2nd INTERNATIONAL

Molecular Plant Protection Congress

ORHANGAZİ • BURSA

May 15-18, 2023

INNOVATIONS IN
PLANT PROTECTION

PROGRAM AND ABSTRACT *BOOK*

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IMPPC2023

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KEYNOTE SPEAKERS

Honorary Keynote Speaker & Opening Lecturer

Craig Mello

University of Massachusettes, USA

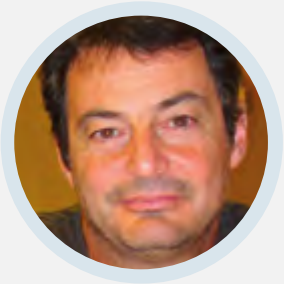
"2006 Nobel Laureate in Physiology or Medicine for discovering RNA interference-RNAi"

Dr. Craig C. Mello received his B.Sc. degree in Biochemistry from Brown University in 1982, and his Ph.D. from Harvard University in 1990. From 1990 to 1994 he conducted postdoctoral research at the Fred Hutchinson Cancer Research Center in Seattle, WA. He has been a member of the University of Massachusetts Medical School faculty since 1995, and a Howard Hughes Medical Investigator since 2000. His pioneering research on RNAi, in collaboration with Dr. Andrew Fire, has been recognized with numerous awards culminating with the prestigious 2006 Nobel Prize in Physiology or Medicine.

Mello and Fire received the Nobel Prize for work that began in 1998, when Mello and Fire along with their colleagues (SiQun Xu, Mary Montgomery, Stephen Kostas, and Sam Driver) published a paper in the journal Nature detailing how tiny snippets of RNA fool the cell into destroying the gene's messenger RNA (mRNA) before it can produce a protein - effectively shutting specific genes down. The Nobel citation, issued by Sweden's Karolinska Institute, said: "This year's Nobel Laureates have discovered a fundamental mechanism for controlling the flow of genetic information." Mello and Fire's research, conducted at the Carnegie Institution for Science (Fire) and the University of Massachusetts Medical School (Mello), had shown that in fact RNA plays a key role in gene regulation. According to Professor Nick Hastie, director of the Medical Research Council's Human Genetics Unit, said: "It is very unusual for a piece of work to completely revolutionize the whole way we think about biological processes and regulation, but this has opened up a whole new field in biology."

Mello is involved in several RNAi-based biotechnology companies. He is a co-founder of RXi Pharmaceuticals where he Chairs the Scientific Advisory Board. In June 2010, he joined the Technology Advisory Board of Beeologics, a company focused on development of RNAi products for honeybee health and various veterinary and agricultural applications, which, according to Mello, "could very well be the first company to obtain FDA approval for an RNAi therapy". In September 2011 Monsanto acquired Beeologics.

Further information could be obtained at:
https://profiles.umassmed.edu/display/129741
https://www.hhmi.org/scientists/craig-c-mello
https://www.nobelprize.org/prizes/medicine/2006/mello/biographical/
https://en.wikipedia.org/wiki/Craig_Mello

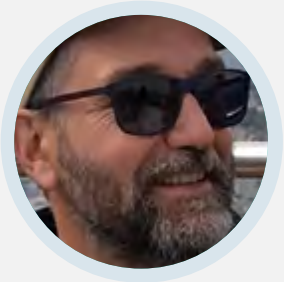


Keynote Speaker

Pierre Abad

INRAE, France

Pierre Abad is Senior Scientist at INRAE. He earned his Ph.D. degree in plant pathology from the University of Paris XI Orsay in 1986. He was head of the plant health department in Sophia Antipolis (France) until 2017. He coordinates the Plant-Nematode Interaction team, which studies plant responses during compatible interactions and nematode parasitism genes. His group demonstrated for the first time the role of a plant susceptibility gene in plant-nematode interaction. This research also encompasses genome structure and evolution as well as evolution of nematode pathogenicity and durability of plant resistance genes. He initiated and coordinated the sequencing project of the root knot nematode genome *Meloidogyne incognita*, which was a double-first: first genome of plant parasitic animal and first genome of a parthenogenetic animal.



Keynote Speaker

Miguel A. Aranda

CEBAS-CSIC, Spain

Miguel A. Aranda graduated from Polytechnics University of Madrid in 1989, and obtained his Ph.D. degree in Plant Pathology in 1995. From 1995 to 1998 he was a postdoctoral researcher at the John Innes Center (JIC, Norwich, UK). In 1999, he joined CSIC (Spain) as tenured scientist, moving Murcia (Spain) in 2002, where he leads the CEBAS-CSIC Plant Virology research group. He has carried out sabbatical stays at JIC (3 months in 2008), UC Berkeley (12 months in 2011-2012) and UC Davis (6 months in 2017). He is currently a Research Professor at CEBAS-CSIC and founder and shareholder of the technology-based company Abiopep S.L. (www.abiopep.com). He is Senior Editor for the Plant-Pathogen Interaction area of Annals of Applied Biology and for the Virology area of Molecular Plant Pathology. Miguel has been working for more than 30 years to understand the biology of plant viruses and how they interact with their hosts. From an applied point of view, his work aims at generating sustainable strategies to control plant diseases induced by viruses, with special emphasis on identifying, characterizing and introgressing genetic resistance to plant viruses in crops. Important contributions of Miguel´s work in this area include the characterisation of resistance genes and resistance mechanisms to viruses in horticultural species of prime importance.

Keynote Speaker

Kevin Ashford

UPL, UK

Originally from a farming family Kevin pursued a career as a qualified industry agronomist for 25 years, specialising as a soil agronomist before taking a position in UPL as the global technical development lead for soil and water technologies. More recently Kevin has led the global technical product development for plant and soil health within UPL. Kevin has a strong background and experience in agriculture which has provided him with key experiences in both the science and the application of industry solutions and techniques applicable for soil health and carbon farming.

Keynote Speaker

Scott Baerson

USDA, USA

Dr. Baerson has extensive experience in the allelopathy and herbicide resistance fields. He has pioneered the use of genomics-based approaches for studying plant root hair cells, and along with his ARS colleagues, elucidated the full genetic and biochemical components of a novel allelochemical biosynthetic pathway in this cell type, representing a significant contribution to our understanding of plant secondary metabolism. He is currently leading the efforts to deploy this pathway for the development of transgenic crops more resistant to weed infestations. Dr. Baerson also made significant contributions to the Roundup Ready brand as an industrial scientist at Monsanto through his work in the gene expression, weed resistance, and specialty crops biotechnology fields. During the course of his career, Dr. Baerson has also been awarded 11 patents, has had his work appear in numerous prestigious journals including Plant Cell, Plant Physiology, New Phytologist, and P.N.A.S, and was the recipient of the prestigious Grodzinsky Award from the International Allelopathy Society.

Keynote Speaker

Xavier Bellés

CSIC-UPF, Spain

Dr. Xavier Bellés is an honorary Professor of the CSIC at the Institute of Evolutionary Biology (CSIC-Universitat Pompeu Fabra), in Barcelona, Spain. His lines of research focus on the study of the evolution of insect metamorphosis, approaching it from the morphological to the molecular scale, including RNAi methodologies for functional genomics studies. In this context, he has dedicated several projects to apply the results obtained to pest control. He has also worked on other physiological processes of the insect, such as reproduction and regulation of feeding. Author or co-author of 382 scientific articles and 11 books, the most recent of which is “Insect Metamorphosis. From Natural History to Regulation of Development and Evolution” (Academic Press, March 2020, 304 pages), a comprehensive treatise on the different types of insect metamorphosis. In his spare time, he works on the taxonomy and systematics of spider beetles.

Keynote Speaker

Mark Belmonte

University of Manitoba, Canada

Dr. Mark Belmonte is a Professor of Biological Sciences at the University of Manitoba. Mark received his B.Sc. (2001) and M.Sc. (2003) from the University of Calgary before moving to Winnipeg where he obtained his Ph.D. in plant science in 2008. After a brief postdoctoral fellowship at UC Davis with John Harada, Mark moved back to Winnipeg to start his own lab in the Faculty of Science where he is a full professor. Dr. Belmonte’s group uses cutting edge next generation molecular tools to improve crop production of some of Canada’s most important agricultural crops. Mark has published his work over 60 times, been the recipient of numerous awards including CBC’s Top 40 under 40, the Canadian Society of Plant Biologists Research Excellence Award and has been recognized for his outstanding contributions to research, teaching and outreach by the Winnipeg Foundation and the University of Manitoba. Mark is devoted to promoting science education and research at outreach events across Canada and takes pride in training the next generation of young scientists.

Keynote Speaker

Assunta Bertaccini

University of Bologna, Italy

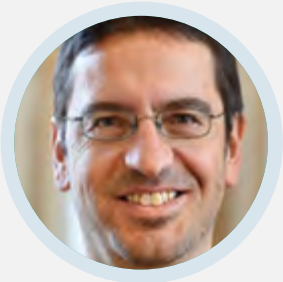
Dr. Assunta Bertaccini has been working as a Plant Pathology professor at the Alma Mater Studiorum – University of Bologna, Italy. Her research is devoted to detection and management of plant diseases associated with phytoplasmas and bacteria. Dr. Assunta Bertaccini has been serving as an editor and reviewer for several scientific international journals with 360 peer reviewed publications and 65 books and book chapters. She is the founder and leader of the International Phytoplasmologist Working Group (IPWG) (http://www.ipwgnet.org/) and a member of SiPAV, APS, IOM, ISHS, Accademia dei Georgofili, International Committee on Systematics of Prokaryotes (ICSP) Subcommittee on Taxonomy of Mollicutes and of the EASIN board.

Keynote Speaker

Robert Brueggeman

Washington State University, USA

Dr. Robert Brueggeman is an Associate Professor at Washington State University and the Robert A. Nilan Endowed Professor of Barley Research and Education. In addition to barley breeding his basic research program focuses on host-pathogen genetic interactions in barley/wheat-fungal pathosystems. In pursuit of understanding the mechanisms of host recognition and pathogen virulence his lab studies these interactions from both the host plant and fungal pathogen perspectives. This research focuses on investigating biotrophic (wheat stem rust) and necrotrophic (net blotch and spot blotch) pathogens that infect both barley and wheat. To understand how programmed cell death-mediated immunity mechanisms in plants provide effective resistance against biotrophic pathogens yet are hijacked by necrotrophic pathogens his lab utilized genetic, genomic and molecular approaches to identify both host resistance and susceptibility genes as well as their corresponding pathogen virulence and avirulence effectors. This research provides the tools for functional analyses that will fill knowledge gaps in the understanding of plant defenses and pathogen effector biology.



Keynote Speaker

Gregor Bucher

Georg August University, Germany

Gregor Bucher studied Zoology and Developmental genetics at the Ludwig-Maximilian-University Munich (1997). During his Ph.D. (LMU, Munich), he studied the function of patterning genes in the red flour beetle *Tribolium castaneum* and discovered parental RNAi (1998-2002). After two years of child care and working as scientific writer, he continued his career in Göttingen (2004), where he established his independent group. In 2013, he was awarded a Heisenberg professorship and since 2017 he has been associate professor at the University of Göttingen. He has been focusing on the genetic basis of development and evolution of insect head and brain. Further, his group has been developing a number of transgenic tools for Tribolium. He initiated and led the first genome wide RNAi screen in an insect outside Drosophila (DFG research unit FOR1234 “iBeetle”) with the aim of overcoming the former candidate gene approach – based on these results, he became interested in the use of RNAi for pest control. He is reviewer for journals in genetics, evolution and development and insect science and for a number of national and international funding agencies. Currently, he serves on the board of the German Zoological Society, is part of the steering committee of the DFG priority program SPP2349 GEvol and is elected member of the DFG panel for Zoology.

Keynote Speaker

Gitta Coaker

University of California, Davis, USA

Dr. Gitta Coaker is a Full Professor at the University of California, Davis. She performed her Ph.D. at The Ohio State University (2003) in the group of Professor David Francis and was a USDA Postdoctoral Fellow at the University of California, Berkeley (2004-2007) with Professor Brian Staskawicz. She joined the faculty at the University of California, Davis in 2007. Dr. Coaker's research program focuses on the interaction between bacterial pathogens and plants. Her work focuses on understanding kinase-mediated immune signaling and pathogen effector targets in both model and crop plants. Her research also investigates vascular pathogens, including vector-borne disease associated with Liberibacter species in citrus, tomato and potato. She was awarded the William H. Krauss Award for Research Excellence (2004), NSF Career Award (2011), Chancellor's Fellow for Research Excellence (2013), Graduate Student Mentoring Award at the University of California, Davis (2020) and the Noel T Keen Award for research excellence in molecular plant pathology (2022).

Keynote Speaker

Neil Crickmore

University of Sussex, UK

Neil is a biochemist/molecular biologist with 35 years' experience of working with the entomopathogenic bacterium *Bacillus* thuringiensis. His primary interest has always been in the mode of action of the pesticidal proteins produced by this bacterium but also in the response of the insect pest to these proteins. Since 1998 he has overseen the naming of these proteins, many of which have been employed in genetically modified crops. In recent years he has led a project to set up an online information resource on the bacteria and their proteins which are used for pest control (www.bpprc.org). He has collaborated widely and holds a visiting professorship position in Beijing.

Keynote Speaker

Aviv Dombrovsky

ARO, Volcani Center, Israel

Dr. Dombrovsky is a Research Scientist at the Institute of Plant Protection, the Agriculture Research Organization (ARO), the Volcani Center. The Dombrovsky laboratory provides 'virological support' to farmers, the agricultural extension service, seed companies and nurseries for the Israeli vegetable industry which is available for worldwide use. The laboratory specializes in the identification of new viral diseases in vegetables and studies the modes of transmission of recently discovered viral diseases in Israel. Topics include virus characterization, the insect vector or mode of transmission/spread, possible agro-techniques to reduce the damage due to the disease.

Keynote Speaker

Ian Dubery

University of Johannesburg, South Africa

Prof. Ian Dubery is a professor of Biochemistry at the University of Johannesburg, South Africa. His research concerns plant biochemistry and agricultural biotechnology with a focus on plant-microbe interactions, inducible defense responses and enhancing innate immunity. He utilizes metabolomics tools and approaches in his research and is the Director of the Research Centre for Plant Metabolomics at the University of Johannesburg.

Keynote Speaker

Stephen O. Duke

University of Mississippi, USA

Stephen Duke is a Principle Scientist at the National Center for Natural Products Research of the School of Pharmacy of the University of Mississippi, after spending more than 40 years with USDA. He is best known for his research on the modes of action and mechanisms of resistance to herbicides. His many awards include Fellow of the American Association of American Scientists and the American Chemical Society. He has published more than 500 peer-reviewed publications and has an h-index of 102 with Google Scholar and 70 with Web of Science. He is currently Editor-in-Chief of Pest Management Science.

Keynote Speaker

Sebastian Eves-van den Akker

University of Cambridge, UK

Sebastian Eves-van den Akker received his B.Sc. in Biology (2007-2010) from the University of Leeds, and his Ph. D. in Plant-Pathology (2010-2014) from the University of Leeds (under the supervision of Prof. P. E. Urwin) and the James Hutton Institute (under the supervision of Prof. J. T. Jones). In late 2014, Sebastian was awarded an Anniversary Future Leaders Fellowship from the Biotechnology and Biological Sciences Research Council (BBSRC) to pursue independent research at the University of Dundee and the John Innes Centre (2015-2018). In 2018, he was awarded a BBSRC David Phillips Fellowship and appointed Head of Group in the Department of Plant Sciences at the University of Cambridge. Sebastian is a geneticist with an interest in inter-kingdom communication. He investigates the genes that control a dialogue between kingdoms of life: the two-way molecular communication between plants and their parasites. The outcome of this communication dictates plant organ development, animal sex determination, and ultimately human food security.

Keynote Speaker

Dolores Fernández Ortuño

Universidad de Málaga, Spain

Dolores Fernández Ortuño has a Ph.D. (2007) in Biology from the University of Malaga (Spain). She is an international expert in the chemical control and fungicide resistance situation of two important phytopathogenic fungi such as *Botrytis cinerea* and *Podosphaera xanthii*. Her scientific career was completed with two long-term stays at Rothamsted Research (United Kingdom) and the University of Clemson (United States). Then, she joined the Department of Microbiology at the University of Malaga as a researcher in the Ramón y Cajal program (2018), obtaining a permanent position as Contracted Professor (2020) and Associate Professor (2022). Her research work is very applied and with great interest for the agriculture, being reflected in numerous JCR publications, book chapters, presentations to national and international conferences and dissemination and scientific transfer activities through articles, guest lectures, interviews, news and several prizes. Currently, her research line aims to provide solutions for the control of *B. cinerea* and *P. xanthii* by identifying new targets, essential proteins for the development and/or pathogenicity of these fungi, and the design of new molecules with fungicidal action.

Keynote Speaker

Elaine Fitches

Durham University, UK

Elaine Fitches graduated with a Ph.D. in insect molecular biology, biochemistry and physiology from Durham University in 1999 and went on to work as a Government research scientist at the Food & Environment research Agency for 17 years. Elaine returned as a Research Fellow to Durham University in 2014 and is currently an Associate Professor in the Department of Biosciences. Her principal research interest lies in novel approaches to control insect pests and most notably the development of protein-based approaches for crop protection. Co-inventor of “Fusion Protein technology”, a patented platform approach that transforms naturally derived neuropeptides that lack oral toxicity, such as paralytic spider venom toxins, into orally and topically effective biopesticides. This technology relies upon the generation of recombinant fusion proteins containing invertebrate specific neurotoxins fused to a “carrier” protein that facilitates toxin transport to the central nervous system of insect pests. The Fitches group are working with industry to develop novel fusion protein based biopesticides and are also investigating potential for the targeted control of insect pests using transgenic plants.

Keynote Speaker

Elizabeth P.B. Fontes

Universidade Federal de Viçosa, Brazil

Elizabeth Fontes is a full professor of Universidade Federal of Viçosa (UFV), Brazil, Coordinator of the National Institute of Science and Technology in Plant-Pest Interactions, Member of the Brazilian Academy of Science (since 2008), and Member of the National Order of Merit Scientific, Commander Class, from the Presidency of Brazil (since 2018). She was the head of the Biochemistry and Molecular Biology Department, UFV, coordinator of graduate programs, Member of the Genetics Committee of the Brazilian National Council for Scientific and Technological Development, and Scientific Director of the Arthur Bernardes Foundation. The primary interest of her lab is deciphering plant defense signaling pathways against biotic and abiotic stresses, specifically in plant responses to geminivirus infection, water deficit, and endoplasmic reticulum stress. Her lab has focused primarily on the plant immune system and the complex molecular network of adaptive responses in plants that integrate the ER-unfolded protein response with the osmotic and cell death signals. More recently, her lab has been engaged in deciphering the crosstalk between antiviral and antibacterial immunity with stress abiotic signaling in plants.

Keynote Speaker

Fernando Garcia-Arenal

Universidad Politecnica de Madrid, Spain

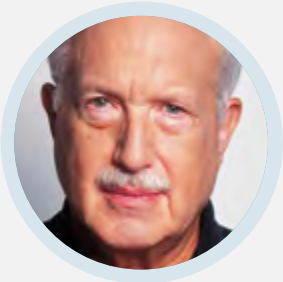
Fernando Garcia-Arenal graduated as Ingeniero Agrónomo from Universidad Politécnica de Madrid (UPM) in 1974, and obtained his Ph.D. degree in Plant Pathology in 1977. From 1981 to 1983, he was a visiting fellow doing research in plant virology at Cornell University's Dept. of Plant Pathology (Ithaca, New York, USA), and in 2001 he did a six-month sabbatical stay at the Dept. of Ecology, Behaviour and Evolution at University of California San Diego (USA). Since 1983, Dr. Garcia-Arenal has been a full professor at UPM. Currently, he leads the research group "Plant-Virus Interactions and Co-Evolution" at Centro de Biotecnología y Genómica de Plantas UPM-INIA. Over the years, interests and contributions Dr. Garcia-Arenal's group have included all aspects of plant virology. However, a major and continuous interest in the group's history has been understanding plant virus evolution as it affects virus disease control. Dr. Garcia-Arenal is author of more than 160 publications in scientific journals, publishing regularly in the most respected journals of the areas of Virology and Plant Pathology.

Keynote Speaker

Godelieve Gheysen

Ghent University, Belgium

Godelieve Gheysen is senior full professor at the Faculty of BioScience Engineering at Ghent University, where she has been head of the Department of Biotechnology for 12 years. Her expertise is plant molecular biology and biotechnology, including science communication to the public. Her research focuses on the molecular analysis of interactions between plants and pathogens with a focus on nematodes and the use of molecular breeding and biotechnology to improve plant resistance to biotic stress. G. Gheysen is a member of the Royal Flemish Academy of Belgium for Science and the Arts (KVAB) and a Fellow of the European Society of Nematologists. In 2013 she obtained the Prometheus Award for Research from Ghent University. G. Gheysen is/was promoter of 48 Ph.D. students. She teaches Molecular Biology, Cell Biology, Gene Technology, Plant Biotechnology and Molecular Aspects of Plant Nematode Relations. She has published >200 A1 papers, was cited about 8000 times, and has an h-index of 53.



Keynote Speaker

Jonathan Gressel

Weizmann Institute of Science, Israel

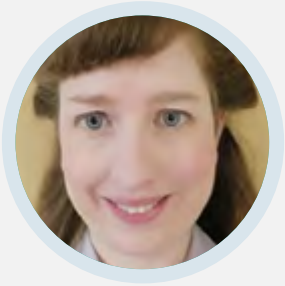
Jonathan Gressel received his M.Sc. and Ph.D. from the University of Wisconsin-Madison and has since been at the Weizmann Institute of Science, now as an emeritus professor. His interests are to see how plant and pesticide sciences can contribute to world food security, with collaborations throughout the developing world. He studied metabolic controls, especially by anti-metabolites and pesticides, and the evolution of herbicide resistance, and modeled strategies to delay resistance. He conceived and helped develop a system to control parasitic Striga (witchweed) using herbicide-treated crop seeds, which is commercialized throughout Africa, He also developed genetic engineering biosafety measures to mitigate transgene movement. He has developed systems to enhance the virulence of biocontrol agents to levels required for agricultural use. He has authored 335 scientific papers and book chapters and is author, or editor of nine books dealing with these issues, including Molecular Biology of Weed Control, and Crop Ferality and Volunteerism. His latest book is "Genetic Glass Ceilings – Transgenics for Crop Biodiversity". He was the Review Editor for the journalsPlant Science, and Pest Management Science and was an associate editor of the journal Food Security. He was awarded the 2010 "Israel Prize", the highest accolade given by the Israeli Government for his Agricultural Research.

Keynote Speaker

Russell Groves

University of Wisconsin, Madison, USA

Dr. Groves's research program tests hypotheses that further the understanding of pest population biology based on sound ecological principles derived from a combination of both field and laboratory research. Here, Groves group balance the development of short-term solutions to these immediate and emerging problems, which out of necessity may require purely empirical and at times ad hoc approaches, with research to develop fundamental concepts and knowledge that will lead to the development of long-term sustainable solutions. Solutions and strategies developed for the commercial and fresh-market vegetable industry must be durable, economical and both environmentally and socially acceptable to remain effective against key, vegetable pest species affecting the industry. Dr. Groves's applied research-based program collaborates with research and extension faculty within the departments of Entomology, Horticulture, Plant Pathology, and Crop Science at the University of Wisconsin as well as scientists from other institutions.

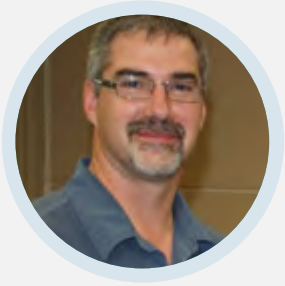


Keynote Speaker

Nichola Hawkins

National Institute of Agricultural Botany, UK

Dr. Nichola Hawkins is a researcher in plant pathology at NIAB, Cambridge, UK. Her research focuses on the evolution of resistance against fungicides and other control measures in fungal pathogens of cereals, including the wheat pathogen *Zymoseptoria tritici*. Prior to joining NIAB, she gained her undergraduate and masters degrees from Imperial College London and her Ph.D. from the University of Reading, and was a postdoctoral researcher at Rothamsted Research in Hertfordshire, UK. She has a particular interest in the evolutionary processes underlying the development of resistance, and the practical implications of fundamental questions such as how repeatable evolutionary pathways are; whether resistance is selected from standing variation or de novo mutations; and whether functional constraints and fitness penalties associated with resistance can be exploited in resistance management. She currently holds a BBSRC Discovery Fellowship, for a project applying experimental evolution methods in fungicide resistance risk assessments.

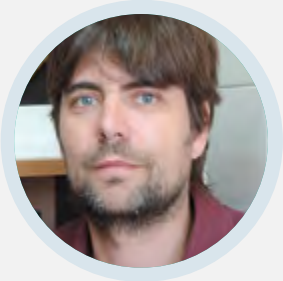


Keynote Speaker

Dwayne Hegedus

Agriculture and Agri-Food Canada, Canada

Dr. Hegedus obtained a BSc degree in Microbiology and Immunology and M.Sc. and Ph.D. degrees in Applied Microbiology from the University of Saskatchewan, Canada, while studying the entomopathogenic fungi (*Beauveria bassiana*). He conducted post-doctoral research at the University of British Columbia, Canada, on the use of gene drive systems (mobile genetic elements) to control insect populations. While there, he co-developed and patented a technology to produce proteins in cultured insect cells which is now used by the pharmaceutical industry to screen new drug candidates. He joined Agriculture & Agri-Food Canada in Saskatoon in 1997 as Insect Biotechnologist. His research involves the application of genomics to the study of insect- and pathogen-host plant interactions.



Keynote Speaker

Salvador Herrero

University of Valencia, Spain

Salva Herrero is Associate Professor at the Department of Genetics and the Laboratory of Biotechnological Pest Control in the Institute of Biotechnology and Biomedicine of the University of Valencia (Spain). His principal research interest is the insect-pathogen interaction. He is interested in understanding how insects respond to entomopathogens, but also how other factors (other pathogens, microbiota, different host plants, etc.) can influence the activity of entomopathogens.

Keynote Speaker

Monica Höfte

Ghent University, Belgium

Monica Höfte is the head of the Laboratory of Phytopathology at the Department of Plants and Crops since 1997 and chair of the Department since 2022. Monica Höfte is a general plant pathologist with a wide interest in both fundamental and practical aspects of plant-pathogen interactions. Her research interests are biological and integrated control of plant pathogens and natural and induced resistance mechanisms against fungi and bacteria in a wide variety of tropical (cocoyam, rice, banana) and temperate crops (lettuce, tomato, bean, cabbage, pepper, grapevine).

Keynote Speaker

Michelle Hulin

The Sainsbury Laboratory, Norwich, UK

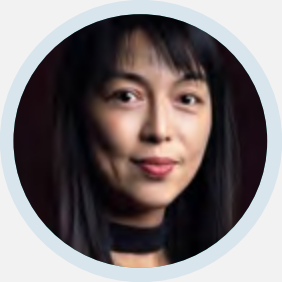
Dr. Hulin is a postdoctoral scientist in the group of Professor Wenbo Ma at The Sainsbury Laboratory in Norwich, UK. Her research focuses on bacterial diseases of plants, specifically characterising the functions of virulence effector proteins that manipulate plant metabolites to promote disease progression. Dr. Hulin uses a combination of population genomics, molecular biology, metabolomics and protein biochemistry to study the role of effectors in disease.

Keynote Speaker

Robert Jackson

University of Birmingham, UK

Robert Jackson has more than 25 years' experience working on microbiology and plant pathology problems. He studied plasmids and type III secretion for his Ph.D. research, discovering a major bacterial pathogenicity gene that can epistatically suppress the effects of avirulence effectors. Since then, his research topics include the study of bacterial pathogenesis, most recently in tree pathology studying Horse Chestnut, Oak, Ash and Cherry; gene regulation and regulatory networks in plant growth-promoting bacteria; the role of surfactants in bacterial motility and biocontrol; the identification and characterisation of bacteriophage for biocontrol; microbiome analyses of invasive alien plant species; and analysis of how bacteria can kill aphids. He collaborates widely in both the UK and globally, and has delivered teaching and research seminars in diverse locations abroad. He has previously served as an elected board member for the British Society for Plant Pathology (BSPP) in 2010-2013 and was involved in developing the Outreach Officer role for the society. He joined the board again in 2019 as Publicity Champion and is President-Elect in 2022, becoming President in 2023. He is also a member of the American Phytopathology Society and served as Senior Editor for Phytopathology between 2012-2014 as well as a Senior Editor for Molecular Plant Pathology from 2015-2021.



Keynote Speaker

Hailing Jin

University of California, Riverside, USA

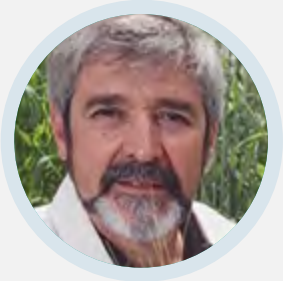
Dr. Hailing Jin is a Professor and the Cy Mouradick Endowed Chair at the Department of Microbiology & Plant Pathology, Center for Plant Cell Biology, Institute for Integrative Genome Biology, University of California, Riverside. Her lab studies the molecular mechanisms of plant immunity and pathogen virulence. The aim of Dr. Jin and her team is to develop effective and environmentally friendly strategies to control plant diseases and ensure adequate food production.

Keynote Speaker

Marek Jindra

Czech Academy of Sciences, Czech Republic

Marek was born in Prague where he graduated from the Charles University. After postdoctoral studies at the University of Washington, Seattle, and at the National Institute of Genetics in Japan, he assumed a group leader position at the Biology Center of the Czech Academy of Sciences, and received professorship at the University of South Bohemia. More recently Marek worked with CSIRO in Australia. Since 2015 he serves as editor of Insect Biochemistry and Molecular Biology. Marek's research interests include hormonal regulation of insect development, particularly metamorphosis, and the role of intracellular receptors and other transcriptional effectors in morphogenesis and homeostasis. To address these problems, he complements Drosophila genetics with work on non-model insects. His main contribution is the genetic and molecular definition of the long-sought receptor for juvenile hormone (JH). He currently pursues mechanisms of JH receptor activation and function. In collaboration with biological chemists, Marek has engaged in high-throughput screening for regulators of JH receptors from multiple insects aiming to develop JH receptor agonists or disruptors for species-selective control of insect pests and disease vectors.

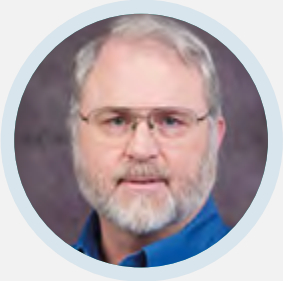


Keynote Speaker

Michael Jones

Murdoch University, Australia

Professor Michael Jones has a degree in Natural Sciences (Biochemistry) and Ph.D. in Plant Biochemistry from Cambridge University, UK. He is internationally recognised in agricultural biotechnology. After 8 years at Rothamsted Research, UK, as Cell Biology Co-ordinator, he became Professor of Plant Sciences at Murdoch University in Western Australia (WA). In 1993 he became Foundation Director of the WA State Agricultural Biotechnology Centre (SABC) and Professor of Agricultural Biotechnology at Murdoch University. He has a wide range of experience of R&D on crop plants, having worked in departments of Biochemistry, Plant Pathology, Developmental Biology and Plant Breeding. He has contributed to nematode-plant interactions, plant virology, molecular markers for crop improvement and transgenic technologies, and pioneered molecular/biotech-based agricultural R&D in WA. Current work is on 'New Breeding Technologies' and gene-editing for crop improvement. He is committed to the translation of research outcomes to commercial implementation, has >300 publications and supervised 70 Ph.D. students, and has co-founded two trait development companies.



Keynote Speaker

Michael Kanost

Kansas State University, USA

Michael Kanost received a B.S. degree in zoology and entomology from Colorado State University and Ph.D. from Purdue University. He was a postdoc at Queen's University in Kingston, Canada with Gerard Wyatt and at University of Arizona with Michael Wells. He has been a faculty member in the Department of Biochemistry and Molecular Biophysics at Kansas State University since 1991. His research has focused on biochemistry of insect immune responses and of insect cuticle formation, with an emphasis on protein function. He is currently an editor of Insect Biochemistry and Molecular Biology.

Keynote Speaker

Rebekah Kelly

AgBiome, USA

Rebekah Kelly is the Trait Program Lead at AgBiome. Since she started at AgBiome in 2014, she has built the trait pipeline with a multidisciplinary team and established a robust gene discovery platform to deliver novel insect control traits. She received a Bachelor of Science degree in Biochemistry from North Carolina State University and a Masters of Science from University of Illinois at Urbana-Champaign.

Keynote Speaker

Kook-Hyung Kim

Seoul National University, South Korea

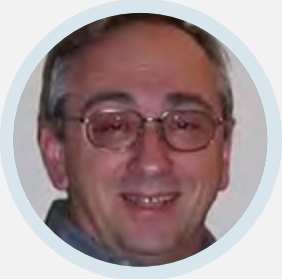
Dr. Kim has completed his Ph.D. from the Department of Plant Pathology at North Carolina State University (NCSU), and postdoctoral studies from the NCSU Department of Biochemistry. He served as the director of the Plant Clinic at Seoul National University for 6 years and as the president of the Korean Society of Plant Pathology. He has published more than 150 papers in reputed journals. He has been serving as the senior editor or as an editorial board member of the Molecular Plant Pathology, Virus Research, Frontiers Journals, Virology, and Scientific Reports.

Keynote Speaker

Glenn F. King

University of Queensland, Australia

Glenn did his Ph.D. at the University of Sydney before postdoctoral studies at the University of Oxford. After academic stints at the University of Sydney and the University of Connecticut Health Center, he joined the Institute for Molecular Bioscience at the University of Queensland in 2007. Glenn is a leader in the field of venoms-based drug discovery, in particular the development of drugs and insecticides derived from spider venoms. His early work on venoms lead to him to found an agricultural biotechnology company (Vestaron Corporation) that has successfully developed bee-safe, environmentally-friendly bioinsecticides. An equally important focus of Glenn's research is the development of venom-derived peptide drugs, which recently led him to co-found a biotechnology company (Infensa Bioscience) that is developing therapeutics to treat stroke and myocardial infarction. Glenn's laboratory maintains one of the largest collection of invertebrate venoms in the world, sourced from more than 500 species of venomous animals including ants, assassin bugs, caterpillars, centipedes, scorpions, spiders, and wasps. Glenn has published 3 books, 19 book chapters, and over 300 peer-reviewed journal articles.



Keynote Speaker

Evsey Kosman

Tel Aviv University, Israel

Evsey Kosman is a mathematician. He develops general and logically consistent approaches and metrics for measuring and decomposing genetic, functional, and phylogenetic variability to address a wide range of topics in Population Genetics, Ecology, and Conservation. His research interests also include analyzing structural relationships of operational units at different hierarchical levels of biological organization and at various spatiotemporal scales. In particular, Evsey does research in Plant Protection and Population Genetics of Plant Pathogens encompassing elaboration of new approaches to study of plant pathogen populations and a comprehensive analysis of specific plant-pathogen systems. Evsey has published 98 peer-reviewed papers in the leading journals and presented above 50 invited lectures at universities and research institutes worldwide.

Keynote Speaker

Michael Kube

University of Hohenheim, Germany

Michael Kube is Professor and Head of the Department of Infection Biology Crops - Livestock at the University of Hohenheim, Germany. He has been working on pathogens for more than two decades. Genomics, pathogen-host interaction and diagnostics of pathogens are central topics of his research, using state-of-the-art technologies for data generation and bioinformatic analysis. His findings are summarised in more than 100 research publications.

Keynote Speaker

Ronald P. Kühnlein

University of Graz, Austria

Ronald P. Kühnlein holds a full professorship for biochemistry at the Institute of Molecular biosciences of the University of Graz, Austria. He is member of the University of Graz field of excellence BioHealth and of BioTechMed Graz and serves a scientific reviewer for various international journals and research foundations. Work of the Kühnlein group pioneered the understanding of the genetic architecture of organismal storage lipid metabolism in the model insect *Drosophila melanogaster*. The Kühnlein laboratory contributed the in vivo functional characterization of central regulators of this process from enzymes such as the TG lipase Brummer to lipid droplet-associated modulators such as Perilipin 1 and 2 to systemic interorgan communication by hormone-controlled signal transduction systems such as the Adipokinetic hormone and its cognate receptor. More recently the group addresses the role of lipids as energy source, structural components or signalling molecules in developmental processes, reproduction and aging with a special focus on steryl ester metabolism. Beyond the Drosophila model, the group studies the lipidome adaptation of an extremophile insect.

Keynote Speaker

Li-Jun Ma

University of Massachusetts, USA

The Ma lab focuses on a model system *Fusarium oxysporum*, a cross-kingdom fungal pathogen that not only causes devastating plant vascular diseases, but can also infect humans. Distinct sets of repeat-rich accessory chromosomes (ACs) – known to play deterministic roles in each host-fungal interaction – have been identified among all pathogenic *F. oxysporum* isolates, including both plant and human pathogens. Experimental evolution study confirms that transposons, enriched in ACs, drive the adaptive evolution in this cross-kingdom fungal pathogen. *Arabidopsis thaliana* independently challenged with a *Fusarium oxysporum* endophyte Fo47 versus a pathogen Fo5176 is employed to investigate the genetic mechanisms that underlie pathogenesis against plant hosts. Metatranscriptomic data reveal a shared pattern of expression for most plant genes (~80%) in responding to both fungal inoculums. At the same time, distinct responding genes depict transcriptional plasticity, as the pathogenic interaction activates plant stress responses and suppresses plant growth/development related functions, while the endophytic interaction attenuates host immunity but activates plant nitrogen assimilation. Collectively, *F. oxysporum* represents an effective model to investigate eukaryotic genome evolution and host-microbe interactions.

Keynote Speaker

Dana R. MacGregor

Rothamsted Research, UK

Dr. Dana R. MacGregor is a plant molecular geneticist with expertise in understanding how plants survive the challenges of their environment and how they pass these beneficial traits on to secure the success of subsequent generations. She is currently focusing on agricultural weeds, Nature's ultimate survivors. She and her team are working on quantifying and undertaking mechanistic investigation of the traits that allow agricultural weeds to allude chemical or cultural controls. Current projects focus on developing lab-based molecular resources, tools and techniques to explore genotype-to-phenotype and phenotype-to-genotype hypotheses in problematic weeds such as *Alopecurus*, *Lolium*, and Amaranthus species. Dana has been at Rothamsted Research since 2018, she is LTHE qualified and an Accredited Supervisor.

Keynote Speaker

Wendy Maddelein

Syngenta, Belgium

Wendy Maddelein is the head of the RNAi platform within Syngenta. As a leading science-based Ag-Tech company, Syngenta aims to help millions of farmers around the world to grow safe and nutritious food, while taking care of the planet. Within the RNAi platform, Syngenta is developing RNA-based biocontrols targeting insect pests. The platform covers all aspects of biocontrol development, going from target discovery, large-scale production over efficacy testing, and formulation. Wendy started her career in 2002 as a molecular biologist in Devgen, a Belgian biotech company working on hybrid rice and RNAi technology. Throughout the years, she obtained extensive knowledge and experience on using RNAi as a research tool for plants, insects and nematodes, but also on the development of RNA-based biocontrols. In 2013, Devgen was acquired by Syngenta and became the Ghent Innovation Center, the center of excellence for RNAi within Syngenta. At this point, Wendy joined Syngenta as team leader for the Molecular Biology team. In 2022, Wendy was appointed platform lead for RNAi within Syngenta. In her role, she oversees the different RNAi-related projects and workstreams, and drives the strategy of the overall RNAi platform.

Keynote Speaker

Jacob Malone

John Innes Centre, UK

Dr. Jacob Malone is a Group Leader in the John Innes Centre in Norwich, UK, where he has studied the molecular mechanisms of plant-microbe interaction since 2011. Dr. Malone is an expert in bacterial signalling and behaviour during host colonisation. Supported by a combination of BBSRC, InnovateUK and direct industry funding, his lab uses microbial genetics, biochemistry and environmental microbiology to examine the regulatory pathways that control bacterial plant colonisation infection and biocontrol, and to understand the selective pressures that shape the microbiome in plant-associated environments. Dr. Malone has published >40 peer-reviewed articles in journals including eLife, PLoS Genetics and Nature Microbiology and has an established track record of leveraging academic findings to enable translational plant and microbial research. Dr. Malone recently co-founded PfBIO, a JIC spin-out company that seeks to capitalise on his findings in the fields of plant microbe interaction and disease biocontrol.

Keynote Speaker

Sophie Mantelin

INRAE, France

Dr. Sophie Mantelin, has worked on the effects of a plant growth-promoting Rhizobacteria on Arabidopsis, characterising the root morphogenetic response and the impact of the inoculation on the plant physiology and N-nutrition during her Ph.D. at the University of Montpellier. As a Post-Doc at the University of California Riverside, she has investigated the role of plant hormones in Mi-1 resistance and/or basal defence in response to root-knot nematodes (RKN) and aphids, and identified new components of the Mi-1-mediated pathway, leading notably to the characterisation of the receptor-like kinase SERK1 as Mi-1 co-receptor. As a researcher at the James Hutton Institute, she investigated the roles of potato cyst nematodes effectors in parasitism, as well as the evolution of potato resistance genes. Since 2021, she has been working at INRAE (France). Dr. Sophie Mantelin is interested in host perception by plant-parasitic nematodes (PPN) and exploit the grapevine-PPN pathosystem as a model, using both RKN (*Meloidogyne* spp.) and virus-vector nematodes (*Xiphinema* spp.) to investigate chemical ecology in nematology.

Keynote Speaker

Pam Marrone

Invasive Species Corporation, USA

Dr. Marrone spent her 30+ year career focused on biological products for pest management and plant health, having started and led three bioag companies (Entotech, AgraQjest and Marrone Bio Innovations (now called Profarm Group), all of which were sold to larger companies. With co-founder Jim Boyd, the former CFO of Marrone Bio, Pam is currently in the process of launching a fourth company, the Invasive Species Control Corporation and its corresponding Invasive Species Foundation, to bring effective, environmentally friendly biological solutions to control destructive invasive species, such as invasive carp, zebra and quagga mussels, bark beetles and toxic algae. She is Chair of the Board of Elicit-Plant and serves on the boards of 180 Life Sciences (NASDAQ:ATNF), Stem Express and Pheronym and advises several agtech/agbio startups, many founded or led by women. Among her many awards, in 2022 she received the American Chemical Society “Kathryn C. Hach Award for Entrepreneurial Success.” She has a B.S. in entomology with Honors and Distinction from Cornell University and a Ph.D. in entomology from North Carolina State University. She is a Fellow of the AAAS and has over 400 patents.

Keynote Speaker

Kostas D. Mathiopoulos

University of Thessaly, Greece

Kostas Mathiopoulos, is Professor of Molecular Biology and Director of the Laboratory of Molecular Biology and Genomics at the Department of Biochemistry and Biotechnology of the University of Thessaly. He received his Ph.D. in Molecular Biology and Microbiology at Tufts University in Boston (1989) and, subsequently, his Master’s in Public Health at Harvard School of Public Health in Boston (1990). He then worked at the National Institutes of Health (Bethesda, USA) and at the University of Rome (Italy) on molecular entomology of the malaria mosquito vector *Anopheles gambiae*. Upon his return in Greece (1998) he continued his research on molecular entomology at the University of Patras and in 2002 he joined the faculty of the Department of Biochemistry and Biotechnology of the U of Thessaly. His research team studies different aspects of molecular biology, molecular ecology, genetics and genomics of insect pests of agricultural and medical importance, towards the development of safe and environmentally friendly methods. The current interests of his Laboratory include: development of RNAi based insecticides; analysis of the structure, function and evolution of the Y chromosome of Tephritid flies; development of genetic sexing strains in medfly and olive fruit fly; study of the olfactory, gustatory and reproduction systems; study of the regulatory role of long non-coding RNAs in the reproductive system of the tiger mosquito.

Keynote Speaker

Mamadou Kane Mboup

Corteva Agriscience, Germany

Mamadou MBOUP earned his Ph.D. in Plant Science from the University of Paris XI Orsay. After multiple experiences in the academia (Munich University, Oxford University and Max Planck institute for plant breeding), he joined the crop protection industry a few years ago leading the laboratory of molecular biology & genetics at the European Research & Development Center of DuPont Crop Protection. He supported DuPont fungicide portfolio and discovery by developing molecular tools for assessing fungicide resistance risk and implementing resistance management strategies. He held the same role at FMC Corporation, extending his activities to insecticide resistance. In 2019, Mamadou Mboup joined Corteva Agriscience as Global Fungicide Resistance Leader.

Keynote Speaker

Hans Merzendorfer

University of Siegen, Germany

Hans Merzendorfer is a Full Professor in the Department of Chemistry-Biology at the University of Siegen, Germany. He studied Biology at the Ludwig-Maximillian-University of Munich, where he also received his Ph.D. in 1999 working on the structure and function of the insect vacuolar ATPase. He did his PostDoc at the University of Osnabrück continuing to explore the molecular physiology of insects with a focus on the midgut but getting increasingly interested in chitin biology. In 2006, he accomplished his habilitation in Animal Physiology, and in 2007, he received a Heisenberg fellowship by the German Research Foundation (DFG) allowing him to stay as a visiting scientist at the Kansas-State-University, USA. After his return to Germany, he became an Adjunct Professor at the University of Osnabrück, and since 2014, he is a Professor for Molecular Biology at the University of Siegen. His research interests are centered on the molecular physiology of membrane proteins including proton pumps, ABC transporters and glycosyltransferases involved in the biosynthesis of chitin. He has published more than hundred research articles, reviews, scientific columns and book chapters.

Keynote Speaker

Steve Meyer

RNAissance Ag, USA

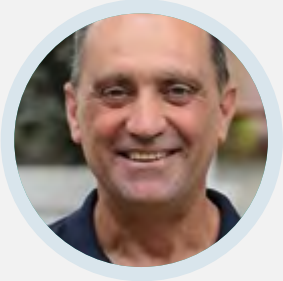
Steve Meyer joined St. Louis-based RNAissance Ag LLC, a subsidiary of TechAccel, in October 2022. Steve brings deep technical experience coupled with international entrepreneurial business experience, including 16 years with Monsanto (now Bayer Crop Science) in a variety of scientific and commercial roles. During his tenure at Monsanto, he conducted biotechnology research that led to the development of multiple commercial products and played a key role in transforming Monsanto's insect control discovery pipeline, leading to his acceptance as a Monsanto Science Fellow. Steve's entrepreneurial journey began in 2019 when he co-founded a vertically integrated medical cannabis business with cultivation, manufacturing, and retail operations in his home state of Missouri. Under his leadership as CEO, the company captured the largest footprint of competitive licenses in the state and raised capital to successfully launch nine operational businesses in just a little over one year. In a quest to continue learning and challenging himself, he exited his cannabis business in 2021, and assumed a role as COO with Lucy Scientific Discovery Inc. (LSDI). Steve has a master's degree in plant biology from Washington University in St. Louis.

Keynote Speaker

Neena Mitter

University of Queensland, Australia

Prof Neena Mitter is the Director of the Centre for Horticultural Science, Queensland Alliance of Agriculture and Food Innovation, the University of Queensland and the Director of the Australian Research Council Industrial Transformation Research Hub for Sustainable Crop protection. She has >150 publications, multiple patents and has supervised >25 Ph.D. students. She has received recognitions such as Fellow of the Australian Academy of Technology and Engineering, Women in Technology Outstanding Life Sciences Award, and Gates Grand Challenges Explorations Award. She is globally renowned for her leadership of innovative platforms namely 'BioClay platform for RNA based crop protection' and 'Clonal propagation of avocado using plant stem cells'. These are ground-breaking platform technologies influencing agricultural production, environmental sustainability, and socio-economic dynamics of farming community. With increased scrutiny on use of chemicals as crop and animal disease control agents, Prof Mitter is focussed on developing clean technologies for the agriculture of tomorrow.

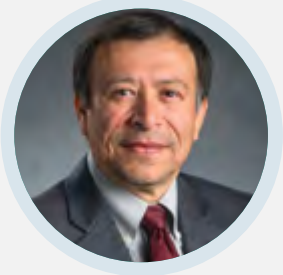


Keynote Speaker

Enrique Moriones Alonso

IHSM-UMA-CSIC, Spain

Dr. Moriones focuses on whitefly-transmitted plant viruses, mainly on tomato yellow leaf curl disease (TYLCD) epidemics caused by begomoviruses and epidemics of tomato chlorosis virus. Research studies include the analysis genetic structure, molecular variability and evolution of associated virus populations, search of host resistance to the virus and to the insect vector, and understanding of plant-virus-vector interactions. Also, the search for crop management practices to reduce crop losses caused by whitefly-transmitted viruses and plant defense mechanisms against viruses are major lines of research. Dr. Moriones received a Ph.D. in Agronomy (July 1991) on molecular and applied Plant Virology from the Universidad Politécnica of Madrid, Spain. From October 1991 until May 1995 he was Head of the Plant Virology Group of the Institut de Recerca i Tecnología Agroalimentaries (Barcelona, Spain). From May 1995 until now he is staff scientist of the Agencia Estatal Consejo Superior de Investigaciones Científicas (CSIC), where he is currently Research Professor and head of the Plant Virology laboratory (Málaga, Spain). Dr. Moriones supervised 11 Ph.D. thesis and published 140 scientific publications in high impact journals.

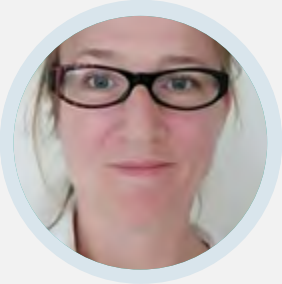


Keynote Speaker

David Mota-Sanchez

Michigan State University, USA

Dr. Mota-Sanchez's research focuses on the evolution of arthropod resistance to pesticides, and insect toxicology. He is working on resistance of Colorado potato beetle, fall army worm and fruit pests to insecticides, and fall armyworm to insecticides and Bt toxins. Dr. Mota-Sanchez is Director of the Arthropod Pesticide Resistance Database (www.pesticideresistance.org) which tracks cases of arthropod resistance globally dating back to 1914. He is also working on IPM, insecticide resistance management, international agriculture and biotechnology particularly with Latin America. He served as an Embassy Science Fellow with the U.S. State Department and USDA FSA in Mexico to increase awareness and understanding of GE crops and provide scientific information that illustrates the economic benefits and social importance of these crops. In addition, he has extension projects to train Latino farmers in IPM and access to USDA programs. He is working also in research and extension of the monarch butterfly in Michigan, and Mexico.



Keynote Speaker

Alex Murphy

University of Cambridge, UK

Dr. Murphy is a Senior Research Associate at the University of Cambridge and carry out research on plant–arbovirus–insect interactions and antiviral resistance mechanisms. Dr. Murphy investigates how virus infection modifies plant interactions with insects with a view to developing sustainable methods of limiting virus transmission in crops. She does this by analysis of insect-perceivable volatile emissions from virus-infected plants combined with observations of insect behaviour. Dr. Murphy also teachs plant pathology to undergraduates and metabolomics to postgraduates, and also organise outreach events to explain to school-aged students the role of plant pathologists in future food security.

Keynote Speaker

Ken Narva

GreenLight Biosciences, Inc., USA

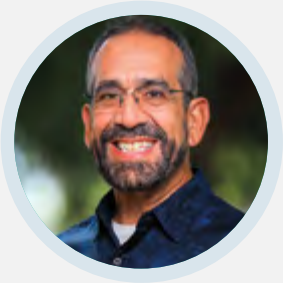
Ken Narva is a leader in the field of Agricultural Biotechnology Research and Development with a passion for innovation aimed at ecologically sound solutions for sustainable food production. Ken earned a Ph.D. in Microbiology from Louisiana State University and a B.S. in Biology from Central Michigan University and is currently a Research Fellow and Head of Entomology at GreenLight Biosciences where he leads the Discovery phase strategy for bio-based insect control products. Ken joined GreenLight Biosciences in 2019. Prior to Greenlight, Ken held leadership roles in Discovery functions at Dow AgroSciences (now Corteva Agriscience) where he delivered globally marketed insect control and agronomic traits for corn, cotton and soybeans. Prior to Dow AgroSciences, Ken was a Discovery Scientist at Mycogen Corporation in San Diego, CA., where he discovered biopesticides for insect control. Before Mycogen, Ken held post-doctoral research positions in small molecule natural products discovery at American Cyanamid in Pearl River, NY, and in plant pathology at the University of Nebraska-Lincoln. Ken is an inventor on over 130 granted U.S patents and an author of over 50 peer reviewed publications.

Keynote Speaker

Ralf Nauen

BayerCrop Sciences, Germany

Ralf Nauen is an insect toxicologist/biochemist working on functional (toxico)genomics, molecular entomology, fundamental and applied aspects of insecticide/acaricide mode of action, selectivity, and detoxification, as well as biochemical and molecular mechanisms of insecticide resistance and its management. He received his Ph.D. from the University of Portsmouth (UK) and is a Bayer Distinguished Science Fellow. In 2013 he was awarded Fellowship of the Entomological Society of America (ESA) and in 2014 he received the prestigious American Chemical Society International Award for Research in Agrochemicals, in recognition of his outstanding and influential research into insecticide and acaricide modes of action and resistance. In 2021 he received the ESA Physiology, Biochemistry and Toxicology (PBT) Section Award. He authored more than 250 scientific papers/book chapters with more than 25,000 citations. He received the Highly Cited Researcher award by the Web of Science 2018-2021. He is appointed Visiting Professor by the Chinese Academy of Agricultural Sciences (CAAS, Beijing, China) and lecturer for agricultural and molecular entomology at the University of Bonn (Germany).

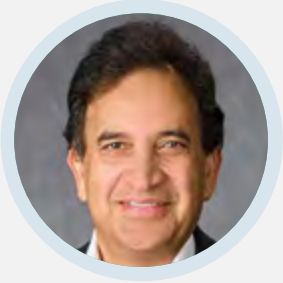


Keynote Speaker

Francisco M. Ochoa Corona

Oklahoma State University, USA

Dr. Francisco M. Ochoa Corona is a Professor at the Institute for Biosecurity & Microbial Forensics, and Department of Entomology & Plant Pathology, Oklahoma State University since August 2008. Dr. Ochoa Corona is a forensic plant pathologist, specializes in developing and delivering reference diagnostics for exotic, naturalized, and indigenous plant viruses. His work is applicable to plant pathogens, and more recently to waterborne plant viruses, insects that can be intercepted at borders, or detected by general surveillance of field settings or within transitional facilities. Ochoa Corona's research in plant pathology contributes scientific input to regulatory officials regarding plant health emergencies and focuses on targeted aspects of forensic plant pathology that are relevant to agricultural biosecurity in Oklahoma, the southern plains, the United States, and other regions of the world such as the South Pacific and Central and South America. Dr. Ochoa Corona joined OSU from the Investigation and Diagnostic Centre (IDC) at Biosecurity New Zealand (BNZ), Ministry of Agriculture and Forestry (MAF), where he was Principal Adviser Virology.



Keynote Speaker

Subba Reddy Palli

University of Kentucky, USA

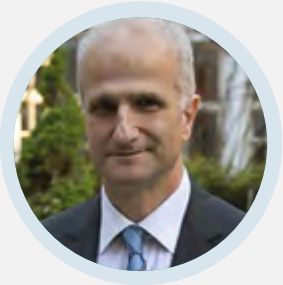
Dr. Subba Reddy Palli, University Research Professor and Chair of entomology at the University of Kentucky. He also Kentucky State Entomologist and serves as the co-director of the Center for Arthropod Management Technologies, NSF Industry and University Cooperative Research Center. Palli received his doctorate from the University of Western Ontario and trained as a postdoctoral fellow at the University of Washington. Subsequently, Palli worked at the Canadian Forest Service and Rohm and Hass Company. He joined the University of Kentucky's Department of Entomology in 2002. He is internationally recognized for his research on hormonal regulation of molting, metamorphosis, and reproduction, development of ecdysone receptor-based gene switches, and RNAi-based pest management. He has published 250 journal articles and book chapters and co-edited a book. He is also a co-inventor on 28 patents. Palli was named as an ESA fellow in 2014 and is also the recipient of the ESA Nan-Yao Su Award, Recognition Award in Insect Physiology Biochemistry, and Toxicology. He received Fulbright-Nehru award in 2015 and was elected as a fellow of American Association for Advancement of Science in 2018. He currently serves on the editorial boards of ten journals and serves on grant review panels of NSF.

Keynote Speaker

Hanu R. Pappu

Washington State University, USA

Dr. Hanu R. Pappu is a professor and the Chuey Chair of plant pathology, and holds the President Sam Smith Distinguished Professorship at Washington State University (WSU). Dr. Pappu's research interests and expertise include the broader area of Crop Protection using conventional and biotechnological approaches. Specifically, his research areas encompass characterization and control of viral diseases of crop plants; development of environmentally friendly and sustainable IPM strategies for reducing the impact of destructive viral diseases of crops; capacity building in developing countries; and technology transfer. Specific areas of interest are genomics, proteomics, epidemiology, breeding for virus resistance, virus diagnostics, and host-virus interactions. His current research focus is on using genome engineering technology such as CRISPR for crop improvement. Professor Pappu published more than 210 refereed journal articles, and gave numerous invited presentations at national and international conferences. He obtained more than US$5 million in extra-mural grants from federal, regional and state funding agencies over the last five years.



Keynote Speaker

Francesco Pennacchio

University of Napoli “Federico II”, Italy

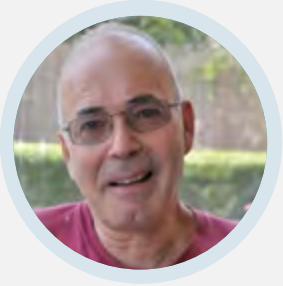
Professor of Entomology at the University of Napoli Federico II (Italy) and Visiting Professor at Newcastle University (UK), in 1989 he received a Ph.D. in Entomology at the University of Napoli Federico II, and, from 1989 to 1991, he was research associate at the Department of Entomology, Texas A&M University, College Station, TX, U.S.A. The study of the molecular physiology of insect multitrophic interactions is at the core of his research interests, along with biotechnologies for insect control that can be developed based on this knowledge. His work particularly focuses on insect immunity and immunosuppression strategies by parasites and pathogens, and on how environmental stress can alter insect immunocompetence. In 2014 he was awarded the Cozzarelli Prize by the National Academy of Sciences of U.S.A. for his work on elucidating the molecular mechanism through which the neonicotinoids adversely affect the insect immune response and promote replication of a viral pathogen in honeybees bearing covert infections. He currently serves as President of the Italian National Academy of Entomology. He is member of EMBO, of the Council for International Congresses of Entomology, and co-editor in chief of “Journal of Insect Physiology”.

Keynote Speaker

Massimo Reverberi

Sapienza University of Rome, Italy

Massimo Reverberi graduated cum laude in Biology in 1996, Ph.D. in Botany in 2001 in Sapienza, Università di Roma, where he is currently associate Professor in Plant Pathology, from 2009, a permanent member of the Ph.D. school in Environmental and Evolutionary Biology and from 2022 President of the course of Agro-biotechnological Sciences. His studies focus on the interaction environment-plant-pathogens regarding the relation among oxidative stress, lipid signals and the biosynthesis of several mycotoxins in different pre- and post-harvest fungal pathogens and how to design biostimulants/bioremediators for solving fungal (their metabolites) contamination of plants and foodstuffs. He participated to several European project on the control of the biosynthesis of some mycotoxins in different foodstuffs and on the application of the integrated control against fungi responsible for post-harvest spoilages. He has authored or co-authored more than 90 peer-reviewed, ISI-indexed publications on various aspects of plant pathology, mycology and microbiology (Hi 27). He is president and co-founder of an Academic Start-up, SARA EnviMob, a company dealing with application of bioinformatics in agriculture inter alia.



Keynote Speaker

Baruch Rubin

Hebrew University of Jerusalem, Israel

Prof. Rubin, is Professor Emeritus of Weed Science and Agronomy, Faculty of Agriculture, Food and Environment of the Hebrew University of Jerusalem. Former Director of the Institute of Plant Sciences and Genetics, thought three courses in Weed Science and supervised 112 M.Sc. and 35 Ph.D. students. His research interests are in weed biology, invasive weeds, herbicide-resistance and behavior of herbicides in plants, soil, water and environment. Currently, his lab and research group are active with 3 post-docs and 2 M.Sc. students. Published more than 200 peer-reviewed papers, book chapters and reviews. Worked at MSU, Michigan as a Research Fellow (1976-1978); on sabbatical leaves in; UC Berkeley, CA, USA (1983-1984); Long Ashton Research Station, UK (1989-1990); Zeneca Agrochemicals, UK (1996-1997); AHRI – Australia (2002-2003), and USP, Piracicaba, Brazil (2012). Was President of the International Weed Science Society (IWSS), Vice President of IAAPS, served as member of EWRS Scientific Committee. He is the Honorary President of the Weed Science Society of Israel, Honorary Member of WSSA, and received Honorary Awards from: WSSA, WSSI; IAPPS; Weed Science Society of India, the Israel Cotton Board and the International Weed Science Society (IWSS).

Keynote Speaker

Shinichiro Sawa

Kumamoto University, Japan

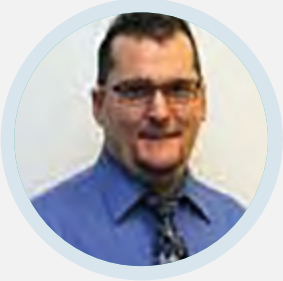
Shinichiro Sawa obtained his Ph.D. from Kyoto University, Department of Botany, where he identified the FIL gene, an abaxial determination gene, in 1999. He then served as an assistant professor at Tokyo Metropolitan University (1999-2002), and focused on ABA and IAA synthetic genes. He has worked as an Associate professor at The University of Tokyo 2002- 2010, and focused on identifying vascular formation-related genes and CLE peptide. He has been working as a Professor at Department of Molecular Agriculture, Kumamoto University. His main interests are Plant morphogenesis, including peptide functional analysis; and biotic interaction between plant and root knot nematodes. He is currently engaged in the identification of genes that regulate plant development. Some of the genes that he is exploring include abaxial-adaxial identification genes, as well as vascular formation-related genes.

Keynote Speaker

Marc F. Schetelig

Justus-Liebig-University Giessen, Germany

Prof. Dr. Marc F. Schetelig is a renowned scientist in the field of insect biotechnology. He currently holds the position of Professor of Insect Biotechnology in Plant Protection at Justus-Liebig University Giessen, where he is also a member of the Institute for Insect Biotechnology. With extensive experience in the development of eco-friendly pest control solutions, Prof. Schetelig specializes in transferring technologies for the Sterile Insect Technique (SIT) to agricultural and medically-relevant insects. He has also conducted research on the evaluation of pesticides on malaria-transmitting mosquitoes (Anopheles species) and the stability and risk assessment of transgenic systems. Prof. Schetelig earned his Dr. rer. nat. degree from the Department of Developmental Biology at Georg-August-University Göttingen, Germany. He completed his diploma in Biochemistry at the University of Bayreuth, Germany, where he majored in biochemistry, genetics, plant physiology, microbiology, and biophysical chemistry. Throughout his career, Prof. Schetelig has held various positions, as a Researcher at the Göttingen Center of Molecular Biosciences, Molecular Biologist in Pest Control at the United States Department of Agriculture (USDA-ARS), and Research Group Leader at Fraunhofer Society in Aachen. He has served as an expert for the FAO, IAEA, and WHO on numerous occasions. Additionally, he has contributed to several international scientific research projects and has been the coordinator of various national and international research programs, including the Research and Innovation Action (RIA) Horizon Europe (EU) Project REACT, an Emmy Noether group funded by the DFG, and an Attract group funded by the Fraunhofer Society.

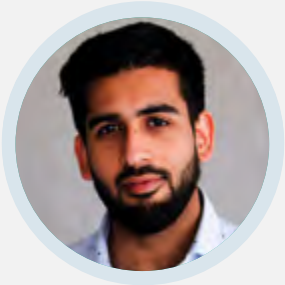


Keynote Speaker

Kyle Schneider

Vestaron, USA

Dr. Kyle Schneider received his bachelor's degree in chemistry from Grand Valley State University in 2009, where he performed structural studies on bacterial antibiotic resistance mechanisms. He next attended Yale University where he received his M.Sc. in Biochemistry and Molecular Biophysics. Subsequently, Schneider studied the molecular mechanisms of weak protein-protein interactions in signaling pathways under Dr. Eric Weiss at Northwestern University where he received his Ph.D. in 2015. In 2016, Schneider accepted a Scientist position at Vestaron where he has worked since to develop next-generation peptide pesticides for crop protection. Schneider is the recipient of several prestigious awards and honors, including the Barry M. Goldwater Scholarship ('08), National Science Foundation Graduate Research Fellow ('10), and National Academy of Engineering Frontiers of Engineering Awardee for the nations' top 100 engineers under 45 ('20) . In addition to academic papers and work as a peer-reviewer, Schneider is an inventor on five patents in crop protection and has written book chapters and essays on the biologics revolution in pesticides. He resides in Kalamazoo, MI, USA with his wife and three children.



Keynote Speaker

Ameer Shakeel

AgroSphere, USA

Ameer is a biomedical engineering graduate. Ameer spearheads the research and technical development of our products. He is passionate about conducting meaningful research that translates to real world applications. Ameer is an inventor of and also leads the development of AgroSpheres' proprietary RNA manufacturing & delivery technology. AgroSpheres' technology breakthrough in enabling RNA stability, delivery and uptake in recalcitrant models such as lepidopterans has led to the company securing several collaborations with the biggest global AgTech companies. The delivery mechanism of the technology enables it to unlock the potential of novel modalities such as RNAi.

Keynote Speaker

Nobuhiro Suzuki

Okayama University, Japan

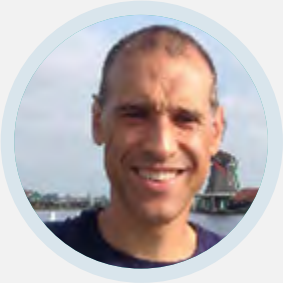
Dr. Nobuhiro Suzuki received his Ph.D. (1989) in virology from Tohoku University in Sendai, Japan, and currently serves as a full professor in the Institute of Plant Stress and Resources, Okayama University. Suzuki Laboratory focuses on characterization of diverse viruses infecting phytopathogenic fungi and exploration of their interplays. Recent achievements include the discovery of a neo-virus lifestyle exhibited by a (+)ssRNA virus and an unrelated dsRNA virus in a plant pathogenic fungus and of multilayer antiviral defense in fungi involving Dicer. Prior to coming to Kurashiki, Okayama Prefecture, he was a visiting fellow of the laboratory of Professor Donald L. Nuss at the University of Maryland Biotechnology Institute (UMBI) for four years (1997-2001) to study molecular biology of hypoviruses that serve as biocontrol agents in Europe. Before visiting UMBI, he served as an assistant professor and a lecturer in the Biotechnology Institute at the Akita Prefectural College of Agriculture for 11 years (1988-1998) where he conducted a project on molecular characterization of rice dwarf virus (RDV), a member of the family Sedoreoviridae. He received awards from the Japanese Phytopathological Society and Japanese Society for Virology for his outstanding achievements in plant and fungal virology. He serves as an Editor of Virus Research, Frontiers in Virology, Journal of General Plant Pathology, and Biology.

Keynote Speaker

Daniel R. Swale

University of Florida, USA

Dr. Daniel Swale received his B.S. in Biological Sciences at Christopher Newport University, a M.S. degree in Life Sciences from Virginia Tech, a Ph.D. degree in Insect Toxicology from University of Florida, and a Postdoctoral Fellowship in Neuropharmacology at Vanderbilt University Medical Center. Currently, he is a tenured Associate Professor in the Emerging Pathogens Institute and the Department of Entomology and Nematology at the University of Florida. His current research program lies at the interface of physiology, toxicology, and molecular genetics to provide knowledge on the modes of action, discovery and development, and resistance of various drugs and insecticides. Specifically, the Swale Lab studies the physiotoxicology of ion channels and ion transporters, and mechanisms that pathogens alter physiological pathways in the arthropod vector to enhance pathogenesis of pathogens, alter arthropod behavior, or alter vector competency. Knowledge gained by our various projects will aid in exploiting the plasticity of insect systems to facilitate the development of novel therapeutics for arthropod control (e.g. vectors of human pathogens) or for enhancement of arthropod systems (e.g. honey bee health).



Keynote Speaker

Gianluca Tettamanti

University of Insubria, Italy

Professor of Zoology at University of Insubria, Italy. Research assistant at King's College London in 1998 and 2004, he received a Ph.D. in Evolutionary Developmental Biology in 2003. His research activity is focused on different aspects of insect development and physiology for the development of biotechnological applications. The main topics addressed are: 1) the study of cell death processes during metamorphosis in holometabolous insects; 2) the use of dipteran larvae for the bioconversion of organic waste and protein production for feedstuff and biotechnological applications; and 3) the identification of molecules for the development of bio-inspired strategies for the control of pest insects. Author of more than 120 articles. Associate editor of Journal of Insects as Food and Feed and member of the editorial board of many international journals.

Keynote Speaker

Mahmut Tör

University of Worcester, UK

Professor Mahmut Tör has been working on molecular plant-microbe interactions, for more than twenty-five years. After graduating in Agricultural Science at Çukurova University in Türkiye, he went to the UK to study for an M.Sc. and Ph.D. in Plant Pathology at Wye College, University of London. It was there he became fascinated in the, then, new area of molecular biology of plant diseases, which led to his future career in this field. Since that time, he has worked as a post-doctoral researcher, a project leader, a manager and mentor for post-docs, supervisor for students and technicians, a group leader, a university lecturer and a collaborator within international scientific consortiums. He has worked at the Universities of London, Akdeniz (Türkiye), and Warwick and, for the last twelve years, at the University of Worcester. His research has been funded by both national and international funding bodies and has led to the publication of numerous articles in international journals. He has mentored more than 70 researchers and collaborated with well-known scientists across a number of academic disciplines and been involved in establishing a new scientific society to bring together plant and animal scientists fighting disease. Active at the national and international level within his field, he routinely referees grant proposals for UK, USA, Canadian, Dutch and Turkish funding agencies and manuscripts for many different international journals. He is a Visiting Professor at Hangzhou Normal University, China, serves on the editorial boards of several scientific journals, and has been a member of different grant committees.

Keynote Speaker

Patrick J. Tranel

University of Illinois at Urbana-Champaign, USA

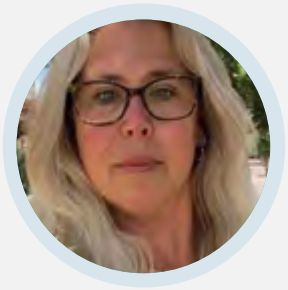
Dr. Patrick Tranel is the Ainsworth Professor and Associate Head in the Department of Crop Sciences at the University of Illinois. His research program uses molecular and genomic tools to address weed science issues. His lab is internationally recognized for its numerous contributions that have increased our understanding of the evolution and underlying mechanisms of herbicide resistance. Dr. Tranel collaborates extensively with more applied weed scientists at the University of Illinois and elsewhere, fostering a research program that is timely and relevant to weed management practitioners. He is a Fellow of the North Central Weed Science Society and the Weed Science Society of America, and he serves as Associate Editor/Editorial Board Member of three journals.

Keynote Speaker

Thomas Van Leeuwen

Ghent University, Belgium

Dr. ir. Thomas Van Leeuwen is professor at the Department of Plants and Crops of Ghent University, Belgium. Prof. Van Leeuwen devotes his research to the elucidation of adaptation mechanisms in crop pests, mainly mites such as the spider mite *Tetranychus urticae*. In the last decade, he was one of the first scholars to underpin the molecular mechanisms of acaricide resistance. With the availability of a high-quality genome sequence, his team and collaborators acquired considerable expertise in genomic mapping, which allowed to elucidate resistance mechanisms without any prior hypothesis, thereby also uncovering the molecular mode of action of several classes of insecticides and acaricides. Although acaricide resistance is the primary subject, investigations into the mechanisms of plant adaptation and extreme polyphagy are also a main interest. Recently, after obtaining an ERC consolidator grant, prof. Van Leeuwen focusses on the molecular genetic mechanisms of gene regulation in the context of xenobiotic resistance. This entails the determination of cis- and trans regulatory variation, expression QTL mapping and the role of gene copy number variation. His research also expands into the fundamental development of reverse genetic tools (RNAi, Crispr/Cas9) tailored to spider mites and other difficult to transform insects.



Keynote Speaker

Jeanmarie Verchot

Texas A&M, USA

Dr. Jeanmarie Verchot, Professor Plant Virology at Texas A&M University in the Department of Plant Pathology. She recently served as Fellow for the Institute for Plant Biotechnology at Texas A&M University from 2019-2021. Prior to this appointment she was named Center Director for the Texas A&M AgriLife Research and Extension Center-Dallas from 2017-2019. Dr Verchot was a Professor of Plant Pathology at Oklahoma State University and Chief Scientific Officer for VF Canna LLC before joining Texas &M Agrlife. Verchot obtained a bachelor's in molecular genetics from Rutgers University in 1987 and her doctorate in microbiology from Texas A&M University in 1995. As a PI Dr Verchot has led investigations to understand potexvirus cell-to-cell movement, the role of ER stress in virus infection involving potyviruses and potexviruses, infectious clone technology for investigations of Rose Rosette Virus in roses. Dr Verchot has served as Associate Editor for Plant Molecular Biology, Councilor for Plant Virology to the American Society of Virology, and has led various national and international symposia on the topic of plant virus-host interactions.

Keynote Speaker

John Vontas

Agricultural University of Athens, Greece

John Vontas (www.aua.gr/vontas) is currently the Director of Institute Molecular Biology and Biotechnology, Foundation for Research and Technology (IMBB-FORTH), Crete, Greece and also full Professor at the Agricultural University of Athens (AUA) since 2014. He obtained his Ph.D. in Insect Genetics (1997) from AUA. Consecutive Marie Curie fellowships took him to Cardiff University (1998-2001), Liverpool School of Tropical Medicine (2002) and IMBB-FORTH (2002-2004). He was appointed Lecturer at AUA (2005), Associate Professor at the University of Crete (2008-2013). He worked at the Innovative Vector Control Consortium (IVCC) in 2013-2014. He teaches in national and international courses and has supervised >25 Ph.D. students and many Post Doctoral researchers, who pursue careers in academia and industry. His research focus on biotechnology based approaches for the control of disease vectors and agricultural pests. He has published many papers and gave a large number of invited talks worldwide. He is Academic Editor in Pesticide Biochemistry and Physiology and on the Editorial Board of main journals in his field.

Keynote Speaker

Aiming Wang

Agriculture and Agri-Food Canada, Canada

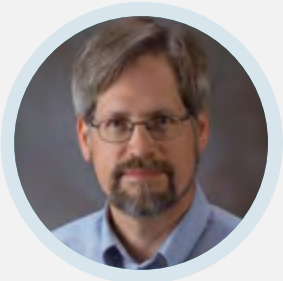
Dr. Aiming Wang completed his Ph.D. in plant molecular biology and virology from the University of British Columbia in 1999. Currently, he is Senior Research Scientist at the London Research and Development Centre, Agriculture and Agri-Food Canada, and Adjunct Professor of the Department of Biology, Western University. Dr. Wang's research program is directed to study the viral pathogens that cause devastating diseases on soybean, cereals, horticultural crops, and vegetables. His research has been concentrated on the elucidation of the viral infection process and molecular virus-plant interactions, and development of genetic resistance, vaccines, and other novel antiviral technologies. Dr. Wang has published over 130 peer-reviewed research papers, 35 book chapters and over 250 other articles and edited seven books/special issues. He has trained 21 graduate students and 26 post-docs/visiting professors. Dr. Wang is the recipient of various awards, such as Queen Elisabeth II Diamond Jubilee Medal from Government of Canada, Golden Harvest Award from Agriculture and Agri-Food Canada, the Ruth Allen Award from the American Phytopathological Society and the Outstanding Research Award from the Canadian Phytopathological Society.

Keynote Speaker

Ping Wang

Cornell University, USA

Dr. Ping Wang is a Professor in the Department of Entomology at Cornell University. His research interest lies in understanding the biochemical and molecular interactions of the insect midgut with host plants and microbial pathogens. Current research projects in his lab are focused on genetics and molecular mechanisms of insect resistance to insecticidal toxins from the soil bacterium *Bacillus thuringiensis* (Bt). His lab uses genetic, biochemical and molecular approaches, and genomic and proteomic technologies to identify and functionally understand the insect midgut genes and their protein products involved in the pathways of toxicity of Bt toxins, and to understand the molecular genetics of Bt resistance in a lepidopteran pest, the cabbage looper *Trichoplusia ni*.



Keynote Speaker

James H. Westwood

Virginia Tech, USA

Jim Westwood is a Professor in the School of Plant and Environmental Sciences at Virginia Tech, where his research program focuses on parasitic plants. Jim's research interests have centered on parasitic weeds, initially focusing on the broomrapes (*Orobanche* and *Phelipanche* spp.) and later including dodders (Cuscuta). He has developed model systems for parasitic plant research that paved the way for molecular and genomic studies of these plants. His group was the first to report host-parasite exchange of mRNAs, and his work is reshaping understanding of how parasitic plants have evolved and interact with their hosts. Jim earned a B.A. from Concordia College (Moorhead, MN) and M.S. from the University of Minnesota, then served in the U.S. Peace Corps in West Africa before completing a Ph.D. at Purdue University. Jim has served as president of the International Parasitic Plant Society and leader of the Parasitic Plant Genome Project. He is a Fulbright Fellow alumnus (France).

Keynote Speaker

Steve Whyard

University of Manitoba, Canada

Steve Whyard is a Professor in the Department of Biological Sciences, University of Manitoba, Canada. Dr. Whyard received his Ph.D. in Biology from Queen's University in 1993, studying molecular mechanisms of insecticide resistance in pest insects. He then spent 10 years in CSIRO Australia, conducting research on the development of novel strategies to control pest insect and other invasive species. He acquired extensive experience with RNA interference (RNAi) technologies while in Australia, developing techniques for RNAi as a molecular biology research tool as well as considering its utility in pest animal control technologies. Following his return to Canada, he has developed a research program that is focused on understanding the molecular controls that govern invertebrate development, sex determination, and sexual differentiation, and continues to be involved in developing RNAi technologies applicable to pest insect control. As an advocate of RNAi technologies, he has been fortunate to collaborate with many other researchers across the globe and has enjoyed helping colleagues develop RNAi-based tools or applications in a broad range of organisms, including invertebrates (nematodes, mollusks, arthropods), vertebrates (fish, mice), plants and fungi.

Keynote Speaker

Kun Yan Zhu

Kansas State University, USA

Dr. Kun Yan Zhu received his Ph.D. degree in Biology from Utah State University in 1992 and conducted postdoctoral research at the University of Massachusetts at Amherst from 1992 to 1995. He joined Kansas State University as assistant professor of entomology in 1996, was promoted to associate professor in 2002, and then full professor in 2007. He was named university distinguished professor of entomology in 2017. His research interests are in the scientific interface between insect toxicology and molecular biology, including mechanisms of insecticide resistance, insect chitin biosynthesis and metabolism, mechanisms and applications of RNA interference, and new approaches for insect pest management. He has authored 225 peer-reviewed journal papers, 15 book chapters and 423 presentations, 162 of which were invited. He has served as an associate editor or editorial board member for 13 scientific journals. He is a Fellow of both the American Association for the Advancement of Science (AAAS) and the Entomological Society of America.

Keynote Speaker

Heiko Ziebell

Julius Kühn-Institut, Germany

Trained as an orchid gardener, Heiko Ziebell studied horticulture in Hannover, Germany and fell in love with plant viruses. Since his diploma thesis he worked with many different plant viruses at the University of Cambridge (UK), where he gained his Ph.D. and Cornell University (USA). He is very interested in host - virus and virus - vector interactions. Currently, he is the head of one of the National Reference Laboratories for Harmful Organisms in Plants at the Julius Kuehn Institute in Germany. He is responsible for the virus diagnostics in vegetables, legumes and other crops.

Dear Colleague,

Molecular approaches are currently among the most popular topics in biological sciences and provide many opportunities in the solution of various problems. We have witnessed common use of these approaches in the field of plant protection in the last decades. Many research projects related to entomology, plant pathology and weed sciences have been conducted using genomics, transcriptomics, proteomics, functional genomics, DNA-based diagnosis techniques, gene expression analyses and recombination studies. Significant progress has been achieved in the solution of pest, disease and weed problems using molecular concepts, such as RNA interference and Crisper/Cass, or tools, such as microbials or peptides, enzymes & proteins. In this manner, the "1st International Molecular Plant Protection Congress (IMPPC)" was held in Adana in 2019, and had hosted 42 top notch experts in the field of molecular plant protection as keynote speakers, and 14 global and local agriculture and biotechnology companies. The congress had a great impact all over the world and created an important awareness. In this context, we wish to continue the awareness and momentum gained with the "2nd International Molecular Plant Protection Congress- IMPPC2023". The IMPPC2023 will be held at Hektaş Agricultural Innovation, Training and Experience Center, Orhangazi-Bursa, Türkiye between May 15-18, 2023, under the coordination of Ankara University, Turkish Ministry of Agriculture and Forestry and Hektaş Ticaret Türk A.Ş.

The opening lecture of IMPPC2023 will be given by Professor Craig Mello (University of Massachusetts, USA), 2006 Nobel Laureate in Physiology or Medicine for discovering RNA interference-RNAi. Eight-seven scientists, who are among the world's leading experts in the fields of "Molecular Entomology & Plant Pathology & Weed Science will deliver keynote talks. In addition, up to 42 biotech, agricultural and life science companies will be located in the exhibition hall to introduce their company profiles and innovations in plant protections.

The theme of IMPPC2023 is "innovations in plant protection". The congress will highlight the innovative plant protection products from dsRNA to peptide-based pesticides, from microbials to new generation chemicals. The purpose of the congress is to provide a platform for researchers and shareholders from industry to ministries in order to share their latest findings and innovations amongst each other and exchange the ideas. The official language of the congress will be English and the abstracts will be provided in the congress book.

We welcome you to "The Second International Molecular Plant Protection Congress" and hope you will have great time in Orhangazi!

Sincerely yours,

On Behalf of the Congress Organization Committee
Umut Toprak, Chair, Ph.D, Ankara University, Ankara, Türkiye

IMPPC2023 *PROGRAM*

15 MAY 2023 MONDAY

10:00-17:30 REGISTRATION Main Entrance
10:00 DEPARTURE FROM HOTELS TO CONGRESS CENTER (Detour)
12:00 DEPARTURE FROM CONGRESS CENTER TO HOTELS (Detour)
14:00 DEPARTURE FROM HOTELS TO CONGRESS CENTER (Detour)
16:00 DEPARTURE FROM CONGRESS CENTER TO HOTELS (Detour)
17:00 DEPARTURE FROM HOTELS TO CONGRESS CENTER (Detour)
18:00 FINAL DEPARTURE FROM HOTELS TO CONGRESS CENTER
19:30-21:30 WELCOME COCKTAIL & OPENING OF HEKTAŞ AGRICULTURE AND SCIENCE MUSEUM
21:30 DEPARTURE FROM CONGRESS CENTER TO HOTELS
22:00 DEPARTURE FROM CONGRESS CENTER TO HOTELS
22:30 FINAL DEPARTURE FROM CONGRESS CENTER TO HOTELS

16 MAY 2023 TUESDAY

08:00 DEPARTURE FROM HOTELS TO CONGRESS CENTER
08:30 DEPARTURE FROM HOTELS TO CONGRESS CENTER
09:00 FINAL DEPARTURE FROM HOTELS TO CONGRESS CENTER
08:30-17:30 REGISTRATION Main Entrance
08:30-17:30 Posters should be attached to the boards.
10:30-12:00 OPENING CEREMONY Main Hall
12:00-13:30 LUNCH
12:15 DEPARTURE FROM CONGRESS CENTER TO HOTELS (Detour)
14:00 DEPARTURE FROM HOTELS TO CONGRESS CENTER (Detour)
13:30-15:00 OPENING LECTURE ***Main Hall*** **O1. Honorary Lecture:** "A Worms tale: From mysteries of inheritance to new technologies for medicine and agriculture" ***Craig Mello, University of Massachusetts, USA*** **Moderator: Umut Toprak**
15:00-15:30 COFFEE BREAK

15:30-16:40 **PLANT MYCOLOGY 1** **SESSION 1 Hall 2** **Moderators:** Dolores Fernández Ortuño Yusuf Yanar	**15:30-16:50** **PLANT VIROLOGY 1** **SESSION 2 Hall 4** **Moderators:** Hanu R. Pappu Kadriye Çağlayan	**15:30-16:50** **PLANT NEMATOLOGY 1** **SESSION 3 Hall 3** **Moderators:** Sophie Mantelin Shinichiro Sawa	**15:30-17:00** **WEED SCIENCE 1** **SESSION 4 Hall 5** **Moderators:** Dana R. MacGregor James H. Westwood	**15:30-17:00** **ENTOMOLOGY 1** **SESSION 5* Main Hall** **Moderators:** Russell Groves Feza Can ** Sponsored by The Royal Entomological Society*
15:30-15:50 **O2. Li-Jun Ma-** KEY "Genome compartmentalization and fungal pathogenesis"	**15:30-15:50** **O7. Heiko Ziebell-** KEY "The importance of plant health in a global world"	**15:30-15:50** **O13. Pierre Abad-** KEY "Epigenetic signatures associated with nematode adaptation to plant resistance"	**15:30-15:50** **O17. Jonathan Gressel-** KEY "A novel approach to pesticide discovery that better confronts resistance: Inhibitors that target protein-protein interactions"	**15:30-15:50** **O23. Ken Narva-** KEY "Discovery, development and commercialization of RNA-based biopesticides"
15:50-16:10 **O3. Hailing Jin-** KEY "Cross-kingdom RNA trafficking between plants and fungal pathogens"	**15:50-16:10** **O8. Alex Murphy-** KEY "Disruption of insect mediated transmission of plant viruses"	**15:50-16:10** **O14. Sebastian Eves-van den Akker-** KEY "AI-powered holistic and dynamic pathology to deliver new sources of resistance"	**15:50-16:10** **O18. Baruch Rubin-** KEY "Herbicide-resistant weeds are a threat to the sustainability of arable farming"	**15:50-16:10** **O24. Steve Whyard-** KEY "Alternative structured double-stranded RNAs can enhance RNAi in insects"
16:10-16:20 **O4. Abdullah Al-Sadi** "Fungal and bacterial antagonists from deserts show high efficacy in the management of *Pythium aphanidermatum*-induced diseases in tomatoes and cucurbits"	**16:10-16:20** **O9. Serpil Erilmez** "Genetic diversity of Cucumber mosaic virus infecting pepper in Türkiye"	**16:10-16:30** **O15. Godelieve Gheysen-** KEY "Transgenic East African highland banana plants are protected against Radopholus similis through host-delivered RNAi"	**16:10-16:30** **O19. Scott Baerson-** KEY "Exploiting allelopathy for biotechnology-derived weed control"	**16:10-16:30** **O25. Gregor Bucher-** KEY "The quest for the best dsRNA target sequences for pest control by a genome wide screen"
16:20-16:30 **O5. İlker Kurbetli** "*Phytophthora dianthi* sp. nov., a new species causing root rot and vascular necrosis of carnation in Türkiye"	**16:20-16:30** **O10. Nihan Güneş-**STU "Determination of PVY resistance and expression of resistance associated genes in tomato plants"			
16:30-16:40 **O6. Gürkan Başbağcı** "Molecular characterization of *Rhizoctonia* species associated with chickpea in Türkiye"	**16:30-16:40** **O11. Muhammad Shafiq Shahid** "Native and non-native *Bemisia tabaci* B haplotype whiteflies are implicated in the spread of endemic and introduced begomoviruses in Oman"	**16:30-16:50** **O16. Michael Jones-** KEY "RNAi vs. Gene-editing for plant nematode resistance?"	**16:30-16:40** **O20. Nedim Mutlu** "Development of resistance against Broomrape (*Orobanche* spp., *Phelipanche* spp.) using Crispr-Cas9 technology in tomato (*Solanum lycopersicum*)"	**16:30-16:40** **O26. Umut Toprak** "The mystery of the self-cannibalize heroes: Silencing Autophagy related 1 (ATG1) and Autophagy related 8 (ATG8) in *Leptinotarsa decemlineata* (Coleoptera: Chrysomelidae)"
	16:40-16:50 **O12. Mohamad Chikh-Ali** "The dynamics of PVY infection during the growing season of the San Luis Valley, Colorado"		**16:40-16:50** **O21. Bahadir Şin-**STU "Determination of the resistance status of wild mustard (*Sinapis arvensis* L.) collected from wheat cultivation areas in Amasya, Çorum, Tokat and Yozgat provinces against Tribenuron methyl by molecular methods"	**16:40-16:50** **O27. Solmaz Ghanbari-**STU "Can Insulin-like peptide 1a (ILP1a) and Insulin-like peptide 4 (ILP4) be good potential targets for RNAi-based pest control in *Leptinotarsa decemlineata* (Coleoptera: Chrysomelidae)?"
			16:50-17:00 **O22. Esra Çiğnitaş-**STU "Molecular identification of *Fusarium* spp. on infected broomrape (*Phelipanche* spp.) seeds"	**16:50-17:00** **O28. İdil Osan-**STU "The regulation of lipid metabolism in *Leptinotarsa decemlineata* (Coleoptera: Chrysomelidae) through RNAi: Insights from gene silencing experiments"

17:30 DEPARTURE FROM CONGRESS CENTER TO HOTELS

19:00-21:00 SESSION 6 "The entrepreneur Street"* F.A.R.M. Square

O29. Pam Marrone- KEY
Co-founder & Executive Chair, Invasive Species Corporation

"Pursuing biologicals for pest management and plant health: A lifelong entrepreneurial journey"

Moderator: Umut Toprak
* Bevarage & Snacks are complimentary

21:30 DEPARTURE FROM CONGRESS CENTER TO HOTELS

22:30 FINAL DEPARTURE FROM CONGRESS CENTER TO HOTELS

17 MAY 2023 WEDNESDAY

07:30 DEPARTURE FROM HOTELS TO CONGRESS CENTER

08:00 FINAL DEPARTURE FROM HOTELS TO CONGRESS CENTER

08:30-10:00 **PLANT MYCOLOGY 2** **SESSION 7 Hall 2** **Moderators:** Dwayne Hegedus Pervin Kınay Teksür		**08:30-10:00** **PLANT VIROLOGY 2** **SESSION 8 Hall 4** **Moderators:** Bayram Çevik Alex Murphy	**08:30-10:00** **PLANT BACTERIOLOGY 1** **SESSION 9 Hall 3** **Moderators:** Gitta Coaker Ian Dubery	**08:30-09:50** **ENTOMOLOGY 2** **SESSION 10 Main Hall** **Moderators:** Subba Reddy Palli Dürdane Yanar
08:30-08:50 **O30. Mark Belmonte-KEY** "Using RNA interference to protect crops against fungal pathogens		**08:30-08:50** **O36. Hanu R. Pappu-KEY** "Host-Virus interactions in the omics era: What is the host telling us?"	**08:30-08:50** **O43. Jacob Malone-KEY** "Pan-genome analysis identifies intersecting roles for *Pseudomonas* specialized metabolites in potato pathogen inhibition"	**08:30-08:50** **O49. John Vontas-KEY** "Functional approaches for elucidating insecticide resistance mechanisms"
08:50-09:10 **O31. Mahmut Tör-KEY** "Control of downy mildew pathogens using spray induced gene silencing"		**08:50-09:10** **O37. Fernando Garcia-Arenal-KEY** "Virus emergence, host range evolution and crop resistance durability"	**08:50-09:10** **O44. Robert Jackson-KEY** "Different mobile genetic elements influence pathogen evolution"	**08:50-09:10** **O50. Ralf Nauen-KEY** "Characterization, impact and spread of diamide insecticide resistance in lepidopteran pests with special reference to ryanodine receptor alterations"
09:10-09:30 **O32. Dolores Fernández Ortuño-KEY** "RNAi strategy, an alternative to conventional fungicides for the control of Botrytis and the cucurbit powdery mildew diseases?"		**09:10-09:20** **O38. Kadriye Çağlayan** "Elucidate genetic diversity of Raspberry bushy dwarf virus (RBDV) in *Rubus* spp. in Türkiye" **09:20-09:30** **O39. Bengi Topkaya** "Analysis of Citrus chlorotic dwarf-associated virus (CCDaV)- Citrus interactions"	**09:10-09:30** **O45. Monica Höfte-KEY** "Toxin-producing Sarocladium and *Pseudomonas* spp. associated with rice: Mutualists or parasites?"	**09:10-09:30** **O51. Thomas Van Leeuwen-KEY** "Transcriptional regulation of detoxification in the polyphagous arthropod pest *Tetranychus urticae*"
09:30-09:40 **O33. Mümin İbrahim Tek-STU** "CRISPR based gene-drive strategy for engineering of disease resistance in plants"		**09:30-09:40** **O40. Başak Ulaşlı** "Molecular characterization of *Colomerus* vitis (pgst.) (Acarina: Eriophyidae) and their potential role as vector of grapevine pinot gris virus (GPGV) In Turkish vineyards"	**09:30-09:40** **O46. Gamze Bölük-Sarı-STU** "Three novel species into Pectobacteriaceae family from Hawaii (*Pectobacterium colocasium* sp. nov., *Pectobacterium hawaiiense* sp. nov. and *Dickeya colocasiae* sp. nov.)"	**09:30-09:40** **O52. Emre İnak** "Greenhouse trials and screening of target-site mutations of *Bemisia tabaci* populations in Türkiye"
09:40-09:50 **O34. Elifgül Aksu-STU** "Functional analysis of candidate sffector PTTG_06852 of wheat leaf rust fungi by rna silencing"		**09:40-09:50** **O41. Nevin Akdura** "Revealing the apple virome using HiPlex technology in Hakkari, Türkiye"	**09:40-09:50** **O47. Yasemin Bektaş** "Seed priming activity of β-aminobutyric acid (Baba) against *Clavibacter michiganensis* ssp *michiganensis* (Cmm) in tomato (*Solanum lycopersicum* L.)	**09:40-09:50** **O53. Marcus Guest** "The evolving roles of worm and moth genetics In pesticide discovery"
09:50-10:00 **O35. İlayda Küçük-STU** "Functional analysis of effector candidate PTTG_01827 of wheat brown rust by gene silencing"		**09:50-10:00** **O42. Songül Yalçın Ateş** "Optimisation of degenerate primers for detection of Peach latent mosaic viroid (PLMVd) analysis by RT-qPCR"silencing"	**09:50-10:00** **O48. Mine Saraçoğlu** "Isolation and identification of bacterial diseases in Central Anatolia Region onion (*Allium cepa* L.) cultivation areas and onion storages and pathogenicity studies"	

10:00-10:30 COFFEE BREAK

10:30-11:40 **PLANT MYCOLOGY 3** **SESSION 11 Hall 2** **Moderators:** Aziz Karakaya Nichola Hawkins	**10:30-12:10** **PLANT MYCOLOGY 3** **SESSION 12 Hall 2** **Moderators:** Özer Elibüyük Elizabeth Fontes	**10:30-12:00** **PLANT BACTERIOLOGY 2** **SESSION 13 Hall 3** **Moderators:** Robert Jackson Monica Höfte	**10:30-11:50** **WEED SCIENCE 2** **SESSION 14 Hall 5** **Moderators:** Jonathan Gressel Scott Baerson	**10:30-11:30** **ENTOMOLOGY 3** **SESSION 15 Main Hall** **Moderators:** Kostas D Mathiopoulos Ping Wang
10:30-10:50 **O54. Robert Brueggeman-KEY** "Rpt5 encodes a receptor-like protein that provides the broadest and most effective net form net blotch resistance in barley"	**10:30-10:50** **O59. Miguel A. Aranda-KEY** "Loss-of-susceptibility to pepino mosaic virus in tomato"	**10:30-10:50** **O67. Gitta Coaker-KEY** "Host manipulation by phloem-limited bacteria"	**10:30-10:50** **O74. Patrick J. Tranel-KEY** "Sex determination in dioecious Amaranthus weeds"	**10:30-10:50** **O79. Glenn F. King-KEY** "Tying insect pests in knots: deployment of spider-venom knottins as bioinsecticides"
10:50-11:10 **O55. Evsey Kosman-KEY** "A uniform logically consistent analysis of population structure of plant pathogens and a general warning about hazardous invasion of aggressive individuals"	**10:50-11:10** **O60. Enrique Moriones Alonso-KEY** "Molecular epidemiology: an essential tool to improve farmers' decision-making in plant protection against plant viruses"	**10:50-11:10** **O68. Michelle Hulin-KEY** "Bacterial pathogens hijack host metabolism to promote virulence"	**10:50-11:10** **O75. James H. Westwood-KEY** "Plant-plant communication: The parasitic plant dodder (*Cuscuta campestris*) uses RNA to control its hosts"	**10:50-11:10** **O80. Elaine Fitches-KEY** "Exploiting spider venom neuropeptides to develop novel biopesticides"
11:10-11:20 **O56. Selcen Doğan-STU** "Development of yellow rust resistant wheat lines with the combination of Real-time PCR, haploid and speed breeding Technologies"	**11:10-11:20** **O61. Kübra Yıldız-STU** "Crispr/cas9-mediated gene Editing using multiplexed grnas to develop resistant against begomoviruses and powdery mildew"	**11:10-11:20** **O69. Bihter Avşar** "Improved heterologous expression, purification, and structural characterization of plant heterotrimeric G-protein γ subunits for crop improvement"	**11:10-11:20** **O76. Dana R. MacGregor-KEY** "Genomic data and tools to test hypotheses are required to understand weediness"RNA to control its hosts"	**11:10-11:30** **O81. Kyle Schneider-KEY** "Transforming crop protection with cysteine rich natural peptides – A pipeline of possibilities"
11:20-11:30 **O57. Özgür Altundaş-STU** Biostimulant effects of ınoculation with *Piriformospora indica* and arbuscular mycorrhizal fungi on wheat	**11:20-11:30** **O62. Keri Wang** "Development of a plant vaccine for management of tomato brown rugose fruit virus"	**11:20-11:30** **O70. Murad Ghanim** "ER-associated molecular responses underlying *Liberibacter solanacearum* transmission by the carrot psyllid"		
11:30-11:40 **O58. Mutlu Şen-STU** "Development of molecular diagnosis method of safflower pathogen *Puccinia carthami*"	**11:30-11:40** **O63. Bayram Çevik** "Exploring the use of RNA interference for controlling tomato brown rugose fruit virus"	**11:30-11:40** **O71. İrem Altın** "Copper resistance screening in *Erwinia amylovora* and transcriptional response of the bacteria to copper compounds in Sakarya, Türkiye"	**11:30-11:50** **O77. Stephen O. Duke-KEY** "Approaches to finding new herbicide target sites"	
	11:40-11:50 **O64. Songül Yalçın Ateş** "Detection of Tomato brown rugose fruit virus (ToBRFV) using newly designed primers and probe by RT-qPCR method"	**11:40-11:50** **O72. Turgay Ünver** "Development of a phytomicrobiome analysis toolkit to dechipher molecular plant-microbe interactions"		
	11:50-12:00 **O65. Gözde Erkış Güngör-STU** "Expression analysis of some tomato defense genes against Tomato brown rugose fruit virus infection"	**11:50-12:00** **O73. Magdalena Górecka** "To be or not to be a toxin – How does the HopAG1 effector upset the host?"	**11:50-12:00** **O78. Selim Karagöl-STU** "Molecular characterization of *Corylus colurna* species from Bolu and Kastamonu Provinces"	
	12:00-12:10 **O66. Cansu Şimşek** "Detection of Tomato brown rugose fruit virus (ToBRFV) using Real-Time PCR (RT-PCR)"			

12:00-13:30 LUNCH

12:15 DEPARTURE FROM CONGRESS CENTER TO HOTELS (Detour)

14:00 DEPARTURE FROM HOTELS TO CONGRESS CENTER (Detour)

13:30-15:00 PLANT MYCOLOGY 4 SESSION 16 Hall 2 **Moderators:** Salih Maden Hailing Jin	13:30-15:00 PLANT VIROLOGY 4 SESSION 17 Hall 4 "Emerging plant viruses" **Moderators:** Aiming Wang Jeanmarie Verchot	13:30-15:00 PLANT BACTERIOLOGY 3 SESSION 18 Hall 3 **Moderators:** Michael Kube Michelle Hulin	13:30-15:00 ENTOMOLOGY 4 SESSION 19 Main Hall **Moderators:** Emre İnak Kun Yan Zhu	13:30-15:00 ENTOMOLOGY 5 SESSION 20 Hall 5 **Moderators:** Ferit Turanlı Wendy Maddelein
13:30-13:50 **O82. Nichola Hawkins-KEY** "How predictable is pathogen evolution under fungicide selection?"	**13:30-13:40** **Opening remarks**	**13:30-13:50** **O92. Ian Dubery-KEY** "Metabolomics of plant defense: The *Avena sativa* – *Pseudomonas coronafaciens* interaction	**13:30-13:50** **O99. David Mota-Sanchez-KEY** "Magnitude of field-evolved resistance of arthropods to pesticides: a comprehensive analysis by decade of use"	**13:30-13:50** **O105. Hans Merzendorfer-KEY** "Chitin biosynthesis: an attractive target for eco-friendly insecticides"
	13:40-14:00 **O88. Aiming Wang-KEY** "Towards control of existing, emerging and reemerging plant viruses"			
13:50-14:10 **O83. Mamadou Kane Mboup-KEY** "How to extend fungicides effective life without broad-spectrum fungicides"	**14:00-14:20** **O89. Aviv Dombrovsky-KEY** "Disinfection efficacy of Tobamovirus-contaminated soil and developing a novel platform for root protection applies"	**13:50-14:10** **O93. Jacob Malone-KEY** "Polysaccharide biosynthesis and its contribution to *Pseudomonas syringae* plant infection"	**13:50-14:10** **O100. Russell Groves-KEY** "The dynamic emergence phenology of the Colorado potato beetle; implications for resistance and pest management"	**13:50-14:10** **O106. Gianluca Tettamanti-KEY** "The circular economy in the agri-food sector: The contribution of black soldier fly"
14:10-14:30 **O84. Dolores Fernández Ortuño-KEY** "An overview of the fungicide resistance situation of the cucurbit powdery mildew, *Podosphaera xanthii*, in Spain"		**14:10-14:20** **O94. Damla Ertimurtaş-STU** "Genetic diversity of *Xanthomonas arboricola* pv. *juglandis* strains affecting walnuts in Türkiye revealed by rep-PCR and MLSA"	**14:10-14:30** **O101. Daniel R. Swale-KEY** "Inhibition of inward rectifier potassium (Kir) channels in the salivary gland prevents plant feeding and pathogen transmission by the cotton aphid, *Aphis gossypii*"	**14:10-14:30** **O107. Ronald Kühnlein-KEY** "Functional analysis of sterol and steryl ester metabolism in the *Drosophila melanogaster* insect model"
	14:20-14:40 **O90. Kook-Hyung Kim-KEY** "Characterization of Rsv3 gene and understanding Rsv3-mediated resistance mechanism in soybean mosaic virus-soybean pathosystem"	**14:20-14:30** **O95. Şafak Kalındamar** "Complete whole genome sequence and genomic analysis of *Pseudomonas cerasi* NTM-B-29 strain isolated from hazelnut orchard in Türkiye"		
14:30-14:40 **O85. Gamze Erdurmuş** "Fenhexamide resistance and molecular species identification of *Botrytis* spp. isolates"		**14:30-14:40** **O96. Edanur Öksüz-STU** "Hybrid genome assembly and annotation of *Xanthomonas arboricola* pathovar *corylina* NTM-B-28 strain isolated from hazelnut tree in Türkiye"	**14:30-14:40** **O102. Mustafa Murat Yeşilırmak-STU** "Determination of sodium channel kdr mutations and biochemical mechanism detection in *Cydia pomonella* populations from Eğirdir/Isparta in the lakes region of Türkiye"	**14:30-14:40** **O108. Maria E. Yakimova-STU** "High quality genome assembly of major pest of boreal forests, *Dendrolimus sibiricus* Tschetv. (Lepidoptera; Lasiocampidae)"
14:40-14:50 **O86. Tuğba Teker-STU** "Screening of tebuconazole, carbendazim, and fludioxonil resistance in *Fusarium* spp., the causal agent of cereal diseases in Türkiye"	**14:40-15:00** **O91. Elizabeth Fontes-KEY** "A signaling hub coordinating antiviral immunity and growth-promoting events"	**14:40-14:50** **O97. Didem Canik Orel** "Gene regions comparison for identification of bacterial pathogens in terms of Lettuce pathogens"	**14:40-14:50** **O103. Burcu Yaman-STU** "Determination of spiromesifen+abamectin resistance and detoxification enzymes of *Panonychus ulmi* koch populations collected from apple orchards in Isparta Province"	**14:40-14:50** **O109. İnci Şahin Negiş** "Using ITS region DNA barcoding to distinguish between *Kakothrips priesneri* Pelikan"
14:50-15:00 **O87. Omar Al-Sudairy-STU** "Newly synthesized benzimidazole–2–carbamate molecules show suppressive activities against plant pathogenic fungi and oomycetes"		**14:50-15:00** **O98. Murat Öztürk** "Molecular characterization of *Pectobacterium atrosepticum* lisolates causing potato blackleg and soft rot disease"	**14:50-15:00** **O104. Esengül Özdemir** "Incidence and spread of pyrethroid resistance mutations in *Varroa destructor* populations in Türkiye"	**14:50-15:00** **O110. Romana Iftikhar** "Mitochondrial genetic diversity of *Thrips tabaci* (Thysanoptera: Thripidae) in onion growing regions of the USA"
15:00-15:30 COFFEE BREAK				

	15:30-16:40 **PLANT VIROLOGY 5** **SESSION 21 Hall 2** *"Emerging plant viruses"* **Moderators:** Aiming Wang Elizabeth Fontes	**15:30-16:50** **PLANT NEMATOLOGY 2** **SESSION 22 Hall 3** **Moderators:** Pierre Abad Godelieve Gheysen	**15:30-16:50** **ENTOMOLOGY 6** **SESSION 23 Main Hall** **Moderators:** Francesco Pennacchio Salvador Herrero	**15:30-16:50** **ENTOMOLOGY 7** **SESSION 24 Main Hall** **Moderators:** Steve Whyard Ken Narva
	15:30-15:50 **O111. Jeanmarie Verchot-KEY** "Emerging viruses and using global host transcriptomics to differentiate pathways underlying disease"	**15:30-15:50** **O114. Sophie Mantelin-KEY** "Host Imprint on plant perception in the root-knot nematode *Meloidogyne incognita*"	**15:30-15:50** **O120. Rebekah Kelly-KEY** "Biological-based insecticides for pest management"	**15:30-15:50** **O126. Neena Mitter-KEY** "RNA based biopesticides for sustainable crop protection – Bio Clay technology"
	15:50-16:10 **O112. Nobuhiro Suzuki-KEY** "Yadokari/yadonushi nature: A virus in a virus in a fungus in a plant"	**15:50-16:10** **O115. Shinichiro Sawa-KEY** "Root-knot nematode modulates plant CLE3-CLV1 signaling as a long-distance signal for successful infection"	**15:50-16:10** **O121. Michael Kanost-KEY** "Fungal cell wall β-1,3-glucan stimulates immune cascades and is a target of an antifungal peptide in *Manduca sexta*"	**15:50-16:10** **O127. Wendy Maddelein-KEY** "RNAi as a biocontrol solution for soy stink bugs"
	16:10-16:30 **O113. Francisco Ochoa-Corona-KEY** "Multiple detection of 33 Poaceae-infecting viruses by e-probe diagnostic nucleic acid analysis"	**16:10-16:20** **O116. Gamze Aksay-STU** "In vitro nematicidal activity of arugula (*Eruca sativa* l.) against stem and bulb nematode (*Ditylenchus dipsaci* kühn, 1857)"	**16:10-16:20** **O122. Musa Kırışık** "Molecular identification of entomopathogenic fungi from western flower thrips [*Frankliniella occidentalis* (Pergande)]"	**16:10-16:30** **O128. Ameer Shakeel-KEY** "AgroSpheres manufacturing and delivery technology to address field stability and targeted delivery of dsRNA to enable efficient RNAi in lepidoptera"
		16:20-16:30 **O117. Taylan Çakmak** "New host plant report of root-knot nematode *Meloidogyne* (Goeldi, 1892) species, from Türkiye"	**16:20-16:30** **O123. Funda Şahin-STU** "Isolation and identification of entomopathogenic fungi from coastal districts of Ordu province, Türkiye"	
	16:30-16:40 **Closing remarks**	**16:30-16:40** **O118. Elif Yavuzaslanoglu** "Effect of extraction conditions on in vitro nematicidal activity of brown mustard (*Brassica juncea* L.) against stem and bulb nematode (*Ditylenchus dipsaci* kühn, 1857)"	**16:30-16:40** **O124. Ardahan Eski** "Efficacy of indigenous entomopathogenic bacteria and fungi against the Western flower thrip, *Frankliniella occidentalis* (Pergende) (Thysanoptera: Thripidae)"	**16:30-16:50** **O129. Steve Meyer-KEY** "Low-cost, scalable dsRNA manufacturing through microbial fermentation solves decade-long challenge and unlocks commercial potential of RNAi BioSolutions"
		16:40-16:50 **O119. Gülsüm Uysal-STU** "Dosage effect of pepper carrying N and Me1 genes to *Meloidogyne incognita*"	**16:40-16:50** **O125. Dürdane Yanar** "Biocontrol potential of some entomopathogenic fungal isolates against *Myzus persicae* (Sulzer) (Hemiptera: Aphididae)"	
17:30 DEPARTURE FROM CONGRESS CENTER TO HOTELS (Detour)				
19:30 DEPARTURE FROM HOTELS TO CONGRESS CENTER (Detour)				
22:30 FINAL DEPARTURE FROM CONGRESS CENTER TO HOTELS (Detour)				

IMPPC2023 PROGRAM

18 MAY 2023 THURSDAY

07:30 DEPARTURE FROM HOTELS TO CONGRESS CENTER

08:00 FINAL DEPARTURE FROM HOTELS TO CONGRESS CENTER

08:30-09:50 PLANT MYCOLOGY 5 SESSION 25 Hall 2

Moderators:
Massimo Reverberi
Semra Hasançebi

08:30-08:50
O130. Dwayne Hegedus-KEY
"Receptor-like kinases BAK1 and SOBIR1 are required for necrotizing activity of *Sclerotinia sclerotiorum* necrosis-inducing effectors"

08:50-09:10
O131. Kevin Ashford-KEY
"Laminarin innovation pathways"

09:10-09:20
O132. Deniz Çakar
"Determination of vc and mating types of *Cryphonectria parasitica* isolates by multiplex PCR, obtained from thirteen chestnut growing provinces of Türkiye"

09:20-09:30
O133. Ülkü Baykal
"Characterization of barcode sequences from complete nuclear rRNA sequences of the hazelnut (*Corylus avellana*) powdery mildew fungus *Erysiphe corylacearum*"

09:30-09:40
O134. Durmuş Erdurmuş
"Characterization of *Trichoderma* spp. obtained from Sakarya plateaus, Türkiye and efficiency of these isolates as biocontrol agents against *Neopestalotiopsis rosae* in strawberry"

09:40-09:50
O135. Osman Telli
"Effect of light on the life cycle, development and pathogenicity of *Hyaloperonospora arabidopsidis*"

08:30-09:50 ENTOMOLOGY 8 SESSION 26 Hall 4

Moderators:
David Mota-Sanchez
Pam Marrone

08:30-08:50
O136. Neil Crickmore-KEY
"Challenges and potential solutions for overcoming insect resistance to *Bacillus thuringiensis* based biopesticides"

08:50-09:10
O137. Ping Wang-KEY
"Bt resistance in *Trichoplusia ni*: mechanisms of resistance to multiple Bt toxins in a generalist insect"

09:10-09:20
O138. Gözde Büşra Eroğlu
"Isolation and molecular identification of local entomopathogenic bacteria from *Pieris brassicae*"

09:20-09:30
O139. Vildan Bozkurt
"Isolation and diagnosis of potentially entomopathogenic bacteria from larvae of Asian walnut moth *Erschoviella musculana* Erschoff (Lepidoptera: Nolidae)"

09:30-09:40
O140. Anna Subbotina-STU
"Sex specificity in defense mechanisms of *Lymantria dispar* against *Bacillus thuringiensis*"

09:40-09:50
O141. Betül Yılmaz-STU
"Formulation and characterization of a local *Bacillus thuringiensis* ssp. *israelensis*: A Promising alternative to chemical control of *Culex pipiens* (Diptera: Culicidae)"

08:30-10:00 ENTOMOLOGY 9 SESSION 27 Main Hall

Moderators:
Marek Jindra
Michael Kanost

08:30-08:50
O142. Subba Reddy Palli-KEY
"Development of genomics-based approaches for control of fall armyworm"

08:50-09:10
O143. Xavier Bellés-KEY
"Major developmental transitions during insect ontogeny are associated with dramatic changes in the network architecture of miRNA-mRNA interactions"

09:10-09:30
O144. Kostas D Mathiopoulos-KEY
"The use of lncRNAs in insect control. Lessons from the tiger mosquito"

09:30-09:50
O145. Kun Yan Zhu-KEY
"Breaking down the barriers: Strategies to enhance RNAi efficiency in insects"

09:50-10:00
O146. Shuhei Hashiro
"Development of dsRNA production technology using *Corynebacterium glutamicum* for RNAi-based pesticides"

10:00-10:30 COFFEE BREAK

10:30-11:50 **PLANT MYCOLOGY 6** **SESSION 28 Hall 2** **Moderators:** Li-Jun Ma Mark Belmonte		**10:30-11:50** **PLANT BACTERIOLOGY 4** **SESSION 29 Hall 3** **Moderators:** Mine Saraçoğlu Jacob Malone	**10:30-11:30** **ENTOMOLOGY 10 SESSION 30 Hall 4** **Moderators:** Neena Mitter Glenn F. King	**10:30-11:50** **ENTOMOLOGY 11** **SESSION 31 Main Hall** **Moderators:** Neil Crickmore Elaine Fitches
10:30-10:50 **O147. Massimo Reverberi-KEY** "Natural compounds from mushrooms to challenge plant pathogens"		**10:30-10:50** **O152. Assunta Bertaccini-KEY** "Phytoplasmas and plant diseases: a transkingdom relationship"	**10:30-10:50** **O158 . Salvador Herrero-KEY** "Plant volatiles as mediators of the insect interaction with baculovirus"	**10:30-10:50** **O163. Marek Jindra-KEY** "Species-selective agonists of juvenile hormone receptor - en route to eco-friendly IGRs"
10:50-11:10 **O148. Mahmut Tör-KEY** "Translational research on pulse downy mildews: Deploying resistance genes, pathogenomics and microbial biocontrol"		**10:50-11:10** **O153. Michael Kube-KEY** "Insights into pathogen-host interactions from phytoplasma genomes"	**10:50-11:00** **O159. Dönüş Gencer** "Isolation and Identification of a new Cypovirus from *Dasychira pudibunda* (Lepidoptera, Lymantriidae) in Türkiye"	**10:30-10:50** **O164. Marc F. Schetelig-KEY** "Zero pesticide pest control - genetic markers for efficient SIT programs in agriculture"
			11:00-11:10 **O160. Vyacheslav Martemyanov** "New *Dendrolimus sibiricus* cypovirus-1: from molecular features to field bioassay" in Türkiye"	
11:10-11:30 **O149. Hailing Jin-KEY** "Voyage of fungal pathogen small RNAs into plants"		**11:10-11:20** **O154. Filiz Randa Zelyüt** "Multilocus sequence typing of 'candidatus *Phytoplasma solani*' ınfecting cucurbits from Türkiye"	**11:10-11:20** **O161. Mahmut Mete Karaca-STU** "Effects of tetracycline treatments on biological parameters and endosymbionts of *Bemisia tabaci* MEAM1"	**11:10-11:30** **O165. Francesco Pennacchio-KEY** "Insect multitrophic interactions for bioinspired plant protection"
		11:20-11:30 **O155. Barbaros Mülayim-STU** "Comparative genome analysis of phytoplasma in plants with different fruit types"	**11:20-11:30** **O162. Dilşan Boylu-STU** "Quantitative Real Time PCR (qRT-PCR) analysis of *Wolbachia* infection in different developmental stages of *Tuta absoluta* populations from Antalya"	
11:30-11:40 **O150. Bayram Kansu** "The pathogenic and phylogenetic relationships of endophytic *Lecanicillium* spp. isolates from turfgrass seeds"		**11:30-11:40** **O156. Yiğit Sabri Ünlü-STU** "Molecular detection of phytoplasma associated disease in Türkiye"		**11:30-11:40** **O166. David Sedlak** "High-throughput discovery of species-selective juvenile hormone receptor agonists"
		11:30-11:40 **O156. Yiğit Sabri Ünlü-STU** "Molecular detection of phytoplasma associated disease in Türkiye"		
11:40-11:50 **O151. Merve Yiğit** "Determination of *Fusarium* wilt (*Fusarium oxysporum* schlecht. F. sp. melon-genae) resistance using molecular marker in double haploid eggplant popula-tions"		**11:40-11:50** **O157. Abdullah Al-Sadi** "Exotic plant disease outbreaks in the Arabian Peninsula: Challenges and opportunities"		**11:40-11:50** **O167. Bahram Naseri** "Effect of pyriproxyfen, a juvenile hormone analog, on diapausing larvae of *Ephestia kuehniella* (Zeller) (Lepidoptera: Pyralidae)"

12:00-13:30 LUNCH	**18:00** DEPARTURE FROM CONGRESS CENTER TO HOTELS
12:15 DEPARTURE FROM CONGRESS CENTER TO HOTELS (Detour)	**18:30** DEPARTURE FROM CONGRESS CENTER TO HOTELS
14:00 DEPARTURE FROM HOTELS TO CONGRESS CENTER (Detour)	**19:00** DEPARTURE FROM HOTELS TO CONGRESS CENTER
13:30-15:30 POSTER SESSION Exhibition Hall *All presenting poster authors should be present at their posters.*	**19:30 FINAL DEPARTURE FROM HOTELS TO CONGRESS CENTER** **19:30-00:30** GALA DINNER Hektaş Ballroom
15:30-16:00 CLOSING SESSION Main Hall	**22:30** DEPARTURE FROM GALA DINNER TO HOTELS
16:00 DEPARTURE FROM CONGRESS CENTER TO HOTELS	**23:30** DEPARTURE FROM GALA DINNER TO HOTELS
16:30 DEPARTURE FROM CONGRESS CENTER TO HOTELS	**00:30** DEPARTURE FROM GALA DINNER TO HOTELS
17:00 DEPARTURE FROM HOTELS TO GALA DINNER	**01:00 FINAL DEPARTURE FROM GALA DINNER TO HOTELS**
17:30 DEPARTURE FROM HOTELS TO GALA DINNER (Detour)	

POSTER SESSION

All poster should be attached to the boards by 16 MAY 2023 TUESDAY, 08:30-17:30.
All presenting poster authors should be present at their posters on 18 MAY 2023 THURSDAY, 13:30-15:30.

P1. Bahram Naseri Physicochemical traits of sugarcane cultivars affected digestive *enzymatic profile of Sesamia nonagrioides* (Lefebvre) (Lepidoptera: Noctuidae) larvae

P2. Javad Salmanı-Moghanlou Effect of different wheat cultivars on digestive enzymes activity of *Trogoderma granarium* (Everts) (Coleoptera: Dermestidae) larvae

P3. Seda Biryol Mycoformulation developed using *Metarhizium anisopliae* (Ascomycota: Hypocreales) based on solid-state fermentation method against *Myzus persicae* (Hemiptera: Aphididae)

P4. Shinichiro Sawa Chemotaxic manipulation as a strategy to protect crop plants from root-knot nematode infections

P5. İsmail Demir Effects of some entomopathogenic fungi on the citrus longhorned beetle, *Anoplophora chinensis* (Coleoptera: Cerambycidae)

P6. *STU* Ceren Doğan Molecular genetic basis of pesticide resistance in phytoseiids as biological control agents

P7. *STU* Nihan Güneş Molecular characterization of Tomato spotted wilt virus (TSWV) and Cucumber mosaic virus (CMV) affecting tomato and pepper crops in Izmir Province

P8. Merve Kara Molecular identification of powdery mildew disease agent *Golovinomyces orontii* on periwinkle (*Vinca major*) plants growing in Türkiye

P9. *STU* Iva Rosić Population dynamics of *Bacillus amyloliquefaciens* SS-38.4 in the phyllosphere of sugar beet and its biocontrol activity against Pseudomonas syringae pv. aptata P21

P10. *STU* Marina Anteljević Phylogenetic analysis of *Pseudomonas syringae* isolates from the Danube River Basin revealed association with past epidemics in Serbia

P11. Dilay Hazal Ayhan Distinct genetic differences between plant and human pathogenic isolates of *Fusarium oxysporum*

P12. Selma Ülgentürk Investigation of the efficacy of some biopesticides against oleander scale, *Aspidiotus nerii* in laboratory conditions

P13. Randy Kutcher Detection and differentiation of *Xanthomonas translucens* pv. *translucens* and pv. *undulosa* from wheat and barley by duplex quantitative PCR

P14. *STU* Utku Şanver Molecular analysis of copper tolerance and genetic diversity in *Pseudomonas syringae* pv. *syringae*, the causal agent of cherry bacterial canker disease

P15. Marek Jindra Unique peptidic agonists of a juvenile hormone receptor with species-specific effects on insect development and reproduction

P16. *STU* Anna Subbotina Molecular diagnostics of *Dendrolimus sibiricus* cypovirus-1 in alternative host

P17. *STU* Hakkı Taşdelen Molecular methods for the identification of Amaranthus species

P18. *STU* Fadime Yetis The molecular characterization of viruses found in honeybee colonies infested with *Varroa destructor* in Türkiye

P19. *STU* Halim Can Kayikci The role of ncRNAs in parasitic plant infection and some strategies of struggling in tomato breeding

P20. Massimo Reverberi Biocontrol treatments confer protection against *Phytophthora infestans* infection of potato by inducing defense hormone biosynthesis

P21. İrem Altın Proteomic characterization of bacteriophage peptides of pathogenic *Xanthomonas arboricola* pv. *juglandis* using Matrix-Assisted Laser Desorption Ionization-Time-of-Flight Mass Spectrometry

P22. *STU* Tuğba Uslu Detection and molecular characterization of viruses infecting tomatoes grown in greenhouses in the highlands of inner western Anatolia

P23. *STU* Gamze Mertoğlu Recent studies on molecular identification of *Phytoseiidae* species (Acari: Mesostigmata) in Türkiye

P24. David Sedlak Action of species-selective juvenile hormone receptor agonists on insect development

P25. İbrahim Mıstanoğlu Genetic characterization of *Meloidogyne incognita* isolates using KASP markers

P26. *STU* İslam Yildiz Development of a Local *Bacillus thuringiensis* ssp. *kurstaki*-Based Biopesticide Effective on the Lepidopteran Pests

P27. Tevfik Özalp Molecular identification of root-knot nematodes in banana growing areas of Antalya province

P28. Serpil Erilmez First report of Tomato brown rugose fruit virus infecting greenhouse tomato in the Aegean Region of Türkiye

P29. *STU* Mahmut Mete Karaca Effects of *Wolbachia* infection status on parasitism performance of *Encarsia lutea* on the silverleaf whitefly *Bemisia tabaci* MEAM1

P30. Deniz Göl Gene knockdown in Arabidopsis downy mildew using small RNA duplexes to assess gene functions

P31. *STU* Oğuzhan Yeni Detection of the sunflower pathogen *Plasmopara halstedii* by loop-mediated isothermal amplification

P32. *STU* Büşra Kara Comparative genomic analysis of Spiroplasma citri in naturally infected citrus samples and in vitro cultures in Türkiye

P33. Damla Ulusoy Eradication processes of Tomato brown rugose fruit virus on tomato seeds

P34. Jack Bell Using Alphafold2 to aid the early design of protein-based bioinsecticides.

P35. *STU* Mehmet Arslan Investigation of thiram-induced cellular responses in Fusarium reference strains

P36. *STU* Berkay Erdur Investigation and classification of fungal pathogens isolated from olive orchard in Türkiye

P37. Havva Nur Cayak Development of multiplex primer and probe against Tomato brown rugose fruit virus (ToBRFV), Tomato spotted wilt virus (TSWV) and Pepino mosaic virus (PepMV) disease factors in tomato and pepper plants

P38. Bihter Avşar An investigation of disease resistance genes in *Corylus avellana* cv. Tombul by resistance gene enrichment sequencing (RenSeq) method

P39. *STU* İlkem Tutku Türkmen Agrobacterium-mediated transformation of tomato with the coat protein gene of tomato brown rugose fruit virus

P40. Ali Mehrvar Diversity of indigenous Actinomycetota of Iran and assays of their culture extracts toxicity on some plant pests

P41. Ali Mehrvar Brine shrimp nauplii play a rapid biomarker role in the chemical screening investigations

P42. *STU* Martyna Jonak NAD+ involvement in the virulence of *Pseudomonas syringae* effector HopAG1

P43. M. Sait Adak Importance of crop wild relatives as potential source for resistance to biotic stress factors in plant breeding

P44. *STU* Hatice Sevde Yüceler Use of plant viruses and VLPs in vaccine production

P45. *STU* Şevket Ölmez Emerging fungal threat for cotton production in Türkiye

P46. Emrullah Güldemir Field screening of Anthracnose resistance in watermelon breeding lines under Bursa-Türkiye conditions

P47. Ayşe Şeker Determination of disease resistance using molecular markers among tomato breeding lines from diverse origin

P48. Osman Telli In vitro analysis of the antigonistic effects of beneficial endophytic bacteria isolated from olive leaves against *Phytophthora infestans* and *Monilinia laxa*

P49. *STU* Metin Burak Tatlıses Comparison of 3D protein structures of fungal effector candidates with defined effectors

P50. *STU* Alperen Dilekli RNAi mediated functional analysis of wheat yellow rust (*Puccinia striiformis* f. sp. *tritici*) effector candidate gene

P51. *STU* Pınar Öztekin Spider venoms: Exploring their potential as bioinsecticides

P52. *STU* Nesrin Ormanoğlu A Novel approach to control stored product pests: RNA interference

P53. *STU* Nesrin Ormanoğlu Mechanism of phosphine resistance in stored product pests

IMPPC2023

ABSTRACTS

O-01 (OPENING LECTURE)

A worms tale: From mysteries of inheritance to new technologies for medicine and agriculture

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The Ancient Greek statesman Solon advised the extremely happy but ill-fated king Croesus, who later lost both his kingdom and his life; "*count no man happy until he's dead, call him at best lucky."* Like Croesus, but in reverse, my career illustrates the fickle nature of luck. My Ph.D. took 8 years, my first paper was scooped and never published. When I finally graduated, I couldn›t get a fellowship due to my lack of publications. Andrew Fire and I were independently trying to achieve DNA-transformation of the tiny worm *C. elegans.* It was hard to get it working, we struggled, but came to know and trust each other along the way. That trust would later allow us to work together to discover RNA interference. My ability to laugh at myself in the face of failure, and to learn from each setback, not only brought me a great friend in Andy, but also brought luck and perhaps even happiness. It is liberating to know that *when you don't have a kingdom to lose, you most certainly have one to gain!* I will describe how our studies of RNAi have uncovered new insights into the ways organisms use RNA to regulate the flow of genetic information both vertically (from parent to offspring) and horizontally (between species). These discoveries are now driving the development of cutting-edge technologies that hold immense potential for advancing medicine and agriculture.

Key words: RNAi, DNA transformation, RNA interference

O-02 (KEYNOTE SPEECH)

Genome compartmentalization and fungal pathogenesis

Li-Jun Ma
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The Ma lab focuses on a model system *Fusarium oxysporum*, a cross-kingdom fungal pathogen that not only causes devastating plant vascular diseases but can also infect humans. Distinct sets of repeat-rich accessory chromosomes (ACs) – known to play deterministic roles in each host-fungal interaction – have been identified among all pathogenic *F. oxysporum* isolates, including both plant and human pathogens. Experimental evolution study confirms that transposons, enriched in ACs, drive the adaptive evolution in this cross-kingdom fungal pathogen. *Arabidopsis thaliana* independently challenged with a *Fusarium oxysporum* endophyte Fo47 versus a pathogen Fo5176 is employed to investigate the genetic mechanisms that underlie pathogenesis against plant hosts. Metatranscriptomic data reveal a shared pattern of expression for most plant genes (~80%) in responding to both fungal inoculums. At the same time, distinct responding genes depict transcriptional plasticity, as the pathogenic interaction activates plant stress responses and suppresses plant growth/development related functions, while the endophytic interaction attenuates host immunity but activates plant nitrogen assimilation. Collectively, *F. oxysporum* represents an effective model to investigate eukaryotic genome evolution and host-microbe interactions.

Key words: *Fusarium oxysporum*, cross-kingdom fungal pathogen, accessory chromosome, single-cell metatranscriptomics

O-03 (KEYNOTE SPEECH)

Cross-kingdom RNA trafficking between plants and fungal pathogens

Hailing Jin
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Small RNAs (sRNAs) are short non-coding RNAs that mediate gene silencing in a sequence-specific manner. We discovered that some sRNAs from eukaryotic pathogens, such as *Botrytis cinerea*, can be transported into host plant cells and suppress host immunity genes for successful infection (Weiberg et al., Science 2013). We further demonstrated that such cross-kingdom RNAi is bi-directional. Plants can also send sRNAs into pathogens using extracellular vesicles to silence fungal virulence genes as part of its immune responses (Cai et al., Science 2018). We found that plants have multiple classes of extracellular vesicles, and exosome is the major class responsible for sRNA delivery. We identified a group of RNA binding proteins that contribute to the selective sRNA loading into extracellular vesicles (He et al., Nature Plants, 2021). Furthermore, we have recently discovered that some plant mRNAs can also be secreted by extracellular vesicles and enter fungal cells. By using Translating Ribosome Affinity Purification profiling and polysome analysis, we observed that the delivered host mRNAs are associated with fungal polysomes, indicating that they are translated in the fungal cells. Furthermore, ectopic expression of transferred host mRNAs in B. cinerea showed that their proteins localised to mitochondria and were detrimental to fungal infection. Thus, extracellular vesicles play an important role in cross-kingdom RNA trafficking between plants and fungal pathogens.

Key words: Cross-kingdom RNAi, RNA trafficking, extracellular vesicles, plant fungal interaction

O-04

Fungal and bacterial antagonists from deserts show high efficacy in the management of *Pythium aphanidermatum*-induced diseases in tomatoes and cucurbits

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Vegetable crops are widely cultivated in Oman, and the production of some vegetables has increased by 1500% over the last 40 years. Despite the importance of vegetable crops in the economy of growers, soilborne diseases have been a major challenge to their production, resulting in losses that were reported to reach 70-100% in several locations in the country. They are caused by different fungal and oomycete species, the most common of which are *Pythium* species. Although management of soilborne diseases has relied on the use of fungicides, the frequent application of fungicides has been associated with some environmental problems and the development of fungicide resistance. Our laboratory investigated the efficacy of more than 200 fungal and bacterial antagonists against *Pythium*-induced disease in tomatoes and cucurbits, including several strains from desert plants. Several fungal (e.g. *Talaromyces, Aspergillus,* and *Trichoderma*) and bacterial (*Pseudomonas* and *Bacillus*) strains showed high efficacy in suppressing growth and spore production of *Pythium aphanidermatum*. In addition, they resulted in morphological abnormalities in *Pythium* spores and mycelium. GC-MS analysis of metabolites showed that the strains produced different types of antimicrobial and antifungal compounds. Bioassay tests showed that the strains, which were effective in the laboratory, suppressed damping-off and wilt diseases of tomatoes and cucurbits under greenhouse conditions. Findings from the study show that several fungal and bacterial strains from desert plants are potential biocontrol agents against *Pythium* diseases of tomatoes and cucurbits.

Key words: *Pythium, Trichoderma, Talaromyces, Bacillus, Pseudomonas*, biocontrol, endophytes

O-05

Phytophthora dianthi sp. nov., a new species causing root rot and vascular necrosis of carnation in Türkiye

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A new species of *Phytophthora* was isolated from root rot and vascular necrosis on carnations (*Dianthus caryophyllus*) collected from the carnation greenhouses in Türkiye. The species was characterized by: papillate, non-caducous sporangia with sometimes double papillae; sporangia were ovoid/obpyriform/ellipsoid/nearly spherical; commonly lateral attachment of sporangiophores; presence of spherical chlamydospores; and heterothallic nature. The new species did not grow at or below 9°C or at or above 32°C; optimum growth temperature was 25°C in carrot agar. In phylogenetic analyses based on data from three nuclear (ITS, β-tubulin; Heat shock protein 90) and four mitochondrial (cytochrome c oxidase subunit 1; cytochrome c oxidase subunit2; NADH dehydrogenase subunit 1; ribosomal protein L10) regions, isolates formed a monophyletic clade. The morphological characteristics and phylogenetic relationships indicated that the isolates were of a new species, which was therefore named *Phytophthora dianthi* sp. nov. (CBS accession: 149136, 149137, 149138). Pathogenicity tests by soil infestation revealed that the isolates caused root rot and vascular necrosis resembling the symptoms originally observed, reducing root weights of carnation plants within 3 months.

Key words: *Dianthus caryophllus*, *Phytophthora*, root rot, vascular necrosis, phylogeny

O-06

Molecular characterization of *Rhizoctonia* species associated with chickpea in Türkiye

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Ninety-six isolates of *Rhizoctonia* spp. were obtained from chickpea roots in Denizli, Uşak, Isparta and Kütahya provinces of Türkiye in 2016-2017 growing seasons. Seventy-three of them were multinucleate *Rhizoctonia* (MNR), four of them were binucleate *Rhizoctonia* (BN) and 19 of them were *Rhizoctonia bataticola*. Based on morphological characteristics, MNR isolates belonged to anastomosis groups (AG) 4 and 5. ITS gene region of all the isolates were amplified by polymerase chain reaction (PCR) using ITS1 and ITS4 primers. As a result of the sequence analysis, 23 isolates belonged to *Rhizoctonia solani* AG 4-HGII, 50 isolates belonged to *R. solani* AG 5, four isolates belonged to binucleate *Rhizoctonia* AG K and 19 isolates belonged to *R. bataticola*. Accession numbers of all the isolates were loaded to GenBank. The isolates were examined for their phylogenetic analysis by on a group basis separately and also all as one. The dendograms revealed that all the isolates clustered with together references generated from other country in the clades. This study is the most comprehensive study on *Rhizoctonia* species isolated from chickpea by using molecular tools in Türkiye.

Key words: Chickpea, *Rhizoctonia*, anastomosis groups, ITS gene region, phylogenetic analysis

O-07 (KEYNOTE SPEECH)

The importance of plant health in a global world

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Plants or plant-based products are the most important staple of human and animal nutrition. Currently, 8 billion (8×10^{12}) people need to be fed worldwide, with around 10 % of the world's population being undernourished (www.faostat.org). Agriculture and horticulture producing highly nutritious food and plant-based food items are therefore crucial for sufficient feeding of the world. However, climate change, war, pests and diseases are many factors leading to shortage of healthy crops. As we are understanding more and more the complex relationships between plants as hosts for viruses, bacteria, fungi, nematodes, insects and so on, uncontrolled global trade and the exchange of seeds and other planting material is causing another threat to global production of crops. Tomato brown rugose fruit virus is a recent example where a newly emerging pathogen has quickly conquered tomato production areas worldwide in a short period of time thus threatening the successful production of this crop. Can we prevent similar outbreaks of newly emerging pathogens in the future? The advantages of plant health regulations and the obstacles implementing these regulations will be discussed in this presentation.

Key words: Plant health, plant health regulation, quarantine pathogens, global trade

O-08 (KEYNOTE SPEECH)

Disruption of insect mediated transmission of plant viruses

Alex Murphy[1,*], Francis Wanonje[2], Sun-Ju Rhee[1], Josiah Musembi Mutuku[3], Cyrielle Ndougonna[4], Marian Combala[4], Wamaitha Mwathi[5], Paul Kuria[5], Ethelyn Echep[6], Ken Okwae Fening[6], Justin Pita[4], John Carr[1]

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Plant-infecting viruses are major threats to food security and constitute the single largest group of emerging crop pathogens. Invertebrates transmit 70% of plant viruses and provide a weak link in the transmission chain that can be targeted for protection of crops. Hemipteran insects, particularly aphids and whiteflies, are the largest group of vectors for plant viruses but, interestingly, are themselves subject to infection by entomopathogenic viruses. This talk will focus on Dicistroviruses, positive-sense RNA entomopathogenic viruses that we have consistently identified in our next generation sequencing data from crop, weed and vector samples from across East and West Africa. These insect viruses have potential as biological controls because some dicistroviruses can spread systemically within plant vascular tissue without replicating or causing plant disease. Instead, these *in planta* reservoirs of virus particles can infect hemipteran insects feeding on the plant and cause symptoms including misperception of plant volatile cues, diminished fecundity, paralysis, and death. In this talk we will discuss our virus discovery work, including the first detection in Africa of a dicistrovirus in the whitefly *Bemisia tabaci*, and our development of an infectious clone for aphid lethal paralysis virus, which we are using to study the effects of dicistrovirus infection on aphids.

Key words: Dicistrovirus, aphid, whitefly, vector

O-09

Genetic diversity of Cucumber mosaic virus infecting pepper in Türkiye

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Cucumber mosaic virus (CMV) is a type of virus in the Bromoviridae family that can infect a wide range of crops including vegetables, legumes, and ornamentals. This virus is economically important and can cause reduced yields and quality losses. The present study identified and analysed the genetic sequence of CMV isolates from pepper plants in Türkiye. Results revealed the diversity of CMV isolates and their phylogenetic relationship to other CMV isolates from different geographical sources. This will help to understand the strain-level differences in their spread and impact across many ornamental and vegetable host species. Leaf and fruit samples with CMV-like symptoms were collected from four provinces in Türkiye (Balıkesir, Çanakkale, İzmir and Manisa).A total of 425 samples were collected and 323 of them were found to be CMV-infected. 30 ELISA-positive samples were purified using total RNA and analyzed using RT-PCR with CMV-specific primers. The PCR products were directly sequenced in both directions using the appropriate CMV primers. Thirty sequences of the CMV coat protein gene were obtained and compared with homologous sequences from GenBank to evaluate the genetic diversity of the virus in Türkiye. It was determined that the base sequence of the coat protein gene of CMV isolates showed nucleotid similarities between 97.45-98.91% when compared to other CMV isolates published from the gene bank so far. Phylogenetic and *in sillico* restriction analysis of the sequences revealed that the strains are genetically diverse and can fall in different subgroup clades.

Key words: Cucumber mosaic virus, pepper, genetic diversity, Türkiye

O-10-STU

Determination of PVY resistance and expression of resistance associated genes in tomato plants

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Tomato is a well-developed model system for molecular genetic studies and a natural host of potato virus Y (PVY). In recent years, it has been reported that the eukaryotic translation initiation factor 4E gene family is associated with resistance to the Potyvirus genus. In Türkiye, the agent has been detected in many tomato production areas including diverse regions. The resistance status of some wild Solanum species and some tomato cultivars were evaluated for reaction to a $PVY^{N:O}$ isolate. Few amino acid changes in the eIF4E protein explain resistance to PVY. For this reason, the polymorphism of eIF4E in the genotypes was determined. Pot-1 locus, which plays a role in PVY resistance in tomato, was shown to be associated with eIF4E. Genetic linkage of them was investigated by using the dCAPS marker (eIF4E-SpeI) in the tomato genotypes used. Viral genome-linked protein (VPg) protein plays a role in breaking resistance genes in some PVY-resistant genotypes. The virulence status of the virus isolate was determined by sequencing VPg. The expression of eIF4E-related genes suggests their role in the tomato-PVY interaction. The expression status of eIF4E1, eIF4E2 and eIF(iso)4E genes during $PVY^{N:O}$ infection in *Solanum arcanum* LA2157 was analyzed at different time points by Real-time Quantitative PCR. GAPDH, UBI, UK and ACT genes were used to determine the reference gene which shows the least variation during PVY infection. Since the responses of plants to virus infection are similar, the results of this study will contribute to the understanding of this issue in other plants.

Key words: Potato virus $Y^{N:O}$, tomato, eIF4E, plant-virus interactions

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O-11

Native and non-native *Bemisia tabaci* B haplotype whiteflies are implicated in the spread of endemic and introduced begomoviruses in Oman

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The *Bemicia tabaci* B mitotype belongs to the North Africa-Middle East (NAFME) cryptic species and is represented by at least eight haplotypes, NAFME 1-8. Among them 6 and 8 have become invasive and occur outside their zone of endemism in northern Africa, Middle East, and South-central Asia. Haplotype life histories and begomovirus-vector specificity of invasive and native NAFME haplotypes are not well-studied. Here, the association between native and non-native begomoviruses and NAFME B haplotypes in Oman was investigated. Unique nucleotide polymorphisms in the 3′-mitochondrial COI sequence differentiated the three NAFME haplotypes, 2, 3, and 5, at a frequency of 31, 3, and 66 percent, respectively. Fourteen begomoviruses were provisionally identified by phylogenetic analysis of the begomoviral 'core coat protein' gene, with 64% and 36% representing native and introduced species, respectively. Logistic regression and correspondence

analyses indicated that neither the exotic nor native viruses were uniquely associated with any haplotype, suggesting relaxed virus-vector specificity. Even so, the introduced chili leaf curl virus-NAFME 5 and Oman native NAFME 2-tomato yellow leaf curl virus-OM (TYLCV-OM) combinations were found to be 'strongly'- and 'closely'-associated, respectively. These results do not rule out the potential for co-evolved transmission competency to have facilitated the regional spread of ChLDV by NAFME 5 and of TYLCV-OM by NAFME 2, albeit, with lower competency. Thus, NAFME 5-mediated transmission of predicted native and non-native viruses appears to have enabled the establish and spread of begomoviruses extant in Oman and locales in nearby cross-roads of South Asia and east coastal Africa.

Key words: Biotype, haplotype, MEAM1, cryptic species, whitefly vector

O-12

The dynamics of PVY infection during the growing season of the San Luis Valley, Colorado

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Potato virus Y (PVY) is a major concern to potato production worldwide due to its impact on potato yield and quality. During the growing season, PVY is transmitted by more than 60 aphid species in a nonpersistent manner. Aphids can acquire and transmit PVY within minutes, which limits the effectiveness of insecticides to reduce PVY transmission. The San Luis Valley (SLV), Colorado, is the second-largest fresh potato growing region in the U.S. and account for about 95% of the total production in Colorado, generating annual revenues of approximately $225 M. In the SLV, PVY is the leading cause of seed potato rejection, which has caused a constant decline in seed potato production in the valley over the past two decades. To help potato growers control PVY, we monitored the dynamics of PVY infection pressure during the growing season of 2022 using tobacco bait plants. The first PVY infection was detected in the week of June 13 which coincides with the emergence of potato crops in the valley. PVY infection increased toward the beginning of August and then declined toward the end of the season. PVY strain composition was studied to identify PVY strains prevalent in the valley. Three PVY strains were identified in bait plants and potato fields, namely, PVYO, PVYN-Wi and PVYNTN. The results of this research will be discussed.

Key words: Potato virus Y, aphid, seed potatoes

O-13 (KEYNOTE SPEECH)

Epigenetic signatures associated with nematode adaptation to plant resistance

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Plant parasitic nematodes of the genus Meloidogyne are crop pests of global importance. As such, *M. incognita* is the emblematic species as it is present all over the world with a wide range of species. Currently the use of resistant plants is the most effective to control nematodes. However, there is an increase in the emergence of virulent lines of *M. incognita* worldwide, able to bypass the resistance of the commonly used tomato Mi1-2 gene, despite their asexual mode of reproduction (obligatory mitotic parthenogenesis). It has been suggested that epigenetic modifications may be involved in the virulence character, with most of the strongest evidence so far coming from research conducted on *M. incognita* isolates using isofemale lineage analysis. In a simplified definition, epigenetics is the study of biological mechanisms that turn genes on and off in a reversible manner, for example in response to any external stimulus. Using high-throughput sequencing technologies to characterize epigenomes, we investigated whether exposure to the Mi1-2 resistance gene affects epigenetic marks. Our analysis of virulence character in *M. incognita* isolates from different geographical origins revealed that the avirulent and virulent lineages differ in their epigenomes and that the virulent lineages share common epigenetic signatures. Some of these findings point to previously identified genes, such as effectors.

Key words: Potato virus Y, aphid, seed Plant resistance, virulence, apomixis, epigenetics, histone post-transcriptional modifications

O-14 (KEYNOTE SPEECH)

AI-powered holistic and dynamic pathology to deliver new sources of resistance

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Plant-parasitic nematodes are a major threat, and in some crops the dominant threat, to food security throughout the world. A central tenet of the discipline is to advance our understanding of plant-parasitic nematode biology in sufficient detail to alleviate their threat to food security. There is an expectation that the development of functional genetic tools will accelerate the progress of research on plant-parasitic nematodes, and thereby the development of novel control solutions.

This talk will describe both recent and rapid progress in developing low-cost, AI-powered, phenotyping. In developing this technology to address a bottle neck in our research, something more important emerged the ability to be truly holistic (i.e. phenotyping every individual pathogen in the whole host)

and dynamic (i.e. across the complete lifecylce of the pathogen) in our analysis of host infection. We think this approach sets a precedent for pathology in general, and will allow genetic dissection of entirely new aspects of host-microbe interactions.

Key words: Plant parasitic nematodes, plant pathology, host microbe interactions

O-15 (KEYNOTE SPEECH)

Transgenic East African highland banana plants are protected against *Radopholus similis* through host-delivered RNAi

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The burrowing nematode *Radopholus similis* is considered a major problem of intensive banana cultivation. It can cause extensive root damage causing plants to fall to the ground, this problem is therefore named the toppling disease of banana. Soaking *R. similis* in double stranded (ds) RNA of the nematode genes *Rps*13, chitin synthase (*Chs*-2), *Unc*-87, *Pat*-10 or beta-1,4-endoglucanase resulted in reduced reproduction on carrot disks, from 2-fold (*Chs*-2) to 7-fold (*Rps*13). The East African Highland Banana cultivar *Nakitembe* was then transformed with constructs for expression of dsRNA against the same genes, and for each construct 30 independent transformants were tested with nematode infection. Four months after transfer from *in vitro* culture to the greenhouse, the banana plants were inoculated with 2000 nematodes per plant and three months later, they were analysed for several parameters including plant growth, root necrosis and final nematode population. All plants with dsRNA constructs against the nematode genes were on average showing lower nematode multiplication and root damage than the non-transformed controls or the banana plants expressing dsRNA against a weevil gene. The highest observed protection was from dsRNA-Rps13-expressing plants where the best 10 lines offered above 88% protection against root necrosis attributed to nematode infection. In conclusion, RNAi seems to efficiently protect banana against *R. similis* caused damage, opening perspectives to control this pest.pressing plants where the best 10 lines offered above 88% protection against root necrosis attributed to nematode infection. In conclusion, RNAi seems to efficiently protect banana against *R. similis* caused damage, opening perspectives to control this pest.

Key words: Banana, *Radopholus similis,* RNAi, transgenic, nematode

O-16 (KEYNOTE SPEECH)

RNAi vs. Gene-Editing for plant nematode resistance?

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I was a co-founder of a trait development company (Nemgenix Pty Ltd) which focussed on using host-induced gene silencing (RNAi) to confer resistance to plant-parasitic nematodes and aphids. Examples of studies on root-knot, cyst- and root lesion nematodes and the green peach aphid will be presented. The benefits and limitations of commercial implementation of RNAi technology will be discussed, together with consideration of the potential of developing resistance using gene-editing (GEd) technology. The potential for commercialising crops using these technologies very much depends on whether they are classified as GMOs or non-GMOs. The current international status of de-regulation of GEd produce (i.e. a classification as non-GMOs) will be presented, with a focus on the Asia-Pacific region. When de-regulated, GEd produce can be treated like any other products of conventional plant breeding. This will enable trade in gene-edited produce between countries which have de-regulated GEd. It appears that increasingly more of the world's nations are proceeding to a rational approach of regulating GEd crops, following the principle that like products should be regulated in the same way. Thus it appears pest resistance based on GEd may provide a better pathwayto commercial implementation.

Key words: RNAi, nematode resistance, GMO, Gene-Editing, de-regulation, trade

O-17 (KEYNOTE SPEECH)

A novel approach to pesticide discovery that better confronts resistance: Inhibitors that target protein-protein interactions

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Pesticide discovery programs have aimed at finding chemicals targeting substrate binding pockets of single enzymes, yet the pesticides most recalcitrant to evolutionary forces have multiple target sites. Enzymes composed of subunits that assemble post-transcriptionally, or bind to another enzyme by protein-protein interactions to form active complexes had been thought to be "undruggable", yet disrupting their interaction would be analogous to having two target sites as simultaneous mutations are required in both partners so as not to bind the inhibitor while still interacting with each other. The pharmaceutical industry has recently pioneered using newly emerged computational technologies to visualize protein-protein interactions and elucidate small molecules that prevent such interactions. The herbicide paraquat, discovered over 60 years ago acts by the disruption of electron transfer from photoreduced Photosystem I to ferredoxin NADP-reduc-

tase. Projini Ag-Solutions brought this technology to pesticide discovery using proprietary software to screen virtual libraries of millions of small chemical structures for those that will disrupt critical hot spots in vital protein-protein interactions. Projini targeted the complex of serine acetyltransferase and O-acetylserine sulfhydrylase that converts serine to cysteine and used their software to synthesize some compounds that kill plants as leads to further syntheses. They used isothermal calorimetry and fluorescence polarization to validate binding to and disrupting of the complex, and whole plant boassays to demonstrate phytotoxicity. The time has come to evolve new pesticide discovery paradigms such as disrupting protein-protein interactions, which open vistas to many new dual targets, to better confront the evolution of target site resistance.

Key words: Multi site inhibitors, protein-protein-interactions, pesticide discovery, allaying resistance

O-18 (KEYNOTE SPEECH)

Herbicide-resistant weeds are a threat to the sustainability of arable farming

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Herbicides are the most effective and widely adopted weed management practice. Misuse of herbicides enhanced the evolution of herbicide-resistant weeds (HRW), which threatens the sustainability of the agroecosystem. In spite of the advances in understanding of herbicide resistance mechanisms, the number of HRW constantly increasing causing economic and environmental damage. Climate changes, stricter regulations and increased number of banned herbicides exacerbate the situation, resulting in increased selection pressure caused by herbicides acting with fewer mechanisms. Weeds confer resistance due to inherited alteration of the herbicide-binding site (TSR) occurring under strong selection pressure. The risk of evolved TSR is higher when the herbicide inhibits a specific and vital process. Non-target site mechanism (NTSR), often based on enhanced activity of different enzyme families catalyzing detoxification processes that may result in multiple herbicide resistance. Obligatory exogamous weeds (e.g., *Lolium* spp.) disseminate the HR trait by pollen grains, are the most dangerous. Invasive weeds may "carry" HR traits and transfer them within and between countries and continents. Lack of workers and increased farm size increase over-dependence on herbicides so their use continues to increase. In order to reduce the detrimental impact of HRW and ensure food security, the ag community should be more proactive. Improved herbicide formulations should be developed to overcome uptake and translocation barriers; New multisite less-specific herbicides should be designed and novel synergists antagonizing metabolic detoxification processes are crucially needed. Above all, farmers should diversify the current control practices by adopting novel non-chemical management methods such as precision application and robotics.

Key words: Target site resistance (TSR), non-target site resistance (NTSR), selection pressure, detoxification, regulation

O-19 (KEYNOTE SPEECH)

Exploiting allelopathy for biotechnology-derived weed control

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Growers have been increasingly challenged in recent decades by the emergence of herbicide resistant weed biotypes, which have now been reported for 23 of the 26 known herbicidal modes of action. It is therefore imperative that every effort is made to identify new modes of action, as well as develop novel technological approaches for weed control. Fortunately, nature has produced a wealth of specialized metabolites such as allelochemicals possessing significant herbicidal activity, which could be adapted or directly utilized for this purpose. Biotechnology-derived approaches such as plant-incorporated protectants, defined as pesticides produced by plants via genetic modification, could also be developed which exploit these pathways and produce natural product-based herbicides *in planta*. Insect and virus resistant plant varieties have been widely adopted by growers, however currently no plant-incorporated protectant herbicides are available for weed management, despite the obvious environmental and economic benefits such technologies could offer. We are currently pursuing the development of the allelochemical sorgoleone, which is exclusively produced in root hair cells of *Sorghum* spp., as a plant-incorporated protectant herbicide. Sorgoleone represents one of the most extensively investigated allelochemicals, and numerous studies have demonstrated its efficacy as a potent broad-spectrum plant growth inhibitor active against many agronomically important monocotyledonous and dicotyledonous weed species. Additionally, sorgoleone appears to affect multiple targets *in vivo* and thus would be less susceptible to evolved weed resistance, making it a promising candidate for development as a plant-incorporated protectant herbicide.

Key words: Herbicide resistance, natural products, mode of action, plant-incorporated-pesticide, allelopathy

O-20

Development of resistance against broomrape (*Orobanche* spp., *Phelipanche* spp.) using CRISPR/-cas9 technology in tomato (*Solanum lycopersicum*)

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Weeds are among the most important factors that cause significant yield and quality losses in tomato (*Solanum lycopersicum*). Thanks to the strigolactone (SL) compounds synthesized from the tomato roots of the fully parasitic broomrape (*Orobanche*/*Phelipanche* spp.), they weaken the plant and even cause plant death by feeding from the root after germination in the soil. In this study, it was aimed to obtain genetically resistant tomato lines against broomrape with the CRISPR/Cas9 system designed to modify the "Carotenoid cleavage dioxygenase 7" (SlCCD7) gene, which is involved in the SL pathway in tomato. As a result of the transformation via the Agrobacterium-mediated method, a mutation causing a biallelic heterozygous deletion of 18 and 186 nucleotides (nt) occurred in the T0 generation. The 186 nt unique mutation resulted in an inframe modification between Thr42-Val105 in the SlCCD7-exon 1 region that resulted in the deletion of 62 amino acids. In the T1 generation, 2 of the 4 plants with 186 nt homozygous deletion were identified as marker-free (not carrying Cas9 gene). In plants carrying 186 nt homozygous deletion, broomrape resistance was obtained without undesirable agro morphological changes. Genetic resistant lines against broomrape can be used for commercial purposes in upland-greenhouse cultivation, open field industry and table tomato cultivation where solarization is not possible. It is predicted that the use of resistant varieties will greatly reduce the yield and quality losses caused by the parasitic weed.

Key words: Gene editing, Agrobacterium-mediated transformation, ccd genes, strigolactone pathway

O-21-STU

Determination of the resistance status of wild mustard (*Sinapis arvensis* L.) collected from wheat cultivation areas in Amasya, Çorum, Tokat and Yozgat provinces against tribenuron methyl by molecular methods

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Different crop plants are grown for the plant nutrition of people around the world. One of these agricultural products is wheat. Agricultural products obtained from wheat gained importance for being used in several ways, such as feeding human beings and ani Although wheat is an important agricultural production material, product losses of up to 100% due to diseases, harmful animal organisms, and weeds have been revealed by many researchers. Even the weeds seen in wheat can cause the entire product to become unusable. The producers generally prefer herbicides since wheat is not a hoe plant; accordingly, there is a limited control method. Due to the regular use of the same group of herbicides, herbicide resistance problem arises in weeds. In this study, wild mustard (*Sinapis arvensis* L.) seeds were collected from 310 different locations from wheat fields in Amasya, Çorum, Tokat and Yozgat provinces to investigate the current resistance status of weed against Tribenuron methyl, which is used extensively in this region. As a result of the bioassay tests, it was determined that 13 of the wild mustard populations collected from 310 fields survived at the registered dose (10 g/ha) of herbicide. According to these results, a dose-response test was performed, and point mutation against ALS group herbicides was investigated molecularly. As a result of the PCR and sequencing study, it was determined that there was a point mutation for Leucine in the amino acid Trp-574 in one population. In this study, resistance to an ALS group herbicide of wild mustard found in wheat growing areas of Amasya, Çorum, Tokat and Yozgat provinces was investigated, and Trp-574 mutation was detected for the first time in Türkiye in a population collected from the Tokat region.

Key words: *Sinapis arvensis*, Trp-574, resistance, tribenuron methyl

O-22-STU

Molecular identification of *Fusarium* spp. on infected broomrape (*Phelipanche* spp.) seeds

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Broomrapes (*Orobanche* spp. and *Phelipanche* spp.) are holoparasitic plants that are completely dependent on the host plant for water and nutrients. *P. aegyptiaca* and *P. ramosa* are the most destructive broomrapes species worldwide, causing

serious damage on Solanaceae crops mainly in Mediterranean countries. Therefore, the discrimination of broomrape species are crucial in term of the specific struggling strategy determination such as biological control. In this context, we used the ribosomal protein S2 (rps2) specific molecular markers for observation of differences between *P. aegyptiaca* and *P. ramosa*. Thus, we can determine the management strategy by using *Fusarium* isolates. In this study, nine isolates of *Fusarium* spp. were isolated from *Phelipanche aegyptiaca*. seeds from the heavily infested tomato-growing greenhouses in the South of Türkiye. Three of them were identified based on internal transcribed spacer (ITS) and translation elongation factor (TEF) gene regions sequence by using the ITS1/ITS4 and EF1-728F/TEFLLE-R primers and the isolates were classified as belonging to *F. fujikuroi* at the rate of 99.80% and 100%, respectively. The aggressiveness of the isolates on *P. aegyptiaca* seeds were assessed by the seed inhibition and radicle growth tests. The isolates were found to be pathogenic on the seeds and the disease severity (%) were determined up to 70%. Our recent studies indicate that *F. fujikuroi*, can give a potential contribution to the biocontrol of *P. aegyptiaca.* This is the first report on *Fusarium* spp. on infected *Phelipanche* spp. seeds based on molecular identification, in Türkiye.

Key words: *Phelipanche aegyptiaca, Fusarium fujikuroi*, parasitic weed, molecular identification

O-23 (KEYNOTE SPEECH)

Discovery, development and commercialization of RNA-based biopesticides

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RNA interference (RNAi) is a ubiquitous, naturally occurring mechanism of eukaryotic gene regulation that has received intense study for over twenty-five years since being first discovered in the nematode, *Caenorhabditis elegans.* RNAi is initiated by various forms of duplex RNA that are processed into small interfering RNAs (siRNA). siRNAs direct RNA-induced silencing complex (RISC) to cleave target mRNA in a sequence-specific manner, resulting in suppression of the encoded protein. RNA-based actives open the potential for a wide range of applications in medicine and agriculture. For crop protection, RNA is being developed as a new mode of action to control agricultural pests and pathogens by targeting genes for cellular function or disease. RNA-based biopesticides fit well with sustainable agriculture initiatives aimed at reducing environmental impact and ensuring food security. RNA is an attractive alternative to broadly toxic synthetic chemistry due to its low persistence in the environment and sequence specificity that targets pests. Innovation across disciplines of bioinformatics, RNA biological manufacturing processes, and cellular delivery are being integrated to drive progress for agricultural RNA products soon to be commercialized. GreenLight Biosciences overcame RNA cost hurdles by inventing a large-scale, cost-effective cell free production process for RNA. The first product from Greenlight Biosciences, Calantha™ , targets *Leptinotarsa decemlineata*, the Colorado potato beetle. The active ingredient in Calantha™, known as ledprona, recently received a recently proposed IRAC MoA classification as the first RNA-mediated protein suppressor. This presentation will highlight the product performance of Calantha™ and provide an update on Greenlight Biosciences' pipeline including RNA-based insecticides, fungicides and acaricides.

Key words: Biopesticides, RNAi, RNA based biopesticides

O-24 (KEYNOTE SPEECH)

Alternative structured dsRNAs can enhance RNAi in insects

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Double-stranded RNA-based insecticides offer the potential to control pest insects with minimal impacts on non-target species, which makes them an appealing alternative to the many broad-spectrum chemical pesticides currently in use. Our lab has been focusing on the development of ingestible double-stranded RNA (dsRNAs) for insect control, and one of the unique challenges of this delivery methods is the destruction of the dsRNA within the insect gut before the molecules can enter the gut cells. Our recent research has determined that some structured dsRNAs are more resistant to insect gut nucleases, which could improve their efficacy for insect control. In addition, we have observed that the alternative structured dsRNAs can enter the cells by a clathrin-independent mechanism, and thus bypass the usual route of entry that conventional dsRNAs use to mediate their effects. Combining different structured RNAs with various adjuvants, we have identified effective formulations that improve the efficacy of foliar dsRNA sprays or topically-applied insecticides to protect crops from a variety of insects. The alternative structured dsRNAs, in addition to being equally, if not more effective than linear dsRNAs, offer the possibility to develop RNAi control strategies for insects that are either resistance to or naturally refractory to conventional dsRNAs.

Key words: RNA interference, insect control, cellular uptake

O-25 (KEYNOTE SPEECH)

The quest for the best dsRNA target sequences for pest control by a genome wide screen

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RNAi is an emerging technology for eco-friendly and species-specific pest control. One of the challenges is the identification of the best RNAi target sequences, i.e. those that lead to the death of the target at minimal concentrations and with minimal side effects on other species. The difficulty in performing large-scale screens in pest species has limited the number of genes that have been tested in the past. One way to gain an Genetic model systems are more easily subjected to genome wide RNAi screens, but it has remained an open question, in how far target genes identified in one species can be transferred to other species. In a genome wide RNAi screen, we have identified the most efficient RNAi target genes in the red flour beetle *Tribolium castaneum*. We present the results of that screen and show, what we learned about efficient target genes in our ongoing follow-up analyses. Further, we discuss the variability that is found when transferring RNAi target genes to other pest species. At the end, we outline a procedure to establish RNAi in pest species and to identify the best target genes.

Key words: RNAi, target genes, beetle, *Tribolium castaneum,* establish RNAi

O-26

The mystery of the self-cannibalize heroes: Silencing Autophagy related 1 (ATG1) and Autophagy related 8 (ATG8) in *Leptinotarsa decemlineata* (Coleoptera: Chrysomelidae)

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Autophagy is involved in certain physiological processes in insects including development, starvation, and response to pathogen's infection. Among the ATG genes, the autophagy genes ATG1 and ATG8 are crucial for autophagy induction and autophagosome assembly, respectively. ATG1 is sufficient to evolve the autophagic process: overexpression of this gene triggers downstream pathways and leads autophagy in a kinase-dependent manner. ATG8 is a key gene in autophagosome foundation and can be utilized as a definite marker for autophagy, given its localization on the autophagosome membrane. In addition, this gene is an evolutionally maintained degradation function beyond an indeed starvation-reactive process observed in eukaryotic cells. In the current study, we first investigated the expression patterns of *L. decemlineata*, one of the most harmful pests of Solanaceae plants worldwide and focused on the potential physiological role of ATG1 and ATG8 in relation to development and starvation. In particular, ATG8 was expressed higher during starvation; however, ATG1 expression was higher when the insects were feeding. Silencing ATG1 by RNA interference (RNAi) led to noticeable increases in triglyceride levels, and body weight with retardation in pupal development, mortality and pupal deformation. The use of RNAi could have promising potential in the control of *L. decemlineata*. This research is funded by Oyak Biyoteknoloji.

Key words: Autophagy, Colorado potato beetle, RNA interference

O-27-STU

Can Insulin-like peptide 1a (ILP1a) and Insulin-like peptide 4 (ILP4) be good potential targets for RNAi-based pest control in *Leptinotarsa decemlineata* (Coleoptera: Chrysomelidae)?

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The insulin signaling pathway is extremely preserved in insects and it has been considered in detail in the recent years and shown to play crucial roles in neuronal growth, synaptic development, and the management of neurotransmitter release. In addition, in some insects, ILPs can directly and indirectly regulate AKH. It has been also known that the FoxO gene is the main transcriptional effector of the insulin signaling pathway and is normally suppressed in the presence of insulin. In the current study, we used RNA interference to produce dsILP1a and dsILP4 and use it on the Colorado potato beetle, *Leptinotarsa decemelineata*, a well-known pest of potato plants worldwide. We investigated the noticeable effect of ILP knockdown on FoxO as silencing ILP4 and ILP1a led to an increase in the FOXO expression during pupation. The knockdown of these genes affected the beetle lifespan, development, and vitality; as well as, energy metabolism (total triglyceride and trehalose levels). Silencing both genes led to weight loss, lower triglyceride levels, higher trehalose levels, and noticeable mortality. Our preliminary data indicates that RNAi process has promising potential in the control of the beetle. This research is funded by Oyak Biyoteknoloji.

Key words: ILP, RNA interference, FoxO, Colorado potato beetle

O-28-STU

The regulation of lipid metabolism in *Leptinotarsa decemlineata* (Coleoptera: Chrysomelidae) through RNAi: Insights from gene silencing experiments

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The Colorado potato beetle (*Leptinotarsa decemlineata*) is a destructive pest which inflicts substantial losses to crops worldwide by feeding primarily on potato foliage throughout its larval and adult stages. The insect relies on its lipid reserves to carry out essential activities such as flying, feeding, and reproduction. One of the key genes involved in the regulation of lipid storage and mobilization is lipases, which break down lipids into free fatty acids and diacylglycerols. In this study, we used the RNA interference technique to characterize a gene encoding a phospholipase A(1)-like protein, which is named PLA1 (LdPLA1), in *L. decemlineata*. We investigated the effect of silencing the LdPLA1 gene over the development of *L. decemlineata*. We successfully silenced LdPLA1 by feeding and injecting the 1st and 3rd stages of larvae and found that the energy metabolism (triglyceride levels) increased after silencing LdPLA1 followed by a noticeable increase in the body weight. Additionally, there was a high mortality rate in the pupal stage of this insect following dsRNA injection. Strikingly, silencing of the *LdPLA1* in larvae resulted in a noteworthy reduction in the egg production of adult females. This observation implies that the impairment of lipolysis caused by gene silencing could potentially affect fecundity. Overall, these findings provide new insights into the regulation of lipid metabolism through RNAi in the Colorado potato beetle.

Key words: Colorado potato beetle, RNA interference, PLA1, Lipase

O-29 (KEYNOTE SPEECH)

Pursuing biologicals for pest management and plant health: A lifelong entrepreneurial journey

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Biologicals for crop protection and plant and soil health are going mainstream after decades of being niche products. All categories of biological crop inputs - bioprotection, biostimulants and bionutrients - are growing at double digits annually, outpacing their synthetic chemical counterparts. While perceptions of efficacy compared to synthetic chemicals linger, there is increasing recognition that when integrated into crop production and pest management programs, bioprotection products can offer higher yields and quality with additional benefits of exemption from residue requirements for easier export, delay in the development of pest resistance to chemicals, shorter field re-entry, biodegradability, lower carbon footprint, increased on-farm soil health and biodiversity, and low risk to non-target organisms, including pollinators. Challenges to faster adoption of bioprotection products is lack of awareness and education in how to deploy their unique modes of action in integrated programs and misperceptions of cost and efficacy. As a serial bioag entrepreneur starting my first company more than 30 years ago, I had many challenges to being ahead of the market, bringing a higher level of science to biopesticide development, and changing the paradigm of how biologicals are used by farmers. Add to that, I was one of very few women entrepreneurs in agricultural biotech. Today, the scene for bioag and agtech entrepreneurs has changed significantly, with billions of dollars being invested annually into startups. There are also many incubators and accelerators helping entrepreneurs on all aspects of starting and growing a bioag/agtech business, including connections to investors and other resources. With so many more problems to solve in food and agriculture, there has never been a better time to become an entrepreneur or work for an innovative startup company. This talk will provide an overview of the status and potential for biologicals and perspectives on my entrepreneurial journey developing multiple products and scaling companies.

Key words: Biologicals, Biological control, biocontrol, biopesticides, biological pesticides, natural products, entrepreneurs, entrepreneurship, startups, founders

O-30 (KEYNOTE SPEECH)

Using RNA interference to protect crops against fungal pathogens

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Sclerotinia sclerotiorum, the causal agent of white mold, infects over 600 species of plants worldwide. *Sclerotinia* is a persistent problem for global food production that has traditionally been managed using broad-spectrum fungicides. However, current fungicide strategies have proven less effective and crop rotations fail due to the promiscuous host range of *Sclerotinia* and the formation of durable resting structures known as sclerotia. Thus, there is an immediate need to manage *Sclerotinia* using novel species-specific control methods. Our strategy exploits the inherent cellular defense process known as RNA interference (RNAi). Upon encountering a double stranded RNA (dsRNA) molecule, the cell processes the dsRNA specifically targeting transcripts with sequence homology. Using a re-designed bioinformatics approach, we identified *Sclerotinia*-specific target genes. RNAi knockdown was confirmed using quantitative real-time PCR on RNA isolated from fungal liquid cultures. dsRNA molecules were screened for growth inhibition on the plant using a system representative of field conditions that showed up to 85% reduction in lesion spread. We then generated transgenic *Brassica napus* (canola) over-expressing good quality dsRNA and showed a more profound and prolonged tolerance to the fungus. Finally, I will provide insight into the uptake mechanisms and utility of next generation molecular fungicides and their applicability to control plant pathogens.

Key words: *Botrytis cinerea*, *Brassica napus*, RNA interference, RNA sequencing, *Sclerotinia sclerotiorum*

O-31 (KEYNOTE SPEECH)

Control of downy mildew pathogens using spray induced gene silencing

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Downy mildews (DM) are obligate oomycete pathogens in the order of Peronosporales and they are responsible for serious losses in yield and quality reduction in many important arable and horticultural crops including sunflower, onion, pea, faba bean, lettuce, spinach, hops, grapes, brassicas and cucurbits. Genetic investigations into these pathogens could not be explored by high-throughput mutagenesis. Recent studies have shown that plants communicate with interacting fungal and oomycete pathogens by using small RNAs (sRNAs). Exploitation of RNAi machinery by Host Induced Gene Silencing (HIGS) and Spray Induced Gene Silencing (SIGS) in DMs have shown promising results to investigate the role of pathogen genes in their native environment. In this collaborative research, we are using siRNA-based gene silencing approach to reveal pathogenicity and developmental genes, which can then be targeted using SIGS technology for DM control. Details of approach we have taken, genes that can be targeted and the possibility of translating this research into crop protection will be discussed.

Key words: Downy mildew, small RNA, gene silencing, HIGS, SIGS

O-32 (KEYNOTE SPEECH)

RNAi strategy, an alternative to conventional fungicides for the control of botrytis and the cucurbit powdery mildew diseases?

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Botrytis cinerea and *Podosphaera xanthii*, the causal agents of the gray mold and the cucurbit powdery mildew diseases, respectively, are one of the main limiting factors of horticultural crops production worldwide, consuming up to 40% of fungicides in its control. However, these fungi have been categorized by the Fungicide Resistance Action Committee as phytopathogens with a high risk for fungicide resistance development, a fact that has been demonstrated in our country. In addition, and according to the "farm to fork" strategy of the recent European Green Deal, the diversity of fungicides available to growers will be reduced by 50% in 2030. For this reason, alternative control tools and molecules with fungicide activity are needed. In our research group, we intend to check if the efficacy of the emerging RNA interference (RNAi) strategy, called "spray-induced gene silencing" (SIGS), could be a valid sustainable solution and an alternative to the use of conventional fungicides for the control of *B. cinerea* and *P. xanthii*. For this purpose, several double-stranded RNA (dsRNAs) have been designed against targets genes involved in the virulence/pathogenicity of both pathogens. To improve the application of these oligonucleotides in the field, their encapsulation to create nanoparticles is being carried out. If we succeed, new molecules with fungicidal action, could be included to obtain a sustainable plant protection control programs in the field.

Key words: Gray mold, *Botrytis cinerea*, cucurbit powdery mildew, *Podosphaera xanthii*, RNAi, SIGS, nanoparticles

O-33-STU

CRISPR based gene-drive strategy for engineering of disease resistance in plants

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Gene-drives are a powerful new gene-editing tool that allows for the management of detrimental organisms, such as the malaria vector *Anopheles gambiae*, by creating heritable mutations or spread of a genetic payload through genetic manipulation of pest populations. The development of site-specific genome-editing tools has improved gene-drives and made them a promising approach for addressing agricultural, ecological, and human health problems. This technology can be used to manage pests and weeds that reduce yield and quality in agricultural production. Additionally, there is potential to generate disease resistant cultivars using CRISPR gene-drives with only routine pollination after a single transformation assay, eliminating the need for repetitive gene-editing experiments or backcrossing. In this study, we designed two CRISPR/Cas9 based gene-drives with constitutive or inducible promoters to disrupt the function of *CsaMLO8*, the major gene associated with powdery mildew susceptibility in *C. sativus*. We used an *in silico* approach to select targets for knock-in and gene-drive designing for pre-experimental guidance and identify edited plants for post-experimental analysis. Additionally, our study aims to investigate the impact of sex bias and promoter type on the efficiency of gene-drives and the type and heredity of induced mutations. Our overall objective is to assess the potential of CRISPR based gene-drives as a tool for plant breeding and other methods to control harmful organisms that reduce agricultural yield or quality. We expect to provide valuable insights into effective strategies for generating disease-resistant cultivars in a shorter time and at a lower cost by using CRISPR-based gene-drives.

Key words: Cucumber, CRISPR, disease resistance, gene-drives, gene-editing, plant resistance, powdery mildew

O-34-STU

Functional analysis of candidate effector PTTG_06852 of wheat leaf rust Fungi by RNA silencing

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Puccinia triticina Eriks (*Pt*) is one of the important wheat pathogen that causes leaf (brown) rust disease and globally great yield losses by transporting of urediospores to very long distances by the wind. The effector proteins are important target to combat of the disease because they are virulence factor having high mutation rate. However, most of the detected/predicted effector candidates could not be functionally analyzed. The aim of the study is functional analysis of the effector candidate PTTG_06852 identified by proteomic approach in our previous study by HIGS. In this method, silencing of the target fungal gene was carried out by the host's own RNAi mechanism. In the study, 510 bp PTTG-06852 specific DNA fragment was designed and used for RNAi silencing by cloning into the BSMV vector and the 2 leaf stage seedlings were inoculated with BSMV. The seedlings with observed gene silencing effects were inoculated with *Pt* race1. Uredinia formation was observed on the plant leaf surface by phenotypically at 10 dpi. Besides the urediospor germination and hyphal development were investigated on infected leaves at 6 dpi by trypan blue staining and PTTG-06852 transcript level was detected by qRT-PCR. While the germ tube and hyphae formation of the spors were reduced in the putative silenced seedlings, qRT-PCR results showed that transcript level also decrease. The preliminary result of phenotypic, microscobic and molecular analysis showed that PTTG_06852 is the real effector of *Pt* race1 and seriously effect disease development. Hovewer biological replicates of the study are goingon for confirmation.

Key words: *Puccinia triticina Eriks (Pt.),* effector, brown rust, HIGS, RNAi, BSMV

O-35-STU

Functional Analysis of Effector Candidate PTTG_01827 of wheat brown rust by gene silencing

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Wheat brown/leaf rust is a fungal disease. The causing agent, *Puccinia triticina* Eriks (*Pt*) create yield loss by reducing the plant's ability to photosynthesise. Effectors are proteins/peptide molecules secreted by pathogens to suppress host defenses and modulate host physiology in order to enhance their virulence success. Therefore, detection of the effectors seems one of the most promising way for contolling of the disease. In this study, it was aimed to detect of the effector by functionally analysing of the candidate gene. For this, candidate effector PTTG-01827 that was identified by our previous proteomics study was silenced and functionally analized. HIGS method was used for the fungal gene silencing. HIGS is the process of silencing fungal genes using RNAi technologies, one of the natural defence mechanisms of plants. In the study, 350 bp long DNA fragments specific to the PTTG-01827 effector candidate were obtained and cloned into BSMV vector. The HIGS method was optimised to silence the target genes. The seedlings of sensitive wheat cultivars Morocco were inoculated with recombinant BSMV including PTTG-01827 fragments and dsRNA molecules of the effector candidate were amplified in plant cells. Subsequently, the plants were inoculated with *Pt* race1 at 10 dpi of the BSMV and the effector mRNAs of *Pt* race1 were targeted with the transferred dsRNAs. Changes in the infection type were analysed and confirmed by qRT-PCR and microscobic investigation. As a result of HIGS, a decrease in *Pt* sporulation and slowing down of hyphae development were observed and confirmed by PTTG transcript level.

Key words: Brown Rust, HIGS, effector, RNAi

O-36 (KEYNOTE SPEECH)

Host-Virus interactions in the omics era: What is the host telling us?

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The Omics era has enabled deeper understanding of the plant-virus-vector interactions at several levels – at the transcriptomics, proteomics, and metabolomics. We have been using two different RNA viruses –Tomato spotted wilt virus (TSWV) and Potato virus Y (PVY) to gain insights into response of hosts to virus infection using omics approaches. Tomato spotted wilt virus (TSWV) encodes a non-structural protein, NSs, which acts as a viral suppressor. The NSs-interacting proteins in *N. benthamiana* were identified via affinity purification and mass spectrometry (AP-MS). Results showed that NSs preferentially interacts with plant defense-related proteins such as calmodulin (CaM), importin, and several others. As two major nodes in the PPI network, CaM and importin subunit were selected for the further verification of their interactions with NSs via Y2H screening. Our work suggests that the downstream signaling, transportation and/or metabolic pathways of host-NSs-interacting proteins may play critical roles in NSs-facilitated TSWV infection. In case of PVY, we performed Y2H screen of *Nicotiana benthamiana* cDNA library using PVY-encoded NIa-pro as the bait. The *N. bentha*miana Indole-3-acetic acid-amido synthetase (IAAS) was identified as an interactor of NIa-pro protein. IAAS converts free (active) IAA to the inactive, conjugated form, which plays a crucial regulatory role in auxin signaling. Transient silencing of IAAS in *N. benthamiana* plants interfered with the PVY-mediated symptom induction and virus accumulation. Conversely, overexpression of IAAS enhanced the symptoms induction and virus accumulation in the infected plants. Our findings demonstrate that PVY NIa-pro protein potentially promotes disease development via modulating auxin homeostasis.

Key words: Tospoviruses, potyviruses, host-virus interactions

O-37 (KEYNOTE SPEECH)

Virus emergence, host range evolution and crop resistance durability

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Viral diseases often decrease crop production by 80% at the local or regional scales. Particularly harmful are emergent viral diseases that, as for humans and domestic or wild animals, account for ~50% of emergent plant diseases. Control strategies for viral diseases are few, being limited to reducing the amount and dispersion of inoculum and to the use of genetically resistant crop varieties. Virus emergence in the population of a new host involves ecological and evolutionary factors, including host range evolution. Host range is central to predicting disease risk, and is not independent of ecosystem complexity. Our analyses of multi-host – multi-pathogen systems demonstrate how plant viruses with broad host ranges respond to host diversity in different communities within heterogeneous landscapes, and show habitat-specific host specialisation. Host specialisation may be hindered by across-host fitness trade-offs, which have been much studied in experimental systems. However, information on their role in host-range evolution in nature is scant. We have analysed the role of across-host fitness trade-offs in host range evolution in a specific case of emergence: the appearance and fixation in virus populations of genotypes that break genetic resistance of host plants. Our studies show that pleiotropic effects of host range mutations may affect different components of the virus fitness, favouring or hindering the evolution of resistance breaking. The magnitude and sign of such pleiotropìc effects was modulated by external ecological factors. Predicting emergence under such complex scenarios is quite a challenge, which requires going beyond the genetics of plant-virus interactions.

Key words: Virus emergence, resistance-breaking, across-host trade-offs, host range

O-38

Elucidate genetic diversity of Raspberry Bushy Dwarf Virus (RBDV) in *Rubus* spp. in Türkiye

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Raspberry bushy dwarf virus (RBDV), recently renamed to *Idaeovirus rubi*, is one of the most common viruses infecting *Rubus* species worldwide but there is still limited number of genome sequences available in the GenBank database and majority of the sequences include partial sequences of RNA-1 and RNA-2. The distribution and incidence of RBDV in main raspberry and blackberry growing provinces in Türkiye were monitored during 2015-2019 and 537 *Rubus* spp. samples were tested by both DAS-ELISA and RT-PCR. Among tested samples, 36 samples tested positive for RBDV by DAS-ELISA (6.70%) and 67 samples by RT-PCR (12.47%). Turkish isolates shared 93-97.7%, 84.3-98.9% and 85-99.2% nucleotide sequence identities with available sequences in the GenBank, in partial RNA-1, movement protein (MP) and coat protein (CP) genes, respectively. In the phylogenetic tree constructed for RNA-1, MP and CP sequences, all Turkish raspberry isolates clustered in a distinct clade. However, the blackberry isolates showed considerable variation in nucleotide sequences and were placed in three distinct groups. The divergent blackberry isolates showed high variability in MP (84.5-89.3%) and CP (85.5-89.7%) regions and were placed in a distinct group. The rest of blackberry isolates clustered together with sweet cherry RBDV isolates adjacent to the grapevine clade or together with raspberry isolates. The comparative analysis conducted on three RNA segments of RBDV highlighted high sequence diversity of Turkish RBDV isolates. This study also emphasizes the importance of regular monitoring of RBDV infections in Türkiye, with special regard to those *Rubus* spp. and grapevine accessions employed in conservation and selection programs. In particular, the presence of new RBDV genetic variants and infection of *Rubus* species must be taken into account in order to choose a correct detection protocol and management strategy.

Key words: Blackberry, raspberry, raspberry bushy dwarf virus, variability, RNA-1, coat protein, movement protein, phylogenetic analysis

O-39

Analysis of Citrus Chlorotic Dwarf-Associated Virus (CCDaV)- Citrus interactions

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Citrus chlorotic dwarf associated virus (CCDaV) is one of emerging virus adversely effecting yield and quality in citrus production. In this study CCDaV-BATEM-M isolate was identified, biological and molecular characteristics of this isolate were determined. The comparison of the CP gene at amino acid and nucleotide level revealed that the isolates share %99-100 similarity to other isolates from Türkiye and other countries in the world. Then, resistance status of commonly grown citrus species in Türkiye to CCDaV were determined at 3, 6, 9 and 12 months post inoculation (mpi) by absolute quantitation using real-time PCR. Analysis shown that while lemon was the most sensitive, trifoliate orange was the most resistant species to CCDaV. In addition, the expression of some R genes were analyzed in the most resistant and susceptible citrus species to determine R genes associated with CCDaV resistance. Lemon and trifoliate orange plants were inoculated with CCDaV by grafting and total RNA was isolated from leaf samples collected from the infected and control plants at at 3, 6 and 9 mpi. The expressions of 15 selected R genes in the infected and controls plants were determined by real-time RT-PCR. The expression analyses revealed some R genes are differentially expressed in resistant trifoliate orange and susceptible lemon in response to CCDaV infection. The results showed that six differentially expressed R genes in resistant and susceptible plants identified in this study may be important for CCDaV resistance.

Key words: Resistance, gene expression analysis, R genes, Real-time RT-PCR, citrus

O-40

Molecular characterization of *Colomerus vitis* (Pgst.) (Acarina: Eriophyidae) and their potential role as vector of grapevine Pinot gris virus (GPGV) in Turkish vineyards

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Grapevine is an important crop in the worldwide. The grape erineum mite, *Colomerus vitis* can cause extensive damage due to grape bunches and leaves lack normal development and yield can be reduced. The mite may also vector grapevine pinot gris virus (GPGV), which causes leaf deformation and mottling, stunted shoot growth and in a certain extent fruit yield and quality. It is a new emerging virus reported in many countries in Europe and also in Türkiye. In this study, *C. vitis* collected from buds in GPGV-infected vines were characterized both morphological and molecular techniques. Morphological studies revealed that the eriophyids collected from leaf erinea and buds belonged to the species *C. vitis*. PCR analysis by using mitochondrial cytochrome oxidase subunit I (COI) gene specific primers confirmed morphological observations and a fragment of 709 bp of the mitochondrial tDNA COI gene was successfully amplified and selected 5 samples were sequenced. The sequences of PCR products showed that Turkish *C. vitis* isolates were seperately grouped together and the intraspecies diversity of them was found lower than other world isolates. The presence of GPGV in *C. vitis* collected from GPGV-infected grapevines was detected by the infection rate of 1.38% (6 individuals/434 tested mites) by RT-PCR analysis. Experimental transmission trials of GPGV to healthy grapevines by using *C. vitis*, collected from GPGV infected grapevines was performed. Although no symptoms were observed in eriophyed inoculated healthy vines during one year observations, RT-PCR analyzes showed that 2 out of 10 inoculated vines were found infected by GPGV. This is the first report on molecular identification by using COI gene region of *C. vitis* obtained from grapevines and showing their potential role in GPGV transmission in Türkiye.

Key words: Grapevine, eryophid, vector, phylogenetic analysis, Türkiye

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O-41

Revealing the apple virome using hiplex technology in Hakkari, Türkiye

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Türkiye is a major apple fruit producer in the crossroads of Europe and Middle East. Several reports have described the presence of multiple viruses affecting apple production in Türkiye including ASGV, ASPV, ACLSV, and ApMV. However, little is known about the presence of the recently discovered bunya-like viruses citrus concave gum-associated virus (CCGaV), apple rubbery wood 1 (ARW1), apple rubbery wood 2 (ARW2), as well as apple luteovirus 1 (ALV-1), and apple hammerhead viroid (AHVd), all of which have been previously reported in apples trees from other apple-producing countries. Here we report the presence and local distribution of these viruses and viroid across twenty different small self-subsistence orchards around Hakkari. Leaves from 100 unique apple trees were collected in June 2022 and processed in USDA-APHIS using the HiPlex technology that targets a wide range of viruses and viroids of fruit trees through an amplicon-based high throughput sequencing strategy. Our results indicated that AHVd and ALV-1 were most prevalent (44% and 26%) followed by CCGaV (20%), ARW2 and ARW1 with 14% and 12% respectively. Sanger confirmation was done for a subset of these samples. Implications about the presence of these virus agents will be discussed. This is the first report of these recently discovered viruses and viroid from apples in Türkiye.

Key words: Apple, plant viruses, diagnostics, amplicon sequencing

O-42

Optimisation of degenerate primers for detection of Peach Latent Mosaic Viroid (PLMVD) analysis by RT-qPCR

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Peach latent mosaic viroid (PLMVd), which is included in the Pelamoviroid genus belonging to the Avsunviroidae family, is in the list of the Plant Quarantine Regulation (Annex-1/A) in Türkiye. PLMVd is an economic important viroid that generally causes disease in stone fruit trees. Since PLMVd is transmitted by mechanical inoculation and by peach aphids (*Myzus persicae*), early and sensitive diagnosis in seedling production areas is very important for pre-orchard and fruit production orchards. In this study, it was aimed that to optimisation of PLMVd specific, reproducible and selective degenerate primers and probe for detection of all isolates of PLMVd by RT-qPCR method. The primers were designed by using full genomes of PLMVd from National Center for Biotechnology Information (NCBI) and using several softwares such as Basic Local Alignment Search Tool (BLAST), Clustal Omega and Primer3. The BLAST showed that the degenerate primers strongly matched with wide range of isolates of PLMVd. Limit of detection (LOD) studies were carried out within the scope of optimization of primers and method validation. In LOD studies using RNAs of lyophilized and fresh peach leaf samples, the detection limit of PLMVd specific degenerate primers was determined to be 10-4.

Key words: Optimisation, degenerate primers, PLMVd, stone fruits, LOD

O-43 (KEYNOTE SPEECH)

Pan-genome analysis identifies intersecting roles for *Pseudomonas* specialized metabolites in potato pathogen inhibition

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Agricultural soil harbors a diverse microbiome that can form beneficial relationships with plants, including the inhibition of plant pathogens. *Pseudomonas* spp. are one of the most abundant bacterial genera in the soil and rhizosphere and play important roles in promoting plant health. However, the genetic determinants of this beneficial activity are only partially understood. Here, we genetically and phenotypically characterize the *Pseudomonas fluorescens* population in a commercial potato field, where we identify strong correlations between specialized metabolite biosynthesis and antagonism of the potato pathogens *Streptomyces scabies* and *Phytophthora infestans*. Genetic and chemical analyses identified hydrogen cyanide and cyclic lipopeptides as key specialized metabolites associated with *S. scabies* inhibition, which was supported by in planta biocontrol experiments. We show that a single potato field contains a hugely diverse and dynamic population of *Pseudomonas* bacteria, whose capacity to produce specialized metabolites is shaped both by plant colonization and defined environmental inputs.

Key words: Rhizosphere, common scab, biocontrol, *Pseudomonas*, microbiome, secondary metabolism, cyclic-lipopeptides

O-44 (KEYNOTE SPEECH)

Different mobile genetic elements influence pathogen evolution

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Bacterial pathogens can evolve by the acquisition or loss of genes that contribute to pathogenicity. We have previously shown that strains of *Pseudomonas syringae* pathogens of bean carry a genomic island encoding a type III effector gene that can trigger plant immunity. The immune response leads to excision of the genomic island from the chromosome and loss of the island in the bacterial population, leading to the emergence of strains that are able to cause disease in the plant. Notably, the genomic island could also transfer to island-less recipient strains of *P. syringae*, demonstrating that the genomic island is able to carry effector genes to other strains and thus could contribute to pathogen evolution through effector acquisition. In more recent work on pathogens of cherry, we have observed that some lysogenic phages could be found in the chromosome of *P. syringae* that carry a type III effector gene. Treatment of bacterial cells with stressors, including UV light, could induce lysogen excision from the chromosome. Mixing of the host bacterium with a phage-less *P. syringae* host on a plant leaf and with UV stimulation, led to transfer of the phage and effector gene to the phage-less strain. Together, these show that two different stimuli and selection pressures can trigger genetic element mobility that can influence pathogen evolution.

Key words: Bacteria, pathogens, pathogen evolution, *Pseudomonas syringae*

O-45 (KEYNOTE SPEECH)

Toxin-producing Sarocladium and *Pseudomonas* spp. associated with rice: mutualists or parasites?

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Rice sheath rot is an emerging disease complex caused by a wide range of fungal and bacterial pathogens with *Sarocladium* oryzae and *Pseudomonas fuscovaginae* being the main culprits. Both are seed-borne and can cause necrotic lesions on the uppermost leaf sheath. Diseased plants produce brown, sterile or empty seeds, or form no panicles at all. *S. oryzae* is known to produce helvolic acid and cerulenin toxins, but our research suggests that only helvolic acid is linked to disease severity in plants. *Sarocladium* isolates however show strong antifungal activity against other rice pathogens, including *Pyricularia oryzae*, due to cerulenin production. Interestingly, natural *Sarocladium* isolates from rice show varying degrees of pathogenicity and toxin production. *P. fuscovaginae* on the other hand, produces two cyclic lipopeptides, syringotoxin, and fuscopeptin, which have been linked to pathogenicity. But syringotoxin also exhibits potent activity against fungal pathogens including the rice sheath blight pathogen *Rhizoctonia solani.* Moreover, we have identified *P. fuscovaginae*-like strains on rice roots that behave as mutualists. These rhizosphere strains are potent biocontrol agents against fungal pathogens. Our hypothesis is that *Sarocladium* spp. are endophytes, while *P. fuscovaginae*-like organisms are rhizobacteria but that both can become pathogens under certain conditions, which we will further explore.

Key words: Rice sheath rot, biological control, *Sarocladium, Pseudomonas*, toxins

O-46-STU

Three novel species into Pectobacteriaceae family from Hawaii (*Pectobacterium colocasium* sp. nov., *Pectobacterium hawaiiense* sp. nov. and *Dickeya colocasiae* sp. nov.)

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Pectobacterium and *Dickeya*, pectinolytic phytopathogens, are responsible for soft rot, blackleg symptoms, and economic losses in a wide host range of plants. PL65, PL152, and PL155 were isolated from infected taro corms, and PL48, PL64, and PL63 were isolated from infected kales from Hawaii. Bacterial pathogens were identified as *Dickeya* spp. and *Pectobacterium* spp. by using Multi Locus Sequence Analyses (MLSA) based on five housekeeping genes (dnaA, gapA, gyrB, atpD, and purA), however, the species designation of these strains was unclear. The 16S rRNA analysis with type strains of other known *Pectobacterium* and *Dickeya* species showed that PL152, PL65, and PL64 are a close relationship with *P. fontis*, *D. zeae* and *P. brasiliense*, respectively. These strains were subjected to polyphasic analysis to determine their genomic and phenotypic characteristics. The Next Generation Sequencing technologies, Oxford Nanopore MinION, Illumina NovaSeq, and PacBio RS II. were used for whole genome sequencing. The concurrent results of average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH), with calculated values lower than 96 and 70% (taxonomic gold standards), respectively. Phylogenetic analysis based on core gene sequences provides a clearly justified description of a potential novel species within the genus *Pectobacterium* and *Dickeya*. The phenotypic characteristic of potential novel strains using BIOLOG differentiated them from the type strains. The results showed no significant difference to determine among the species. Here, we proposed three novel species into Pectobacteriaceae family: *Dickeya colocasiae* sp. nov. [PL65T(=ICMP 24361T)], *Pectobacterium colocasium* sp. nov. [PL152T(=ICMP 24362T)], and *Pectobacterium hawaiiense* sp. nov. [PL64T(=ICMP 24363T)].

Key words: Pectobacteriaceae, soft rot, novel species, next Generation Sequencing technologies, Oxford Nanopore MinION, Illumina NovaSeq, and PacBio

O-47

Seed priming activity of β-Aminobutyric Acid (BABA) against *Clavibacter michiganensis* ssp. *michiganensis* (*Cmm*) in tomato (*Solanum lycopersicum L.*)

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Abiotic and biotic stress factors cause yield and quality losses in agricultural production. Increasing world population and decreasing agricultural lands also reduce the overall production potential. To increase the yield and quality, it is necessary to protect plants against stress factors. Seed-priming is the practice of improving germination and seedling development by subjecting the seed to certain pre-treatments before germination. Seed-priming applications are used to improve germination ratio and seedling establishment, as well as yield and other end products. Plant defense elicitors stimulate the plant's natural immune system when applied to the plant externally, thereby inducing the plant against phytopathogens. β-Aminobutyric Acid (BABA) is one of these plant defense elicitors. In our study, the effect of BABA-seed priming on *Clavibacter michiganensis* ssp *michiganensis* (*Cmm*), which causes bacterial cancer in tomato (*Solanum lycopersicum* L.), was investigated. Tomato seeds were subjected to seed-priming for 72 hours with 12 mM BABA (BABA-Priming) or water as the control group. Germinated seedlings without any priming were used as the positive control. Plants were infected with *Cmm* when they reached to 3-4 leaf stage. As a result of the study, BABA-priming significantly reduced the severity of the disease compared to the control. In addition, BABA priming as a spray or water priming provides effective protection compared to the control. To understand the molecular mechanism of this suppression, plant samples were taken from two different time points (0h and 7th day) and transcriptional changes of important plant immunity genes (*NPR1*, *PAL*, *PR1*, *WRKY70*, *WRKY33b*, *TPK1b*, and *PR5*) were examined. According to qRT-PCR results, *NPR1* gene expression increased significantly in BABA-primed seedlings compared to the control. *NPR1* gene expression increased approximately 5-fold with BABA-priming application at the 0th hour. BABA-priming also caused an up-regulation in *PR1* gene expression. Foliar spraying of BABA (BABA-priming+BABA-Sp) to BABA-seed-primed plants resulted in a 9-fold increase in *PR1* gene expression. Along with the regulation of other genes, BABA-priming improved plants' tolerance against *Cmm*. In line with the results obtained in our study, it is predicted that BABA-seed priming may contribute to the literature and have potential use in plant protection.

Key words: β-Aminobutyric Acid, plant immune system, seed-priming, *Solanum lycopersicum* L., *Cmm*, plant defense elicitor, gene expression

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O-48

Isolation and identification of bacterial diseases in Central Anatolia Region onion (*Allium cepa* L.) cultivation areas and onion storages and pathogenicity studies

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Onion bacterial diseases cause serious economic losses during storage as well as in the field. During the onion development period, yield losses due to bacterial diseases reach 40% if the climatic conditions are suitable. Bacterial problems of onions have become more important lately for reasons that are not completely clear. In this context, during the 2019-2020-2021 growing seasons, surveys were carried out in warehouses and onion growing areas in Ankara and Eskişehir provinces. After isolation of pure culture, 46 of 508 isolates obtained from Ankara and Eskişehir provinces gave positive results in hypersensitive reaction tests in tobacco or pectolytic activity in potatoes. The 16S rDNA gene region of these samples was amplified using universal primers 27F and 1492R. The raw sequence data of the isolates sent to the sequence as a result of PCR were checked by BLAST analysis in a universal database and similarity rates with the species available in the gene bank (NCBI) were checked. Consensus sequences were formed by arranging the obtained raw sequence data and subjected to Clustal W analysis. 12 different species belonging to the bacteria of the genera *Pseudomonas, Bacillus, Pantoea, Pectobacterium, Klebsiella, Rahnella, Acinotobacter, Proteus, Chryseobacterium, Enterobacter, Paenibacillus were identified.* In total, 84% of the bacterial isolates were not pathogenic on onion, with only isolates of *Pantoea, Pectobacterium, Proteus* and *Bacillus,* proving pathogenic. Identifying and characterizing the nature of onion microflora, including bacterial pathogens of onion, is vital to developing rapid disease detection methods and effective diseases management.

Key words: Onions, bacterial pathogens, *Pantoea*, *Pectobacterium*

O-49 (KEYNOTE SPEECH)

Functional approaches for elucidating insecticide resistance mechanisms

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The intense use of insecticides has resulted in the selection of resistance in mosquitoes and agricultural pests to such an extend that their control becomes exceedingly challenging. Target site mutations or increased detoxification are the major mechanisms responsible for the phenotype. However, often even for genes and mutations that have repeatedly been associated with resistance, and even sometimes characterized in vitro, their contribution to the phenotype remains elusive, while it is the co-evolution of independent resistance mechanisms that leads to striking phenotypes. We use functional genetics (Gal4-UAS system, CRISPR) to characterize the role of genes and their mutations in insecticide resistance in mosquitoes and agricultural pests. Through bioassays we quantify the levels of resistance conferred by each mechanism and their combination. Some representative case studies include: A) the functional validation through CRISPR of different voltage gated sodium channel (VGSC) mutations in *An. gambiae* pyrethroid resistance and investigation of their combined effect with the over-expression of detoxification enzymes; B) investigation of the contribution of putative target site resistance mutations (on the Ryanodine Receptor, the VGSC and the ABCC2 transporter, associated with resistance against diamides, indoxacarb and Bt respectively) in major lepidopteran pests, through CRISPR induced mutations in *Drosophila*. These studies improve our understanding for the genetic basis of resistance and support practical applications, for example by determining the diagnostic value of genetic markers, when present alone or in combination in field populations.

Key words: Functional genetics, insecticide resistance mechanisms, synergism, mosquitoes, lepidoptera

O-50 (KEYNOTE SPEECH)

Characterization, impact and spread of diamide insecticide resistance in Lepidopteran pests with special reference to ryanodine receptor alterations

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Diamide insecticides, selectively acting on insect ryanodine receptors (RyR), were commercialized approx. 15 years ago. They particularly target lepidopteran pest species in diverse agronomic and horticultural cropping systems. Diamides are globally registered in many countries and provide reliable control levels in most settings. However, their frequent application, due to a lack of effective alternative modes of action, has resulted in the evolution of diamide resistance in some of the world's most destructive lepidopteran species, including diamondback moth, tomato leafminer, rice stem borer and beet armyworm. High levels of diamide resistance, compromising diamide efficacy at recommended label rates, have been shown to be particularly conferred by RyR target-site mutations affecting diamide binding. Recently RyR target-site mutations were also described in fall armyworm, *Spodoptera frugiperda*, a pest native to the Americas which only a few years ago invaded the Eastern Hemisphere. The presentation reviews past, present and future research on diamide insecticide resistance mechanisms in lepidopteran pests, with special reference to RyR target-site alterations. Furthermore, principles enabling the prediction of the impact and spread of diamide resistance, based on population genetics and molecular studies will be discussed as well as resistance management strategies to delay the evolution of diamide resistance.

Key words: Diamide insecticides, resistance, Lepidoptera, fall armyworm, ryanodine receptor

O-51 (KEYNOTE SPEECH)

Transcriptional regulation of detoxification in the polyphagous arthropod pest *Tetranychus urticae*

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The spider mite *Tetranychus urticae* is a global pest known to feed on 1,100 different hosts from 140 plant families, including most major crops. The species is one of the most notorious organisms for insecticide/acaricide resistance development, and elucidated resistance mechansims include target-site resistance and acaricide detoxification, which together lead

to very high levels of resistance. We have previously shown that spider mites can mount a strong transcriptional response when adapted to a novel hosts or after development of acaricide resistance. However, whether these transcriptional responses are mainly regulated in *cis* (by selection at many loci), or by a few *trans* acting factors, remains unclear. Using dedicated crosses between inbred lines and determination of allele-specific expression, we have started to unravel gene regulation mechanisms on a genome wide scale and the global architecture of gene expression variation in a generalist herbivore.

Key words: eQTL, gene regulation, acaricide resistance

O-52

Greenhouse trials and screening of target-site mutations of *Bemisia tabaci* populations in Türkiye

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The sweet potato whitefly, *Bemisia tabaci* (Gennadius, 1889) (Hemiptera: Aleyrodidae) is a globally distributed pest that can feed on hundreds of host plants resulting in substantial economic losses. In addition, this pest can transmit more than 200 virus diseases. Chemical insecticides are the major control method to suppress this pest across globe. However, *B. tabaci* can develop resistance very quickly due to its short life cycle, high fecundity, multivoltine nature. Monitoring of resistance and resistance mechanisms have been considered as a key for a robust resistance management program. In the present study, we evaluated the efficacy of four commonly used insecticides (acetamiprid, sulfoxaflor, spirotetramat, cyantraniliprole) on larval and adult stages of eight *B. tabaci* populations in greenhouse field conditions. Sulfoxaflor and cyantraniliprole were the most effective insecticides against larval stage, whereas, acetamiprid efficacy was significantly higher than other insecticides for adults. Also, well-known mutations at the target-site of commonly used insecticides were screened in twenty whitefly populations. As a result, several mutations in acetylcholinesterase, voltage gated sodium channel as well as acetyl-CoA carboxylase were determined in field-collected Turkish whitefly populations.

Key words: Insecticide resistance, pharmacodynamic resistance, resistance management, point mutations

O-53

The evolving roles of worm and moth genetics in pesticide discovery

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Model invertebrate genetics has made valuable contributions to our understanding of pesticidal mechanisms of action over the past decades. It has enabled the verification of the mechanism of action for chemistries such as Cyclobutrifluram and Spiropidion, critically linking mode of action hypothesis to biological effect. Genome editing and next generation sequencing have enhanced forward and reverse genetic capabilities in model species but have also opened the door to conducting these studies in some pest species. As we move towards identifying active ingredients with improved selectivity the utility of the traditional model invertebrates will become diminished, given that pesticide activity is a pre-requisite for genetic studies. In our lab we have been focusing on the use of the lepidopteran *Plutella xylostella*, a pest of brassica. *Plutella* causes billions of dollars of losses per year and is therefore a pest of importance. Its relatively small size, short life cycle and ease of maintenance make it appealing for use as a model. Having genetic capabilities in high value crop pests also influences our approach to pesticides discovery. The traditional discovery approach is led by biological activity in the target pest. The availability of genetic tools and genomic resources are enabling molecular target led approaches to pesticide discovery. In my presentation, I will focus on the valuable contribution of model species, the development of capabilities in *Plutlla xylostella,* and how this is impacting our approach to traditional pesticide discovery approaches as well as molecular target led discovery.

Key words: *Plutella*, *Caenorhabditis elegans*, insecticide, nematicide, genome editing, BSA

O-54 (KEYNOTE SPEECH)

Rpt5 encodes a receptor-like protein that provides the broadest and most effective net form net blotch (*Pyrenophora teres* f. *teres*) resistance in barley

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Net form net blotch (NFNB), caused by the necrotrophic fungal pathogen *Pyrenophora teres* f. *teres* (*Ptt*), causes significant yield loss of barley worldwide. Resistance to NFNB conferred by the *Rpt5* resistance gene (*R*-gene) from barley line CI5791 is the broadest and most effective resistance reported. However, the dominant susceptibility gene (*Spt1*) is also present at this locus in additional lines. The *Rpt5*/*Spt1* locus has been reported in many studies and appears to contain multiple alleles of *Rpt5* and *Spt1*. We performed high-resolution mapping of *Rpt5* in a CI5791 x Tifang F_2 population, revealing that double recombination occurs surrounding the locus in approximately one percent of recombinant gametes with no individuals harboring recombination within the ~2 Mb delimited region. *Rpt5* and *Spt1* candidate genes within the ~2 Mb delimited region harbor unprecedented levels of polymorphism, suggesting pathogen pressure is driving diversification, as diverse virulence and avirulence *Ptt* effectors target the *Rpt5*/*Spt1* locus. Two *Rpt5/Spt1* candidate genes with predicted *R*-gene function, a receptor like protein (RLP) and receptor like kinase (RLK), were identified and selected for functional validation. Golden Promise transformants containing the *Rpt5* allele from line CI5791 showed a significant shift towards resistance. Thus, the RLP is *Rpt5,* and we have identified the first NFNB resistance gene in barley. This research has begun to uncover the complex molecular mechanisms underlying this resistance/susceptibility locus and more broadly provides valuable insight into how plants resist necrotrophic pathogens.

Key words: Net form net blotch, Rpt5, disease resistance

O-55 (KEYNOTE SPEECH)

A uniform logically consistent analysis of population structure of plant pathogens and a general warning about hazardous invasion of aggressive individuals

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Valid comprehensive inferences in study of variation of a given system can be reached only if selected approaches to data analysis are able to utilize correctly and consistently all available information. Exhaustive descriptive analysis of different facets of variation of hierarchically organized population is considered. All methods and metrics are based on proper assessments of dissimilarities between individuals for different types of data (virulence, molecular, functional data etc.) and distances between populations. This research addresses the following main issues.

1. Attributes of population variation and structure.
    1.1. Different facets of variability.
    1.2. Variation within a population.
        1.2.1. Dispersion within a population (average-based versus assignment-based for individual profiles with and without association between traits, respectively).
        1.2.2. Diversity within a population.
        1.2.3. Combined dispersion-based variation within a population - effective number of different individuals.
        1.2.4. ingularity of individual types and warning system.
    1.3. Variation among populations.
        1.3.1. Differentiation among populations.
        1.3.2. Distance between populations (average-based versus assignment-based for individual profiles with and without association between traits, respectively).
    1.4. Structural variation of a total population.
2. Virulence markers – virulence structure and variability.
    2.1. Variation of plant–pathogen interaction with infection type data.
    2.2. Linkage disequilibrium and employment of proper methods and metrics.
    2.3. Effective number of different populations and virulence polymorphism.
3. Molecular markers – genetic structure and variability with SNPs and SSRs.
4. Functional traits – trait-based structure and variability.

Key words: Dispersion, diversity, combined dispersion-based variation, effective numbers, structural variation, singularity of individuals and populations

O-56-STU

Development of Yellow Rust resistant wheat lines with the combination of Real-Time PCR, haploid and speed breeding technologies

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Yellow rust is one of the most common and destructive fungal problem on common wheat (*Triticum aestivum* L.) and durum wheat (*T. turgidum* L.var. *durum*) worldwide. The yield losses caused by yellow rust can reach up to %70 in susceptible varieties. There are about 55 resistance (R) genes defined by the Yr code from different ancestors of wheat, which are known to provide resistance for a wide range of yellow rust pathotypes. Among them Yr15 originated from *T. dicoccoides* is reported as the most effective source to confer resistance to a broad spectrum against more aggressive strains. Since it offers an economical and efficient solution, introgression of Yr15 into cultivated bread and durum wheat is an important issue and has been studied for years. In the present study, we aimed to transfer yellow rust resistance gene Yr15 into a high yielding but susceptible spring wheat varieties by using sequence specific fluorescent probe based real-time PCR analysis, coupled with haploid and speed breeding technologies. For this purpose, probe designs were carried out to determine the presence of the Yr15 gene. Then, crosses between resistant and susceptible sources were carried out in bread and durum wheat varieties. The study has been carried out in combination with MAS using Real-Time PCR in every generation as well as haploid and rapid breeding practices. In conclusion, it is predicted that a period of 3 years will be gained in reaching to homozygous Yr15 resistant wheat varieties. MAS for Yr15, speed breeding and double haploid are expected to shorten the time required to develop yellow rust resistant wheat varieties.

Key words: Wheat stripe rust, *Puccinia striiformis* f.sp. *tritici*, Yr genes, marker assisted selection

O-57-STU

Biostimulant effects of inoculation with *Piriformospora indica* and arbuscular mycorrhizal fungi on wheat

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While plant protection has utmost importance for sustaining long-term, environmentally friendly, and sustainable agricultural production, it is still at the center of ongoing debate due to usage of chemical pesticides that may cause resistance development. Improvement of nature-based solutions such as usage of beneficial fungi to protect plants from pests, diseases and abiotic stress factors might stop the debate and generation of public concern. For example, *Piriformospora indica* is a well-known symbiotic fungus that suppresses pathogen invasion, reduce diseases severity, and enhance plant defense mechanisms by altering the expression of stress-related genes such as MAPK and WRKY, producing secondary metabolites and regulating signaling pathway. Because the fungus has unique features that are not only desirable for biocontrol agents but also biostimulator, we investigated its biostimulant potential. Physiological background of *Piriformospora indica*-mediated tolerance enhancement against combined salinity and boron toxicity on commercial durum and bread wheat was evaluated in the first experiment. In the second experiment, the impact of interplay of arbuscular mycorrhizal fungi and *Piriformospora indica* on wheat yield was studied. After validation of *Piriformospora indica* inoculation by PCR, effects of the inoculation revealed significant shoot biomass enhancement under salinity stress and boron toxicity with *Piriformospora indica* inoculation mediated by increasing mineral acquisition, Na+ exclusion, triggering antioxidant defense mechanisms, alleviating membrane damage, and enhancing antioxidant capacity. The second experiment has shown that synergism between arbuscular mycorrhizal fungi and *Piriformospora indica* enhanced grain yield by 45% when compared to mock treatment. Thus, our result showed the biostimulant potential of *Piriformospora indica*.

Key words: *Piriformospora indica*, arbuscular mycorrhizal fungi, salinity, boron toxicity, wheat

O-58-STU

Development of molecular diagnosis method of Safflower Pathogen *Puccinia carthami*

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Safflower is one of the important oil plants. *Puccinia carthami* is a fungal phytopathogen which leading to significant yield loses and economic damage in safflower. It stands out as serious threat to safflower production. The diagnosis of phytopathogens at erarly stage is important for disease control and avoid of the yield loses. Molecular diagnosis is best way for early detection diverse ofthe phytopathogens. While various methods are widely used to detect *P. carthami* such as physiological and microscopic methods, molecular detection are very limited. In this study, PCR-based molecular methods was developed for detection of *P. carthami* by targeting twodifferent genomic region and different primer pairs. In the study, pathogen spores was collected by swep from safflower leaves and used for gDNA extraction. Five primer pairs were used that 4 of them were designed spesific to variable β-tubilin gene and ITS regions. In addition, one of the primer pairs (RA68) was selected from literature which was reported for *P. triticina* for testing of the Puccinia species specifity. Pc.ITS-1 and Pc.ITS-2 of the tested 5 primers in the study produced distinctive DNA fragments only for *P.carthami*, while Pc-ITS-3 aplified specific DNA fragments for 3 Puccinia species. Thus, a molecular

method has been developed that will enable rapid and complete diagnosis of *P.carthami* according to classical methods. One of the primer pairs (Pc.ITS-3) was used to validate this method and spesific detection was successfully achived. The species-specificity of the primer sets originally designed in this study was confirmed by other plant pathogens.

Key words: *Puccinia carthami*, PCR-based methods, safflower, Rust, Fungi, ITS region, β-tubulin region, Primer

O-59 (KEYNOTE SPEECH)

Loss-of-susceptibility to pepino mosaic virus in tomato

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The identification of sources of resistance to plant viruses is traditionally achieved by screening germplasm belonging to the target species and/or close relatives. This approach might be unsuccessful in occasions, as appears to be the case for pepino mosaic virus (PepMV) in tomato. PepMV affects tomato crops worldwide, causing a disease of serious economic repercussions. The existence of potential sources of natural resistance to PepMV has been described, but resistance seems to be partial, to be controlled by complex genetics and/or to be specific to the viral strain. We have addressed alternative strategies for the development of varieties resistant to PepMV, including the screening of an EMS mutagenized collection of tomato lines, and the targeting of genes encoding potential susceptibility factors identified through molecular approaches. After a screening of a collection of mutagenized tomato families, we identified a mutant showing reduced virus accumulation and no symptoms after PepMV inoculation. Resistance was mapped to a locus in chromosome 2 where a missense mutation caused the putative truncation of the hyperosmolality-gated calcium permeable channel 4.1 (OSCA4.1) protein. A CRISPR/Cas9 *slosca4.1* mutant was resistant to PepMV, but not to tobacco mosaic virus or potato virus X. On the other hand, we identified in a yeast-two hybrid screening the interaction between the PepMV coat protein and the tomato glutathione S-transferase 38 (SlGSTU38). The analysis of a *slgstu38* mutant generated using CRISPR/Cas9 showed that SlGSTU38 functions as a PepMV-specific susceptibility factor in a cell autonomous manner, re-localizing to virus replication complexes during plant infection. Knocking out SlGSTU38 triggered ROS accumulation in leaves and the deregulation of stress-responsive genes. Neither *slosca4.1* nor *slgstu38* mutants had any other readily observable phenotype than resistance to PepMV, making them invaluable in resistance breeding programs.

Key words: PepMV, potexvirus, resistance, SlOSCA4.1, SlGSTU38

O-60 (KEYNOTE SPEECH)

Molecular epidemiology: An essential tool to improve farmers' decision-making in plant protection against plant viruses

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Epidemics of plant viruses are very dynamic with dramatic changes in time associated to virus evolution. Mutation, recombination or genetic reassortment are driving forces in virus evolution. Moreover, exchanges of genetic diversity among geographically independent evolutionary niches can also occur associated to human movement and plant trade. Genetic or molecular plant protection approaches will then be challenged by a variable virus population. Therefore, understanding of the evolution and dynamics of populations is essential for effective protection against plant viruses. Molecular epidemiology offers an alternantive for a rapid surveillance of changes in virus populations that can help to identify host and virus factors that determine epidemic success to improve farmers' decision-making in crop protection. Begomoviruses (genus *Begomovirus*, family Geminiviridae), and among them tomato yellow leaf curl disease-associated viruses such as isolates of the Tomato yellow leaf curl virus (TYLCV) species severely constrain tomato crops worldwide. Begomoviruses have very dynamic populations associated to frequent genetic exchanges because of recombination between virus variants or to geographical migration that are driving diversification and evolution of TYLCV and related viruses. Recombination was demonstrated to be crucial guiding host adaptation and emergence of begomoviruses, making these viruses such successful plant pathogens. The use of molecular epidemiology to understand the evolution and to design effective and robust control of the damage caused by these viruses in tomato will be discussed.

Key words: Plant virus, begomovirus, tomato, tomato yellow leaf curl virus

O-61-STU

CRISPR-Cas9-mediated gene editing using multiplexed grnas to develop resistant against Begomoviruses and powdery mildew

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CRISPR-Cas systems are RNA-guided genome editing tools that typically consist of a target-specific chimeric sgRNA and the widely used Cas9 endonuclease. Cas9 creates DNA double-strand breaks (DSBs) that induce mutations and that causes targeted gene (s) in the genome to be knocked-out. CRISPR Cas9 genome editing tool has been applied to improve the agronomic traits, resistance to biotic factors, and other characteristics of tomatoes. Tomato is an important vegetable crop cultivated in the world and Türkiye ranks fourth in the amount of tomato production. Begomovirus-associated diseases and Powdery Mildew (PM) (caused by *L. taurica* ve *O.neolycopersici*) are the most common diseases in that threaten tomato production. In previous studies, genes associated with susceptibility of tomato to Begomoviruses (SlNAC1-SlPelo) and PM (SlMlo1) have been discovered in tomato plants. In this study, we explore the possibility of using the CRISPR/Cas9 system to provide tomato plants with molecular resistance against the aforementioned pathogens. To induce mutations in these genes, a total of 6 different gRNAs has been designed by CRSPR-GE software and their effects on the selected exons were confirmed with Sanger sequencing. The gRNAs were amplified and cloned into pDIRECT_23C plasmid vector (Addgene plasmid #91140) using the Golden gate cloning method. Plasmid pDIRECT_23C construct containing gRNAs and CRISPR-Cas9 region was transferred to E. coli DH5α cells by Heatshock method. Plasmid was transferred to electrocompetent Agrobacterium tumefaciens strain GV3101 by electroporation method. the CRISPR vector will be transferred to the tomato plant via Agrobacterium-mediated transformation and transformed explant regeneration for tissue culture.

Key words: Begomoviruses, CRISPR/Cas9, powdery mildew, resistance, tomato

O-62

Development of a plant vaccine for management of tomato brown rugose fruit virus

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Tomato brown rugose fruit virus (ToBRFV) can overcome all known genetic resistance genes resulting in all commercial tomato varieties being susceptible to the virus and reducing yields up to 70%. Virus cross protection is an acquired immunity phenomenon that plants, when infected with a mild virus isolate/strain, develop tolerance to further infection by a severe challenging isolate/strain of the same virus or related virus species. It has been reported that the mild virus strains have been successfully used to manage plant virus diseases efficiently in commercial greenhouses and fields to reduce crop yield losses. To develop the attenuated ToBRFV strains, we first successfully constructed an infectious ToBRFV whole genome clone from a wild-type strain. A total of five ToBRFV mutants were developed by mutagenesis of the ToBRFV clone and tested in both laboratory and commercial greenhouse conditions. The tomato plants inoculated with all five ToBRFV mutants did not develop symptoms under laboratory conditions. The protection efficacy was carried out in a commercial tomato greenhouse by challenging the mutant-treated plants of a cherry tomato variety with a wild-type ToBRFV. Three mutants induced mild symptoms compared with positive controls while two mutants did not induce typical ToBRFV symptoms in the first 6 weeks. Tomato plants treated with the mutants showed tolerance to infection of the wild-type ToBRFV strain as the yield of the treated plants increased up to 56.9% and the fruit weight increased up to 46.75% at week 10 of harvest. The second trial is in progress testing on TOV tomatoes.

Key words: Tomato brown rugose fruit virus, ToBRFV, vaccine, cross protection

O-63

Exploring the use of RNA interference for controlling tomato brown rugose fruit virus

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Tomato brown rugose fruit virus (ToBRFV) is an emerging tobamovirus that causes serious problems in tomato production in many regions of the world, including Türkiye. ToBRFV is able to break Tm-2^2 resistance gene provided resistance to other tobamoviruses in tomato over 40 years. Although resistance to ToBRFV has been described in some genetic sources, this resistance has not yet been integrated into commercial cultivars. Therefore, the potential use of RNA interference as an alternative control strategy against ToBRFV was investigated in this study. For this purpose, first, two conserved regions in the ToBRFV genome were selected and dsRNAs targeting these regions were synthesized by *in vitro* transcription. Then, MgAl-layer double hydroxide (LDH) nanosheets with average size of 50 nm were chemically synthesized. The dsRNAs and the LDH nanosheets were mixed at different ratios to show dsRNA binding to LDH nanosheets and stability dsRNA loaded into the LDH nanosheets. A mixture of ToBRFV dsRNA1 and the LDH nanosheets, called NaNoRugose, was prepared and tested for its effect on ToBRFV infection and replication in a commercial tomato cultivar. Ten seedlings of the tomato cultivar were first sprayed with the LDH nanosheet, NaNoRugose or water, two hours after spraying all seedlings were inoculated with ToBRFV. Then, RNA was isolated from seedling 30 days post inoculation and tested by RT-qPCR along with

standards for detection of ToBRFV and absolute quantification of virus. The results showed that NaNoRugose significantly reduced the viral load but could not completely prevent the infection of ToBRFV.

Key words: Tomato, RNAi, ToBRFV, LDH, nanoparticles, biopreparate

Acknowledgment: This study was supported by TÜBITAK TEYDEB Project No. 2220073

O-64

Detection of Tomato brown rugose fruit virus (ToBRFV) using newly designed primers and probe by RT- qPCR method

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Tomato brown rugose fruit virus (ToBRFV) is belonging to family of Virgaviridae and genus of Tobamovirus. ToBRFV is an agent listed quarantine organism for many regions, including the European Union and it is listed on Alert list (A2 list) of European Plant Protechtion Organisation (EPPO). ToBRFV is an important viral disease that causes economic losses especially in tomato and pepper plants. Since the virus can spread rapidly mechanically, its early detection with sensitive and rapid diagnosis methods is very important in terms of production. In this study, it was aimed that to design more specific, reproducible and selective primers and probe which detects most of new isolates of ToBRFV in the world and mainly Türkiye. The primers were designed by using more than 200 full genomes of ToBRFV from National Center for Biotechnology Information (NCBI) and using several softwares such as Basic Local Alignment Search Tool (BLAST), Clustal Omega and Primer3. The BLAST showed that the primers strongly matched with wide range of isolates of ToBRFV. The primers were performed by using One Step RT-qPCR method that it was perfectly matched with ToBRFV isolates which were isolated tomato and pepper plants. The BLAST was also showed that the primers match less than 90% similiar to closely related species (TMV, ToMV, ToMMV, CGMMV) and host genomes (tomato and pepper).So that, RT-qPCR analysis for TMV, ToMV, ToMMV, CGMMV have still been performed.

Key words: Tobamovirus, detection, ToBRFV, primers, tomato, pepper, RT- qPCR

O-65-STU

Expression analysis of some tomato defense genes against Tomato brown rugose fruit virus infection

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Tomato brown rugose fruit virus (ToBRFV) is recently emerged virus causing significant economic losses in tomato in many growing regions including Türkiye. ToBRFV overcomes Tm-2^2 gene which have provided resistance to other Tobamoviruses in tomato for many years. There is no known resistance to ToBRFV in commercial tomato cultivars and integration of resistance identified in some genetic resources to commercial cultivar will require time. Therefore, understanding ToBRFV-tomato interaction is necessary for developing alternative strategies for controlling ToBRFV. Since response of tomato defense genes to ToBRFV infection was not determine previously, the expression of same tomato defense genes were analyzed in response to ToBRFV infection in two tomato cultivars. First, five seedlings of tomato cultivars Torry with Tm-2^2 and Ofri without Tm-2^2 gene were infected with ToBRFV and virus-free mock inoculations were used as controls. Total RNAs were isolated from leaf samples from these plants at 1,7, 14 and 21 days post infection (dpi). The expression analysis of 13 selected tomato defense genes showed that the expression of pathogenesis related protein 6 (PR6), peroxidase (POX), and catalase (CAT) genes were significantly induced in response to ToBRFV infection. While the expression of the phenylalanine ammonia-lyase (PAL5) gene was repressed in ToBRFV infected plants, no significant changes were observed in the expression of other selected genes. When the expression of these genes were compared in two different tomato cultivars infected with ToBRFV, some differences in the expression of CAT gene were observed between two cultivars.

Key words: ToBRFV, Tomato, Defense genes, Real-time RT-PCR, Gene expression

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O-66

Detection of Tomato brown rugose fruit virus (ToBRFV) using Real-Time PCR (RT-PCR)

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Tomato brown rugose fruit virus (ToBRFV) is a virus that causes quality and yield losses in tomato and pepper plants in Europe, North America, and Asia. In general, ToBRFV does not show symptoms until the color of the fruits changes, hence difficult to detect in early stages of inoculation. Furthermore, the virus is a member of the *Tobamovirus* genus, which includes widespread genetically close viruses such as Tobacco mosaic virus (TMV), Tomato mosaic virus (ToMV), Pepper mild mottle virus (PMMoV), etc. leading difficulties in proper diagnosis. Therefore, a set of specific primers and probes was in need to detect ToBRFV for qualitative and quantitative RT-PCR (qPCR) studies. Genomic sequences of ToBRFV accessions from different hosts and localities were aligned and checked for conserved regions. Furthermore, conserved regions were also checked against all known members of the *Tobamovirus* genus for cross amplification. At the end, the design was based on a conserved region on replicase gene between the nucleotides 1691-1776 bp (reference accession: NC_028478.1) producing 86 bp product. Theoretical design was applied in a one-step RT-PCR assay using Bio-Rad CFX96 RT-PCR machine under 90 minutes for quick diagnosis. The result showed the assay can detect ToBRFV in tomato and pepper tissues samples reliably. Furthermore, the assay was not cross amplifiable for TMV, ToMV, and PepMV positive samples. Therefore, the test showed high specificity for ToBRFV due to its sequence-specific design, thus, RT-PCR can provide a conclusive diagnosis. This detection technique is anticipated to be crucial in the breeding of lines that may be ToBRFV resistant.

Key words: *Tobamovirus, Solanaceae*, Real-Time PCR, molecular detection

O-67 (KEYNOTE SPEECH)

Host manipulation by phloem-limited bacteria

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Vector-borne plant diseases (VBDs) have worldwide ecological and economic impact. Some of the most widespread and devastating VBDs are associated with *Liberibacter* spp. which are obligate, phloem-colonizing bacterial pathogens that are transmitted by psyllid vectors onto plant hosts. *Candidatus* Liberibacter solanacearum (CLso) is an emerging pathogen associated with multiple economically important diseases in Solanaceous and Apiaceous plants, while Ca. Liberibacter asiaticus (CLas) is the most devastating citrus pathogen. We have computationally identified Liberibacter effectors, analyzed their expression in vector and host, as well as determined their sub-cellular localizations. While Liberibacter is restricted to plant phloem sieve elements, we revealed its effectors can move cell-to-cell through plasmodesmata. Here, I will discuss our research focusing on identification and characterization of effector host targets from both CLso and CLas. Unlike effectors from foliar pathogens, most Liberibacter effectors are unable to suppress plant defense, indicating they have unique activities whose host targets are different than canonically studied effectors.

Key words: Vector-borne disease, *Liberibacter*, effector

O-68 (KEYNOTE SPEECH)

Bacterial pathogens hijack host metabolism to promote virulence

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Nicotinamide adenine dinucleotide (NAD^+) is a crucial component in both prokaryotic and eukaryotic immune systems. Recently, the discovery that Toll/interleukin-1 receptor (TIR) proteins function as NAD^+ hydrolases (NADase) has linked NAD^+-derived small molecules with plant immune signaling. Here we investigated how the model bacterial pathogen Pseudomonas syringae may manipulate host NAD^+ metabolism as a virulence strategy. We searched for type III effectors (T3Es) with potential NADase activity. Thirteen T3Es were identified, including five new candidates, that possess potential NAD^+-hydrolyzing domains. Most *P. syringae* strains that cause disease encode at least one NAD^+-manipulating T3E. One novel T3E, named HopBY showed structural similarity to both TIR and adenosine diphosphate ribose (ADPR) cyclase.

HopBY efficiently hydrolyzes NAD^+ in vitro and in planta specifically producing 2'cADPR. This signaling molecule is also produced by TIR immune receptors of plants and other bacteria. Intriguingly, this effector promoted bacterial virulence, indicating that 2'cADPR may not be the signaling molecule that directly initiates immunity. I will discuss our ongoing work to study the diversity of NADase enzyme active sites involving molecular docking and targeted mutagenesis. This work aims to shed light on the battle between host and pathogen centered around NAD^+ metabolism and provide insight into the diversity of NAD^+-derived molecules involved in plant immunity.

Key words: Bacteria effector metabolism evolution

O-69

Improved heterologous expression, purification, and structural characterization of plant heterotrimeric G-protein γ subunits for crop improvement

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Heterotrimeric G-proteins are composed of α, β and γ subunits that have roles as molecular switches to turn on intracellular trafficking by external stimuli. They are involved in multiple biological processes ranging from early seedling development, organ shape determination, hormone perception, ion-channel regulation to stress adaptation and immune responses. In plants, heterotrimeric G-protein (Gγ) subunits are diverse, and they have structural plasticity to provide functional selectivity to the heterotrimer. Although the Gβ and Gγ subunits dimerize to function in the signaling pathway, the interaction mechanism of various Gγ subunits with the Gβ subunit partners is still elusive. To better understand the interaction mechanism, one approach is to separate the subunits for the re-assembly in vitro. Hence, developing a reliable method for achieving the efficient production and purification of these proteins has become necessary. In this study, Gγ1 and Gγ2 proteins from *Oryza sativa* and *Arabidopsis thaliana* were successfully identified, cloned, expressed in bacteria, and purified as recombinant proteins with the fusion tags. Preliminary structural characterization studies without the Gβ partners showed that Gγ1 proteins have disordered structures with coiled-coil, α-helix extensions, and loops, whereas the Gγ2 protein has a more dominant β-sheet and turns structure. The proposed optimized expression and purification protocol can contribute to investigations on the Gβγ binding mechanism in plant Gprotein signaling. The investigations on selective binding are critical to shed light on the role(s) of different plant Gγ subunit types in biological processes.

Key words: Plant G-proteins, AGG1, RGG1, RGG2

O-70

Endoplasmic reticulum (ER)-associated molecular responses underlying *Liberibacter solanacearum* transmission by the carrot psyllid

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Carrot Yellows (CY) is a devastating disease that has been a major constraint to carrot cultivation in many countries, causing significant yield losses. *Candidatus* Liberibacter solancearum (CLso) is the causative agent of CY and is transmitted by the carrot psyllid *Bactericera trigonica*. Management of diseases caused by *Liberibacter* species including CY, the citrus greening disease (Huanglongbing), and the Zebra Chip disease depends on chemical control for lowering the psyllid vector populations, leading to health, economic and environmental problems. Understanding the transmission of CLso by psyllids is fundamental to devising sustainable management strategies. Persistent transmission of vector-borne pathogens involves critical steps of adhesion, cell invasion, and replication inside the insect gut cells before passage to the hemolymph. Our previous studies have used microscopy and expression analyses and confirmed a role of the Endoplasmic Reticulum (ER) in inducing immune responses and subsequent molecular pathways that lead to programmed cell death (apoptosis) upon CLso infection in the insect gut. Key genes involved in ER stress-related pathways were found to be differentially regulated in CLso-infected psyllids. Feeding CLso-infected and uninfected psyllids with different ER stress agents resulted in significant regulation of PERK, one of the three sensors that activate the unfolded protein response (UPR). These results demonstrate that CLso actively regulates and manipulates gene expression in the insect gut during transmission and this site is a strong candidate for targeting and regulating the transmission.

Key words: Liberibacter, psyllid, transmission, endoplasmic reticulum

O-71

Copper resistance screening in *Erwinia amylovora* and transcriptional response of the bacteria to copper compounds in Sakarya, Türkiye

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Fire blight is the most harmful bacterial disease impacting pear (*Pyrus communis*), apple (*Malus domestica*), and several rosaceous ornamentals, which is brought on by the Gram-negative bacterium *Erwinia amylovora*. Copper-resistant strains of *E. amylovora* may emerge as a consequence of ongoing use of copper-based treatments in pear and apple protection pro-

grams. *Cop*A is known as an inner membrane pump that extrudes copper (Cu^{+}) from the cytoplasm to the periplasm with the help of an exterior membrane pump that exports copper from the periplasm to the extracellular matrix,. Thus, pathogens can regulate the levels of copper in cells to prevent harm. In this study, we examined the *in vitro* effects of various concentrations of copper sulfate (100, 200, 300, 400, and 500 ppm) on the development and growth of 28 *E. amylovora* strains originating from Sakarya/Türkiye in order to ascertain the possible occurrence of copper resistance in this area. Additionally, we showed that *cop*A (F: TAAAAGCGGATTGCTTTGCT, R: CACCTCTTGCGCTTATTTCC), which is crucial for enduring copper stress both *in vitro*, is transcriptionally regulated by copper. Our research revealed that all strains grew normally on NA that had been 100 ppm copper sulfate added, suggesting some degree of resistance to copper ions. 19 strains produced colonies with typical size and appearance at 400 ppm, while 4 strains produced colonies with smaller sizes and slower growth. This might be due to copper-based chemicals have been used extensively and frequently in Sakarya to control fire blight population in field. Regarding the *Cop*A gene, 16 isolates demonstrated that genomic DNA was amplified using PCR to create a fragment measuring 2703 bp.

Key words: Fire blight, *Erwinia amylovora*, copper resistance, *cop*A, Türkiye

O-72

Development of a phytomicrobiome analysis toolkit to dechipher molecular plant-microbe interactions

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Advances in next-generation sequencing (NGS) technologies and bioinformatics led to producing a massive amount of data on the plant-associated microbiome. Emerging databases are continually being constructed for microbial genomes and barcode genes. Phytomicrobiome representing the bacteria, fungi, archaea, and protozoa associated with the plant environment and various plant tissues is an important community for plant growth and health. Here, we present a novel approach to characterize the phytomicrobiome in an individual sample associated with plant such as soil, compost, root, rhizome, leaf, and stem. In corporation with NGS and developed software it is possible to determine the phytomicrobiota members at species level. To date we have created and analyzed over 200 phytomicrobiome datasets to deshipher the plant-linked microbial community members in which microbial plant pathogens are also included by the developed "Phytomicrobiome DNA Kit". Various bacterial species associaed with different families such as Bacillaceae, Pseudomonadaceae, Streptomycetaceae, and Microbacteriaceae were identified as well as the fungi groups as Peronosporaceae, Ceratobasidiaceae, and Aspergilaceae in the analyzed samples. It was also possible to taxonomically charaterize archeabacteria species in the compost specimens. The phytobiome kit benefits RefSeq, Silva and Greengenes databases as genomic source and Kraken2 as a taxonomical classification tool. Thus, the presented kit, as an all-in one tool from the sampling to the taxonomical assignment, offers a unique approach for phytomicrobiome identification without culturing the microbes.

Key words: Plant-microbe interaction, Shotgun genome sequencing, *Metagenomics*, Microbial composition, Operational taxonomic classification, Kraken2 algorithm

O-73

To be or not to be a toxin – How does the HopAG1 effector upset the host?

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Despite being intensively studied pathogenic bacteria such as *Pseudomonas syringae* are still considered as one of the major determinants of losses in worldwide plant production. *P. syringae* strains usually employ a set of up to 40 effectors to subvert host defense. HopAG1 effector family appears commonly in *P. syringae* strains but its mechanism of action remains unknown. In our studies, we try to answer a question whether HopAG1 acts as a toxin or is specifically recognized by components of host defense system. When expressed in *Nicotiana benthamiana* HopAG1 induces massive damages of leaf tissue. Therefore, we compared the dynamics of cell death development caused by HopAG1 with those evoked by other effectors with the previously described mechanisms of action – HopBF1 known as a toxin and HopQ1 whose expression leads to a hypersensitive response in *N. benthamiana*. Our observations indicated that HopAG1-dependent tissue collapse phenocopied HopBF1. However, expression of HopAG1 in *N. tabacum* and *N. clevelandii* did not lead to leaf damage, suggesting that the effector does not act as a general toxin. The effector recognition in plants involves several signaling pathways. Therefore, we focused on pinpointing the components of signaling required for HopAG1 recognition. Expression of HopAG1 in ΔEDS1 and NahG plants (lacking EDS1 and with lowered salicylic acid (SA) level, respectively) led to development of similar symptoms as in the wild-type *N. benthamiana*, suggesting an involvement of other pathways, which will be further explored.

Key words: *Pseudomonas syringae*, effector recognition, HopAG1

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O-74 (KEYNOTE SPEECH)

Sex determination in dioecious *Amaranthus* weeds

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Palmer amaranth (*Amaranthus palmeri*) and waterhemp (*Amaranthus tuberculatus*) are weeds that are challenging to manage with contemporary control methods and they are dioecious, making them ideal candidates for genetic control strategies. For example, development and employment of a gene drive for maleness could lead to local population collapse. Towards this long-term goal, we are investigating the mechanisms of sex determination in these species. Previous research identified a male-specific Y (MSY) region in each species that shared limited synteny with each other, suggesting dioecy evolved separately in the two species. To identify which of the 100-plus genes present within the MSY regions are the key sex-determination genes, we conducted comparative transcriptomics between sexes of both Palmer amaranth and waterhemp, and comparative genomics with other dioecious *Amaranthus* species. Results from both studies are consistent with at least two dioecy evolutionary events within the genus leading to distinct sex-determination systems. In Palmer amaranth, we identified a gene encoding a pentatricopeptide repeat (PPR) protein that is present within the MSY and highly expressed in males. A homologous gene was also male-specific in *Amaranthus watsonii*, a dioecious species closely related to Palmer amaranth. We propose that this gene acts as a sex-determination factor by suppressing expression of feminizing genes that are in proximity of the MSY. A putative sex-determination gene has not yet been identified in waterhemp; repression of feminizing genes might occur via epigenetic modifications.

Key words: *Amaranthus*, dioecy, sex determination, genetic control, Palmer amaranth, waterhemp

O-75 (KEYNOTE SPEECH)

Plant-plant communication: The parasitic plant dodder (*Cuscuta campestris*) uses RNA to control its hosts

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Parasitic plants have been shaped by evolutionary pressures of the parasitic lifestyle that have led to the development of novel plant features such as haustoria, but have also suffered reductions in anatomy and photosynthetic ability. A prominent feature of parasitic plants is their ability communicate with other plants, so as to facilitate location and identification of suitable hosts as well as to manipulate host physiology to acquire nutrients and suppress defenses. Here I will discuss the stem parasite *Cuscuta campestris* (Field dodder), which form open connections to their host plants that allow the transfer of not only water and nutrients, but macromolecules such as RNAs and proteins. We have found that translocated *Cuscuta* messenger RNAs encode proteins that are also found in the host and that these proteins are able to affect host physiology. It appears that at least some parasite-encoded proteins are translated in host cells and may function in plant-plant interactions. Other work indicates that *Cuscuta* microRNAs function in the host to suppress expression of host genes in ways that benefit the parasite, suggesting that they act as effectors in the interaction. Taken together, this work supports the concept that RNA functions in signaling over long distances and between different species.

Key words: Field dodder, *Cuscuta campestris*, parasitic plant, RNA, plant communication

O-76 (KEYNOTE SPEECH)

Genomic data and tools to test hypotheses are required to understand weediness

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Today's Weed Scientists are fortunate to have access to genomic data for problematic weeds. These data are unequivocally leading to better knowledge and understanding of the fundamental biology of weediness, weed population genetics, and ecology. However, the more we know, the clearer it becomes that a genome alone is not sufficient. For instance, a single genome is much less informative than a pangenome or multiple genomes from sister species, and the outputs from analysis of genome(s) indicates correlations rather than demonstrates causation; therefore these new data generate new hypotheses that require further testing. For instance, our recent publication shows that genetic basis of non-target site resistance in black-grass (*Alopecurus myosuroides*) differs between populations, where populations presenting similar herbicide resistance phenotypes have significant differences in differentially expressed genes or QTLs associated with resistance. Ours and other experiments have identified candidate genes and pathways correlated with weedy traits, but thus far, most studies finish with these correlations rather than demonstrating causation. To get beyond correlations and test hypotheses concerning causation, Weed Science requires tools to functionally validate genes of interest rapidly and accurately. Our lab aims to bring agricultural weeds into the molecular laboratory and generate the necessary resources and techniques that will allow us to test genotype-to-phenotype hypotheses directly in weedy species. For instance, using the troublesome arable weed black-grass (*Alopecurus myosuroides*), we adapted methods for virus-induced gene silencing or virus-mediated overexpression to transiently reduce or induce gene expression in planta respectively. This presentation will discuss those breakthroughs, reiterate why they are necessary, and give examples of how genomic resources and genetic tools has enabled better molecular-level understanding of weediness and weedy traits.

Key words: Weedy Traits, Alopecurus, Genomics, virus-mediated reverse genetics, Molecular Biology

O-77 (KEYNOTE SPEECH)

Approaches to Finding New Herbicide Target Sites

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Rapidly evolving and spreading herbicide resistance is increasing the need for herbicides with new molecular targets for use in resistance management strategies. This review will cover several approaches to discovery of new herbicide target sites. Natural compounds continue to be a source of potent phytotoxins with novel target sites. Romidepsin and spliceostatin C will be discussed as examples of successfully screening a phytotoxic biological source containing two compounds with novel target sties. The natural phytotoxin citral will be discussed as a natural phytotoxin for which the novel binding target was determined by an *in silico* approach. The approach of finding the novel targets and then finding inhibitors will discussed, with emphasis on predicting viable, new herbicide targets. Potential target identification by determination of *in vivo* enzyme substrate/product and/or enzyme concentrations will be outlined. Herbicide targets from pharmaceutical molecular targets will be briefly mentioned. Finally, new target sites on old enzymatic targets will be discussed, with emphasis on use of negative cross resistance to develop manage resistance. Phytoene desaturase will be discussed as a target for this approach.

Key words: Herbicide, mode of action, natural product, pharmaceutical, phytotoxin, target site

O-78-STU

Molecular Characterization of *Corylus colurna* species from Bolu and Kastamonu Provinces

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This study was carried out *Corylus colurna* species grown in the provinces of Bolu and Kastamonu in 2020-2022. it was studied on the hazelnut genotypes that stand out with their rootstock feature in the Turkish hazelnut population. 48 promising hazelnut genotypes were selected. 17 ISSR primers were used to determine the molecular characteristics of the genotypes. Amplification did not occur in 1 of these primers ((CAC)6), and polymorphic bands were obtained from the other 16 primers. All of the 16 primers used in the study and generating amplification were determined as polymorphic. Primers produced a total of 189 bands. 185 of these bands were identified as polymorphic. The mean of polymorphism is 91.64%. The mean polymorphism rate per primer was determined as 11.12, while the mean polymorphic band was 10.88. The primer producing the most bands was (AG)7YC with 21 bands, while the primer producing the least band was DBDA(-CA)7 with 6 bands. The highest number of polymorphic bands was (AG)7YC with 21 polymorphic bands, and the primer with the lowest number of polymorphic bands was DBDA(CA)7 and (CA)8R. The polymorphism rate values of the primers ranged from 86% to 100% (Average 91.64%). Polymorphism rate was found to be 100% in 12 of the primers. The polymorphism information content values of the primers used in the study ranged from 0.64 ((CA)8R) to 0.92 ((CAC)3GC). The effective band frequencies of the primers used in the study ranged between 1.51 (VHV(GT)7G) and 2.39 ((GT)6GG), and the average effective band frequency was 1.81. It has been observed that these genotypes have different growth forces as weak, medium and strong. Different growth forces affect the resistance to pathogens. For this reason, as a continuation of the study, cultivar registration will be carried out and biotic and abiotic stress resistance will be tried to be determined in future studies.

Key words: Hazelnut, growth force, polymorphism, ISSR

O-79 (KEYNOTE SPEECH)

Tying insect pests in knots: deployment of spider-venom knottins as bioinsecticides

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Spider venoms are complex chemical arsenals that contain a rich variety of insecticidal toxins. However, most spider venoms are dominated by disulfide-rich peptides known as knottins. The knotted three-dimensional (3D) architecture of these mini-proteins provides them with exceptional stability under field conditions and resistance to insect proteases. Moreover, in contrast with other bioinsecticides, which are often slow-acting, spider knottins are fast-acting neurotoxins. In addition to being potently insecticidal, some knottins have exceptional taxonomic selectivity, being lethal to key agricultural pests but innocuous to vertebrates and beneficial insects such as bees. The intrinsic and Bt-enhanced oral activity of these peptides, combined with the ability of aerosolised knottins to directly kill sapsucking insects, has enabled Vestaron Corporation to develop them commercially as eco-friendly bioinsecticides[1]. Deployment of cryo-electron microscopy to determine the 3D structures of these knottins in complex with their ion channel receptors has opened the door to rational design of knottins with improved potency and selectivity.

Key words: Bioinsecticide, knottin, venom peptide, spider venom, eco-friendly, ion channel

O-80 (KEYNOTE SPEECH)

Exploiting Spider venom neuropeptides to develop novel biopesticides for control of Hemipteran pests

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Spider venoms contain cysteine-rich peptides that interact with ion channels in the nervous system (NS) of prey causing paralysis. High potency, stability, and specificity of action towards invertebrates makes such peptides ideal candidates for development as bioinsecticides. However, whilst these peptides may be lethal when injected, efficacy is typically low when delivered orally to insects due to failure to access their target sites of action in the NS. We have developed a novel method that enables the oral and contact delivery of venom derived peptides to their site of action via fusion to a "carrier" protein that directs transport of an attached toxin across the insect gut to the circulatory system. We have recently demonstrated that this approach also enhances the contact insecticidal efficacy of venom derived toxins and this is thought to be attributable to GNA mediated delivery to the NS. The Asian citrus psyllid *Diaphorina citri* (Hemiptera: Psyllidae) vectors the phloem-limited bacterial pathogen *Candidatus* Liberibacter asiaticus, the main causative agent of Huanglongbing (HLB) also known as citrus greening disease. HLB, for which there is no cure, has become established in all major citrus-growing regions and is now the most globally destructive disease of citrus. Disease management relies heavily upon chemical control to suppress vector populations. This reliance has led to the emergence of resistance in field pest populations and highlights the need to develop biopesticides with novel target sites of action. Here we present data from laboratory trials to support the use of fusion proteins as a means of controlling sap sucking pests through exogenous application.

Key words: Hemiptera, fusion protein, knottin peptides, snowdrop lectin

O-81 (KEYNOTE SPEECH)

Transforming crop protection with cysteine rich natural peptides – A pipeline of possibilities

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Estimates suggest that yearly more than 20% of all crops are lost to pest damage, forcing farmers to spend more than $9 billion on pesticides in just the US alone. The agrochemical industry, however, is under intense regulatory scrutiny across the world as governments work to limit the negative environmental impact of industrial synthetic chemicals. The result is fewer tools available for growers and increased risk to the global food chains. Recently, Vestaron commercialized the safe and effective SPEAR® peptide bioinsecticide. Peptide bioinsecticides work by similar mechanisms to their synthetic chemical counterparts, but possess greater specificity for target receptors and pests, no long-term environmental persistence, and are broken down into environmentally safe amino acids. Here, I will provide an overview of Vestaron's biopesticide pipeline and describe case-studies on the protein engineering required to commercialize peptides for crop protection; including for Vestaron's next active ingredient, BASIN®, expected to launch in US markets later this year.

Key words: Peptides, biopesticide, bioinsecticide

O-82 (KEYNOTE SPEECH)

How predictable is pathogen evolution under fungicide selection?

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The emergence and spread of resistance against pesticides and other control measures is a major challenge in crop protection. It is also an example of parallel evolution, with resistant phenotypes evolving repeatedly across multiple pest and pathogen species. However, the degree of genotypic parallel evolution varies between pesticide classes. Among the fungicides, resistance against QoIs is highly repeatable at a molecular level, with one point mutation reported in over 80% of species with known field resistance mutations. In contrast, 75% of CYP51 mutations in field isolates with reduced azole sensitivity are known from a single species. Working with the wheat pathogen *Zymoseptoria tritici*, I am using in vitro selection to experimentally test the repeatability of resistance evolution under different fungicide use scenarios, alongside functional genetics approaches to quantify the fitness effects of resistance mutations under different enviromental conditions. By defining the factors that can make resistance genotypes less predictable, such as different mutations being selected by different compounds within a class, or resistance-fitness trade-offs depending on the selective environment, we can improve resistance risk assessments and better target resistance monitoring methods and management guidelines to those genotypes which are most likely to be seen in the field.

Key words: Fungicides, pesticide resistance, fungi, plant pathogens, evolution

O-83 (KEYNOTE SPEECH)

How to extend fungicides effective life without broad-spectrum fungicides

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Multisite fungicides are an important component for effective disease control and managing fungicide resistance as they also prevent or delay rapid evolution of resistance. Over the last decades, multisite fungicides have been under regulatory pressure in some geographies because of insufficient selectivity and potential negative impact on ecosystems. Several multisite fungicides have disappeared in some countries, making both disease and fungicide resistance management more difficult. Meanwhile, many single-site fungicides are no longer providing effective control against targeted pathogens because resistance has frequently evolved. The crop protection industry must reinvent itself by offering innovative solutions and strategies for controlling plant diseases and managing resistance to existing and new fungicides. In this context, Corteva is bringing new molecules and biologicals to the global fungicide market. Those innovative fungicides offer new MoAs in markets where most molecules are getting eroded, and others are threatened by new regulatory constraints. A key challenge is to protect such molecules from losing effectiveness in the short term.

Key words: Fungicide resistance, multisite fungicides

O-84 (KEYNOTE SPEECH)

An overview of the fungicide resistance situation of the cucurbit powdery mildew, *Podosphaera xanthii*, in Spain

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Diseases are a major source of crop and plant damage that can be caused by a number of plant pathogenic organisms, being fungi the number one cause of crop loss worldwide. Fungicide treatments are, and will remain, essential for maintaining healthy crops and high-quality yields. They are a key component of integrated crop management; however, their continuous use has caused in many fungal pathogens the appearance of resistant isolates soon after their introduction in the market. Plant pathogenic fungi employ several distinct mechanisms to establish insensitivity against fungicides with different modes of action. Hence, fungicide resistant strains may cause enormous economic losses. Monitoring for fungicide resistance is vital to determine whether resistance management strategies are working. During this talk we will focus on an important phytopathogenic fungus for the Spanish agriculture, the cucurbit powdery mildew *Podosphaera xanthii*, its fungicide resistance situation to the main anti-powdery mildew and how to optimize the use of fungicides to control this important disease in the field.

Key words: Cucurbit powdery mildew, *Podosphaera xanthii*, *LAMP*, fungicide resistance

O-85

Fenhexamide resistance and molecular species identification of *Botrytis* spp. isolates

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Botrytis cinerea (teleomorph *Botryotinia fuckeliana*) is a polyphagous pathogen that can cause damage in many vegetable species. *Botrytis cinerea* Pers. causes yield losses by infecting the leaves, stems, flowers or fruits of the plant. Fungicides with different mode of action are used to control this disease. *Botrytis pseudocinerea* has been detected together with *B. cinerea* but at lower densities in various fruit and vegetable production areas. In some studies conducted in recent years in the world, an increase in the density of *B. pseudocinerea* has been observed due to the intensive use of fungicides. Since *B. cinerea* and *B. pseudocinerea* have similar morphological and pathological characteristics, they cannot be easily distinguished under field conditions. Although *B. pseudocinerea* is hypersensitive to many fungicides, it is hereditarily resistant to the active substance fenhexamide. This resistance is reported to be associated with a 24bp deletion in an intron in the CytB gene of the fungus, which affects the formation of the G143A mutation, which has a major effect on resistance to QoI group fungicides. In this study, the susceptibility level of *Botrytis* spp. isolates isolated from greenhouses in Antalya province, where tomato cultivation and plant protection product application are intensively practiced, to fenhexamide in vitro conditions was determined by microtiter test method. According to the test results, the isolates were found to be susceptible to fenhexamide at different levels. Species identification was made at molecular level using g2944_137_F / g2944_273_R primers specific for the 24bp deletion, which is the difference in the genotypic structure of the two species, and it was determined that all of the isolates belonged to *B. cinerea* species.

Key words: *Botrytis cinerea*, *Botrytis pseudocinerea*, microtiter, fungicide resistance, fenhexamide

O-86-STU

Screening of tebuconazole, carbendazim, and fludioxonil resistance in *Fusarium* spp., the causal agent of cereal diseases in Türkiye

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Fungicide treatment is an indispensable part of efficient food production by ensuring agricultural sustainability. The Fungicide Resistance Action Committee (FRAC) provides fungicide resistance management guidelines in which antifungal agents are sorted by mode of action. In this study, inhibitory effects of tebuconazole, carbendazim, and fludioxonil, within different groups of FRAC Code list, against *Fusarium graminearum* PH-1 and *F. culmorum* FcUK99 reference strains were investigated. Inhibitory concentrations of tebuconazole for PH-1 (MIC:1.75, MIC_{25}:0.437, MIC_{50}:0.875, MIC_{75}:1.31 µg/ml) and for FcUK99 (MIC:1.2, MIC_{25}:0.3, MIC_{50}:0.6, MIC_{75}:0.9 µg/ml) were determined. In both strains, MIC, MIC_{25}, MIC_{50}, and MIC_{75} of carbendazim were 1.4, 0.35, 0.7, and 1.05 while values of fludioxonil were 0.45, 0.112, 0.225, and 0.337. Binary mixture treatments of antifungals in MIC_{25} revealed that carbendazim and fludioxonil antagonized the inhibitory effect of tebuconazole on PH-1 whereas carbendazim+fludioxonil was a synergistic effect. Fludioxonil showed a higher antagonistic effect than carbendazim. All binary combinations of antifungals had synergistic effects against FcUK99. The triple combination completely inhibited fungal growth. The MIC_{50} values of each fungicide on reference strains were used as discriminatory doses in the determination of the sensitivity level of 38 *F. graminearum* and 30 *F. culmorum* isolates obtained from infected wheat in Türkiye. Tebuconazole was the agent to which the field isolates showed the highest resistance, while fludioxonil was the most sensitive. Outcomes will contribute to cereal disease management and risk assessment by suggesting appropriate fungicide usage within the plant protection programs in Türkiye

Key words: *Fusarium graminearum, F. culmorum*, tebuconazole, carbendazim, fludioxonil

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O-87-STU

Newly synthesized benzimidazole–2–carbamate molecules show suppressive activities against plant pathogenic fungi and oomycetes

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Most bioactive compounds are designed and synthesized by heterocyclic chemistry. Benzimidazole and its derivatives are important heterocycles that are critical subunits for pharmaceutical and biological molecules. This study was carried out to investigate the effect of 44 newly synthesized benzimidazole compounds on *Alternaria alternata, Rhizoctonia solani, Cochliobolus hawaiiensis, Fusarium solani, Lasiodiplodia pseudotheobromae* and *Pythium aphanidermatum,* which are pathogens of major crops worldwide. Well diffusion method was done using 100 µL of two different concentrations of benzimidazole compounds (1000 and 5000 ppm). The molecules designated as EBI.bB4, EBI.eB1, EBI.fB2, EBI.gB1, EBI.gB2, EBI.aB4.S, EBI.aB5.S, EBI.eB1.S and EBI.gB1.S showed suppressive effects on fungal and oomycete growth at 1000 and 5000 ppm. When these fungicides were tested against *Trichoderma harzianum*, a beneficial biocontrol fungus, the fungus was not affected. This suggests that these newly synthesized fungicides may work synergistically with *T. harzianum* in suppressing growth of the pathogenic fungi. Scanning electron microscopy showed that the fungicides resulted in malformation, bursting, swelling and hyphal tip collapse of the mycelia. The study shows that nine new fungicides show promising results in reducing growth and resulting in deformations of the mycelia of *A. alternata, R. solani, C. hawaiiensis, F. solani, L. pseudotheobromae* and *P. aphanidermatum* pathogens. The benzimidazole compounds had no effect against the biocontrol agent *T. harzianum*.

Key words: *Pythium,* cucumber, hyphal burst, well-diffusion, pesticides

O-88 (KEYNOTE SPEECH)

Towards control of existing, emerging and reemerging plant viruses

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Viruses account for nearly half of the plant endemics and are considered as major plant pathogens that threaten global food security. In the past 20 years, our research covered several groups of existing and emerging viruses that infect legumes, strawberry, greenhouse vegetables and fruit trees with a focus on potyviruses. Potyviruses are the largest group of known plant-infecting RNA viruses including many notorious viruses such as plum pox virus (PPV). We have characterized host factor genes that are essential for infections by potyviruses. We have further conducted proof-of-concept experiments in manipulation of them for disease control using PPV as a case study. In collaboration with colleagues, transgenic plum highly resistant to PPV was successfully developed by targeting either the PPV genome or the plum eIF(iso)4E gene, a host factor gene of PPV. Since peach, the primary host of PPV, is recalcitrant to genetic transformation, established technologies such as precise genome editing and RNA silencing (RNAi) that require genetic transformation are not applicable. We thus studied the possibility to create PPV resistance by silencing a host factor gene of PPV through virus-induced gene silencing (VIGS). We thus developed a PNRSV (prunus necrotic ringspot virus)-based vector and modified the vector to target the eIF(iso)4E gene. This modified vector knocked down the expression of eIF(iso)4E and prevented PPV infection in peach. For the mutagenesis approach, we successfully generated a peach mutant population and screened out several PPV-resistance lines. In addition, we generated a peach mutant population and successfully screened out several PPV-resistant lines.

Key words: RNAi, VIGS, host factor, plum pox virus, tomato brown rugose fruit virus

O-89 (KEYNOTE SPEECH)

Disinfection efficacy of Tobamovirus-contaminated soil and developing a novel platform for root protection applies

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The tobamoviruses tomato brown rugose fruit virus (TOBRFV) and cucumber green mottle mosaic virus (CGMMV) have caused severe crop damage worldwide. Soil-mediated dispersion of the mechanically transmitted tobamoviruses constitutes a major hindrance toward mitigating disease spread in crops carefully planted under sanitized conditions. Tobamoviruses are viable for months in soil and plant debris and for more than a year adhere to the clay. However, a low percentage of infectious foci occur in soil following a tobamovirus-infected growing cycle, rendering disinfection studies of several contaminated plots inconclusive for large-scale crop productions. Regarding ToBRFV we have found a low percentage of ca. 3% soil-mediated infection when the soil contained root debris from a previous 30-50 day growth cycle of ToBRFV-infected tomato plants. We have therefore formulated a rigorous platform for studying disinfectant efficacy in greenhouses by pouring a virus inoculum into planting pits prior to disinfectant treatment and by truncating seedling roots before planting, which was otherwise conducted under sanitized conditions. In addition, we have length the pre-growth cycle to 90-120 days. These rigorous conditions were employed to challenge the efficiency of four innovative root-coating technologies in mitigating soil-mediated ToBRFV infection while avoiding any phytotoxic effect. We tested four different formulations, which were prepared with or without adding various virus disinfectants. We have found that under conditions of 100% ToBRFV infection of uncoated positive control plants, the best results, were observed in the presence of the disinfectant chlorinated-trisodium phosphate (Cl-TSP).

Key words: Tobamoviruse, TOBRFV, CGMMV, cucumber green mottle mosaic virüs, tomato brown rugose fruit virus

O-90 (KEYNOTE SPEECH)

Characterization of *Rsv3* gene and understanding *Rsv3*-mediated resistance mechanism in soybean mosaic virus-soybean pathosystem

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Soybean mosaic virus (SMV) is one of the most prevalent viruses infecting soybean plants. Management of SMV depends on good agricultural practices and the use of resistant cultivars. However, the emergence of resistance (R)-breaking strains of SMV urges the characterization of alternative resistance genes on soybean pants. We have identified the *Rsv3* gene which confers strong strain-specific extreme resistance (ER) to SMV from soybean cultivar L29. Mixed infections and viral synergism, however, occur by two or more viruses leading to increased susceptibility to at least one of the viruses. ER against SMV, governed by the Rsv3 R-protein, manifests a swift asymptomatic resistance against the avirulent strain SMV-G5H. Still, the mechanism by which Rsv3 confers ER is not fully understood. We obtained evidence that viral synergism might break this resistance by impairing downstream defense mechanisms triggered by Rsv3 activation. We found that activation of the antiviral RNA silencing pathway and the

proimmune MAPK3, along with the suppression of the proviral MAPK6, are hallmarks of Rsv3-mediated ER against SMV-G5H. Surprisingly, infection with bean pod mottle virus (BPMV) disrupted this ER, allowing SMV-G5H to accumulate in *Rsv3*-containing plants. BPMV subverted downstream defenses by impairing the RNA silencing pathway and activating MAPK6. Further, BPMV reduced the accumulation of virus-related siRNAs and increased the virus-activated siRNA that targeted several defense-related NLR genes. These results illustrate that viral synergism can result from abolishing highly specific *R* gene resistance by impairing active mechanisms downstream of the *R* gene.

Key words: Soybean mosaic virus, resistance genes, *Rsv3*, resistance mechanism, soybean

O-91 (KEYNOTE SPEECH)

A signaling hub coordinating antiviral immunity and growth-promoting events

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Begomoviruses (*Geminiviridae* family) cause severe diseases in dicotyledonous worldwide. As ssDNA viruses replicating in the nuclei of infected cells, the nascent viral DNA must move to the cytoplasm and then to the adjacent cell to cause disease. The begomovirus nuclear shuttle protein (NSP) facilitates the nucleocytoplasmic transport of viral DNA and acts with the movement protein (MP) to translocate viral DNA to uninfected cells. NSP also functions as a virulence factor that suppresses antiviral immunity against begomoviruses. Here, we discuss the NSP virulence function as a suppressor of the NSP-interacting kinase 1 (NIK1)-mediated antiviral immunity. Previously, we have made some progress toward deciphering this signaling pathway mediated by a leucine-rich repeat receptor-like kinase (NIK1), which has been identified through interaction with the geminivirus nuclear shuttle protein (NSP). We showed that NIK1 relays biotic signals to the RPL10/LIMYB signaling module to control translation as an antiviral immunity mechanism and negatively regulate antibacterial immunity. Currently, we further extended the characterization of this biotic stimuli-induced cell surface signaling pathway and identified the nature of the viral PAMPs that activate the antiviral signaling. We also demonstrated that the NIK1/RPL10/LIMYB signaling circuit is activated by abiotic stresses, including osmotic stress and high temperature, to control translation and photosynthesis coordinately. We have solid evidence to propose that NIK1 represents a signal-transducing hub activated by different stimulus-sensing transmembrane receptors to regulate growth-promoting events under biotic and abiotic stresses. Therefore, NIK1 may function as a coreceptor, relaying information from various sensing receptors towards growth control under different stresses.

Key words: Begomovirus, antiviral immunity, photosynthesis, translation, NSP-interacting kinase 1, NIK1, Nuclear shuttle protein, NSP

O-92 (KEYNOTE SPEECH)

Metabolomics of Plant Defense : The *Avena sativa – Pseudomonas coronafaciens* Interaction

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Metabolites are considered the end-products of regulatory processes at a cellular level, and their levels are regarded as the ultimate response of the biological system to biotic- and abiotic stresses. Hence, the metabolome serves as a metabolic fingerprint of the biochemical events that occur in a biological system under specific conditions. In this study, an untargeted metabolomics approach was applied to elucidate biochemical processes implicated in oat plant responses to *Pseudomonas syringae* pv. *coronafaciens* (*Ps-c*) infection and to identify signatory markers related to defence responses and disease resistance against halo blight. Metabolic changes in two oat cultivars (Dunnart and SWK001, differing in susceptibility to *Ps-c*), were investigated at the 3-leaf growth stage and metabolome changes monitored over a 4-day post-inoculation period. Metabolites present in methanolic extracts were analysed using an ultra-high-performance liquid chromatography (UHPLC) system coupled to a high-definition mass spectrometer (MS) analytical platform. The multi-dimensional data were processed using multivariate statistical analysis and chemometric modelling. The chemometric models indicated time- and cultivar-related metabolic changes, defining the host response to the bacterial inoculation. Further multivariate analyses of the data were performed to profile differential signatory markers, which included amino acids, phenolics, phenolic amides (avenanthramides), fatty acids, flavonoids, alkaloids, lipids, terpenoids, saponins (avenacosides) and plant hormones. Metabolic alterations involved in oat defence responses to *Ps-c* were thus elucidated and key signatory metabolic markers defining the defence metabolome were identified. The study generated results in support of marker-assisted breeding and contributes toward a more holistic view of oat metabolism under biotic stress.

Key words: *Avena sativa*, LC-MS, metabolomics, multivariate data analysis, oat, *Pseudomonas syringae* pv. *coronafaciens*, secondary metabolites

O-93 (KEYNOTE SPEECH)

Polysaccharide biosynthesis and its contribution to *Pseudomonas syringae* plant infection

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Pathways enabling surface adhesion, stress tolerance, and epiphytic survival are key to the survival of foliar pathogens on the harsh environment of the leaf surface. Understanding the roles and regulation of these pathways is therefore important to understand the initial stages of bacterial plant infections. To address this, we characterised the poorly understood α-glucan biosynthetic pathway in the phytopathogenic bacterium *Pseudomonas syringae* pv. *tomato* (Pst), then examined the intersecting contributions of several polysaccharide loci to epiphytic survival and infection. Functionally redundant, combinatorial phenotypes were observed for several polysaccharides, with α-glucan conferring desiccation tolerance to Pst in combination with alginate. Meanwhile, exopolysaccharides were shown to contribute to leaf surface adhesion. Pst polysaccharides were shown to be tightly coordinated by multiple environmental signals. Nutrient availability, temperature, and surface association strongly affect the expression of different polysaccharides under the control of a network of transcriptional and second messenger signalling pathways. Our results indicate that polysaccharides play important roles in overcoming environmental challenges to Pst during the early stages of plant infection.

Key words: *Pseudomonas syringae*, exopolysaccharides, bacterial signalling, foliar infection, environmental signals, biofilm

O-94-STU

Genetic diversity of *Xanthomonas arboricola* pv. *juglandis* strains affecting walnuts in Türkiye revealed by *rep*-PCR and MLSA

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Walnut blight (WB) caused by *Xanthomonas arboricola* pv. *juglandis* (*Xaj*) and Brown Apical Necrosis (BAN) are the most serious diseases caused premature walnut fruit drops in Aegean and Marmara region in Türkiye. *Xaj* and together with *Fusarium*/*Alternaria* as causal agents of BAN. The aim of this study was to determine to prevalence of WB-BAN and genetic variability of *Xaj* according to geographically differences. During 2018-2019 season samples were collected from symptomatic leaves and fruits. According to biochemical assays and immature nut pathogenicity test, all isolates were identified as *Xaj*. Molecular studies were conducted with *Xaj* isolates which showed typical symptoms of WB-BAN and had high virulence. Furthermore, *Xaj* strains which represent each region were identified using 27F/1492R universal primers for 16S rDNA sequence. 31 isolates showed between %99.83-100 homology to *Xaj*. Genomic fingerprinting by *rep*-PCR was carried out genetic diversity between WB and BAN associated bacteria from Manisa, Balıkesir, Çanakkale. At a similarity coefficient of 0.89, 31 *Xaj* isolates divide into nine groups. MLSA using *atpD, rpoD, gyrB, fyuA, dnaK, efp, glnA* housekeeping genes showed genetic diversity between *Xaj* among different region. In the dendrogram, *Xaj* strains grouped in 3 different clades. *Xaj* strains obtained from WB in Balıkesir were grouped in Clade-1. Although *Xaj* BAN strains from different region (Manisa and Çanakkale) and *Xaj* Kula-10 WB strain (Manisa) grouped in Clade-1. This is the first study on genetic diversity of *Xaj* strains in Türkiye which provides basis for understanding variation among *Xaj* population and developing innovative disease management strategies.

Key words: *Xanthomonas arboricola* pv. juglandis, MLSA, *rep*-PCR, BAN, walnut blight

O-95

Complete whole genome sequence and genomic analysis of *Pseudomonas cerasi* NTM-B-29 strain isolated from hazelnut orchard in Türkiye

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Pseudomonas cerasi is an emerging bacterial plant pathogen affecting pear, cherry, and hazelnut trees. *P. cerasi* causes bacterial blight showing necrosis and dieback in hazelnut trees. We previously isolated fluorescent *P. cerasi* strain from infected hazelnut trees in the northeast Black Sea region of Türkiye. Here, we present the complete genome sequence and genomic analysis of *P. cerasi* NTM-B-29 strain. The size of a single circular chromosome is 5,71 Mb with 59,4% G+C content. NTM-B-29 has 4,835 protein-coding sequences, 54 tRNAs, and 4 rRNAs. Phylogenetic analyses based on average nucleotide identity taxonomically identified NTM-B-29 strain with prunus pathogens *P. cerasi* PL963 and 58T strains, and hazelnut pathogen *P. cerasi* H-346-S strain. Orthologous gene clusters analysis showed that NTM-B-29 strain gained unique features from genomic islands. NTM-B-29 strain tends to gain more genomic islands but fewer insertion elements and prophages. NTM-B-29 strain encodes CRISPR regions, but it has no Cas proteins. NTM-B-29 strain has hrp/hrc gene cluster on the hrp pathogenicity island that encodes type III secretion system. NTM-B-29 strain also possesses type II, III, IV, and VI secretion systems. Virulence factor analysis revealed that NTM-B-29 strain encodes type IV pili for adherence, biofilm, and an extensive repertoire of type III secretion systems effectors. Genome sequence analyses of NTM-B-29 strain revealed czcABC/czcRS gene clusters for copper resistance. Taken together, whole genome sequence and genomic analysis data provide comprehensive insights into the understanding of the pathogenicity of *P. cerasi* NTM-B-29 strain in hazelnut.

Key words: *Pseudomonas cerasi*, hazelnut pathogen, whole-genome sequencing, bioinformatics

O-96-STU

Hybrid genome assembly and annotation of *Xanthomonas arboricola* pathovar *corylina* NTM-B-28 strain isolated from hazelnut tree in Türkiye

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Xanthomonas arboricola pathovar *corylina* (Xac) is a bacterial plant pathogen causing bacterial blight in hazelnut orchards. Xac infections can cause yield loss in hazelnut cultivation. Whole-genome sequences of Xac isolates are important to understand the pathogenicity of Xac strains. Although several whole genome sequences of Xac strains were released, there is no complete genome sequence of Xac strains reported from Türkiye. Previously, we reported the isolation of the Xac NTM-B-28 strain caused bacterial blight in the northwest Black Sea region of Türkiye. Here, we produced hybrid whole-genome assembly and annotation of the Xac NTM-B-28 strain using Illumina and Oxford Nanopore technologies. The size of a single circular chromosome is 5,4 Mb with 5,399 protein-coding sequences. Average nucleotide identity-based phylogenetic analyses revealed that the NTM-B-28 strain shares 99,57% similarity with Xac CFBP1159 and Xac IVIA3978 strains. NTM-B-28 horizontally gained type IV secretion system via a genomic island. Moreover, NTM-B-28 has type I, II, III, and V secretion systems. Virulence factors analysis revealed that the NTM-B-29 strain encodes type IV pili for adherence and type II secretion systems effectors. Xac NTM-B-28 strain also encodes copLAB gene cluster for copper resistance. The genome sequence of the Xac NTM-B-28 strain provides valuable insights into the genetic diversity and pathogenicity of Xac and could facilitate the development of effective strategies for hazelnut disease management.

Key words: *Xanthomonas arboricola* pathovar *corylina*, hazelnut pathogen, whole-genome sequencing, bioinformatics.

O-97

Gene regions comparison for identification of bacterial pathogens in terms of Lettuce pathogens

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16S ribosomal RNA (16S rRNA) sequences have been used extensively in the classification and identification of Bacteria and Archaea and to establish taxonomic relationships between prokaryotic strains. Seventy-eight strains show soft rot, leaf spots, water-soaked leaf areas, and necrosis symptoms lettuce strains were analyzed for the identification of the causative bacterial pathogens by using 16SrRNA gene, *gyr*B (DNA gyrase subunit B), *rec*A, (recombination A) and *rpo*D (RNA polymerase sigma factor) housekeeping gene regions. Amplicons were sequenced and the results were compared with the reference sequences and the deposited sequences in GeneBank. The causative bacterial pathogens belong the Genus *Erwinia* and *Pseudomonas*. 16SrRNA gene region was able to reveal at Genus and species level at 63 of the strains higher than 99.4%. *gyr*B gene region identified 69 of the strains and *rec*A gene region was able to identified 67 of the strains with a similarity rate higher than 99%. The highest identification level was observed on *rpo*D gene region with a similarity rate of 99.6-99.9% in species level. *Pseudomonas fluorescence* group was found the most complicated to identified. When the regions were compared in terms of Genus *Erwinia* and *Pseudomonas*, 16SrRNA gene region identified 85% and 80% of the strains, *gyr*B gene region 96% and 95% of the strains, *rec*A gene region 95% and 90%, *rpo*D gene region 100% and 98% at species level, respectively. We recommend *rpo*D gene region as the most effective and reliable gene region beside 16SrRNA gene region to identify the bacterial plant pathogens at species level especially for the *Pseudomonas fluorescence* group.

Key words: *16S rRNA* gene, housekeeping genes, *Pseudomonas fluorescence* group, lettuce

O-98

Molecular characterization of *Pectobacterium atrosepticum* strains causing potato blackleg and soft rot disease

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The characteristics of eight strains from macerated potato tubers collected in Türkiye between 2018-2021 were studied. Cavity-forming colonies were obtained from infected potato tubers on CVP medium. Of them, eight strains produced reducing substances from sucrose, grew in 5% NaCl, and failed to grow in nutrient agar at 37°C. Based on their physiological and biochemical characteristics and confirmation of the genus-specific primer Y1/Y2, they were identified as *Pectobacterium* spp. The strains produced 434 bp spesific PCR products with primers Y45/Y46 to detect *P. atrosepticum*. Artificial inoc-

ulation of the isolates with their related hosts resulted in the same symptoms on potato from which the same bacteria were re-isolated and identified. Among the strains, two groups were obtained from ERIC and BOX PCR fingerprinrting. The nucleotide sequences of the *dna*X gene of the strains identified them as *P. atrosepticum*.

Key words: *Pectobacterium atrosepticum*, soft rot, potato, PCR detection, ERIC and BOX PCR, dnaX gene

O-99 (KEYNOTE SPEECH)

Magnitude of field-evolved resistance of arthropods to pesticides: A comprehensive analysis by decade of use

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Climate change is increasing the number of pest generations per year and expanding invasive species ranges in new regions. A combination of these factors plus a growing human population that requires an increasing demand for food and feed for animal production is resulting in an increasing number of field-evolved resistance cases to insecticides. Resistance is one of the most critical pest management challenges in agriculture production and human and animal health protection. To respond to these challenges the use of active ingredients in larger quantities and/or deployment of transgenic crops with traits to control pests will be intensified. Currently there are 626 species and 18,004 cases of resistance (www.pesticeresistance.org). In this talk I will present a comprehensive analysis and insights of arthropod resistance adaptation from 1914 to 2023 by insecticide mode of action, taxonomic category, and geographical area. Emphasis will be placed in resistance development by decade.

Key words: Pesticide resistance, pest management, insecticide resistance

O-100 (KEYNOTE SPEECH)

The dynamic emergence phenology of the Colorado Potato Beetle (*Leptinotarsa decemlineata*); İmplications for resistance and pest management

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The Colorado potato beetle (*Leptinotarsa decemlineata*) is a major agricultural pest of solanaceous crops. An effective management strategy employed by agricultural producers to control this pest species is the use of systemic insecticides. Recent emphasis has been placed on the use of neonicotinoid insecticides. Despite efforts to curb resistance development through integrated pest management approaches, resistance to neonicotinoids in *L. decemlineata* populations continues to increase. One contributing factor may be alterations in insect fatty acids, which have multiple metabolic functions and are associated with the synthesis of xenobiotic-metabolizing enzymes to mitigate the effects of insecticide exposure. In this study, we analyzed the fatty acid composition of *L. decemlineata* populations collected from an organic production field and from a commercially managed field to determine if fatty acid composition varied between the two populations. We demonstrate that a population of *L. decemlineata* that has a history of systemic neonicotinoid exposure (commercially managed) has a different lipid composition and differential expression of known metabolic detoxification mechanisms relative to a population that has not been exposed to neonicotinoids (organically managed). The fatty acid data indicated an upregulation of Δ6 desaturase in the commercially managed *L. decemlineata* population and suggest a role for eicosanoids and associated metabolic enzymes as potential modulators of insecticide resistance. We further observed a pattern of delayed emergence within the commercially managed population compared with the organically managed population. Variations in emergence timing together with specific fatty acid regulation may significantly influence the capacity of *L. decemlineata* to develop insecticide resistance.

Key words: Resistance mechanisms, diapause, Colorado potato beetle

O-101 (KEYNOTE SPEECH)

Inhibition of inward rectifier potassium (kir) channels in the salivary gland prevents plant feeding and pathogen transmission by the cotton aphid, *Aphis gossypii*

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Feeding by hemipterans, such as the cotton aphid (*Aphis gossypii*), results in significant damage to agricultural crops and economic losses. Importantly, feeding events are dependent on salivary gland secretions that led us to to directly test the hypothesis that pharmacological inhibition of inward rectifier potassium (Kir) channels would result in salivary gland failure and reduced sap ingestion. The insect specific Kir inhibitors, VU041 and VU730, reduced the length of the salivary sheath in a concentration dependent manner, indicating that the secretory activity of the aphid salivary gland is dependent on Kir channel function. Next, we employed the electrical penetration graph (EPG) technique to measure the effect Kir inhibition has to aphid feeding biology. Foliar application of VU041 or VU730 significantly ($P<0.05$) increased the time to first probe, total probe duration, and eliminated ingestion of phloem compared to untreated aphids. We tested the ability to formulate VU041 and VU730 to increase systemic movement throughout the plant. Treatment of lower leaves with formulated Kir inhibitors and EPG recordings of aphids infested on upper leaves indicated systemic movement as both inhibitors led to a significant ($P<0.05$) reduction of phloem salivation and ingestion. Furthermore, formulated VU730 significantly ($P<0.05$) reduced xylem ingestion and led to significant mortality at 24 hours post infestation. The altered feeding behavior and absence of phloem feeding is relevant for horizontal transmission of plant viruses and the influence of Kir inhibitors to reduce acquisition or transmission of phloem-restricted viruses was determined and will be discussed.

Key words: Insecticide, antifeedant, pathogen transmission, salivary gland

O-102-STU

Determination of sodium channel kdr mutations and biochemical mechanism detection in *Cydia pomonella* populations from Eğirdir/Isparta in the lakes region of Türkiye

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Cydia pomonella L. is controlled mostly with chemical insecticides and failures of chemical control have been reported in Türkiye and elsewhere. Research on the molecular basis of insecticide resistance in *C. pomonella* has revealed the involvement of target-site and metabolic mechanisms. Deltamethrin resistance status for seven populations of fifth-instar larvae, was evaluated by bioassays, synergistic studies, biochemical and knockdown point mutation analyses. The resistance ratios calculation by dividing LD_{50} values field populations with LD_{50} value of the susceptible population revealed high level resistance (21.84 and 22.3-fold) to deltamethrin, respectively, in MAREM and Tepeli populations. The PBO as a microsomal monooxygenase inhibitor (P-450), DEM as a GST inhibitor, and TPP as an EST inhibitor were used as synergists. The synergistic ratios were 1.14, 1.34 and 1.09 for MAREM 1.47, 1.39 and 1.75 for Tepeli, respectively in TPP, PBO and DEM. When the GST, P-450 and EST activities were evaluated using at least 10 larvae by a microplate reader, values for detoxification enzymes were increased 1,71 and 1,48 fold for EST; 1,96 and 1,75-fold for P-450; 0,86 and 0,85-fold GST in the MAREM and Tepeli populations respectively. Trans-membrane segments 4 to 6 of the domain II region of para sodium channel gene containing previously identified voltage-gated sodium channel target site mutation was amplified by PCR and sequenced. The sequence analyses confirmed that L1014F kdr mutation (CTT to TTT) corresponding to Leucine to Phenylalanine amino acid substitution of the voltage-gated sodium channel in *C. pomonella* was determined in the MAREM population.

Key words: *Cydia pomonella*, resistance, deltamethrin, kdr mutation, codling moth

O-103-STU

Determination of spiromesifen+abamectin resistance and detoxification enzymes of *Panonychus ulmi* koch (Acari: Tetranychidae) populations collected from apple orchards in Isparta province

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Spider mites develop resistance to many pesticides in a short time with their short biology, high reproductive potential and their arrhenotokie reproduction behave. In recent years, the companies of pesticide producing which have been developing mixed pesticide formulations by mixing different active ingredients in order to prevent or delay resistance in spiders and other pests. However, it is not known whether this mixture of pesticides is a solution to prevent the development of resistance or whether it causes a more complex problem. In the study, 13 populations were collected from different apple orchards in the province of Isparta. It was determined the populations which developed resistance to the spiromesifen+abamectin (S+A) mixture formulation or not. For this purpose, the LC_{90} value of the susceptible population was determined after used as a diagnostic dose. *Panonychus ulmi* populations collected from apple orchards were treated with the diagnostic dose of the S+A mixture, and populations which have less than 80% mortality were considered resistant to the S+A mixture. Marem-1, Tepeli-2 Gelendost-2 and populastions were determined developed resistance to S+A. In conclusion the resistance rates were 7.66, 4.44, 3.12 fold, respectively. The synergistic effects of S+A and DEM, TPP and PBO synergists were investigated for Marem-1 population. Synergistic effect was determined for all sinergists. Esterase, GST, P450 enzymes activities were evaluated on *P. ulmi* populations. All enzyme values were determined for Marem-1, Tepeli-2, Gelendost-2 populations. The results of enzyme acitivies; for esterase 15.75, 25.15 and 34.98 RFU/30min/mg protein, for GST 12.32, 12.62, 10.16 RFU/30min/mg protein and for P450 3.21, 1.42, 1.55 RFU/30min/mg protein values, respectively. mined developed resistance to S+A. In conclusion the resistance rates were 7.66, 4.44, 3.12 fold, respectively. The synergistic effects of S+A and DEM, TPP and PBO synergists were investigated for Marem-1 population. Synergistic effect was determined for all sinergists. Esterase, GST, P450 enzymes activities were evaluated on P. ulmi populations. All enzyme values were determined for Marem-1, Tepeli-2, Gelendost-2 populations. The results of enzyme acitivies; for esterase 15.75, 25.15 and 34.98 RFU/30min/mg protein, for GST 12.32, 12.62, 10.16 RFU/30min/mg protein and for P450 3.21, 1.42, 1.55 RFU/30min/mg protein values, respectively.

Key words: *Panonychus ulmi*, resistance, spiromesifen+abamectin, detoksification enzymes

O-104

Incidence and spread of pyrethroid resistance mutations in *Varroa destructor* populations in Türkiye

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Varroa destructor is the most widespread ectoparasite of Western honey bee *Apis mellifera* L. and poses a significant threat to bee health globally. *Varroa* mites are controlled with synthetic acaricides, in particular pyrethroids. However, prolonged and frequent usage of synthetic acaricides has resulted in the development of resistance. In this study, we report on the presence of resistance mutations in the voltage-gated sodium channel in *V. destructor* populations from Eastern and South-Eastern Anatolian beekeeping areas. Resistance mutations at the same position, L925V/M/I, that were previously associated with pyrethroid resistance, were found in more than 70% of the populations. A general correlation between the presence of mutations and the history of acaricide usage was observed for the sampled hives. Combining the previously available data from Türkiye, resistance status of pyrethroids across the country was discussed. Revealing the presence and geographical distribution of pyrethroid resistance mutations in *V. destructo*r populations from Turkish apiaries will contribute to create more effective mite management programmes. Last, we showed that haplotype diversity, based on two mitochondrial genes;cytochrome c oxidase subunit I (cox1) and NADH dehydrogenase subunit 4 (nd4), was low.

Key words: *Apis mellifera*, *Varroa destructor*, genetic variations, pyrethroids, resistance

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O-105 (KEYNOTE SPEECH)

Chitin biosynthesis: an attractive target for eco-friendly insecticides

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Chitin is an essential structural component of various types of extracellular matrices in arthropods, mollusks, nematodes and fungi. However, it is largely lacking in vertebrates and higher plants due to the absence of the key enzyme of chitin biosynthesis, i.e. the chitin synthase. Therefore, compounds that impair chitin biosynthesis have been considered environmentally safe arcaricides, insecticides and fungicides at least for amphibians and mammals. Chitin synthesis inhibitors, which interfere with chitin biosynthesis in arthropods and fungi, meanwhile represent an important class of compounds in pest management. Chitin synthesis inhibitors that have been developed into commercially used substances include oxazolines, thiazolidinones, tetrazines and benzoylphenyl urea, which are in use as arcaricides and insecticides, as well as pyrimidine nucleoside peptides, which have anti-fungal activities. First mechanistic insight into their mode of action has been revealed by the discovery of resistance mutations for arcaricides and insecticides, and recently by solving the structures of fungal chitin synthases in complex with nikkomycin Z. In addition, the genes encoding chitin synthases have been shown to be promising targets for RNA interference based approaches of pest control. Many studies in insects have focused on the role of the chitin synthase involved in cuticle formation and molting. We focus on chitin synthases necessary for peritrophic matrix formation in the insect midgut, which is a mucus-like chitinous extracellular matrix essential to maintain the epithelial barrier function. Disruption of this barrier results in intestinal inflammation due to the activation of innate immune-signaling pathways.

Key words: Chitin synthase, epithelial barrier, innate immunity, peritrophic matrix, *Tribolium castaneum*

O-106 (KEYNOTE SPEECH)

The circular economy in the agri-food sector: the contribution of black soldier fly

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In the last fifty years, agriculture has become more resource intensive to efficiently sustain the world population growth. This approach, relying heavily on fossil inputs, is generating a serious environmental impact. In this framework, circular economy could help the transition from conventional-linear agriculture into a more sustainable one, thus reducing, reusing, and recycling the inputs and outputs from agricultural activity. A relatively new technology for the valorization of agri-food waste, which globally amounts to 1.3 billion tons/year, is the use of the black soldier fly (BSF), *Hermetia illucens*, whose saprophagous larvae can grow on a variety of organic waste and side streams including fruit and vegetable waste, by-products of the food processing chains, plant tissue waste, and dairy waste. BSF larvae efficiently reduce the waste volume, transforming it into protein-rich biomass that can be used as animal feed or bioplastics production, but they are also a valuable source of fats and bioactive compounds with high biotechnological potential, as chitin and antimicrobial peptides. Finally, the use of BSF frass as fertilizer closes the loop for the full valorization of this organic waste. Although the BSF sector is almost mature and new applications based on this insect are rapidly developing, a deep knowledge on the physiological mechanisms underlying the life and feeding habits of this insect could significantly contribute to boost the growth of this

insect-mediated technology. In this presentation some biological aspects related to the amazing bioconversion capabilities, adaptations, and defense mechanisms of these larvae will be discussed in an applied perspective.

Key words: *Hermetia illucens*, immune system, insect gut, agri-food waste, waste management

O-107 (KEYNOTE SPEECH)

Functional analysis of sterol and steryl ester metabolism in the *Drosophila melanogaster* insect model

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Sterols are essential lipids implicated in a variety of biological functions, including membrane homeostasis, signalling, and hormonal control of metabolism. Insects are sterol-auxotrophs which particularly depend on the organismal management of dietary sterols including the conditional storage and mobilization of steryl esters (SE) in intracellular lipid droplets of the fat body. We use the unrivalled genetic tools of the model insect *Drosophila melanogaster* to disclose regulatory strategies of sterol and steryl ester regulation at the molecular, cellular, organ and organismal level to address their corresponding biological functions. Specifically, we use knockdown and knockout mutant flies to characterizes the most important enzymes for sterol/steryl ester interconversion: hormone-sensitive lipase (Hsl) and sterol *O*-acyltransferase (SOAT). We demonstrate that Hsl is essential for organ-specific SE mobilization in the context of intergenerational sterol transfer from mother to embryo. Consistently, Hsl function warrants optimal fecundity and by this reproductive success under dietary sterol limitation. In SOAT mutant flies SE stores are depleted, which causes developmental and lifespan impairments.

Key words: Sterol, steryl ester, *Drosophila melanogster*, hormone-sensitive lipase (Hsl), sterol *O*-acyltransferase (SOAT), fecundity, lifespan

O-108-STU

High quality genome assembly of major pest of Boreal Forests, *Dendrolimus sibiricus* Tschetv. (Lepidoptera; Lasiocampidae)

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Dendrolimus sibiricus considered as the most important pest within the genus inhabit boreal forests of Asia providing most harmful outbreaks, covered millions hectares. Outbreaks promote wildfires that end up destroying vast areas of the forest ecosystem and endangering nearby human communities. Thus *D. sibiricus* considered as one of the important pests of boreal forests attracting attention of many researchers in the light of potential invasion of this species in another regions. In this work, we made the de novo assembly of *Dendrolimus sibiricus* genome based on the Pacbio HIFI sequencing. Also we made RNA-seq of representative transcriptome for genome annotation using short-sized sequencing Illumina. The resulting assembly is characterized by a continuity comparable to the level of individual chromosomes (N50 = 21.5 MB), the size of the genome was 609 MB. The annotation contains about 14,000 high-like models of protein-coding genes, which differs a little from the number of those in closely related species. Genome-scale information gives us the fundamental basis for following study of this species where specific molecular tools could be applied. Complete genome sequencing allows to study gene expression of target genes, which are responsible for insect resistance against insecticides or natural enemies. *D. sibiricus* has facultative summer diapause, that make difficult to predict the outbreaks of this species. Gene expression analysis following complete genome sequencing will reveal the pathways involved in the triggering of summer diapause. Finally complete genome sequences would make clearer the species status of D. sisbiricus which now is under discussion.

Key words: *Dendrolimus sibiricus*, genome assembly, pest control, complete genome sequencing, transcriptome, Siberian moth

O-109

Using ITS region DNA barcoding to distinguish between *Kakothrips priesneri* pelikan

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Thripidae family is a diverse group of insects with global distribution and significant economic importance as pests of agricultural crops. Accurate identification and classification of Thripidae species are critical for their effective management and control. To aid in this effort, DNA barcoding using the ITS gene region has proven to be an efficient and reliable tool for identifying and differentiating Thripidae species. The high variability rate of the ITS region makes it particularly effective for identifying and classifying closely related species, providing valuable insight for understanding and preserving the taxonomic diversity of the Thripidae family. The present study aims to explore the effectiveness of the ITS gene region for DNA barcoding of *Kakothrips priesneri* Pelikan species. For the first time, the ITS data obtained from this study showed the placement of *Kakothrips priesneri* in both commonly methods, used DNA barcoding (BLAST and MEGA), produced positive results for the ITS analysis, indicating that the region may be suitable for the *Kakothrips* species.

Key words: *Kakothrips,* DNA barcoding, BLAST, phylogenetic tree, ITS

O-110

Mitochondrial genetic diversity of *Thrips tabaci* (Thysanoptera: Thripidae) in onion growing regions of the USA

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Onion thrips (*Thrips tabaci* Lindeman, Thysanoptera: Thripidae) causes severe damage to many horticultural and agronomic crops worldwide. *T. tabaci* is a key pest of *Allium cepa* in the USA. However, there is limited information available on the genetic variation within and between *T. tabaci* populations in the USA. In the current study, 83 *T. tabaci* specimens were collected from *A. cepa* from 15 different locations comprising four states of the USA. A total of 92 COI gene sequences of *T. tabaci* from *A. cepa* were analyzed to understand the genetic diversity and structure of *T. tabaci* collected from onion host. Seven distinct haplotypes of *T. tabaci* infesting *A. cepa* were identified from the current collection, while nine *T. tabaci* sequences retrieved from GenBank comprised 5 haplotypes. Overall, 15 haplotypes of *T. tabaci* infesting *A. cepa* were identified in the world that includes the ten haplotypes in the USA. In the phylogenetic analysis, all the populations collected during the study clustered with thelytokous lineage, while *T. tabaci* sequences retrieved from GenBank corresponded to leek-associated arrhenotokous lineage. The highest genetic variation was found in Elba and Malheur populations with 3 haplotypes identified in each. The results suggest that haplotypes 1 and 7 are more frequently prevailing haplotypes in the North-Western USA, with haplotype 1 being the predominant all over the country. The eastern USA appears to have a more diverse group of haplotypes. The populations from Hungary constituted distinct haplotypes and a haplotype from Kingston linked it with the predominant haplotype.

Key words: Onion thrips, haplotypes, cytochrome oxidase subunit I (COI), arrhenotoky, thelytoky

O-111 (KEYNOTE SPEECH)

Emerging viruses and using global host transcriptomics to differentiate pathways underlying disease

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Most negative-strand RNA viruses (NSV) infect animals and humans while a smaller group of the plant-infecting counterpart is expanding, with many causing devastating diseases worldwide, affecting a large number of major staples and high-value food crops. The major plant-infecting viruses of the family Fimoviridae are causing diseases in trees including mountain Ash, Oak, Aspen, Maple, Pear, and the unique Palo Verde that is native only to the Sonoran Desert in Southwestern USA and Northwestern Mexico Advances in RNA-sequencing technology have enabled increasing numbers of reports of emerging virus species and new hosts globally, including new NSV species infecting roses, blackberry, raspberry, fig, pigeon pea, maize. As virus surveillance and diagnosis increase, there is a need for additional research tools to investigate these new pathosystems and understand their infection cycles. New efforts are bringing RNA sequencing technology to monitor host responses to detectable viruses and characterizing gene expression profiles associated with virus diseases in plants as in medicine. Measuring host responses associated with latent infection or active disease is essential to defining the contribution of host genetics to the outcomes of virus infection. In this new renaissance of pathogen discovery and widespread genomics technology, the use of genetic and transcriptomic data offers the opportunity to more rapidly evaluate host responses that potentially link to disease as well as cellular defenses to limit infection. As virus surveillance and diagnoses increase, there is a need for additional research tools to investigate these new pathosystems to understand their infection cycles. New efforts are bringing RNA sequencing technology to monitor host responses for detectable viruses and also for characterizing gene expression profiles associated with virus diseases in plants as in medicine. Measuring host responses associated with latent infection or active disease is essential to defining the contribution of host genetics.

Key words: RNA virus, infectious clone, Emaravirus, transcriptomics, virus-host interactions, ER stress

O-112 (KEYNOTE SPEECH)

Yadokari/yadonushi nature: A virus in a virus in a fungus in a plant

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We have previously discovered a virus neo-lifestyle exhibited by a (+)ssRNA virus, yadokari virus 1 (YkV1), and an unrelated dsRNA virus, yadonushi virus 1 (YnV1) in a Japanese strain of the phytopathogenic ascomycete, *Rosellinia necatrix*. YkV1 has been proposed to replicate in the capsid hijacked from YnV1 as if it were a dsRNA virus. Four distinct yadokariviruses YkV2, YkV3, YkV4a and YkV4b have been discovered in two Spanish *R. necatrix* strains, co-infected by multiple diverse dsRNA viruses. These dsRNA viruses, belonging to the order *Ghabrivirales*, show low levels (<22%) of RNA-directed RNA polymerase (RdRP) sequence identity, while yadokarivirus RdRPs show 21~66% sequence identity. Here, we identified partner viruses for each yadokarivirus. First, we prepared *R. necatrix* transformants carrying single yadokarivirus cDNAs, and transfectants singly infected with the dsRNA virus partner candidates. Second, every possible combination of the transformants and transfectants was co-cultured to allow for mutual virus lateral transfer. YnV1 could assist YkV1 replication, but not other dsRNA viruses. Similarly, YkV3 and YkV4 were supported only by a megbirnavirus RnMBV3 and a megatotivirus RnMTV1, respectively. The partners were mutually interchangeable between the two YkV4 strains and the three RnMTV1 strains. These combined results show that the neo-lifestyle of yadokariviruses is widespread and that while each yadokarivirus has a species-specific partnership with a dsRNA virus, yadokariviruses as a whole can partner diverse dsRNA viruses. Furthermore, we show different interactions observed among different pathosystems involving four players, and discuss them from phytopathogical perspectives.

Key words: Fungal virus, *Rosellinia necatrix*, yado-kari virus, yado-nushi virus, dsRNA virus

O-113 (KEYNOTE SPEECH)

Multiple detection of 33 *Poaceae*-infecting viruses by e-probe diagnostic nucleic acid analysis

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Globalization increased the biosecurity risk of unwanted viral introductions initiating single or mixed infections of *Poaceae,* which cause yield-loss of concern to the U.S.A. quarantine. Serology or molecular methods target mainly single-virus infections making monitoring laborious and time-consuming. This study describes E-probe Diagnostic Nucleic Acid Analysis (EDNA) combined with high-throughput-sequencing (HTS) applied to quarantine plant disease detection. EDNA uses MiFi®, a user-friendly graphical interfase for convenient access to HTS data analysis via web browser. MiProbe™, a MiFi® component, identifies unique virus genomic signatures using electronic probes (e-probes) for use with MiDetect™ for detection of sets of pre-determined viruses in HTS data. E-probes with high genome coverage were designed with MiProbe™ for 33 viruses reported to infect *Poaceae*. Another database including seven *Poaceae* host genomes (barley, corn, miscanthus, sugarcane, sorghum, switchgrass, and rice) was included for increased e-probe specificity. All e-probes were BLAST screened with the NCBI nt database to confirm specificity and to remove non-specific sequences (curation). HTS simulation was generated *in silico* spiking host background with different concentrations of viruses using MetaSim. The limit of detection of e-probes was assessed with the HTS simulated data. Eleven out of 33 viruses were tested *in vitro* in nine confirmed infected samples by HTS (Oxford-Nanopore-MinION). The HTS data obtained *in vitro* were screened with MiDetect™ using the *Poaceae* virus-specific e-probes. MiFi® detected all viruses in the *in-vitro* generated HTS data, and positive detections were confirmed with mapping to reference using Genious Prime©. MiFi® simplify bioinformatic analysis and has potential for routine diagnostics.

Key words: EDNA, e-probes, Poaceae, high throughput sequencing (HTS), virus detection

O-114 (KEYNOTE SPEECH)

Host imprint on plant perception in the Root-knot Nematode *Meloidogyne incognita*

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Soil-born plant pathogenic nematodes can cause great damage to crops, either directly by feeding and establishing in the roots or by transmitting devastating viruses. Those microscopic worms parasitize roots and need their host to feed and/or reproduce. Finding the plant is therefore the first and essential prerequisite for those nematodes to establish parasitism. Infective nematode larvae (stage 2 juvenile; J2) can perceive plant chemical signals in soil and follow the gradients towards the roots. However, the nature of those signals, their cognate receptors in nematodes and sensory neurons mediating the nematode chemo-dependent behavioural responses (chemotaxis) are still largely unknown. By combining behaviour study, molecular genetics, cell biology and phytopathology my project is to exploit two plant parasitic models, *Meloidogyne* and *Xiphinema* species, to investigate how these pathogens perceive their host and what is the impact of the host itself on the modulation of their sensory capacity. Using experimental evolution of the model *M. incognita* and a newly developed chemotaxis system, I'll show you that the host plant profoundly impacts the nematode behaviour towards root extracts and that the host imprint significantly affects the nematode transcriptional response. In the long term, one can wonder how building knowledge of nematode chemical ecology can beneficiate the development of control strategies towards these pests in the field.

Key words: Chemotaxis, host imprint, *Meloidogyne incognita*, perception, plant parasitic nematodes

O-115 (KEYNOTE SPEECH)

Root-knot nematode modulates plant CLE3-CLV1 signaling as a long-distance signal for successful infection

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Plants utilize many long-distance and systemic signals to modulate growth and development, as well as responding to biotic and abiotic stresses. Parasitic nematodes infect host plant roots and cause severe damage to crop plants worldwide. However, the molecular mechanisms that regulate parasitic nematode infections are still unknown. Here we show that plant parasitic root-knot nematodes (RKN), *Meloidogyne incognita* modulate the host CLAVATA3 (CLV3)/EMBRYO SURROUNDING REGION (CLE)-CLV1 signaling module to promote the infection progression. Plants deficient in the *CLE* signaling pathway show enhanced RKN resistance, whereas *CLE* overexpression leads to increased susceptibility toward RKN. Grafting analysis shows that *CLV1* expression in the shoot alone is sufficient to positively regulate RKN infection. Together with the results from the split-root culture system infection assay and the CLE3-CLV1 binding assay, we conclude that mobile root-derived CLE signals are perceived by CLV1 in the shoot, which subsequently produce systemic signals to promote gall formation and RKN reproduction. We have recently reported a model where the sink organ (roots) actively signals the source organ (leaves) via root-to-shoot long-distance mobile CLE peptides, to maintain the root's sucrose level and growth (Okamoto et al., 2022 Plant Physiol.), and the nematode might take over this endogeneous systemic signal for their successful infection. This is the first report demonstrating pathogens manipulating the host's endogenous peptide signal in land plants as part of the infection process. Furthermore, our results also shed light on how peptides may function as long-distance signaling molecules in inter-specific interactions.

Key words: Root-knot nematode, systemic signal, peptide signal, CLE peptide

O-116-STU

In vitro nematicidal activity of Arugula (*Eruca sativa* L.) against stem and bulb nematode (*Ditylenchus dipsaci* kühn, 1857)

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Annually 157 billion dollars economic loss is attributed to the nematodes. The stem and bulb nematode causes significant economic losses for a wide range of plant species worldwide. The onion race of nematode is the main pest of the onion and garlic plants. It causes a yield loss of up to 65% just in Türkiye. Management of the nematode is challenging due to the wide host spectrum. Rotation crops and resistance varieties are limited. The use of agro-chemicals is reduced in the world for environmental concerns and adverse effects on human health. Therefore, natural plant protection agents are necessary for eco-friendly management applications. Arugula has a high potential for nematicidal activity with its natural compound contents. This study aimed to investigate the nematicidal activity of arugula extract against the stem and bulb nematode *in vitro*. I this study, the extraction conditions of different plant parts as well as application dosage and exposure time on nematodes were determined. Overall, the whole plant had more nematicidal activity obtained in different extraction conditions. 15.0 to 67.2% nematicidal activity was found with different dosages

of the arugula extract on *D. dipsaci*. The nematicidal activity significantly increased on the 4th day, which was found to be between 11.4 to 50.4%. The arugula plant extract showed nematicidal activity comparable with the positive control, which is non-fumigant nematicide fenamiphos. Therefore, it can be considered as a promising natural biocontrol product for *D. dipsaci* management. Further investigation of the nematicidal activity is necessary under greenhouse and field conditions.

Key words: Plant parasitic nematode, nematicidal activity, arugula, natural compounds

O-117

New host plant report of root-knot nematode *Meloidogyne* (Goeldi, 1892) species, from Türkiye

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Root-knot nematodes are members of the genus *Meloidogyne* and they are an economically important polyphagous group of highly adapted obligate plant parasites, are distributed worldwide and parasitize nearly every species of higher plant. Species of *Meloidogyne* are pests of major crops, vegetables, fruit, and ornamental plants grown in tropical, subtropical, and temperate climates. In Türkiye, it has been observed that the root-knot nematode population has an increasing tendency in terms of its distribution. For this reason, a survey was conducted in Çanakkale and Balıkesir provinces, which are located in the northwest of Türkiye and have an important place in edible, medicinal and aromatic plant production. 158 soil and plant samples were taken from the areas where especially winter crops are grown in Çanakkale and 35 medicinal and aromatic plant samples were taken from Balıkesir province. As a result, 23 out of 158 samples from Çanakkale and 2 out of 35 samples from Balıkesir were found infested with *Meloidogyne* species. Diagnoses were made by combination of morphological, morphometric and molecular methods using second stage infective juvenile and female individuals obtained from contaminated plants. From Çanakkale province, *Meloidogyne javanica*, *M. hapla* and *M. incognita,* from Balıkesir province*, M. arenaria* and *M. incognita* species were identified. This survey reveals the first host-plant record of *M. arenaria* in lemon balm, *M. incognita* in calendula and *M. hapla* in parsley plant in Türkiye.

Key words: *Calendula officinalis,* identification*, Melissa officinalis, Meloidogyne arenaria, M. incognita, M. hapla, Petroselinum crispum*

O-118

Effect of extraction conditions on *in vitro* nematicidal activity of brown mustard (*Brassica juncea* L.) against stem and bulb nematode (*Ditylenchus dipsaci* kühn, 1857)

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Stem and bulb nematode causes economic losses on onion and garlic production all over the world. The nematode causes a yield loss of up to 65% just in Türkiye. One of the most practical and fast-acting methods for the management of plant parasitic nematodes is the use of chemicals. Due to the concerns for the environment and human health, the use of synthetic chemicals is restricted in the world. Instead, the use of eco-friendly natural products attracts considerable interest. *Brassica juncea* is well known for its nematicidal activity; however, there is not detailed investigation on the potential of *B. junceae* for the management of stem and bulb nematode. In this study, the extraction conditions of *B. juncea* were investigated for its nematicidal activity against *D. dipsaci in vitro*. In the experiment, two different types of the plant (dry and fresh), extraction methods (sonicated and conventional), and three different extraction temperatures (-10°C, +4°C, +70°C) were investigated. The highest nematicidal activity was obtained at sonicated and conventional extraction techniques with the extraction of fresh plants at 70°C. Immotile nematode percentages of 89.2 and 87.8% in these treatments were significantly higher than positive controls, respectively. The optimization of the extraction conditions is the first step in the development of a plant protection agent. The extraction temperature and the method conditions were determined with this study.

Key words: Plant parasitic nematode, nematicidal activity, brown mustard, natural compounds

O-119-STU

Dosage effect of pepper carrying *N* and *Me1* Genes to *Meloidogyne incognita*

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Meloidogyne incognita is one of the most common and devastating root-knot nematodes (RKNs) of vegetables, mainly in pepper (*Capsicum annuum*). The use of resistant genes in the management of RKNs is one of the effective and practical methods. However, the dosage of genotypes carrying the *Me1* and *N* genes have caused the selection of nematode populations capable of overcoming the resistance carried these genes. Thus, it is necessary to investigate the pathogenicity of nematodes to integrated control strategies. The aim of the study was to evaluate reaction of *Me1* and *N* gene on pepper to *Meloidogyne incognita* S6 isolate under the controlled conditions. In the study, as resistant pepper material of both homozygous and heterozygous of *Me1* and *N* gene were used and the study was conducted randomized block design with five replicates twice. Second stage juveniles of *M. incognita* S6 isolate were inoculated at 1000 J2s per plant. Eight weeks after inoculation plant roots were evaluated according to quantified parameters; the number of egg mass, number of galls and gall index (0-5) per root. In addition, molecular markers linked to *Me1* and *N* genes were used for validation of genes. The results show that *M. incognita* S6 isolate was not overcame both homozygous and heterozygous of *Me1* and *N* gene. Furthermore, it seems that the resistance level of the gene might not affected by nematode population. Further studies are underway to pepper-nematode interactions to determine the effects of differences in nematode isolates.

Key words: Root-knot nematode, *Me1, N*, nematode resistance gene, *Capsicum annuum*

O-120 (KEYNOTE SPEECH)

Biological-based Insecticides for Pest Management

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Significant damage and crop losses are caused by insect pests. With widespread emergence of pest resistance to current products on the market, consumer demand for sustainable products, and with the government initiatives to decrease the usage of chemical residues, new solutions are needed. Biological-based insecticides provide a solution to meet these demands and it is critical they provide efficacy to increase crop yields. Advancements in sequencing technology combined with computational biology, machine learning, and functional genomics, create an opportunity to increase the speed of discovery of efficacious biological-based insecticides. The ability to integrate and analyze complex datasets across technologies is critical to the success for the discovery of new efficient biological solutions. At AgBiome, we leverage our data science capabilities with high-throughput screening to discover and deliver biological-based insecticides to manage pests.

Key words: Biolocigal based insecticides, pest management, insecticides, pests

O-121 (KEYNOTE SPEECH)

Fungal cell wall β-1,3-glucan stimulates immune cascades and is a target of an antifungal peptide in *Manduca sexta*

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Insects respond to microbial infections by activation of serine protease cascades in hemolymph, which activate prophenoloxidase and cytokines, resulting in melanization of pathogens and synthesis of antimicrobial proteins. These responses are stimulated by peptidoglycan in bacterial cell walls and by β-1,3-glucan in fungal cell walls. We have investigated hemolymph plasma proteins in the lepidopteran insect *Manduca sexta*, which bind to β-1,3-glucan and trigger protease cascades or have direct antifungal activity. β-glucan recognition protein 2 (βGRP2) is a plasma protein that contains an N-terminal glucan binding domain and a C-terminal glucanase-like domain. Fungal infections in hemolymph are detected by binding of the N-terminal domain of βGRP2 to β-1,3-glucans, which induces self-association of βGRP2, forming a platform on the fungal surface to trigger the activation of the initiating protease HP14 in the protease cascade leading to activation of prophenoloxidase and the Toll pathway to stimulate synthesis of antimicrobial proteins. One type of microbe-induced hemolymph protein is diapausin, which we found to have antifungal activity. Diapausin concentration increases in hemolymph after injecting the larvae with yeast or bacteria. Purified diapausin is active against yeasts and some ascomycte fungi, including pathogens of insects and plants. Diapausin-1 binds to β-1,3-glucan on the yeast cell wall and interrupts cell separation after cell division, leading to cell clusters. Diapausin-1 may disrupt fungal growth by binding to cell wall β-1,3-glucan and/or impairing β-1,3-glucan synthesis. This study advances our understanding of an insect immune response to fungal infections and may contribute to the identification of new targets for the development of antifungal drugs, strategies for use of fungi for insect pest control, or use in biotechnology to protect plants from fungal infection.

Key words: Immunity, hemolymph, fungal cell wall, yeast, diapausin, pathogen, antifungal, phenoloxidase

O-122

Molecular identification of entomopathogenic fungi from Western Flower Thrips [*Frankliniella occidentalis* (pergande)]

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Frankliniella occidentalis (Pergande) (Thysanoptera: Thripidae), which is the major pest of many vegetable and ornamental plants in greenhouse growing in Antalya, can both directly damage plants by sucking plant sap and indirectly damage as the vector of some important plant viruses. Local isolates of Entomopathogenic fungi (EPF) in geographic areas where pests are found have important advantages in control. As a result of the isolations made from the brought samples; 31 different isolates belonging to 15 different species were obtained from Akanthomyces, Alternaria, Aspergillus, Beauveria, Cladosporium, *Fusarium*, Isaria, Lecanicillium and Sporothrix genera. While ITS2-ITS5 primers of S. pallida K4, Ak. muscarius DOA1 and DOA2 and L. psalliotae DOA3 isolates were used, ITS1-ITS4 primers were used for the identification of all other isolates. S. pallida K4 isolate banded at 450 bp using ITS2-ITS5 primers, while all other isolates banded at approximately 580 bp. According to the results of molecular studies, 12 Alternaria isolates, 8 Cladosporium isolates, 3 Beauveria isolates, 2 Acanthomyces isolates, 2 *Fusarium* isolates, 1 Isaria isolate, 1 Lecanicillium isolate, 1 Sporothrix isolate, 1 Aspergillus isolate showed similarities with the isolates registered in the NCBI gene bank. Genetic similarities/differences between the species were determined as a result of the analysis made with the MEGA 7 (Molecular Evolutionary Genetics Analysis) Phylogenetic Tree Program based on the ITS gene regions of entomopathogenic fungi and DNA sequence analyzes were performed. As a result of the data obtained, it was determined that there were geographical differences between the fungal species.

Key words: Antalya, biological control, entomopathogenic fungi, *Frankliniella occidentalis*, western flower thrips

O-123-STU

Isolation and identification of entomopathogenic fungi from coastal districts of Ordu province, Türkiye

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A total of 250 soil samples were taken from the forest, hazelnut, kiwi, vegetable, and meadow-rangeland areas in the coastal regions of Ordu province, Türkiye. Entomopathogenic fungi were isolated from these soil samles using the *Galleria*-bait method. Eighty five fungal isolates were isolated from these soil samples, after which they were morphologically and molecularly identified. After morphological characterization 64 out of 85 isoletes were identified molecularly. Based on the molecular characterization results, twenty three out of the 64 isolates were *Beauveria bassiana* (35.94%), 11 isolates were *Metarhizium brunneum* (17.19%), 8 isolates were *Metarhizium anisopliae* (12.5%), 6 isolates were *Metarhizium robertsii* (9.38%), 4 isolates were *Purpureocillium lilacinum* (6.25%), 4 isolates were *Clonostachys rogersoniana* (6.25%), 3 isolates were *Fusarium solani* (4.69%), 1 isolate was *Clonostachys rossmaniae* (1.56%), 1 isolate was *Aspergillus flavus* (1.56%), 1 isolate was *Cordyceps cicadae* (1.56%), 1 isolate was *Cordyceps fumosorosea* (1.56%) and 1 isolate was *Fusarium oxysporum* (1.56%). In the coastal area of Ordu province, the most common entomopathogen fungal genus is *Metarhizium* followed by *Beauveria bassiana*.

Key words: Entomopathogenic fungi, isolation, biological control, forest, hazelnut, Black Sea

O-124

Efficacy of indigenous entomopathogenic bacteria and fungi against the Western flower thrip, *Frankliniella occidentalis* (Pergende) (Thysanoptera: Thripidae)

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The Western flower thrip, *Frankliniella occidentalis* (Pergande), is one of the most economically important agricultural pests worldwide and attacks a wide range of vegetable and horticultural crops. The most common control measures for *F. occidentalis* are chemical pesticides. However, varying degrees of resistance are developing due to the overuse of pesticides. Therefore, more and more attention is paid to biological control. To investigate the efficacy of indigenous entomopathogens against *F. occidentalis*, fifteen bacteria and fifteen fungi were tested separately on the larvae and adults. Experiments were conducted using an IRAC-approved bioassay method (IRAC Method No. 010). *Serratia marcescens* Se9 showed the highest mortality than the other bacterial isolates at a concentration of 10^9 cfu/ml in larvae and adults, showing a mortality of 54% and 69% respectively. On the other hand, the fungus *Metarhizium flavoviride* As-18 at a concentration of 10^8 conidia/ml showed mortality of 92% and 74% in larvae and adults, respectively. Concentration-response experiments were conducted with these potential isolates. LC_{50} values of *S. marcescens* Se9 and *M. anisopliae* As-18 for larval stages were calculated as 4×10^6 cfu/ml and 1.6×10^4 conidia/ml, respectively. However, LC_{50} values for the adult stage were higher than for the larval

stage and were calculated as 6.3×10^6 for *S. marcescens* and 7.1×10^4 conidia/ml for *M. anisopliae*. The study found that these two isolates have the potential to be used for biological control of the pest. However, the formulation of the isolates and the application in the field should be carried out with further studies.

Key words: Local entomopathogens, insecticidal effect, *Frankliniella occidentalis*, biocontrol

O-125

Biocontrol potential of some entomopathogenic fungal isolates against *Myzus persicae* (Sulzer) (Hemiptera: Aphididae)

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Aphids are one of the major insect pests of greenhouses and field crops worldwide. Several species of entomopathogenic fungi (EPF), including *Beauveria bassiana*, and *Metarhizium anisopliae*, have been developed commercially to control aphid species. This study was conducted to evaluate the virulence of four isolates and one commercial product (Nostalgist) of EPF, including, *B. bassiana* (GOPT-DYYLD, and GOPT-562), and *Metarhizium brunneum* (ORP-13, and ORP-27) against *Myzus persicae* (Sulzer) nymphal stages on pepper plants using whole plant method in growth chamber at 25°C and 75% relative humidity (RH). These isolates were phenotypically and molecularly identified to the species level based on the nucleotide sequences of the ITS1 and ITS4 region within the 5.8 S rRNA gene. Aphid mortality was recorded after one, two, and three days of post-treatment. Mortality percentages of ORP-27, Nostalgist, DYYLD, ORP-13 and GOPT-562 after 3 days of application were 68.2±0.36, 67.4±1.43, 66.2±0.63, 62.8±0.44, and 60.9±1.29 %, respectively. The obtained results revealed that the lowest LTR50 R value of 1.1 day was obtained with isolate DYYLD followed by ORP-27 and Nostalgist with 1.4 and 1.5 day respectively with dose of 10^8 spores/mL. Among the four entomopathogenic fungal isolates, ORP-27 and DYYLD were found to be the promising virulent isolates. By testing their field efficacy, they can be used as potential biocontrol agent for the management of aphid.

Key words: Biological control, entomopathogenic *fungi, Beauveria bassiana, Metarhizium brunneum*

O-126 (KEYNOTE SPEECH)

RNA based biopesticides for sustainable crop protection – Bio Clay Technology

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In this globalised world of interconnected economies and climate change concerns, we need to ensure that our food crops are protected from pests and diseases as they can account for 20-40% losses in productivity. The ongoing usefulness of chemical pesticides suffers from issues such as residual toxicity, run off, specificity and resistance. RNA based biopesticides or 'RNA sprays' for plants as a next generation crop protection platform without the need for genetic modification is gaining momentum globally. BioClayTM technology using degradable layered double hydroxide clay particles as carriers of double stranded RNA (dsRNA), the trigger molecule of RNA interference, has opened the window of opportunity to deliver RNA sprays as a non-GM, residue free, specific, stable, and environmentally sustainable alternative to chemical pesticides. RNAi effectors delivered as BioClay are stable, do not get washed off and provide protection to the sprayed and unsprayed leaves against the targeted pests and pathogens for extended periods. The clay degrades on the surface of the leaf alleviating concerns about residues. The novel delivery platform is being progressed to target viruses, insect pests and fungi. We have recently shown that BioClay can provide protection against multiple life cycle stages of whitefly (*Bemisia tabaci*), a phloem-feeding global agricultural pest. Real world application of RNA based biopesticides with sustainable credentials for the global consumer will be governed by factors such as cost-effective production of dsRNA, stable delivery, risk identification and mitigation strategies, regulatory landscape, and community acceptance.

Key words: RNA interference, RNA sprays, BioClay, biopesticides, crop protection

O-127 (KEYNOTE SPEECH)

RNAi as a biocontrol solution for soy stink bugs

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Triggering an efficient and commercially relevant RNAi response in piercing-sucking pests through oral uptake of a foliar spray has long seemed a daunting task. It is generally believed that the active ingredient, the double stranded RNA, does not enter the plant cells or vascular system, from which these insects feed. Over the past decade, Syngenta has been

developing an RNA-based product aiming to control stink bug pests in soy plants. From multiple target discovery screens using artificial diet assays, several lead targets were selected for their effectivity in key sting bug species and their potential for selectivity. However, it soon became clear that the translation to a more field realistic foliar spray was not straightforward. The feeding process of these stink bugs poses biodelivery challenges on behavioural, mechanical, and enzymatical levels. The characteristics of the leaf probing, stylet insertion and saliva excretion were examined, as well as their consequence on the RNAi efficacy. Based on this knowledge, co-formulant screens were executed. These resulted in the selection of multiple co-formulants that give a significant benefit to overcoming these biodelivery challenges, and are a major step forward in the development of an RNA-based biocontrol product for soy stink bugs.

Key words: RNAi, RNA interference, stink bugs, biocontrol

O-128 (KEYNOTE SPEECH)

AgroSpheres manufacturing and delivery technology to address field stability and targeted delivery of dsRNA to enable efficient RNAi in lepidoptera

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AgroSpheres fermentation and delivery technology is a fermentation-based technology that produces encapsulated RNA. The RNA is encapsulated in DNA deficient non-replicating spherical minicells. The minicell encapsulated RNA can be formulated to achieve different stability profiles. Stability enhanced minicell-RNAs enable significantly enhanced persistence in and uptake across the lepidopteran midgut. The stability and uptake enhancement enable RNAi mediated transcript degradation and successful insect control in lab, greenhouse and field environments. *Plutella xylostella* is presented as a case study from lab to greenhouse, with an emphasis on mode of action (MOA). The MOA entails uptake across the midgut, accumulation into the columnar cells and onset of insecticidal activity. Furthermore, this MOA was only enabled by stability enhanced minicells. This data highlights the importance of delivery as a mode of action to enable novel biological modalities such as RNAi.

Key words: RNAi, mode of action, *Plutella xylostella*, delivery technology

O-129 (KEYNOTE SPEECH)

Low-cost, scalable dsRNA manufacturing through microbial fermentation solves decade-long challenge and unlocks commercial potential of RNAi BioSolutions.

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RNA interference (RNAi)-based BioSolutions are a promising new approach for controlling pests and diseases in agriculture, home and garden, aquaculture, and animal health markets. RNAi offers a new mode of action to complement existing integrated pest management programs that is highly selective and presents few risks to non-target organisms and the environment. A major challenge to the commercial development and broad implementation of sprayable RNAi BioSolutions has been the extremely high cost of the double-stranded RNA (dsRNA) active ingredients. RNAissance Ag, LLC (St. Louis, Missouri, USA) is dedicated to revolutionizing the agricultural industry by developing RNAi BioSolutions that are both effective and affordable. The company has developed a proprietary bacterial fermentation-based manufacturing technology for high-volume, low-cost dsRNA production. Using this platform, dsRNA yields of up to 12 grams per liter fermentate have been achieved, a massive improvement over other fermentation technologies that have reported yields of 1 gram or less of dsRNA for the same volume. Our technology is easily scalable, leveraging existing industrial fermentation infrastructure, to meet the global production demands to support widespread adoption of RNAi BioSolutions. In this presentation, we describe RNAissance Ag's dsRNA manufacturing technology. By focusing on reducing the cost of production, RNAissance Ag aims to make RNAi BioSolutions accessible, while also promoting sustainable and environmentally friendly farming practices. The potential impact of this technology on global food production is immense, and the company is poised to become a leader in the field of biological pest control.

Key words: RNA interfernce, RNAi, crop protection, dsRNA, biomanufacturing, sustainable agriculture

O-130 (KEYNOTE SPEECH)

Receptor-like kinases BAK1 and SOBIR1 are required for necrotizing activity of *Sclerotinia sclerotiorum* necrosis-inducing effectors

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Sclerotinia sclerotiorum is the causative agent of stem rot in canola/oilseed rape, which is the most serious disease afflicting this crop in many regions of the world. The most distinct symptom of the disease are the necrotic lesions that eventually penetrate into the pith and result in collapse of the stem. Tissue necrosis may be caused by necrosis-inducing proteins, such as the necrosis and ethylene-inducing proteins (Nep1 and Nep2) that have been previously characterized in *S. sclerotiorum* and several other fungal and oomycete plant pathogens. To catalogue the wider suite of necrosis-inducing proteins and/or protein effectors, an informatics exercise was conducted to identify genes encoding small, secreted, cysteine-rich proteins. These were tested for their ability to induce necrosis in *Nicotiana benthamiana* via *Agrobacterium*-mediated infiltration. Six novel necrosis-inducing proteins were discovered, of which all but one required secretion to the host periplasmic place for activity. Localization studies using fusions to the green fluorescent protein and co-localization with organelle markers indicated that most of the necrosis-inducing proteins localized to the endomembrane system; however, endoplasmic reticulum stress and induction of the unfolded protein response were not involved in the necrosis phenotype. Interestingly, virus-induced gene silencing experiments revealed that all of the obligately-secreted necrosis-inducing proteins were dependent on the presence of the plant receptor-like kinases BAK1 and SOBIR1 for activity. This suggests that *S. sclerotiorum* necrosis-inducing proteins very likely interact with host extra-cellular receptors to initiate the sequence of events required for necrosis, a discovery that has important implications in breeding for resistance.

Key words: *Sclerotinia sclerotiorum,* canola, oilseed rape, disease, necrosis, receptors

O-131 (KEYNOTE SPEECH)

Laminarin innovation pathways

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There is a growing requirement for the industry to have a change in mindset towards the traditional ways for looking at plant pathogenic microorganisms, driven by growing pressures for us to be fully sustainable in our inputs to agriculture with the least impact on the environment in every aspect. We see growing pressure to restrict or remove registration of conventional chemistries in the EU and indeed globally and it would be unconscionable for us to not consider how we can change the normal and enter a new way of thinking. UPL has been developing a range of products from differing source to address this demand. Within the scope of R&D strategy and innovation vision of UPL "Vacciplant" is how we have developed a solution from the extraction and purification of laminarin from the brown seaweed *Laminaria digitata* for disease control use. The application of laminarin on a plant will act as an elicitor and thus will activate the plant defenses leading to crop protection against diseases from various origin. The complexity of this elicitor mode of action and its positioning in farmer's fields, leads us to refine our knowledge constantly. Used as an accompaniment to traditional solution, Vacciplant offers to the grower a secure protection strategy from a sustainable biocontrol solution. By changing the mindset we are changing the game as UPL.

Key words: UPL, biocontrol, biosolution, laminarin, sustainability, innovation

O-132

Determination of vc and mating types of *Cryphonectria parasitica* isolates by multiplex PCR, obtained from thirteen chestnut growing provinces of Türkiye

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Chestnut canker caused by a fungus, *Cryphonectria parasitica*, is a serious disease of chestnuts everywhere it grows. The only practical way to prevent the disease is biological control by using hypovirulent isolates of *C. parasitica*, which are infected by a hypovirus. The hypovirus is only transmitted to the virus free isolates, the virulent ones, by hyphal conjugation, which is not so easy because of the presence of many vege-

tative incompatible strains of the pathogen. Biological control can only be applied either between the two fully compatible or genetically identical strains. For this reason, vegetative compatibility (vc) types, which are about 82, has to be determined. The classical vc type determination, based on the pairing the obtained isolates with the previously known vc types on culture media, is time consuming and sometimes does not give sound identification. Fluorescent multiplex genotyping assay offers a simple and high-throughput tool for characterizing the vc and mating types of *C. parasitica* at the population level. In this study, the panels in the fluorescent multiplex genotyping method were modified, and alternatively, we show that the same primer set is appropriate for conventional PCR of both *vic* locus and MAT gene using non-modified primer and agarose gel electrophoresis that can be found in any molecular laboratory. However, these modifications do not include any primer or PCR conditions changes. Validation was performed by successfully genotyping 183 isolates of *C. parasitica* collected from thirteen chestnut-growing provinces of Türkiye. With this method, only the presence of two vc types, EU-1 and EU-12, was determined from all the isolates in the region, while with the classical method some of the isolates could not be matched to any of the European tester isolates or some were placed to different vc types. With this application, mating types of the pathogen were also determined.

Key words: *Castanea sativa*, chestnut blight, multiplex PCR assays

O-133

Characterization of barcode sequences from complete nuclear rRNA sequences of the hazelnut (*Corylus avellana*) powdery mildew fungus *Erysiphe corylacearum*

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Powdery mildew is one of the important fungal diseases of hazelnut plant (*Corylus avellana*) caused by *Erysiphe corylacearum* (Ascomycota, Erysiphales). This obligate biotrophic fungus has significantly reduced the yield of the hazelnut crop in Türkiye. Accurate identification of powdery mildew fungal species, which have the potential to spread to new areas and/or new hosts, is important for rapid detection and early control. Identification of the powdery mildew fungus based on microscopic examination of the teleomorph (sexual stage) and the morphology of the chasmothecium and its appendages is not reliable on its own because the morphology of structure is not as conserved as originally assumed. Ribosomal RNA (rRNA) genes are extensively used as DNA barcodes and consist of a standardized short sequence of DNA (400–800 bp) to identify species. These sequences differ in cellular origin (nuclear, mitochondria, plastid), quality, length, and organismal origin and may represent any region on ribosomal cistron. Only the ITS region of *E. corylacearum* including the ITS1 and ITS2 regions, separated by the 5.8S gene, and is found between the 18S (SSU) and 28S (LSU) genes in the nuclear rDNA repeat unit has been sequenced and deposited in NCBI. This study characterized the *E. corylacearum* complete 18S small subunit (SSU), and 28S large subunit (LSU) rRNA genes generated by next-generation sequencing to provide a reference material for the identification of fungal taxa.

Key words: Powdery mildew, *Erysiphe corylacearum*, hazelnut, barcode gene, rRNA, 18S rRNA, 28S rRNA

O-134

Characterization of *Trichoderma* spp. obtained from Sakarya plateaus, Türkiye and efficiency of these isolates as biocontrol agents against *Neopestalotiopsis rosae* in strawberry

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Trichoderma species are widely used in biological control of plant pathogenic fungi and many different species are produced commercially. Among these species, *Trichoderma harzianum* is the most widely known and used. In this study, *Trichoderma* spp. were isolated from soil samples obtained from Soğucak, Sultanpınarı, Karagöl and İnönu plateaus located in Sakarya province, Türkiye. Twenty-three *Trichoderma* spp. isolates were obtained from 35 soil samples by soil dilution method. Identity of these isolates were confirmed by DNA sequencing of the internal transcribed spacer (ITS). Most of these isolates were classified as *T. harzianum*, the other species as *Trichoderma hamatum* and *Trichoderma koningii.* Efficiency of *T. harzianum* isolates, a well-known biocontrol agent was investigated in vitro by dual culture test against *Neopestalotiopsis rosae*, the causal agent of root rot and leaf spot in strawberry. Based on the results of dual culture test, *T. harzianum* S8-7 isolate had the highest effect with inhibition rate of 55.02%, while *T. harzianum* S12-1 isolate showed the lowest effect with inhibition rate of 37.22%. These results showed that *T. harzianum* isolates had significant potential in biological control of *Neopestalotiopsis rosae*.

Key words: *Trichoderma harzianum, Neopestalotiopsis rosae,* biological control

O-135

Effect of light on the life cycle, development and pathogenicity of *Hyaloperonospora arabidopsidis*

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Light and temperature are two important factors on circadian clock regulation, which imparts a survival advantage by enabling an organism to anticipate daily environmental changes. In plants, light affects immune responses in a way that plants can react more or less effectively to infections by pathogens. However, effect of light on pathogenicity as independent from the plant immune system has not been clear, especially in obligate biotrophic plant-pathogen interactions. We have been working on *Arabidopsis-Hyaloperonospora* interactions and have been searching answers for some of the questions raised as to whether; a) there is a circadian regulation on downy mildew, b) the circadian clocks of plant and the pathogen are synchronised with each other, c) light has an effect on pathogenicity, d) light influences pathogen development and e) there are some effector genes regulated by light. We used pathology, molecular biology and transcriptomics to answer these questions. Our results indicate that the downy mildew pathogen has clock genes, there is a synchrony between plant's and pathogen's clocks, and the pathogen development is affected by light. Latest data will be presented.

Key words: Oomycetes, circadian clock, downy mildew

O-136 (KEYNOTE SPEECH)

Challenges and potential solutions for overcoming insect resistance to *Bacillus thuringiensis* based biopesticides

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Products based on the entomopathogenic bacterium *Bacillus thuringiensis* (Bt) have been extremely successful in controlling a wide range of crop pests. These products primarily consist of either sprayable formulations of the bacterium itself, or genetically modified crops expressing pesticidal proteins encoded by Bt. Extensive use of these products has naturally led to insects developing resistance to them and requiring a wide range of strategies to be devised in order to slow down resistance development, or to overcome it. In this presentation I will discuss the complex basis of Bt resistance in one particular insect pest – the diamondback moth – and the implications that this has for resistance management. I will then describe an experimental evolution procedure that we have developed in an attempt to derive Bt strains capable of controlling resistant insects, in addition I will show how this method can be used in conjunction with protein engineering protocols to help identify mutant pesticidal proteins with enhanced activity.

Key words: *Plutella xylostella,* Bt-crops*, directed evolution.*

O-137 (KEYNOTE SPEECH)

Bt resistance in *Trichoplusia ni*: Mechanisms of resistance to multiple bt toxins in a generalist insect

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The soil bacterium *Bacillus thuringiensis* (Bt) has been the most successfully used microbial insecticide in agriculture, and Bt genes coding for insecticidal toxins are the primary transgenes engineered into current insect-resistant transgenic crops. However, evolution of Bt resistance in insects threatens the sustainable application of Bt-biotechnology in agriculture. Identification and understanding of Bt resistance mechanisms in insects are fundamentally critical for continuing success of Bt-biotechnology and management of insect resistance to Bt toxins. The cabbage looper, *Trichoplusia ni*, is a generalist herbivore with a broad range of host plants and has developed resistance to Bt in greenhouse populations. To understand the molecular genetics of insect resistance to Bt toxins, we use *T. ni* as a representative of the largest Lepidoptera family Noctuidae and a major group of agricultural pests, to develop a biological research system to study the mechanisms and gene mutations conferring Bt resistance. From the greenhouse-derived Bt resistant *T. ni* populations, we have isolated and established *T. ni* strains resistant to the major Bt Cry toxins used in Bt-crops, Cry1Ac, Cry2Ab and Cry1F. The resistance traits to the Cry toxins were characterized. Resistance-conferring gene mutations were mapped and identified by genetic linkage analysis, whole genome sequencing, bulked segregant analysis and other molecular techniques. The Bt resistance-conferring mutations identified were functionally examined and confirmed using mutant *T. ni* strains with specific mutations generated by CRISPR/Cas9 mutagenesis. Major Bt resistance-conferring mutations to Cry1Ac and Cry2Ab in *T. ni* have been identified and additional resistance conferring mutations are to be understood.

Key words: *Bacillus thuringiensis*, Cry toxins, Bt resistance, resistance mechanisms, *Trichoplusia ni*

O-138

Isolation and molecular identification of local entomopathogenic bacteria from *Pieris brassicae*

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Larvae of the large cabbage butterfly, *Pieris brassicae*, are important agricultural pest that feeds on many products such as white and black cabbage, radish, broccoli, turnip, arugula, and cauliflower. To control this species, manufacturers use intensive chemical pesticides. Considering the harm of chemical products to humans and the ecosystem, biological control agents to be isolated and developed from this creature were needed. In this study, *P. brassicae* larvae living in cabbage-planted areas in different localities of Hatay, Türkiye were collected and brought to the laboratory in January 2023. In most of the larvae and even the newly hatched larvae from the collected egg packs, growth retardation, and death by liquefying were observed. When the homogenate obtained after the larvae were crushed in a tissue lyser, motile bacteria were observed when examined under the light microscope, and as a result of gram staining, it was determined that the bacteria were gram-negative. For the molecular identification of bacterial isolates, following DNA isolation, 16SrRNA partial region was amplified with universal primers and sequence analysis was performed. As a result of the initial analysis performed after trimming the bad-read head and end parts of the obtained sequences, it was determined that isolates showed 99% and 98% similarity to *Serratia marcescens* and *Pseudomonas fluorescens* entomopathogenic bacteria, respectively. In particular, the isolation of these bacteria, which have the chitinase toxin gene, from their natural host is promising for the biological control of *P. brassciae*.

Key words: *Pieris brassciae*, cabbage, biocontrol, *entomopathogenic bacteria*

O-139

Isolation and diagnosis of potentially entomopathogenic bacteria from larvae of Asian Walnut Moth *Erschoviella musculana* erschoff (Lepidoptera: Nolidae)

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In the studies carried out in Bartın province, non-viable *Erschoviella musculana* (Lepidoptera: Nolidae) larvae were collected from walnut fruits. As a result of isolation from larvae, *Bacillus*-like cream-white irregular shaped bacterial colonies with different shapes and colors were determined. Irregular shaped, creamy-white colored *Bacillus*-like colonies obtained by isolation were purified on Nutrient Agar (NA). These isolates gave Gram positive, oxidase negative reactions and did not grow at 37 °C. DNA was isolated from pure isolates grown on NA and 16S rRNA gene region was amplified by conventional PCR using 27F forward and 1492R reverse universal primers. PCR products gave bands at ~1500 bp on agarose gel. According to the results of the sequence studies, as a result of the BLASTn comparison with the species in the NCBI database, Larva1 isolate *Bacillus* sp. (accession no: OP493233.1) showed 99.5% similarity. Larva2 isolate *Bacillus subtilis* subsp. *subtilis* (accession no: MT605412.1) 100% and Larva3 isolate *Bacillus subtilis* subsp. *subtilis* (accession no: MT605412.1) showed 99.78% similarity. It was confirmed that the isolates 1, 2, 3 obtained from the larvae were bacteria belonging to the genus *Bacillus*. In this study, the isolate *Bacillus subtilis* subsp. *subtilis* was determined for the first time in the world and in Türkiye. *Bacillus subtilis* is a species with a broad spectrum of biological activity that can control insects as well as plant pathogens. Studies on the biology of the Asian walnut moth and studies investigating the biological activities of different *Bacillus* species isolated from the microbiome of this pest should be continued.

Key words: *Erschoviella musculana*, *Bacillus* sp., biologic control, entomopathogen, walnut

Acknowledgment: This study was carried out within the scope of TÜBITAK (1001) 121O485 project "The Biology and Application of Local Biopreparation Containing *Bacillus thuringiensis* in Control of Asian Walnut Moth *Erschoviella musculana* Erschoff (Lepidoptera: Nolidae)"

O-140-STU

Sex specificity in defense mechanisms of *Lymantria dispar* against *Bacillus thuringiensis*

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The defense mechanisms against pathogens of insects have been widely studied. Although the effect of sex on these mechanisms has been extensively discussed, differences in these mechanisms between the sexes of larvae insects remain largely unstudied. Studying larval sex differences in mechanisms underlying insect defense against pathogens can be valuable for the development and improvement of pest management. Here larval sex differences in defense mechanisms against pathogens have been studied on the spongy moth *Lymantria dispar* L. (Lepidoptera: Erebidae), one of the most widespread forest pests in the Holarctic region. The *Bacillus thuringiensis* - entomopathogenic bacterium widely used as the basis for bioinsecticides, was chosen as a pathogen inducing the emergence of defense mechanisms in larvae insects. We study larval sex differences in the following insect larvae defense mechanisms: parameters of innate immunity - the antibacterial activity in the midgut tissue and cell-free hemolymph and factor involved in insect defense mechanisms - gut microbiome. We also evaluated the sex-specific mortality of *L. dispar* induced by *B. thuringiensis* infection. We find that antibacterial activity in the midgut is activated by infection, but only in females while the mortality level was higher in females. It is known that female numbers significantly contribute to the restoration of the population after insecticide application. Thus found sex-specific differences in larvae immunity would contribute to the creation of more effective (targeted) methods of controlling insect pests aimed at the defense mechanisms of females.

Key words: *Lymantria dispar,* antibacterial activity, gut microbiome, pest control, sex-specific immunity.

O-141-STU

Formulation and characterization of a local *Bacillus thuringiensis* ssp. *israelensis*: A Promising alternative to chemical control of *Culex pipiens* (Diptera: Culicidae)

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Mosquitoes are vectors of pathogens that cause infections such as Malaria, West Nile Fever, Deng Fever, and Zikavirues. The mosquito, *Culex pipiens* (Diptera: Culicidae) is one of the best-known species among these disease vectors. *Culex pipiens* have been controlled with diverse control methods such as biological and chemical control strategies. In particular, organophosphate-based chemicals are used in the chemical control of *C. pipiens*; however, they also lead to increased resistance and adverse impacts on non-target species. In this manner, microbial-based bioinsecticides are promising alternatives to chemical inseciticides. *Bacillus thuringiensis* subsp. *israelensis* (Bti) is widely used for mosquito control. In this study, formulation of two native *Bti* isolates, EN15 and EN24, have been tested on *C. pipiens* third instar larvae compared to the non-formulated counterpart. Formulation of the toxin of both isolates led to increased activity compared to non-formulated toxin. EN15 led to 90% mortality, while EN24 showed lower insecticidal effect. Furthermore, activity of the EN15 product lasts longer than EN24. This research is funded by Oyak Biyoteknoloji.

Key words: *Bacillus thuringiensis* ssp. *israelensis,* mosquito, bioinsecticide

O-142 (KEYNOTE SPEECH)

Development of genomics-based approaches for control of Fall Armyworm

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The fall armyworm (FAW), *Spodoptera frugiperda* is a polyphagous pest that causes economic losses to many crops in Americas and Caribbean countries. It is becoming a major concern around the world. Therefore, we need to develop resources to study the molecular basis of biological processes that make this insect successful in causing crop losses despite our best efforts to control this devastating pest. Both genome and transcriptome sequences for FAW as well as for a cell line derived from this insect have been completed. However, functional genomics studies and research to understand various developmental and physiological processes at the molecular level are not performed in this insect. One of the main reasons

for the lack of information on functional genomics in this insect is due to its recalcitrance to RNA interference (RNAi). RNAi is inefficient in this insect because dsRNases rapidly degrade dsRNA, some dsRNA entering the cells is entrapped in the endosomes, and some critical genes required for efficient RNAi are not present in this insect. We employed nanotechnology to improve RNAi in this insect. The FAW eggs are easy to inject and CRISPR/Cas9–based genome editing technique works well. Multiple transgenic CRISPR/Cas9-based genome editing methods were developed for FAW. Transgenic insects and tissue-specific promoters were used to identify P450s responsible for insecticide resistance in this insect. Recent advances in functional genomics studies in FAW aimed at improving the management of this global pest will be discussed.

Key words: RNAi, Genome editing, transgenic insects, insecticide resistance, fall armyworm

O-143 (KEYNOTE SPEECH)

Major developmental transitions during insect ontogeny are associated with dramatic changes in the network architecture of miRNA-mRNA interactions

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We analyzed the miRNA-mRNA interactions at 11 key stages throughout the ontogeny of the cockroach *Blattella germanica*. We built bipartite networks in each of these stages, where the nodes are the expression of miRNAs and mRNAs, and the edges come from miRNA target predictions. To identify network architecture changes, we determined three properties: connectance, modularity, and nestedness. The results indicate that there are dramatic changes associated to the maternal to zygotic transition, in early embryogenesis, which is characterized by low graph order and low degree of miRNAs and mRNAs, high connectance and high clustering degree, and high nestedness. Also characteristic is the architecture of the miRNA-mRNA interaction in the transition from embryo to nymphs, at the end of embryogenesis, which is characterized by high graph order and degree of miRNAs and mRNAs, and very low nestedness. In contrast, metamorphosis, that is, the transition from nymph to adult, is not associated to special changes in the miRNA-mRNAs interactions. This is counterintuitive, but not fully unexpected in a hemimetabolan species like *B. germanica*, where the nymphs already have the adult body plan. This ancestral metamorphosis type contrasts with the more modified holometabolan type, in which the larvae are different from the adult, and require the pupal stage that bridges the gap between the last larva and the adult. We predict that the architecture of the miRNAs-mRNAs networks will undergo important changes associated to metamorphosis in holometabolans, which involves a deconstruction and subsequent construction of an entirely new morphology.

Key words: microRNA-mRNA interaction, bipartite networks, *Blattella germanica* ontogeny, connectance, nestedness, modularity

O-144 (KEYNOTE SPEECH)

The use of long non-coding RNAs in insect control. Lessons from the tiger mosquito

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Long non-coding RNAs (lncRNAs) have risen into prominence as important regulators of cellular and metabolic processes. The way they regulate gene expression varies, ranging from guiding transcription factors, remodeling chromatin, functioning as sponges for miRNAs, or regulating post-transcriptional mRNA modifications. Due to the absence of coding capacity, lncRNAs demonstrate a notable lack of nucleotide sequence conservation even among closely related species. This lack of sequence conservation, however, offers an extraordinary possibility for the development of species-specific approaches for insect control. Along this line, in an effort to target the fertility of the Asian tiger mosquito, *Aedes albopictus*, we set out to investigate the role of ovary-specific lncRNAs. Through the analysis of transcriptomic data, we identified several lncRNAs that were differentially expressed upon blood feeding; we called these genes Norma (NOn-coding RNA in Mosquito ovAries). Silencing Normas resulted in significant impact on mosquito fecundity and fertility. Particularly, silencing Norma3 resulted in 43% oviposition reduction, smaller ovaries and 53% hatching reduction of laid eggs. Moreover, a significant downregulation of two neighboring mucins was observed in smaller anti-Norma3 ovaries, indicating a potential interplay between Norma3 and the mucins. Our work constitutes the first experimental proof-of-evidence connecting lncRNAs with mosquito reproduction and opens a novel path for pest management. We are employing a similar strategy for the discovery of fertility-related lncRNAs in agriculturally important Tephritids. Since mosquito ovaries develop and Normas are induced upon mosquito blood feeding, we adapted our protocol to non-blood feeding insects. Differentially expressed lncRNAs are under investigation.

Key words: Long non-coding RNAs, fertility, fecundity, species-specific control

O-145 (KEYNOTE SPEECH)

Breaking down the barriers: Strategies to enhance RNAi efficiency in insects

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RNA interference (RNAi) is a natural sequence-specific post-transcriptional gene silencing process mediated by double-stranded RNA (dsRNA) in most eukaryotic organisms. RNAi has been widely considered as a novel strategy for managing insect pests. However, RNAi efficiency varies considerably among different insect species and the instability of dsRNA in the gut and hemolymph is one of the most important factors causing low RNAi efficiency in insects. We identified four dsRNA-degrading nuclease (*dsRNase*) genes in different insect species. RNAi-mediated silencing of *dsRNase* genes can significantly enhance RNAi efficiency against a target gene, indicating that dsRNA-degrading nucleases contribute to low RNAi efficiency in insects. In addition, low cellular uptake of dsRNA and inefficiency of endosomal release after dsRNA is internalized in insect cells are other two important factors causing low RNAi efficiency in insects. Our research shows that clathrin-dependent endocytosis is an important mechanism for dsRNA uptake in insects. To protect dsRNA from dsRNase-mediated degradation and to facilitate a cellular uptake of dsRNA, we developed nanoparticle-based dsRNA delivery approaches. Our study shows that chitosan-based dsRNA nanoparticles can not only dramatically enhance dsRNA stability but also significantly enhance RNAi efficiency in mosquito and western corn rootworm larvae by feeding. Our findings point to useful strategies to enhance RNAi efficiency in insects. These strategies include applications of dsRNase inhibitors, delivery of dsRNA using various nanocarriers, and use of endosomal escape-enhancing agents. Our findings are expected to promote the application of RNAi-based approaches for insect pest management.

Key words: Cellular uptake, dsRNase, nanoparticle, pest management, RNAi efficiency, RNA interference

O-146

Development of dsRNA production technology using *Corynebacterium glutamicum* for RNAi-based pesticides

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RNA interference (RNAi) based pesticides are expected to be utilized as new environmentally friendly agricultural materials that provide pest control effects through RNAi using double-stranded RNA (dsRNA) as the main active ingredient. Our group has originally developed dsRNA production technology using *Corynebacterium glutamicum*. *C. glutamicum* is a non-pathogenic, non-endotoxic, GRAS-certified Gram-positive bacterium that is used in the industrial production of amino acids. To construct dsRNA expression system using *C. glutamicum*, the following 3 points were implemented. (1) Deletion of *rnc* gene, dsRNA-specific RNA-degrading enzyme, (2) Development of high copy number plasmid vectors that greatly exceed the copy number of conventional plasmids in *C. glutamicum*, and (3) Development of a highly active RNA transcription system. We selected a ladybird beetle, *Henosepilachna vigintioctopunctata*, as a model target pest and constructed an efficient production system for *diap1**-dsRNA (360 bp), which suppresses expression of the essential gene *diap1* (encoding death-associated inhibitor of apoptosis protein 1) in *H. vigintioctopunctata*[1]. Batch cultivation using a jar fermentor resulted in *diap1**-dsRNA productivity of more than 1.0 g per liter of culture. When the sterilized microbes containing *diap1**-dsRNA were fed to larvae of *H. vigintioctopunctata*, *diap1* expression in the pest was suppressed, and the leaf-feeding activity of the larvae declined. Based on the above, we have been able to construct a highly productive dsRNA production system using *C. glutamicum*, and we are currently working on further improvement of the system to respond to regulatory issues.

Key words: dsRNA, *Corynebacterium glutamicum*, RNAi-based pesticides, *Henosepilachna vigintioctopunctata, diap*

O-147 (KEYNOTE SPEECH)

Natural compounds from beneficial fungi to challenge plant pathogens

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Climate change and global trade are enlarging the area available for pathogens to exploit crops. Recent outbreaks in plant diseases depict a scenario of growing resistance to agrochemicals and enhanced capabilities of pathogens to cause destructive phenomena (e.g., the *Xylella* case). For the sake of sustainability, we are reducing (or at least aiming to) the agrochemicals load in intensive crop farming. Nevertheless, we must find alternative – effective – solutions to limit plant diseases. This lecture pointed on a 20-years' experience in finding these solutions into mushrooms, notably among the wood-decaying ones. This group of mushrooms can also be edible or at least non-toxic to humans and animals such as *Trametes versicolor.* Starting from this latter, we demonstrated that its culture filtrate contains very active metabolites: namely exopolysaccharides and small peptides. Then we extend this search to other mushrooms such as *Schyzophyllum commune* finding similar clues and suggesting that this group of wood-decaying organisms probably produce batteries of antioxidant and antimicrobial compounds to face a particularly hostile and recalcitrant trophic niche. We employ these bioactive molecules at different degree of purification and produce them from several types of waste materials to limit plant pathogens, specifically those contaminating staple crops with mycotoxins.

Key words: Wood-decaying mushrooms, plant pathogens, *bioactive compounds*, staple crops, mycotoxins

O-148 (KEYNOTE SPEECH)

Translational research on pulse downy mildews: Deploying resistance genes, pathogenomics and microbial biocontrol

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Pulses, in particular peas and broad beans, are important crops both in the UK and worldwide and they are grown as extensive monocultures. Even with long rotations, the crops are vulnerable to major epidemics of economically important pests and diseases, of which downy mildews (caused by the oomycete biotrophic pathogens *Peronospora viciae* f. sp. *pisi* (Pvp) and *P. viciae* f. sp. *fabae* (Pvf) in peas and beans, respectively) are the most serious. In a collaborative project on Pvp and Pvf, we have been carrying out research that leads to translational science. Here, we aim to identify new R-genes for breeding purposes, develop tools for the accurate detection and diagnostics of Pvp/Pvf isolates using genomics, and use biological control agents to suppress downy mildew pathogens. New sources of resistance in pea and faba bean have been identified and the use of genome-wide association studies is underpinning the development of molecular markers linked to the loci involved. Draft reference genomes of both Pvp and Pvf have been assembled. More than 40 isolates of Pvp have been collected and single spored. More than 20 of them have been re-sequenced and SNP analysis are being carried out. Various strains of *Bacillus* and Pseudomonas have been assessed for activity against the pathogen using in vitro and in planta antagonism assays and very promising results have been obtained. The latest data will be presented.

Key words: Downy mildew, R-gene, pathogenomics, MBCA, diagnostics

O-149 (KEYNOTE SPEECH)

Voyage of fungal pathogen small RNAs into plants

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The fungal pathogens deliver small RNAs (Bc-sRNAs) into plant cells to hijack host Argonaute protein 1 (AGO1) to silence host immunity genes. However, the mechanism by which these fungal sRNAs are secreted and enter host cells remains unclear. Extracellular vesicles are membrane-bound vesicles released from cells that can transport cargos, including proteins, nucleic acids, lipids, glycans, and pigments, between cells as a form of intercellular communication. These EVs can provide protection to their cargos from degradation by extracellular enzymes, which is especially important for RNA trafficking. Here, we demonstrate that *B. cinerea* utilizes extracellular vesicles to secrete Bc-sRNAs, which are then enter plant cells through clathrin-mediated endocytosis. The *B. cinerea* tetraspanin protein, Punchless 1, serves as a biomarker for EVs and plays an essential role in fungal pathogenicity. We observed numerous Arabidopsis clathrin-coated vesicles around *B. cinerea* infection sites We used biochemistry, genetics, and cell biology approaches to demonstrate that fungi secrete sRNAs via extracellular vesicles, which then enter host plant cells mainly through clathrin-mediated endocytosis.

Key words: Extracellular vesicles, small RNAs, cross-kingdom RNAi, plant fungal interaction, clathrin-mediated endocytosis

O-150

The pathogenic and phylogenetic relationships of endophytic *Lecanicillium* spp. isolates from turfgrass seeds

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Endophytes are micro-organisms that colonize their host plants cells inter or intra cellularly without producing any specialized disease symptoms there. They do not only contribute in the host plant growth such as in taking water and minerals from soil, but also help to protect their hosts against arthropods and plant pathogens. Fungal endophytes are the most common microorganisms in nature and *Lecanicillium* is one of the most recent distinct genera in the fungal endophytes. In this study, six isolates of *Lecanicillium* were isolated endophyt-

ically from healthy seeds of *Festuca arundinaceae* and *Lolium perenne* collected from different pasturelands of Türkiye and they were identified on their morphological characters on agar medium and partial sequencing of Internal Transcribed Spacers (ITS) in Ribosomal DNA (rDNA), molecularly. To determine the effect of *Lecanicillium* isolates on the growth of plants, lyophilized and grounded fungal mycelium were applied to soil, in pots having seeds of wheat and barley that are closer to turfgrass. Finally, biological control potential of these endophytes against the causal agents of root and crown rot diseases of cereals such as *Fusarium culmorum*, *Bipolaris sorokiniana* and *Rhizoctonia solani* were checked by a dual test *in vitro*. As a results, one *L. antillanum* and two *L. aphonacladii* species were identified on morphological and molecular data basis, while the remains were not showed any similarity with other *Lecanicillium* species on GeneBank. According to *in vitro* and *in planta* results, it is possible that the positive effects of the endophytic *Lecanicillium* spp. can be seen on the plant growth and cause inhibition of soilborne pathogens.

Key words: *Lecanicillium aphonacladii*, turfgrass, *Festuca arundinaceae*, ITS-rDNA, endophyte

O-151

Determination of Fusarium wilt (*Fusarium oxysporum* Schlecht. F. Sp. *melongenae*): Resistance using molecular marker in double haploid eggplant populations

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Fusarium wilt (*Fusarium oxysporum* Schlecht.f. sp. melongenae, FOM) is a major soil-borne pathogen, causing vascular wilt disease in eggplant. A molecular marker tightly linked to single dominant gene (FOM) was developed for use in marker assisted selection (MAS). The aim of the study is to develop eggplant lines resistant against *Fusarium* wilt using a marker assisted backcross breeding and double haploid technique approach. Eggplant population were developed using crossing with donor parents which were carrying the *Fusarium* wilt resistance and were anther cultured. Total 117 eggplant genotypes were obtained via anther culture and 37 of them were spontaneus double haploid. The SCAR426 marker was used to determine the Fom gene on eggplant population. The results showed that 64 of DH / H plants carried the resistance allel (R). The eggplant lines resistant against *fusarium* wilt developed via MAS and anther culture can be used in eggplang breeding programs.

Key words: Eggplant, *Fusarium* wilt, molecular markers

O-152 (KEYNOTE SPEECH)

Phytoplasmas and plant diseases: a transkingdom relationship

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Phytoplasmas or '*Candidatus* Phytoplasma' are bacteria without cell wall living only in the insect hemolymph and in the plant sieve tubes. After more than 20 years from their discovery their role as plant pathogens is still not resolved for lack of Koch postulates fulfillment. Worldwide there are several relevant epidemics in which phytoplasmas play a role as key factors in reducing the production and the revenues of crops. This situation is worsen by their dissemination by propagation and micropropagation materials, insect vectors, and seeds. Economically relevant phytoplasma diseases are reported in both woody and annual crops since these bacteria are present in several diverse environments and in particular in tropical and subtropical areas where the insect vectors play their dissemination to alternate plant and insect host species. There are a number of phytoplasma metabolic features and effectors that were discovered mining several available full and draft genomes that are clarifying the interactions of these bacteria with both plants and insect vectors confirming their two kingdoms adaptation ability. Recent efforts allowed to obtain colonies containing mainly phytoplasmas following their isolation from field-infected or experimentally-infected plants. Moreover, little steps are in progress to define direct phytoplasma biological activity while several pathogenicity related factors were found and confirmed as potentially active in transgenic plants. Molecular tools helped in resolving phytoplasma differentiation and allowed to study their epidemiology for appropriate and environmentally friendly management of associated diseases, moreover their isolation in artificial media should help in clarifying their phytopathological role in severe epidemics worldwide such as coconut lethal yellowing and grapevine yellows.

Key words: '*Candidatus* Phytoplasma', plant disease, insect vector, epidemiology, management

O-153 (KEYNOTE SPEECH)

Insights into pathogen-host interactions from phytoplasma genomes

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Some bacteria have lost properties in the course of reductive evolution. There are a large number of such species among the wall-less bacteria in the class Mollicutes. Typical examples of such extreme evolutionary paths are provided by the vector-transmitting bacteria of the provisional taxon '*Candidatus* Phytoplasma'. These phytopathogenic bacteria are colonising as intracellular parasites the phloem sap of plants and are associated with a variety of important diseases in crops. Since *in vitro* cultivation of these bacteria is not available, genome

research plays an important role. It offers deep insights into adaptive processes, impressively reflected in small genome size, rapid splitting of phylogenetic lineages, codon usage, genome instability, and group-specific equipment in terms of metabolism and virulence factor coding. In particular, research on effector proteins has made great progress in recent decades. Thus, with the help of the recently completely determined genome of the pathogen of *rubus stunt* disease '*Candidatus* Phytoplasma rubi', the proliferation symptom could be linked to a deduced effector protein. The importance of collecting genome data on phytoplasmas will continue to increase rapidly in the coming years. In addition to basic research, it is particularly important for plant protection, which requires these data for the development of new diagnostic assays. There is an obvious need, as climate change is currently enabling phytoplasma vectors to penetrate northern regions. A prominent example is the rapidly increasing incidence of phytoplasmosis in sugar beet and potato cultivation in Germany, resulting in high economic losses.

Key words: Mollicutes, phytopathogenic, reductive evolution, rubus stunt

O-154

Multilocus sequence typing of '*Candidatus* Phytoplasma solani' infecting cucurbits from Türkiye

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The Cucurbitaceae family, which includes many different genera, is cultivated all over the world and plays a significant role in human nutrition. Pathogen-induced cucurbit diseases result in economic losses. Among these pathogens encompass the stolbur group '*Candidatus* Phytoplasma solani,' which has an adverse effect on perennial or annual plants, including cucurbits, and is very prevalent in Europe and the Mediterranean region. In this study, multilocus sequence typing of seven '*Ca.* P. solani' determined in cucurbit growing areas from the Marmara region were detected by molecular assays of *tuf, vmp1*, and *stamp* genes. Molecular characterization studies were performed by nested PCR, sequencing, and phylogenetic analyses. It was determined that all cucurbit strains infected with stolbur were in the *tuf-b1* genotype. For the *stamp* gene, the strains were divided into b-II and b-III *stamp* clusters and showed high nucleotide similarity with five different genotypes. The *vmp1* gene genotypes for the cucurbit strains were V4 and V14, respectively. All these results showed a close relationship with the genotypes of non-ribosomal genes reported from eastern European countries located in the western part of Türkiye.

Key words: *Phytoplasma*, cucurbit, stolbur, *tuf* gene, *vmp1* gene, *stamp* gene

O-155-STU

Comparative genome analysis of phytoplasma in plants with different fruit types

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'Candidatus (Ca.) Phytoplasma' is a plant pathogen belonging to the class Mollicutes and are AT-repeat-rich, transposable, reduced-genome, wall-less bacteria. They are transmitted from plant to plant by insect vectors that feed on phloem. Phytoplasmas cannot be grown in cellfree media; that is, they were not cultured. Therefore, their identification and taxonomy is based on gene sequences and genome analysis. Their AT-repeat-rich genome and potential mobile units (PMUs) in their genomes make genome analysis difficult. Besides, one of the major problems with the taxonomy of phytoplasmas is that the same phytoplasmas show different symptoms in different plants and can be transmitted by another vectors. In this study, the genomes of phytoplasmas with the same 16S rRNA region, isolated from different plants with different symptoms, were analyzed. For this purpose, genetic differences of phytoplasmas showing different symptoms in plants with different fruit types were tried to be revealed by next-generation sequencing. These de novo assembled complete or draft genomes are important for calculation of average nucleotide identity (ANI). A phytoplasma specific workflow was developed and implemented for de novo assembly of reads sequenced with Illumina NovaSeq 6000 (2 x 150). After the gene prediction and annotation were completed, SNP variant analyzes were made among the 14 samples studied.

Key words: Phytoplasma, next-generation sequencing, genome analysis, plant pathogen, de novo assembly, SNP

O-156-STU

Molecular detection of phytoplasma associated disease in Türkiye

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Phytoplasmas, formerly known as mycoplasma-like organisms are uncultivable, phloem-restricted bacteria and spreaded by insects which is mainly leafhoppers, planthoppers, and psyllids. They have been associated to diseases in thousand of plant species, including economically important plants. The threat of phytoplasma associated diseases are increasing due to climate change in Türkiye. Phytoplasmas are one of the most poorly understood plant pathogens in spite of their agricultural importance and/or idiosyncratic features, due to not being developed of in vitro culture, gene delivery and mutagenesis systems. The aim of the study is to detect phytoplasmas by using real time PCR with Eva Green based approach and probe based approach and compare their sensitivity. Symptomatic plant samples were collected from field in 2021 summer and DNA were extracted by modified CTAB pro-

tocol. Real time PCR assay performed with 16S universal primers and 18S plant internal control primers. According to results Eva Green based approach gives %100 non specific amplification including healhty plant groups such as arabidopsis, spinach and even halobacteria. Probe based approach is much more sensitive againist Eva Green based approach. We used different plants such as tomato, potato, daffodil and grapevine and non specific amplification does not observed. BLAST analysis shows universal phytoplasma 16S rDNA primers are binding to plant chloroplast genome. Evolutionarily, ribosomal 16S DNA is highly conserved regions. Plant and bacterial 16S rDNA shows high sequence homology, most cases universal primers lead to false posivites with using Eva Green based approach and needs to develop rapid, accurate and universal detection kit.

Key words: Phytoplasma, detection, real time PCR, sensitivity

O-157

Exotic plant disease outbreaks in the Arabian Peninsula: Challenges and opportunities

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Exotic plant pathogens, especially invasive pathogens, represent a major challenge to agriculture in different parts of the world. The Arabian Peninsula is an arid part of the world, depending on the cultivation of date palms and several fruit and cereal crops native to this area. The expansion in the agricultural area, especilly with vegetable, fruit and ornamental plans, has been a result of the introduction of several new types and cultivars of plants. This resulted in the introduction of new pathogens and the appearance of new devastating diseases that were not present in the region in the past. Phytoplasma diseases, especially witches' broom disease of lime, destroyed over one million lime trees in the Arabian Peninsula over the last three decades. Consequently, countries such as Oman became an importer of limes after being an important exporter of this commodity in the past. Other major disease including Ceratocystis mango wilt, Panama disease (Tropical Race 4) of bananas, phytophthora blight of tomato, citrus greening and citrus tristeza that were introduced in countries in the Arabian Peninsula. They resulted in a decline in the cultivation and production of these crops and severe economic losses to growers. This paper will focus on quarantine in these countries, sources and threats of exotic pathogens, and potential solutions.

Key words: Invasive pathogens, transmission, viruses, fungi, bacteria, phytoplasma, economic losses

O-158 (KEYNOTE SPEECH)

Plant volatiles as mediators of the insect interaction with baculovirus

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In response to insect herbivory, plants have various defense mechanisms at their disposal, including the release of herbivore-induced plant volatiles (HIPVs). These HIPVs serve as signals to alert undamaged tissues and to attract natural enemies of the herbivores. Although some HIPVs can directly harm herbivore survival, they may also play a role in regulating the interactions of herbivores with the environmental microbes, including entompathogens. In this sense, we propose that HIPVs can additionally mediate the three-way interactions between plant-insects-entomopathogens. Our findings indicate that exposure of the caterpillars of the noctuid *Spodoptera exigua* to indole and linalool, but not exposure to (Z)-3-hexenyl acetate, increased the susceptibility to *Spodoptera exigua* multiple nucleopolyhedrovirus (SeMNPV). In another hand, we have observed that during SeMNPV infection, the expression levels of some odorant receptors (ORs) were increased, which was not observed when *S. exigua* was infected with a more generalist baculovirus, the Autographa californica multinucleopolyhedrovirus (AcMNPV). ORs are transmembrane receptors that are specifically expressed in the olfactory sensory neurons housed in the antennae and maxillae of caterpillars. They play a crucial role in olfactory perception and signal transduction by recognizing the single volatile molecules present in a blend. We observed that these transcriptional changes occurred starting at 72 hours post-infection and were consistent across all larval stages. To link these changes to a likely alteration of olfactory-driven behaviors, we functionally characterized two ORs whose transcript levels were altered by SeMNPV infection: OR35 and OR23. While we did not identify any ligands for OR23 in our panel, we found that OR35 was a broad-tuned receptor capable of binding volatiles from multiple chemical classes. We selected linalool, one of the best ligands for OR35, to run further behavioral assays, which showed how SeMNPV infection specifically altered linalool-driven behavior compared to uninfected controls and larvae infected with AcMNPV.These results suggest that plant volatiles and the alteration of their perception by herbivores can be relevant in the evolutionary arm race that regulates multitrophic interactions between plants, their herbivores and their pathogens.

Key words: Baculovirus, Odorant receptors, HIPVs, insect behaviour

O-159

Isolation and Identification of a new Cypovirus from *Dasychira pudibunda* (Lepidoptera, Lymantriidae) in Türkiye

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The pale tussock moth *Dasychira pudibunda* L. (syn. *Callitearа pudibunda* L.) (Lepidoptera, Lymantriidae) caused an epidemic in the beech forests of Inegol (Bursa) in Türkiye in 2018 and 2019, causing significant damage. This species is mainly known as a beech pest, but feeds on a large number of deciduous forest tree species as a polyphagous. As a result of the larvae eating the beech leaves, the trees be left completely without leaves, and as a result, increment loss occurs in the trees. A large number of dead and diseased *D. pudibunda* larvae and pupa specimens were collected from the infested site in a survey study. Morphological and molecular examinations of the cadavers revealed that the infection that could bring the end of the epidemic was a co-infection of baculovirus and cypovirus (CPV). Studies with electron microscopy revealed co-infection of a cypovirus and baculovirus in cadavers. Cypovirus-specific segments were evaluated as evidence of an RNA genome isolation. Genome sequence analysis showed that the new cypovirus was similar to Trichoplusia ni cypovirus 15. The cypovirus isolate was named Dasychira pudibunda cypovirus-D (DapuCPV-D). In this study, a cypovirus from the pale tussock moth was isolated for the first time in Türkiye. The isolate has the potential to be used in biological control studies because it has a very high mortality effect at its source.

Key words: Cypovirus, *Dasychira pudibunda*, *co-infection*, biological control

O-160

New *Dendrolimus sibiricus* cypovirus-1: from molecular features to field bioassay

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In our study, we found a virus strain belonging to the genus Cypovirus (Reoviridae); the strain was isolated from *Dendrolimus sibiricus*: that possesses attractive features as a candidate for mass production of biological agents for lepidopteran-pest control. We describe morphological, molecular, and ecological features of the new Cypovirus strain. This strain was found to be highly virulent to *D. sibiricus* (half-lethal dose is 25 occlusion bodies per second-instar larva) and to have a relatively wide host range (infects representatives of six families of Lepidoptera: Erebidae, Sphingidae, Pieridae, Noctuidae, Plutellidae and Lasiocampidae). Interesting finding is that the A-spike protein responsible for penetration function of virus significantly differ in amino acid sequence from related CPV-1 viruses isolated from another lepidopteran. Phylogenetic analysis of the sequenced DsCPV-1 genome showed that it most likely has arisen as a consequence of a recombination event between strains DpCPV1 and LdCPV-1. The virus strain showed a strong interaction with a nontoxic adjuvant (optical brightener), which decreased the lethal dose for both main and alternative hosts, decreased lethal time, and may expand the host range. Moreover, we demonstrated that the insecticidal features were preserved after passaging through the most economically suitable host. Multiplication of virus via alternative host keep high virulence of virus to susceptible pest species. This was confirmed by both laboratory and field bioassays.

Key words: Cypovirus, complete genome sequencing, lepidopteran pests

O-161-STU

Effects of tetracycline treatments on biological parameters and endosymbionts of *Bemisia tabaci* MEAM1

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The whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) harbors a variety of endosymbionts (depending on species) that play an important role in the pest's biology and evolution. In this study, we investigated temporal changes of the endosymbionts (*Portiera*, *Hamiltonella* and *Rickettsia*) and biological parameters of *B. tabaci* Middle East Asia Minor 1 (MEAM1) after Tetracycline treatments. Same age *B. tabaci* (female and male) were fed with tetracycline solution (50 mg/ml) while control group was fed only with sucrose for 48 hours. Then, one female and one male adult were placed on the lower surface of a cotton leaf enclosed in a clip cage. Individuals were transferred to new cages daily, and the number of eggs laid per day, development time of immature, mortality rates, and sex ratio were determined. Besides, ten *B. tabaci* adults were collected at five different ages (1, 5, 10, 15, and 20 days old), placed in 95-100% ethanol for endosymbiont molecular analysis. Endosymbiont variations were detected with Polymerase Chain Reaction (PCR) using 16 and 23S ribosomal gene region primers. The reduction in the total number of eggs per female showed tetracycline treatments significantly reduced whitefly fecundity in both first (F_0) and second (F_1) generations. Tetracycline treatment was also prolonged the total mean development time of immature stages (32.2 day) and this value was 10 days longer than the control. Tetracycline treatments reduced the longevity of female but not males. Molecular analysis showed that all the three endosymbionts were reduced but not completely eliminated from the *B. tabaci* MEAM1 by tetracycline, and the effect of the tetracycline was varied depending on the species of endosymbionts and the age of the adult whitefly.

Key words: Antibiotic, endosymbiont, MEAM1, Tetracycline, whitefly

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O-162-STU

Quantitative real time PCR (qRT-PCR) analysis of Wolbachia ınfection in different developmental stages of *Tuta absoluta* populations from Antalya

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The tomato pinworm, *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae), is an economically important pest of tomato. The pest harbors cytoplasmically inherited bacterium, *Wolbachia* that was found in a wide range of arthropods. In this study, we developed a quantitative real-time PCR (qRT-PCR) assays to screen *Wolbachia* infection dynamics among different developmental stages of the tomato pinworm. A FAM labeled TaqMan probe targeting *Wolbachia ftsZ* gene was used for qRT-PCR, whereas HEX labeled TaqMan probe targeting pinworm *actin* gene was used for host gene quantity normalization. Larval samples were collected from tomato fields grown in Antalya during 2021 summer season. Some larval samples were grown to precise age under laboratory condition. DNA was extracted from age-specific whole specimen and subject to optimized qRT-PCR assay. Each age-specific stage was represented with at least 20 biological samples. Though quantitatively variable, all pinworm samples tested exhibited 100% *Wolbachia* infection. Using the TaqMan assay, significant differences in *Wolbachia* densities were detected among developmental stages of the pest. Generally, the first larval stage exhibited the lowest *Wolbachia* titer with increasing amounts towards the fourth larval developmental stage. Relative amount of *Wolbachia* was higher in pupal stage than larval stages, but slightly lower than adult stage. Within pupal stage, there was no differences among 1, 3, 6 and 9 day old pupae. Similarly, W*olbachia* amount seemed not to differ 1, 3, 6 and 9 day old moths. The efficiency and applicability of the qRT-PCR assay was discussed for host-endosymbiont dynamics interaction.

Key words: Endosymbiont, Real-Time PCR, *Tuta absoluta*, *Wolbachia*

O-163 (KEYNOTE SPEECH)

Species-selective agonists of juvenile hormone receptor - en route to eco-friendly IGRs

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Juvenile hormone (JH) acts through an intracellular receptor (JHR) consisting of the bHLH-PAS proteins methoprene-tolerant (Met) and taiman (Tai). JH binding to Met induces formation

of a transcriptionally active Met-Tai complex which regulates specific genes. JHR signaling plays vital roles in insect development, physiology, and reproduction. Prior to metamorphosis, JH maintains the larval status; formation of insect adults requires absence of JH during the final juvenile stage. Application of JHR agonists at this time blocks adult development and hence provides effective means of insect control. However, existing synthetic JHR agonists (juvenoid insect growth regulators, IGRs) such as methoprene, fenoxycarb, and pyriproxyfen affect both target and non-target insect species and crustaceans. Therefore, JHR agonists that would selectively target pests or disease vectors are desired. Our recent work shows an unprecedented example of peptidic juvenoids whose effect is limited to one family of true bugs. The peptidic juvenoids activate the bug JHR at picomolar concentrations while doses million times higher have no effect on JHR from insects resistant to these compounds. Molecular dynamics simulations reveal a structural basis for the superior potency of peptidic juvenoids. Our aim is to prepare analogous peptides targeting pests. Another project based on automated high-throughput screening with JH receptors from several insect species yielded JHR agonists that selectively block metamorphosis of these species without affecting others, including the honey bee (details presented by Sedlak et al.). Our data demonstrate that novel JHR agonists with target-specific effect can be developed for sustainable pest control. Supported by 20-05151X (CSF).

Key words: Insect development, juvenile hormone, hormone receptor, agonist, selectivity, high-throughput screening

O-164 (KEYNOTE SPEECH)

Zero pesticide pest control - genetic markers for efficient SIT programs in agriculture

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The sterile insect technique (SIT) is a species-specific and environment-friendly approach to control insect pest populations, which has been successfully applied as a component of areawide integrated pest management programs worldwide. It is based on releases of mass-reared, sterilized male insects, which mate with females in the field. Due to the males' infertility, these matings remain without offspring, and the population size will be reduced over time. However, not all relevant and, in principle, contemplable insect pests can yet be tackled using this beneficial technique, because specific requirements need to be met to make large-scale operational SIT programs safe, efficient, and cost-effective. One of these requirements is to selectively remove females from the rearing population before release, also known as sexing, to enable male-only releases. Developing and using so-called genetic sexing strains (GSS) has significantly improved the sexing procedure for a few species. The most successful GSS was created for the Mediterranean fruit fly using classical mutagenesis. However, its construction and modifications took more than 20 years. Advances in genomics and gene editing techniques enabled us to find and understand the genetic basis of the medfly GSS and to start recreating its properties in other species. With this, it should be possible to construct GSS in new species in a much shorter time and without any transgenes. The differences, advantages, and disadvantages of the 'classic GSS' compared to our 'neo-classical' approach will be discussed.

Key words: Sterile insect technique, insect pest control, area-wide IPM, *Ceratitis capitata*, Tephritids, zero pesticide approach

O-165 (KEYNOTE SPEECH)

Insect multitrophic interactions for bioinspired plant protection

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Reduction of pesticide use in agriculture requires an increasing availability of sustainable tools and strategies of pest control. It is highly desirable that current research efforts aim at developing novel, highly specific biopesticides and bioprotection strategies based on knowledge obtained from the understanding of the molecular mechanisms underlying multitrophic interactions among plants, insects and their natural antagonists. This approach allows to use biocontrol agents as a source of virulence factors or of molecular information on which to base technologies reproducing their negative impact on pests and to develop bioinspired pest control tools for sustainable plant protection. Moreover, understanding the mechanisms underlying insect multitrophic interactions paves the way towards the definition of protection strategies for beneficial insects and the ecosystem services they provide.

Key words: Biocontrol, bioinsecticides, host regulation, parasitoids, pollinators

O-166

High-throughput discovery of species-selective juvenile hormone receptor agonists

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Juvenile hormone (JH) is vital to insect development. While JH prevents precocious metamorphosis, formation of adult insects requires JH absence during their final juvenile stages. Application of JH receptor (JHR) agonists at this time blocks adult development and hence provides effective means of insect control. Several synthetic JHR agonists (juvenoids) serve as pesticides of the insect growth regulator (IGR) class. However, existing compounds such as methoprene, fenoxycarb, and pyriproxyfen affect both target and non-target insect species and crustaceans. To discover JHR agonists with selec-

tive effect on target pest species, we performed automated, high-throughput chemical screening, initially in a Drosophila cell line carrying a JHR-dependent transcriptional reporter. Primary hits were validated through follow-up assays including ligand-receptor binding, dimerization of the JHR subunits, and effects on developing insects. This campaign uncovered novel compounds with JHR agonist activities exceeding those of a reference juvenoid methoprene. To identify species-selective juvenoids, we devised cell-based reporter systems utilizing JHR proteins from several target insects. Diversification of hits from high-throughput screens yielded agonists, some of which preferentially activated JHRs of particular insects while surpassing in potency the universal juvenoid IGR fenoxycarb. When tested in vivo, the discovered compounds blocked metamorphosis of the target species but not of the honey bee. These results demonstrate feasibility of our approach toward discovery of novel and selective JHR agonists for potential use as eco-friendly means of pest control.

Key words: Juvenile hormone receptor, agonist, high-throughput screening, insect development

Acknowledgment: Supported by 20-05151X (Czech Science Foundation) and project LM2018130 (MEYS) to the National Infrastructure for Chemical Biology CZ-OPENSCREEN.

O-167

Effect of pyriproxyfen, a juvenile hormone analog, on diapausing larvae of *Ephestia kuehniella* (Zeller) (Lepidoptera: Pyralidae)

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The Mediterranean flour moth, *Ephestia kuehniella* (Zeller), is a widely distributed pest that causes economic damage by feeding on stored products, especially cereal flour. Pyriproxyfen is one of the most important insect growth regulators used in controlling stored-product insect pests. By imitating the action of juvenile hormone, pyriproxyfen causes insect pests to experience prolonged larval development, failure to emerge as pupae or malformed pupae, absence of embryo development, and in some cases, a reduction in fecundity. This study examined the toxicity of pyriproxyfen on diapausing fifth-instar larvae of *E. kuehniella* at 25 ± 1°C, 65 ± 5% relative humidity, and a photoperiod of 16:8 (L:D) h. The 50% lethal concentration (LC_{50}) of the insecticide was calculated as 7.39 and 5.68 ppm at 72 and 96 h after treatment, respectively. After preparing the desired concentrations based on the preliminary test, the effect of sublethal concentrations (LC_{20} = 2.87, LC_{30} = 4.10, and LC_{40} = 5.56 ppm) of pyriproxyfen was determined on mortality and survival period of diapausing larvae. There was no significant difference in the survival period of diapausing larvae in different tested treatments. The survival percentage of diapausing larvae at one, two, three and ten weeks after treatment was not significantly different from the control. This study shows that the sublethal concentrations of pyriproxyfene have no significant effect on diapausing larvae of *E. kuehniella*, which indicates the high resistance of diapausing larvae to pyriproxyfen.

Key words: Mediterranean flour moth, pyriproxyfen, larval period, larval survival

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P-1

Physicochemical traits of sugarcane cultivars affected digestive enzymatic profile of *Sesamia nonagrioides* (Lefebvre) (Lepidoptera: Noctuidae) larvae

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The sugarcane stem borer, *Sesamia nonagrioides* (Lefebvre) is one of the most destructive pests of sugarcane in many regions of the world including Iran. The use of resistant cultivars is an important management method against *S. nonagrioides*. Effect of six commercial sugarcane cultivars, CP48-103, CP57-614, CP69-1062, CP73-21, SP70-1143, and IRC99-02 was studied on digestive proteolytic and amylolytic activities of S. nonagrioides larvae at 27±1°C, 60±5% R.H., and a photoperiod of 16: 8 (L: D) h. The fifth instar larvae fed on the stem of each sugarcane cultivar were carefully dissected in pre-cooled distilled water under stereomicroscope. The larval midguts (30 midguts for each cultivar) were separated and homogenized on ice using a pre-cooled homogenizer. The homogenates were centrifuged at 4°C, and the supernatants were used as a digestive enzyme source. To evaluate possible correlations between the insect's enzymatic activities and physiochemical traits of the cultivars, the physical (moisture content, trichome density, stem rind hardness) and biochemical (total protein, carbohydrate, tannins, phenolics, and flavonoids content) properties of tested sugarcane cultivars were measured. The highest digestive proteolytic and amylolytic activities of larvae were on cultivar CP69-1062, and the lowest activities were on cultivars CP57-614 and SP70-1143. Both tested digestive enzymes were negatively correlated with the tannins, phenolics, and flavonoids content of the cultivars. Our results indicated that CP57-614 and SP70-1143 were partially resistant cultivars against S. nonagrioides, which could be recommended for cultivation in sugarcane farms where the risk of S. nonagrioides damage is high.

Key words: *Sesamia nonagrioides*, digestive enzyme, sugarcane cultivar, biochemical traits

P-2

Effect of different wheat cultivars on digestive enzymes activity of *Trogoderma granarium* (Everts) (Coleoptera: Dermestidae) larvae

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The goal of this study was to investigate digestive proteolytic and amylolytic activities of *Trogoderma granarium* (Everts) larvae on the grains of various wheat cultivars (N-91-9, Heidari, Aftab, Tirgan, N-92-19, Gaskojen and Kouhdasht) using starch and azocasein substrates, respectively. The fifth instar larvae fed with wheat cultivars were dissected under stereomicroscope. The larval midguts were homogenized on ice using a pre-cooled homogenizer. The homogenates were centrifuged at 4°C, and the supernatants were used as the source of digestive enzymes. Our results showed that the proteolytic activity of larvae was the lowest on cultivars Heidari, Aftab, N-91-9 and N-92-19, and highest on cultivars Tirgan, Gaskojen and Kouhdasht. The amylolytic activity on cultivar Gaskojen was higher than on cultivars Heidari, Aftab and N-91-9. Among different cultivars, the highest protein concentration was in grains of cultivar Gascogen. Moreover, grain hardness index in cultivar N-92-19 was higher than cultivars Aftab, Kohdasht and Gascogen. The findings of this study indicated that Heidari, Aftab, N-92-19 and N-91-9 were unfavorable cultivars for feeding of *T. granarium*. These cultivars could be used as one of the sources of resistance in management programs of *T. granarium*.

Key words: *Trogoderma granarium*, digestive enzyme, grain properties, wheat cultivar

P-3

Mycoformulation developed using *Metarhizium anisopliae* (Ascomycota: Hypocreales) based on solid-state fermentation method against *Myzus persicae* (Hemiptera: Aphididae)

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In this study, protease and chitinase gene content of a local *Metarhizium anisopliae*, KTU-51 (Ascomycota: Hypocreales) strain with high insecticidal activity against *Myzus persicae* (Hemiptera: Aphididae) is one of the most agriculturally important insect pests, was determined by nested PCR method, and its phylogenetic positions were shown according to gene sequences. Mass spore production of the KTU-51 strain was achieved through solid-state fermentation using rice as a substrate. These spores were used to develop an oil-based mycoinsecticide and it was named AFISIDAL-OD MET-TR61. The product produced 78.33% mortality with 1 x 10^8 conidia /ml concentration on *M. persicae* nymphs seven days post-infection. The same concentration caused 79% mortality against aphid in pot experiments performed under laboratory conditions. The results show that the mycoinsecticide developed from the local isolate KTU-51 (*M. anisopliae*) is extremely promising in the biological control of *Myzus persicae*.

Key words: Biocontrol, *Myzus persicae*, *Metarhizium*, mycoinsecticides, oil-based formulation

Acknowledgment: This research was supported by The Scientific Research Committee of Karadeniz Technical University (KTU-BAP) for the project FDK-2017-5896.

P-4

Chemotaxic manipulation as a strategy to protect crop plants from root-knot nematode infections

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Root-knot nematodes (RKN, *Meloidogyne incognita*) are promiscuous plant parasites that infect many economically important crop plants, and cause up to several billions USD-worth of agricultural losses annually in many regions of the world. Traditional RKN control approaches, such as nematicide and soil fumigation tend to show reduced effectiveness over time as RKN acquire resistance, and may leave undesirable impacts on the environment. Infective RKN larvae are known to locate suitable host plants by sensing chemo-attractants and repellants secreted by plant roots, then follow these chemical cues through chemotaxis to find the host. This behavior may be taken advange of to develop novel strategies that protect crop plants from RKN infections. We have found that RKN are attracted to Arabidopsis (*Arabidopsis thaliana*) seeds in a seed coat mucilage extrusion-dependent fashion, and have further identified L-gal-substituted rhamnogalacturonan-I (RG-I) from flax seed coat mucilage as an RKN attractant. Similarly, RG-I derivatives secreted from *Lotus corniculatus* roots were also found to attract RKN, while cell wall carbohydrates purified from one of organic tissues were found to disrupt RKN chemotaxis instead. Aside from cell wall carbohydrates, we found other plant metabolites such as cadaverine, and inorganic compounds such as calcium sulfate and silica gel to also influence RKN chemotaxis. By combing these chemo-attractants and repellants, it may be possible to directly manipulate RKN behaviors in fields, thereby protecting crop plants from RKN infections while minimizing the detrimental side-effects on the soil.

Key words: *Meloidogyne incognita*, chemotaxis, rhamnogalacturonan-I, cell wall carbohydrates, crop protection

P-5

Effects of some entomopathogenic fungi on the citrus longhorned beetle, *Anoplophora chinensis* (Coleoptera: Cerambycidae)

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In this study, some local entomopathogenic fungi including *Metarhizium anisopliae*, *Beauveria bassiana*, *Lecanicillium muscarium* and *Isaria fumosorosea* were tested to control citrus longhorned beetle, *Anoplophora chinensis* (Coleoptera: Cerambycidae). All entomopathogens were applied to adult stage of *A. chinensis* which was highly invasive, destructive, and polyphagous pest at 1 x 10^8 conidia/mL concentration. According to the results of screening tests, mortality of KTU-51 (*M. anisopliae*) reached 100 % and KTU-21 (*M. anisopliae*) reached 90% on the pest on the 12th day. Apart from *M. anisopliae*, it was determined that Hp-4 (*B. bassiana*), which produced 60% mortality just after 12 days of infection, had a 100% mortality effect on the pest on the 15th day of application. Therefore, KTU-51 (the most effective of strains belonging to the genus *Metarhizum*) and Hp-4 (the most effective of strains belonging to the genus *Beauveria*) were selected for dose-response (1 x 10^{5-9} conidia/ml) mortality tests against adult stage of the pest. Based on probit analysis, the LC_{50} values of isolates KTU-51 and Hp-4 were calculated as 3,4 × 10^5 conidia/mL and 2,6 × 10^6 conidia/mL against *A. chinensis* adults, respectively. Based on all these findings, both strains, which are extremely promising as biocontrol agents against A. chinensis, were sprayed against to adult stage of the pest under semi-field conditions

in 40-60 cm screen cages at 1 x 10^{7-9} conidia/mL concentrations. In this experiment, KTU-51 and Hp-4 produced 87.16% and 89.24% mortality on the pest at 10^9 spores/ml concentration within 20 days, respectively.

Key words: *Anoplophora chinensis, Beauveria, Metarhizium*, biological control, entomopathogenic fungi

Acknowledgment: This research was supported by The General Directorate of Agricultural Research and Policy (TAGEM-20/AR-GE/-12).

P-6-STU

Molecular genetic basis of pesticide resistance in phytoseiids as biological control agents

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Some pests have been controlled successfully by members of the Phytoseiidae family. But, several pesticides used against other pests are highly toxic to phytoseiids. Resistant strains in a few number of phytoseiids occurred naturally or by artificial selection has been reported in previous studies. The use of the manipulated predator strains has been known to be a practical and cost effective tactic for the biological control. This review summarized genetic studies related with resistance mechanisms in phytoseiid mites. Based on scarce studies, the resistance developments in phytoseiids were found related with target site mutations, increase detoxification enzyme activities and the insensitive AChE. The resistance development in a naturally chlorpyriphos-resistance *Kampimodromus aberrans* strain was found associated with G119S substitution in its AChE gene. Metabolic resistance depend on enhancing P450 and GST enzymes in the fenpropathrin-resistant *Neoseiulus barkeri* strain was explained with overexpression of two CYP4, three delta class and one Mu class genes of the predator. Similarly, the expression level of CYP4-d in a methidathion resistant strain of *Amblyseius womersleyi* was found significantly higher than in its susceptible strains. While two point mutations in the linker region between domains II and III of VGSC with a polymorphism analysis were also reported in the fenpropathrin-resistant *Neoseiulus barkeri* strain, a mutation in different two linker regions of a deltamethrin-resistance *Phytoseiulus persimilis* strain was pointed out. A target-site gene mutation in AChE of primicarb-resistant *Neoseiulus californicus* strain has been shown in recently. To understand the molecular genetics and physiological basis of resistance development in phytoseiid mites, it is need many critical researches identifying and cloning their useful resistance genes.

Key words: Biological control, molecular studies, pesticides, phytoseiids, resistance

P-7-STU

Molecular characterization of Tomato spotted wilt virus (TSWV) and Cucumber mosaic virus (CMV) affecting tomato and pepper crops in Izmir province

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The objective of this study was to investigate Tomato spotted wilt virus (TSWV) and Cucumber mosaic virus (CMV) in tomatoes and peppers showing virus induced symptoms in vegetable growing districts of İzmir, Türkiye. Surveys were carried out in tomato and pepper plantations, and the incidences of these viruses in collected leaf samples were determined by RT-PCR. Nucleotide identities and phylogenetic relationships of the TSWV and CMV isolates with other isolates obtained from the GenBank database were determined. The results of the current study showed that tomato plants were infected at the same rate (21.50%) with TSWV and CMV. Out of the tested pepper samples, 64.15% were infected with TSWV and 25.47% with CMV. The results showed that, the identity rate of TSWV isolates from tomato was 99-96% at nucleotide level while the isolates from pepper showed 100-95% identity. On the other hand, the nucleocapsid protein gene region of the tomato isolate of CMV had nucleotide similarity rate of 98-95% with other isolates in GenBank, while that of its pepper isolates had 100-98% identity. Also, CMV isolates showed close phylogenetic relationship with the CMV isolates of subgroup IB. This study revealed the presence and molecular characterization of TSWV and CMV in tomato and pepper plants in İzmir province.

Key words: Pepper, RT-PCR, solanaceous crops, tomato, virus

P-8

Molecular identification of powdery mildew disease agent *Golovinomyces orontii* on periwinkle (*Vinca major*) plants growing in Türkiye

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During the summer 2021, powdery mildew infections were observed on periwinkle plants (*Vinca major* L.) growing in university landscapes in Hatay province of Türkiye. Symptoms included circular colonies of white dense mycelia and infected leaves developed gray leaf spots beneath fungal colonies. The leaves yellowed and the mycelium covered the entire surface of the leaf until it turned brown and died. A detailed light microscopy study of disease agent revealed that all morphological characteristics were consistent with previous reports of the powdery mildew fungus *Golovinomyces orontii*. Pathogenicity was confirmed by gently pressing affected leaves of

V. major onto leaves of five healthy plants. Five non-inoculated plants served as controls. Inoculated and non-inoculated plants were kept in a greenhouse at 24 to 30°C. Inoculated plants developed signs and symptoms after 10 days, control plants remained symptomless. The fungus from the inoculated plants was identical morphologically to that observed from initially diseased plants. To confirm the identification, the internal transcribed spacer (ITS) regions of PMV12 were amplified with primers ITS1/4 and ITS5/P3 and sequenced directly. The resulting sequences were deposited in GenBank (Accession Nos. OQ165183 for ITS1/4 and OQ165185 for ITS5/P3). BLAST search of these sequences revealed 100% similarity with the ITS sequences of *Golovinomyces orontii* on plants of *Vinca* sp. (KY660780) and *Vinca major* (KR011138). Based on the morphological characteristics and molecular analysis, the fungus was identified as *G. orontii*. To our knowledge, this is the first report of powdery mildew caused by *G. orontii* on *V. major* in Türkiye.

Key words: *Golovinomyces orontii*, *Vinca major*, powdery mildew

P-9-STU

Population dynamics of *Bacillus amyloliquefaciens* SS-38.4 in the phyllosphere of sugar beet and its biocontrol activity against *Pseudomonas syringae* pv. *aptata* P21

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The success of biocontrol depends directly on the colonization of plant tissue by the biocontrol agent. The objective of this study was to investigate the ability of *Bacillus amyloliquefaciens* SS-38.4 to colonize sugar beet leaves and suppress the leaf spot disease caused by *Pseudomonas syringae* pv. *aptata* P21. Sugar beet leaves were sprayed with the bacterial suspension of SS-38.4 followed by P21 12 hours later (T_1), but also in the reverse order (T_2). Plants treated with SS-38.4 or P21 alone were controls ($C_{38.4}$ and C_{P21}). Strains were isolated one, five and seven days after treatments and confirmed with SS-38.4-SCAR markers and *P. syringae*-specific primers. Results were analysed using two-way ANOVA and Tukey's test ($\alpha = 0.05$). During seven days, populations were stable in both controls ($C_{38.4}$ 3.45 ± 0.31 and C_{P21} 3.72 ± 0.44 log CFU/cm^2). Changes in population number of P21 were noticeable from the fifth day (T1 1.35 and T2 1.43 log CFU/cm^2), while on the seventh day a significant decrease was observed in T_1 (0 log CFU/cm^2) and T_2 (1 log CFU/cm^2). The number of SS-38.4 remained constant in both treatments and similar to control. A significant reduction in disease symptoms was observed on the seventh day in T_1 and T_2 (0 % and 0.23% affected leaf tissue) compared to C_{P21} (3.9 %). Strain *B. amyloliquefaciens* SS-38.4 can establish and maintain a stable population on the sugar beet leaf surface up to seven days after application, while exhibiting a significant suppressive effect on *P. syringae* pv. *aptata* P21.

Key words: Biocontrol, *Bacillus* spp., *Pseudomonas* spp., phytopathogen, phyllosphere colonization

P-10-STU

Phylogenetic analysis of *Pseudomonas syringae* isolates from the Danube River Basin revealed association with past epidemics in Serbia

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Pseudomonas syringae (*Psy*) is a widespread complex of plant pathogenic bacteria. It's a causal agent of diseases in many economically important hosts, including herbaceous and woody plants. The species complex is composed of 13 phylogroups. The aim of our study was to estimate the phylogenetic diversity of *Psy* isolates from the Serbian Danube River basin – a major irrigation source. A partial sequence of the citrate synthase housekeeping gene (*cts*) was amplified for 51 isolates from the collection. All amplicons were sequenced using the Sanger sequencing method. Based on the sequences obtained, a phylogenetic tree was constructed using Mega 11 software to infer the evolutionary history using the neighbour-joining method. The *cts* sequences of 51 isolates were compared with the *cts* sequences of isolates from previously reported epidemics in Serbia using the NCBI BLASTn tool. The analysis resulted in the detection of phylogroups 2, 7, 9, and 13. Most isolates were assigned to phylogroup 2 (70.6%), with the remainder evenly distributed among phylogroups 7, 9, and 13 (9.8% each). Nine isolates of phylogroup 2 showed 100% similarity in *cts* sequence with isolates from diseased cherry plants in different epidemic events in Serbia. Phylogroup 2 is known to be the most widespread phylogroup, of which numerous isolates have been found in non-agricultural habitats but also as disease causal agents on plants. Insights into phylogenetic diversity in the environment are important to explain the ecology of *Psy* and to predict possible disease outbreaks.

Key words: *Pseudomonas syringae*, phylogeny, diversity, species complex, *citrate-synthase gene*

P-11

Distinct genetic differences between plant and human pathogenic isolates of *Fusarium oxysporum*

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Fusarium oxysporum is a cross-kingdom pathogenic fungus that can cause vascular wilt disease in many economically important plants. *F. oxysporum* is also a major cause of blinding corneal diseases worldwide, and of disseminated infections in immunosuppressed individuals. In addition to the diverse immune responses to plant and human pathogens by their hosts, they also face distinct environments, including temperature, pH, and available nutrients. We compared a tomato pathogenic isolate, *F. oxysporum* f. sp. *lycopersici* 4287 (Fol4287), with a human pathogenic isolate that causes blinding corneal disease, *F. oxysporum* MRL8996. We examined how these strains of *F. oxysporum*, belonging to the same species and sharing the majority of genomic regions, respond to distinct causes of stress. Distinct accessory chromosomes were identified for the plant pathogen and human-infecting *F. oxysporum* isolates. Comparisons of accessory chromosomes genes and repeats as well as testing of these two strains under precisely controlled conditions identified specific differences in cross-kingdom pathogenicity. Collectively our studies indicate that MRL8996 is better adapted to elevated temperatures and has a faster growth rate in rich media and nutrient-limited conditions. This strain was also more sensitive to antifungals such as caspofungin, Congo Red, amphotericin B, and voriconazole. Conversely, the plant pathogenic strain Fol4287 tolerates osmotic and cell wall stress conditions better than MRL8996. Further, we performed experimental evolution in heat stress and mouse eye model showed the fast adaptation of this organism to these environments. This observation may reflect the unique adaption of *F. oxysporum* to wide host range.

Key words: *Fusarium oxysporum*, experimental evolution, fungal genomics

P-12

Investigation of the efficacy of some biopesticides against oleander scale, *Aspidiotus nerii* in laboratory conditions

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The oleander scale insect *Aspidiotus nerii* Bouché (Hemiptera:Diaspididae) is a cosmopolitan pest that feeds more than100 families of plants. In this study, the efficacy of Mineral oil 850 g/l, Spirotetramat 100 g/l, Azadiracthin 10 g/l, Orange oil 60 g/l and Carboxylic acids potassium salts 479,8 g/l against all life stages of oleander scale insect on potato tubers and ivy leaves (*Hedera helix*) were investigated in climatic room 26±1°C, 65±1% RH and 16:8 h L:D photoperiod conditions. According to the studies mineral oil caused the highest mortality with 83,59% followed by Carboxylic acids potassium salts, Azadiracthin, Spirotetramat with 82,57%, 54,85%, 53,21% and Orange oil showed the lowest effect with %52,58 against 1 day old first instars of scales on potato tubers. All preparations were ineffective against the second instar nymph, and adult female on potato tubers. However, in ivy leaves trials, mineral oil and Spirotetramat showed the highest effect against crawlers with 100% ratio, followed by Carboxylic acids potassium salts (95,78%), Azadiracthin (82.63%) and Orange oil (76,44%). While the highest effect against second instar was achieved by Mineral oil, Orange oil showed the lowest effect. Unlike other preparations, mineral oil caused the highest effect (90,9%) on the adult female, followed by the Carboxylic acids potassium salts (76,9%) and Spirotetramat, Orange oil and Azadiracthin. Effectiveness of preparations showed variance on 7th, 14th and 21th days after application, depends on the life stages of the scale.

Key words: Scale insect, fatty acids, potassium salts of fatty Acids, azadirachtin, organic farming, environment

P-13

Detection and differentiation of *Xanthomonas translucens* pv. *translucens* and pv. *undulosa* from wheat and barley by duplex quantitative PCR

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Bacterial leaf streak (BLS) caused by *Xanthomonas translucens* has recently become an important disease in North America, threatening wheat (*Triticum* spp.) and barley (*Hordeum vulgare*) crops. So far, specific quantitative PCR (qPCR) for detection and differentiation tests for *X. translucens* pathovars affecting both crops are not available. Two probe-based qPCR systems, namely P-Xtt and P-Xtu, were developed for diagnosis of BLS pathogens *Xanthomonas translucens* pv. *translucens* (Xtt) and pv. *undulosa* (Xtu), respectively. P-Xtt is specific to pv. *translucens*. P-Xtu is specific to pv. *undulosa*, pv. *cerealis*, pv. *secalis* and pv. *pistaciae*. P-Xtt and P-Xtu worked on all accessible strains of pv. *translucens* and pv. *undulosa*, respectively. Both systems could detect 100 copies of the target gBlock DNA. The two systems could be used in singleplex qPCR and duplex qPCR, with similar efficiencies. On genomic DNA from strains of various *X. translucens* pathovars, both singleplex qPCR and duplex qPCR could specifically detect and differentiate pv. *translucens* and pv. *undulosa*. On infected barley and wheat grain samples, the duplex qPCR showed similar efficiency compared to a previously published qPCR system but with the additional capability of pathovar differentiation. The duplex qPCR system developed in this study will be useful in studies on BLS detection, differentiation and quantification of the pathogens for diagnostic analysis and for research on inoculum load effects on seed to seedling transmission.

Key words: Bacterial leaf streak, *Xanthomonas translucens*, qPCR, wheat, barley

P-14-STU

Molecular analysis of copper tolerance and genetic diversity in *Pseudomonas syringae* pv. *syringae*, the causal agent of cherry bacterial canker disease

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Cherry is a significant commercial fruit tree in the Rosaceae family that grows worldwide. The bacterial cancer disease of stone fruits is a major issue in cherry farming regions, caused by the *Pseudomonas syringae* pv. *syringae* (Pss) bacterium, which results in significant losses of cherry crops and yields in the country. Copper compounds are the most common method of controlling Pss; however, the misuse of copper compounds has resulted in the bacterium developing resistance to these compounds. The aim of this study is to identify the Pss isolates' copper tolerance at various copper concentrations, determine the genetic variations between isolates using REP and BOX elements via the REP-PCR method, and examine the link between genetic variability and copper tolerance in bacterial samples collected from cherry cultivation areas with bacterial cancer symptoms in the Izmir Province. The study discovered a high level of copper tolerance in the Bağyurdu, Ören, and Armutlu regions of Izmir Province, and genetic variations were found among Pss isolates in REP and BOX elements, which were associated with copper toleranceCherry is a significant commercial fruit tree in the Rosaceae family that grows worldwide. The bacterial cancer disease of stone fruits is a major issue in cherry farming regions, caused by the *Pseudomonas syringae* pv. *syringae* (Pss) bacterium, which results in significant losses of cherry crops and yields in the country. Copper compounds are the most common method of controlling Pss; however, the misuse of copper compounds has resulted in the bacterium developing resistance to these compounds. The aim of this study is to identify the Pss isolates' copper tolerance at various copper concentrations, determine the genetic variations between isolates using REP and BOX elements via the REP-PCR method, and examine the link between genetic variability and copper tolerance in bacterial samples collected from cherry cultivation areas with bacterial cancer symptoms in the Izmir Province. The study discovered a high level of copper tolerance in the Bağyurdu, Ören, and Armutlu regions of Izmir Province, and genetic variations were found among Pss isolates in REP and BOX elements, which were associated with copper tolerance

Key words: *Pseudomonas syringae* pv. *syringae*, copper Tolerance, genetic variation, REP PCR

P-15

Unique peptidic agonists of a juvenile hormone receptor with species-specific effects on insect development and reproduction

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Juvenile hormones (JHs) act through a receptor complex consisting of methoprene-tolerant (Met) and taiman (Tai) bHLH-PAS domain proteins to induce transcription of genes including *Kr-h1*. Among diverse synthetic JH mimics (juvenoids), peptidic juvenoids stand out as highly potent yet uniquely selective to a specific family of true bugs (Pyrrhocoridae, Heteroptera). While the first peptidic juvenoids were discovered in the early 1970s, their mode of action has remained unknown. Here we demonstrate that, like established JH receptor agonists, peptidic juvenoids act upon Met to induce expression of *Kr-h1* and block metamorphosis in the linden bug, *Pyrrhocoris*

apterus. Peptidic juvenoids induced dimerization between the Met and Tai proteins from *P. apterus* but, consistent with their selectivity, not from other insects. We synthesized 120 new peptide derivatives, some of which acted at picomolar concentrations and thus outperformed the native JH or classical juvenoids (fenoxycarb) by orders of magnitude. Importantly, their potency in inducing Met-Tai interaction correlated with the capacity to block metamorphosis in *P. apterus* larvae and to stimulate oogenesis in reproductively arrested adult females. Molecular models of the ligand-bound pocket of *P. apterus* Met demonstrated that the high potency of peptidic juvenoids correlates with high affinity. This is a result of malleability of the ligand-binding pocket that allows the peptidic ligands to maximize their contact surface. Our data establish peptidic juvenoids as highly effective and species-selective JH receptor agonists. Supported by grants 20-05151X (CSF) and LM2018130 (MEYS).

Key words: Insect development, oogenesis, juvenile hormone, hormone receptor, agonist, ligand binding, selectivity, molecular modeling

P-16-STU

Molecular diagnostics of *Dendrolimus sibiricus* cypovirus -1 in alternative host

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Researchers are providing more and more evidence for the developing an environmentally friendly approach to pest control (raise of resistance, environmental pollution, effect on human health). The Dendrolimus sibiricus Cypovirus -1 (DsCPV-1) also known as cytoplasmic polyhedrosis virus, belonging to the genus Cypovirus (Reoviridae) recently isolated for the first time from *D. sibiricus* has attractive characteristics to be considered as a candidate for mass production of biological pest control agents. This virus has several advantages over existing bioinsecticides such as a wide range of target species, high transmission level, and high productivity and high virulence. An alternative host - *Manduca sexta* was chosen as a suitable species for further cultivation and production of a DsCPV-1 strain for a bioinsecticide product. Here we have developed a molecular diagnostic method for this virus, because light microscopy is not informative enough because of the modification of polyhedra size within the alternative host. We use a real time PCR test system, which allows us to measure the quantity of genomes copies of this RNA virus in the midgut of infected larvae. This method will allow us to control DsCPV-1 multiplication in any susceptible host and avoid confusion in the case of activation of nucleopolyhedra covert infection which looks relatively the same in light microscope. Applying molecular diagnostics of cypovirus will help in the studies of the mechanisms of DsCPV-1 pathogenesis which in turn the improvement of cypovirus's bioinsecticides by enhancing these effects.

Key words: Cypovirus, Real time PCR, pest control, pathogenesis diagnostic

P-17-STU

Molecular methods for the identification of Amaranthus species

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Amaranthus species are annual weeds that are harmful especially in agricultural areas around the world. Accurate identification of Amaranthus species is important for effective weed control, but since Amaranthus species are hybridizable, identification of hybrid species may be difficult, which can sometimes lead to misidentification. In the control of Amaranthus species, correct identification of the species is necessary for the control techniques and herbicides to be used. For example, widely differing responses to glufosinate active ingredient have been reported between *Amaranthus retroflexus* L and *Amaranthus palmeri* S. Wats. In this study, studies on molecular methods that can be used to prevent errors that may arise in the diagnosis of some Amaranthus species with morphological methods were investigated. Molecular markers are used to distinguish genotypes whose phenotypes are mixed under environmental conditions. The use of molecular markers for species differentiation allows for rapid and accurate species identification. Several molecular identification methods have been developed for single-species identification of Amaranthus species. A random amplification of polymorphic DNA (RAPD) method, a restriction fragment length polymorphism (RFLP) method using the internal transcribed spacer (ITS) and species-specific single-nucleotide polymorphisms (SNPs) are the most commonly used of these methods. In this study, comparative analyzes of these methods were made.

Key words: *Amaranthus* spp, diagnosis, amaranthus genetic diversity

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P-18-STU

The molecular characterization of viruses found in honeybee colonies infested with *Varroa destructor* in Türkiye

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Honey bees have an important place to pollinate numerous crops and native plants. This social insect faces several problems. *Varroa destructor* Anderson and Trueman (Arachnida: Acari: Varroidae) is at the top of the list. This parasitic mite feeds on the hemolymph and body fluids of adult and immature honey bees. *V. destructor* causes physical harm to honey bees and it shows an important transmission route for emerging bee virus infections. The viruses have particular symptoms in honeybees and they cause colony loss. Different viral determinations were tested in the honeybees that were infested with *V. destructor* in different studies of Turkiye. The results of the studies show that the association of many viruses with *V. destructor* has been tested in honeybee colonies with different experiments. To determine these viruses have been used by the reverse transcription-PCR (RT-PCR) with approximately 24 different primer sets in Turkiye. The results of the studies show that the most common honeybee viruses are the deformed wing virus (DWV) and black queen cell virus (BQCV) which have been determined to be related to *V. destructor*. At the same time, results show that the other common viruses (Acute Bee Paralysis Virus (ABPV) and Chronic Bee Paralysis Virus (CBPV) are not transferred by *V. destructor*. DWV and BQCV viruses have been determined by using DWV-F-R and BQCV1-2 primer sets in Turkiye. In addition, these two viruses are common in some parts of the world, and nowadays, in the national studies, DWVA and BQCV-F-R primer sets have been used to identify to the viruses respectively.

Key words: Honey bee, *Varroa destructor*, RT-PCR, DWV, BQCV

P-19-STU

The role of ncRNAs in parasitic plant infection and some strategies of struggling in tomato breeding

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The weeds and parasitic plants in general are important biotic stress factors on plant growth, leading to yield and quality losses. Because parasitic weeds, exploit the plants by up taking the water and other nutrient, they repress the crop growth and productivity. Although chemical using based strategies exist, they are both expensive and not environmentally friendly. On the other hand, breeding methods are not only cheaper but also more sustainable in terms of the environments. In this context, ncRNAs based methods are prominent as a breeding strategy. Many studies revealed that there are mRNA exchanging between host and parasite and some micro RNAs can adversely affect the parasitic weeds. Thus, it is conceivable that some breeding strategies can be developed. Even though there are some studies in rice and model plant Arabidopsis thaliana, the similar study in tomato is inadequate. Therefore, these types of studies can be considered as innovator method in tomato breeding.

Key words: Tomato, parasitic weeds, ncRNA, trans-species, breeding

P-20

Biocontrol treatments confer protection against *Phytophthora infestans* infection of potato by inducing defense hormone biosynthesis

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Potato late blight, caused by *Phytophthora infestans*, is a serious potato (*Solanum tuberosum* L.) disease worldwide, and the use of natural compounds to induce the plant resistance represent a promising eco-friendly strategy to reduce the disease impact. Mushrooms represent a formidable source of bioactive compounds, and we focus our attention on the cultural filtrate (CF), rich in polysaccharides and proteins secreted by asexual mycelia of *Trametes versicolor.* CF is a source of several bioactive compounds known as fungal growth inhibitor, modulator of fungal antioxidant system, and elicitor of plant defense. *T. versicolor* CF was sprayed on potato seedlings and was examined the degree of immune response protection against *P. infestans.* We tested also the ß-aminobutyric acid (BABA), known for its ability to induce plant disease resistance towards several types of pathogens, including *Phytophthora infestans.*A mass spectrometry analysis indicated that both CF and BABA induced the accumulation of common hormones facing pathogen attack, we have also evaluated the expression of the genes related to the biosynthesis and signaling of salicylic acid (*PAL1*, *WRKY1* and *PR1*) and jasmonic acid (*JAR1*, *MYC2* and *PR4*). Finally, we showed that the protective effect produced by BABA against *P. infestans* was mimicked by CF treatment. In conclusion, the use of natural compounds to induce the plant resistance bring a sustainable method to control the disease caused by *P. infestans.*

Key words: Potato late blight, *Trametes versicolor*, defence priming, exopolysaccharide, antimicrobial peptides

P-21

Proteomic characterization of bacteriophage peptides of pathogenic *Xanthomonas arboricola* pv. *juglandis* using Matrix-Assisted Laser Desorption Ionization-Time-of-Flight Mass Spectrometry

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This study focused on develop and evaluate a rapid and reliable method for identifying *Xanthomonas arboricola* pv. *juglandis* bacteriophages, based on detecting their specific proteins using matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) profiling. Six bacteriophages were isolated from infected walnut leaves and fruits in Sakarya/ Türkiye. A total of 1,867 non-redundant peptides belonging to 1,048 proteins were identified and analyzed. Among them, 23 phage-origin peptides were found out as specific *X. a.* pv. *juglandis* peptides. These peptides belong to proteins such as phage portal proteins, phage major capsid protein in P2 family, phage holin family protein, phage tail protein, phage virion morphogenesis protein, phage baseplate assembly protein V and uncharacterized phage proteins. Bacteriophage phylogeny was investigated, as well as the relationship between phages encoding the peptides determined and the bacteria they infect. The findings revealed that certain peptides are present in closely related phages, and that bacteriophage phylogeny is linked to the *X. a.* pv. *juglandis* they infect. Because of phage specificity to the bacterial hosts, diagnostic peptides, among others, could be beneficial for the characterization and identification of *X. a.* pv. *juglandis* specific phages, especially peptides that belong to specialized functional proteins.

Key words: Bacteriophage, *X. arboricola* pv. *juglandis*, peptide, MALDI-TOF, Türkiye

P-22-STU

Detection and molecular characterization of viruses ınfecting tomatoes grown in greenhouses in the highlands of inner Western Anatolia

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Tomato is an economically important crops, commonly grown in the greenhouses and open fields in Türkiye all year around. Since the greenhouse tomato productions are limited by extremely high temperatures in the coasts during summer, greenhouse production of tomato in highland conditions increase to close the production gap in recent years. Although viruses infecting tomato in the greenhouses in coasts fairly studied, the presence and distribution of viruses in the highland tomato greenhouses are unknown. In this study, surveys were conducted Afyonkarahisar, Burdur, Denizli, Isparta, Kütahya ve Uşak, provinces and 282 samples showing virus symptoms were collected from tomato greenhouses. The samples were tested separately for 18 different viruses by SYBR Green-based RT-qPCR method, and 224 of the samples were infected at least with one virus. In addition, mixed infections were detected in 98 samples. Burdur (Çavdır), was the region with the most virus infected samples and TSWV, ToBRFV, ToMV, TMV, PepMV and PVY were the most common viruses in the survey areas. Up to 4 isolates representing each detected viruses and different survey areas were selected and the coat protein (CP) genes of the selected viruses were amplified by RT-PCR. The amplified CP genes were purified and cloned and their sequences were determined. The sequences of virus isolates from different regions were compared with the CP genes of virus isolates from different production regions of the world obtained from the GenBank database. The similarity and phylogenetic relationships of virus isolates from Türkiye and other regions were determined.

Key words: Greenhouse cultivation, Tomato viruses, Real-time PCR, Molecular detection, Sequencing and sequence analysis

P-23-STU

Recent studies on molecular identification of *Phytoseiidae* species (Acari: Mesostigmata) in Türkiye

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The predatory mites belong to Phytoseiidae family are effective biological control agents that feed on spider mites and some small pests. Their accurate identification is critical for success of biological control. The commonly used method for identification of phytoseiid species is confront of their morphologic features. As they are microscopic organisms with complex and minute taxonomic characters, various target DNA fragments including 12S rRNA, COI mtDNA, CytB mtDNA, and ITSS were identified as alternative diagnostic tools at the species level within a barcoding framework. In this study, we focus on the latest researches on the molecular barcoding of Phytoseiidae species found in Türkiye. DNA sequence data in this review have been obtained from NCBI GENBANK database. The DNA sequences shared in the database was mostly produced by using COI mtDNA marker and followed by 12S rRNA, ITSS, CytB mtDNA and HSP90, respectively. Among 112 phytoseiid species recorded from Turkiye, 45% of them have already been characterized by molecular identification while 55% of which still need to be sequenced. Based on the DNA sequences belonging to species from 23 different genera, *Typhlodromus* is the most studied genera, and followed by *Neoseiulus*, *Amblyseius*, *Euseius*, and *Phytoseiulus*. Although *Typhlodromus pyri* is not predominant in Turkiye, this species is the most sequenced species among 30 different species in the genus *Typhlodromus*. Considering ecological and habitat variations, present molecular data about Turkish phytoseiid populations is inadequate. In the future, it is necessary to perform more molecular studies covering both Turkish populations and undefined worldwide species.

Key words: Molecular markers, identification, taxonomy, Phytoseiidae, DNA barcoding

P-24

Action of species-selective juvenile hormone receptor agonists on insect development

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Juvenile hormone (JH) maintains larval character of insect juveniles by activating the *Kr-h1* gene through a JH receptor complex (JHR) comprising Met and Tai proteins. Metamorphosis to adults requires absence of JH and *Kr-h1* expression during the final juvenile stage in both hemimetabolous and holometabolous insects. Administering JHR agonists at this time prevents adult development. Synthetic JH mimics that presently serve to control pest and disease vectors display poor selectivity toward target species. To develop selective means for insect control, we screened a chemical library of 90K compounds for activators of JHRs from diverse target species. We have found compounds that bound Met, stimulated assembly of the JHR complex, and blocked adult development in a species-selective manner. When treated with the specific JHR agonists, last-instar hemimetabolous larvae molted to a doomed extra larval instar, whereas treated pupae of holometabolans either formed second lethal pupae (beetles) or arrested without producing viable adults (mosquitoes). In contrast, development of honey bee pupae was unaffected by the compounds targeting other species. Our data demonstrate that novel, species-selective compounds for insect research and control can be developed. Supported by grants 20-05151X (CSF) and LM2018130 (MEYS).

Key words: Insect development, metamorphosis, juvenile hormone, hormone receptor, agonist, selectivity, high-throughput screening

P-25

Genetic characterization of *Meloidogyne incognita* isolates using KASP markers

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Root-knot nematodes (RKNs) are one of the most important plant parasitic nematodes that cause heavy economic losses in cultivated plants. *Meloidogyne incognita* is one of the most widespread species of RKNs in protected vegetables areas in the world. The knowledge of genetic variation within *M. incognita* is necessary for management of nematode infestation, improvement of resistant varieties and understanding genomic evolution of RKNs. In this study, Kompetitive Allele-Specific PCR (KASP) markers developed from genome of *M. incognita* were used to screen genetic variation among 34 isolates of *M. incognita* collected from vegetable growing areas in the West Mediterranean region of Türkiye. The clustering analysis showed that there were differences among isolates in terms of locations and host plants. Results can be used for improvement of resistance varieties and management tactics.

Key words: KASP, *Meloidogyne incognita*, variation

P-26 STU

Development of a local *Bacillus thuringiensis* ssp. *kurstaki*-based biopesticide effective on the lepidopteran pests

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The aim of this study is to develop an environmentally-friendly effective biopesticide to control of lepidopteran pests. In this study, a biopesticide was developed using a local isolate effective against lepidopteran pests. The developed biopesticide contains *Bacillus thuringiensis* subs. *kurstaki* (Btk), a Gram-positive, aerobic, spore-forming, cry toxin-containing and local entemopathogenic bacterium. The Btk was incubated in a laboratory fermenter, and spores and crystal proteins were collected and powdered with a spray dryer with a special formulation. Number of spores, wettability, suspensibility, and moisture content of developed powder biopesticide are determined as 1x1010 cfu/g, 15s, 80% and 8,01%, respectively. The insecticidal activity of Btk-based biopesticide was tested against the larvae of Tomato moth, *Tuta absoluta* (Lep.: Gelechiidae) and European grapevine moth, *Lobesia botrana* Den.-Schiff. (Lep.: Tortricidae) in 4 replicates and at 3 different doses under the field conditions. The highest mortality against the larvae of *T. absoluta* was 82.06% at 200 g/100 L water concentration of Btk-based biopesticide. The highest mortality against the larvae of *L. botrana* was 95.81% at 100 g/100 L water concentration. In conclusion, the Btk-based biopesticide has a great potential for commercialization against lepidopteran pests. This project was supported through a special grant by Oyak Biyoteknoloji, Türkiye.

Key words: *Bacillus thuringiensis* ssp. *kurstaki*, biopesticide, lepidopteran, *Lobesia botrana*, *Tuta absoluta*

P-27

Molecular identification of root-knot nematodes in banana growing areas of Antalya province

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Banana (*Musa* spp.) is a plant that can be grown economically in tropical and subtropical regions. In Türkiye, banana growing is mostly done in the Mediterranean region. Antalya has attracted attention in recent years with its increasing banana production and production areas. Plant parasitic nematodes are one of the most important pests of banana due to the root damage and yield loses. Especially, root-knot nematodes (RKNs), belonging to genus *Meloidogyne*, can cause significant damage on banana. The present study aims on molecular identification of RKNs in banana growing areas of Antalya province. For this purpose, soil samples were taken from 26 banana growing locations with different production backgrounds. Nematodes were extracted from soil using modified Baerman funnel technique and DNA was isolated from nematode pool. Samples have been analyzed with six different species-specific primers belonging to RKNs. Results showed that *M. incognita, M. javanica, M. arenaria* and *M. hapla* were present in 20 samples. Among them *M. incognita* was found as the most prevalent RKN species. Furthermore, this is the first report on the presence of *M. hapla* in banana growing areas of Türkiye.

Key words: Banana, identification, *Meloidogyne* spp., PCR primers

P-28

First report of Tomato brown rugose fruit virus infecting greenhouse tomato in the Aegean Region of Türkiye

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In recent years, a new viral agent that has emerged in greenhouse tomato-grown areas was first reported in Jordan and named as Tomato brown rugose fruit virus (ToBRFV). During the growing season of 2021–2022, a total of 283 symptomatic tomato leaf and fruit samples were collected from different locations (Aydın, Denizli, İzmir, Kütahya, Manisa and Muğla) in the Aegean Region, Türkiye. Plants exhibited symptoms as severe mosaic with dark green wrinkling, blistering, narrowing, and deformation on leaves. Discoloration, irregular brown necrotic lesions, and yellowing spots were observed on tomato fruits. The sample was tested using ELISA kits for the presence of ToBRFV, Tomato spotted wilt virus (TSWV) Potato virus Y (PVY), Tobacco mosaic virus (TMV) (Bioreba, Switzerland) according to the manufacturers' instructions. As a result of DAS-ELISA analysis, ToBRFV was detected in 176 symptomatic plants. Total RNA was extracted from collected leaf and fruit samples using total RNA purification kit (Norgen Biotek Corp. Canada) and tested by ToBRFV-specific real-time RT-PCRs as described in EPPO PM7/146 (European and Mediterranean Plant Protection Organization, 2021). A positive result was obtained also by conventional RT-PCR using ToBRFV-specific primers (Alkowni et al., 2019). PCR products of three randomly selected positive samples were directly sequenced and BLAST analysis of the obtained sequences revealed 99,8 -100% nucleotide identity with the deposit sequence in NCBI from Türkiye (MT 118666.1) and USA (OM892678.1). Strict eradication measures have been taken in contaminated areas. This is first report of Tomato brown rugose fruit virus infecting greenhouse tomato in the Aegean Region of Türkiye.

Key words: Tomato, tomato brown rugose fruit virus, PCR, phylogenetic analysis

P-29-STU

Effects of *Wolbachia* infection status on parasitism performance of *Encarsia lutea* on the silverleaf whitefly *Bemisia tabaci* MEAM1

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Encarsia lutea (Masi) (Hymenoptera: Aphelinidae) is one of the most important natural enemies of the silverleaf whitefly, *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae). *Wolbachia* is a genus of bacteria that causes parthenogenesis and reproductive incompatibility in various Hymenopteran species. The objective of this study was to determine the effect of Wolbachia infection on parasitism performance of *E. lutea* by comparing Wolbachia-infected and uninfected lines. For this purpose, newly emerged female and male *E. lutea* adults were fed with tetracycline or pure sucrose solution (control) for 24 h. Subsequently, one parasitoid couple was placed on the lower surface of a cotton leaf enclosed in a clip cage, and offered with 40 3rd instar *B. tabaci* nymphs for 24h. All the female and male adults were collected and placed in pure ethanol to extract DNA for Wolbachia detection. Wolbachia was not completely removed but reduced in tetracycline-fed *E. lutea* adults with 34.4% infection rate. Although the difference was not statistically significant, higher parasitism rate was obtained in *Wolbachia*-infected line (31.7%) when compared to Wolbachia-uninfected line (25.8%). Further studies are needed to confirm the impact of *Wolbachia* to the mosquito vector. Further studies are needed to confirm the effects of *Wolbachia* on the parasitism performance of E. lutea.

Key words: *Bemisia tabaci*, *Encarsia lutea*, parasitism, Tetracycline, *Wolbachia*

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P-30

Gene knockdown in arabidopsis downy mildew using small RNA duplexes to assess gene functions

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Small interfering RNAs (siRNAs) are 21-23 nucleotide long non-coding RNA duplexes. They elicit gene silencing by RNA interference (RNAi). The knockdown effect of siRNA for a target gene is driven by sequence-specific degradation of complementary mRNA molecules. The siRNA-mediated gene silencing can be used as a reverse-genetic approach to elucidate the function of genes. Downy mildew (DM) diseases caused by oomycetes pathogens result in significant economic losses when during favorable environmental conditions. *Hyaloperonospora arabidopsidis* (Hpa) and its host plant Arabidopsis thaliana provides a useful model pathosystem to investigate the genetic basis of plant-DM interactions. In the present study, RNA sequencing was performed for samples at 0-3-5-7 days post inoculation to identify differentially expressed genes (DEG) of Hpa. Subsequently, synthetic siRNAs targeting selected Hpa genes were designed. Until now, more than 50 genes were tested with germination and infection assays. Among siRNAs tested, some of them inhibited both spore germinations and sporulations. Interestingly, a number of siRNAs enhanced germination and sporulation, while, few siRNAs that did not alter germination or sporulation. Trypan blue staining, biomass analysis and qRT-PCRs are being performed on siRNAs that showed altered phenotypes at present. The promising results provide evidence that the exogenous application of siRNAs targeting pathogen genes has important potential to control DM diseases of crop plants. Latest data will be presented.

Key words: Downy mildew, *Hyaloperonospora arabidopsidis*, siRNAs, gene silencing, differential gene expression

P-31-STU

Detection of the sunflower pathogen *Plasmopara halstedii* by loop-mediated isothermal amplification

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Plasmopara halstedii is a plant pathogen that causes downy mildew disease in sunflower plants, leading to significant yield losses and economic damage worldwide. The pathogen has a complex life cycle. As a result of the pathogen's high adaptability to changes in the environmental situation, it stands out as a serious threat to sunflower production. The detection of *Plasmopara halstedii* is crucial for managing the sunflower disease and preventing its spread. Various methods are used to detect the pathogen, including physiological examination methods, serological methods, molecular detection methods, and microscopic examinations. In this study, loop-mediated isothermal amplification (LAMP), which is one of the molecular methods, was used to detect *Plasmopara halstedii*. The reason this method was chosen is that it does not require thermal cycles, it can be worked with low equipment costs and it is a very advantageous method because it offers a simpler application area to the user compared to other molecular methods with visual detection method. In the experimental part of the study, pathogen extraction was performed primarily from sunflower plant samples. The species determination was performed by PCR method using primer sets specific to *Plasmopara halstedii*. LAMP-based primers designed specifically for *Plasmopara halstedii* were used to validate this method and species specific detection was successfully achieved. It was concluded that the results of LAMP and PCR are consistent with each other. The species-specificity of the LAMP-based primers originally designed in this study was confirmed by other sunflower pathogens.

Key words: *Plasmopara halstedii*, sunflower, loop-mediated isothermal amplification (LAMP), downy mildew

P-32-STU

Comparative genomic analysis of *Spiroplasma citri* in naturally infected citrus samples and *in vitro* cultures in Türkiye

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Citrus stubborn disease (CSD) is one of the most important vector-borne diseases in most citrus growing regions worldwide especially in the eastern Mediterranean and the Middle East. *Spiroplasma citri*, the causal agent of CSD, is a phloem-limited, wall-less bacterium, belonging to reduced genome bacteria group, Class Mollicutes. In the present study, *Spiroplasma citri* was detected and characterized from naturally infected citrus trees grown in different locations in Türkiye and *in vitro* cultures obtained from periwinkle, sesame, turnip and cicadellids. In order to screen and confirm *S. citri*, PCR-based detection was performed by focusing on *spiralin*, P58 putative adhesin-like multigene, and P89 putative adhesin genes of *S. citri*. The detection rate of *S. citri* was consistently higher in the fruit columella than in the leaf midribs for naturally infected field samples. For cultured samples, we have found that primer pairs based on P89 were more sensitive in recognizing *S. citri* in field samples than those based on the *spiralin* gene and P58 gene. Furthermore, the obtained isolates were characterized molecularly by sequence analysis showing 99.75% identity with *S. citri* GII3-3X strain which was originally isolated from the leafhopper *Circulifer haematoceps*, collected in Morocco (1980) and *99.25A % identity with BLH-MB strain which* was originally isolated from a Navel orange tree in Riverside, California (1972). In terms of the current situation of *S. citri* across Türkiye, this study presents an overview of the disease's spread in the citrus-growing regions of *S. citri* in culture and naturally infected citrus.

Key words: *Spiroplasma citri*, citrus stubborn disease, spiralin, P58, P89

P-33

Eradication processes of tomato brown rugose fruit virus on tomato seeds

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Tomato brown rugose fruit virus (ToBRFV) is the most recently evolved and virulent Tobamovirus, it has reported sinced 2014. The ToBRFV spreads quickly with mechanical contact in close proximity, but it is spread through long-distance contact due to the prevalence of seed trade among countries. The lack of a chemical control for virus diseases, as well as limited resistant varieties to ToBRFV in tomato-growing areas, is causing a potential ToBRFV pandemic around the world. This study aims to eradicate tomato seeds from the virus through application of thermal and UV lights. After these, ToBRFV infections were measured using physical methods and PCR analyses. Firstly, infected seeds were gradually heated from 20 °C to 72 °C with a 50 rpm rotation for 3 days in a specially designed thermal machine; the heated seeds had a 0.3% infection rate and the ToBRFV had lost its virulence. Secondly, the ToBRFV-infected seeds were exposed to UV light with a wavelength of 254 nm for 30 minutes; it was determined that UV application 50% inactivated the virus. Aditionally, success of seed eradication could not adversely affect seed germination. These results indicate that thermal heat applications are promising method to control ToBRFV in seed transmissions.

Key words: Eradication, seed, ToBRFV, tomato

P-34

Using Alphafold2 to aid the early design of protein-based bioinsecticides

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By utilising the diverse chemistries present in spider venom neurotoxic peptides, it is possible to produce bioinsecticides that target pests while minimizing off-target effects on beneficial insects. Orally effective insecticides of this kind can be generated by recombinantly fusing toxin peptides to plant-derived carrier proteins, which are capable of traversing the insect gut epithelium and transporting linked toxins to the nervous system. ω-Phylotoxin-Tbo-IT1a (PhTx), a spider venom peptide toxin from the oblong running crab spider (*Tibellus oblongus*), was expressed in yeast and showed promising pesticidal activity towards lepidopteran and hemipteran pests by injection and oral ingestion respectively. By contrast, PhTx displayed no injection, oral, or contact toxicity towards bumble bees. Recombinantly fusing PhTx to the carrier snowdrop lectin (*Galanthus nivalis* agglutinin; GNA) resulted in low expression levels and was degraded when expressed by yeast cells. Analysis using Alphafold2, an AI-based protein structure prediction program, suggested this may be attributable to the close proximity of the toxin relative to GNA resulting in toxin destabilisation. Utilising Alphafold2, iterative modifications were made to both the linker region and the primary sequence

of PhTx to improve the predicted structure. The resulting fusion protein, GNA/PhTx, has been viably expressed in yeast and early bioassay results suggest that Alphafold2 could be a valuable tool for the rational design of protein-based bioinsecticides.

Key words: Bioinseciticde, spider venom, fusion protein, protein design, alphafold

P-35-STU

Investigation of thiram-induced cellular responses in *Fusarium* reference strains

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Diseases, caused by *Fusarium* spp. in economically important plants, result in significant yield losses in many countries. The application of fungicidal active compounds is the most cost-effective approach for controlling of growth of these species and the management of those diseases. In this study, the effects of thiram, one of the fungicide active compounds, on *F. graminearum* PH-1 and *F. culmorum* FcUK99 reference strains were investigated at the cellular level, focusing on cell viability, oxidative stress, and apoptosis. The minimum inhibitory concentration (MIC) of thiram was determined as 165 µg/ml for both strains. MIC_{25}, MIC_{50}, and MIC_{75} doses for both reference strains were calculated with values of 41.25, 82.5, and 123.75 µg/ml, respectively. Radial growth rates were significantly reduced ($p<0.001$) in both strains for all tested concentrations except the MIC_{25} of FcUK99 ($p>0.05$). WST-1 analysis revealed that MIC_{25}, MIC_{50}, and MIC_{75} doses of thiram reduced cell viability of PH-1 at the rate of %18.30, %32.06, and %45.45, respectively, while cell viability of FcUK99 decreased in %33.53, %51.68 and %76.1. Oxidative stress, triggered by this compound was demonstrated by using 2',7'-dichlorodihydrofluorescein diacetate staining. Intense green fluorescence increased in a dose-dependent manner. Similarly, thiram-induced apoptosis was visualized under fluorescence microscopy after acridine orange/ethidium bromide dual staining. Dose-dependent orange fluorescences were increased in both *Fusarium* strains. Our findings suggested that thiram is a disease control agent that effects by triggering oxidative stress and apoptosis among cellular processes in PH-1 and FcUK99 reference strains.

Key words: *Fusarium*, fungicide, thiram, oxidative stress, apoptosis

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P-36-STU

Investigation and classification of fungal pathogens isolated from olive orchard in Türkiye

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Diseases caused by fungal phytopathogens in olive leaves can lead to yield and quality losses in olive cultivation. This study aimed to identify fungal phytopathogens isolated from olive leaves with leaf spot disease symptoms, collected from the olive orchard in Akköy/Çanakkale in 2021. Surface-sterilized leaves were plated on water agar and incubated in the dark at 17°C for 16-20 hours. According to spore morphology, three isolates were described as *Venturia* sp. or *Aureobasidium* sp. while two isolates as *Alternaria* sp.. The 28S rDNA region with 620 bp length and eukaryotic translation elongation factor (*TEF1-α*) gene region with 850 bp fragment were amplified via PCR from genomic DNAs of 14-day-old cultures. Products of *TEF1-α* that were amplified by specifically designed oligonucleotides, were sequenced via the Sanger sequencing method. Alignment analyses revealed that three isolates, previously shown morphologically as *Venturia* or *Aureobasidium,* were identified as *A. pullulans* with aligned scores of 98.80%, 98.64%, and 98.81%, respectively. One isolate was molecularly diagnosed as *Alternaria tenuissima* with a similarity rate of 99.14%. It was suggested the isolate could be one of the phytopathogens of leaf spot diseases. The remaining isolate showed similarity to *Ascochyta* sp., *Neodidymelliopsis longicolla*, and *Didymella glomerata* with rates of 86%, 86.29%, and 86.12%, respectively. Findings provide basic data for the studies to be carried out fight against leaf spot diseases. One of the most important outcomes of this study is the isolation of *A. pullulans* which has an antagonistic relationship with various fungal phytopathogens and produces biotechnologically valuable metabolites.

Key words: Leaf spot diseases, *Olea europa* L., phytopathogen, PCR, *TEF1-α*

Funding: This study was funded by the Scientific Research Projects Coordination Unit of İstanbul University [Project number: 38399].

P-37

Development of multiplex primer and probe against Tomato brown rugose fruit virus (TOBRFV), Tomato spotted wilt virus (TSWV) and Pepino mosaic virus (PEPMV) disease factors in tomato and pepper plants

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Tomato (*Solanum lycopersicum*) and pepper (*Capsicum annuum*) are indispensable vegetable species that have many different uses as human food in our country as well as in the world and contribute to the national economy. Virus diseases are one of the most important problems in tomato production. The inability to apply the chemical warfare method used against viruses and the fact that other control methods are not known by the manufacturer cause virus-related losses to increase. In this study, a Taqman® probe-based Real-time multiplex PCR method with three different primer-probe pairs was developed for the simultaneous detection of three important plant viruses. These viruses that cause a lot of yield loss in tomatoes and peppers are Tomato brown rugose fruit virus (ToBRFV), Tomato spotted wilt virus (TSWV) and Pepino mosaic virus (PepMV). The coat protein sequences of the three viruses mentioned above were obtained from the National Center for Biotechnology Information (NCBI) and BLAST was performed. Then, the common regions were determined and primer and probe designs were made using the Primer3 program. Since the main purpose of our Multiplex qRT-PCR study, which is a method that requires intensive optimization processes, is to provide a sensitive, fast and economical method, dilution series were prepared by determining the optimum conditions that will enable the PCR method to reach these goals. The FAM-channel was selected for ToBRFV, the HEX-channel for Tswv, and the Cy5-channel for Pepmv. The multiplex qRT-PCR experiment was successful with Ct values of 19.09, 21.89 and 21.63, respectively.

Key words: Multiplex qRT-PCR, virus, ToBRFV, TSWV, PepMV, tomato, pepper

P-38

An investigation of disease resistance genes in *Corylus avellana* cv. Tombul by resistance gene enrichment sequencing (RenSeq) method

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Hazelnut, grown primarily in the Black Sea region, is one of Türkiye's most valuable agricultural export crops. 'Tombul' is a cultivar prized for its distinctive taste, high oil content, thick shell, high kernel ratio, and easy-peeled testa. Hazelnut production in Türkiye is negatively affected by biotic stressors including mites, bacteria, and fungi; the newly emerged destructive powdery mildew fungus, *Erysiphe corylacearum*, causes significant crop losses. In the presented study, we generated a chromosome-scale genome assembly of *Corylus avellana* cv. 'Tombul' using a hybrid sequencing approach (Illumina, MinION, Hi-C) to identify disease resistance genes. The reference Tombul genome contained 272 predicted complete NLR genes; re-sequencing of a second individual found 258 NLR genes, only 183 of which were identical to the reference, suggesting that this gene family is highly diverse in hazelnut populations. We identified a small group of wild/uncultivated hazelnut individuals with complete resistance to PM. We adapted the RenSeq technique to hazelnut, producing a sequence capture library of probes from hazelnut NLR coding sequences, and then used long-read MinION sequencing to analyze pooled DNA from resistant and sensitive genotypes. These were then compared to identify candidate resistance genes against *E. corylacearum*, which can be used in future breeding programmes.

Key words: Tombul, *Corylus avellana*, RenSeq, *Erysiphe corylacearum*, powdery mildew

P-39-STU

Agrobacterium-mediated transformation of tomato with the coat protein gene of tomato brown rugose fruit virus

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Tomato brown rugose fruit virus (ToBRFV) has become widespread in tomato production areas in the world and Türkiye in recent years. ToBRFV is easily transmitted mechanically and able to break the Tm2[2] resistance providing resistance to other tobamoviruses. Since a resistance to ToBRFV has not yet been developed in commercial cultivars by conventional breeding methods, the development of alternative resistance methods should be investigated. In this study, research was conducted to develop resistance based on pathogen-derived coat protein-mediated resistance as an alternative resistance against ToBRFV. For this purpose, ToBRFV CP gene was first amplified by RT-PCR and cloned between the CaMV35S pro-

moter and terminator to construct the gene cassette. Then, the gene cassette was cloned into the T-DNA region of the pCAMBIA0380 binary vector and transferred to *Agrobacterium tumefaciens*. Approximately 1800 hypocotyl and 1200 cotyledon fragments obtained from in vitro germinated tomato seeds were transformed by *Agrobacterium*. Approximately 300 shoots were obtained through shoot induction the transformed explants by BAP and 130 shoots survived were transferred to the rooting medium. 14 plantlets obtained from 32 of rooted shoots were transferred to glass jars containing sterile soil supplemented with liquid MS media for adaptation to the soil. Genomic DNA was isolated from five of soil-adapted plantlets and the samples were tested by PCR method using primers specific to ToBRFV CP gene. PCR analysis showed that four of the tested plants contained ToBRFV CP gene in their genome. Potential transgenic plants will be analyzed by ELISA, RT-qPCR and Western blot methods.

Key words: Tomato, ToBRFV, genetic transformation, coat protein mediated resistance

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P-40

Diversity of indigenous Actinomycetota of Iran and assays of their culture extracts toxicity on some plant pests

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A total of 48 indigenous Actinomycetota isolates were obtained from the microbiology collection of the University of Tehran, Iran, and were subjected to the molecular identification. The isolates' DNA were extracted using crushed-biomass method and their 16S rRNA gene (almost complete sequences) were amplified. The obtained sequences and their comparison with those of the closest type-species in the EZBioCloud database showed that 31 isolates with a frequency of 64.58% belong to the genus *Streptomyces* and the rest of the isolates (35.42%) belonged to seven rare Actinomycetota generae including *Kribbella*, *Micrococcus*, *Nonomuraea*, *Saccharothrix*, *Nocardia*, *Micromonospora*, and *Actinomadura*. The phylogenetic relationship of the isolates with the selected type-species were also illustrated by Neighbor Joining trees (MEGA 7.0), showing eight and five clades for *Streptomyces* and rare Actinomycetota, respectively. Furthermore, their ISP2 broth medium culture extracts were also extracted and their toxicity were investigated on the female adults of the two-spotted spider mite, *Tetranychus urticae* (Trombidiformes: Tetranychidae), and the first instar nymphs of the rose-grain aphid, *Metopolophium dirhodum* (Hemiptera: Aphididae), and the dark willow leaf aphid, *Chaitophorus salijaponicus niger* (Hemiptera: Aphididae). Results showed that four highly toxic extracts were belonged to the *Streptomyces* including *S. pratensis, S. atrovirens*, *S. panaciradicis*, and *S. albogriseolus*. All the extracts at 50 mg/ml after 12 h of treatment showed a rage of 55-100% mortality on the pests. However, the great toxicity of the indigenous Actinomycetota extracts suggests that these metabolites can be considered as the highly potent microbial-based insecticides in different plant pest control programs.

Key words: Phylogeny, actinomycetes, secondary metabolites, insecticide

P-41

Brine shrimp nauplii play a rapid biomarker role in the chemical screening investigations

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Saving time and cost are the factors mainly considered in large-scale screening studies. The use of a living organism capable of rapid response to chemical compounds leads to quick toxicity screening. The brine shrimp, *Artemia* (Artemiidae), which is a sister group with the Hexapoda and is commonly used as a model organism in many toxicological experiments were accordingly selected. Twenty-five biosynthesized silver nanoparticles (AgNPs) concentrations (0.1 to 2.5 mg/ml at 0.1-fold intervals), and three concentrations (x, x, and 2x of the field recommended dose) of emamectin benzoate 5% SG, and indoxacarb 15% SC, were evaluated against 40-hour nauplii of *A. urmiana* and *A. franciscana* in three replications. The mean mortality rate was achieved 58.6-82.0% and 100.0% with the LT_{50} ranges of 6.3-17.6 h, and 3.0-5.3 h, for the AgNPs and the insecticides, respectively. Also, the results obtained on the second instar larvae of the Beet armyworm (BAW), *Spodoptera exigua*, and the female adults of the Two-spotted spider mite (TSM), *Tetranychus urticae*, showed a similar trend with a mortality rate of 22.1-54.9% and 86.8-100% on the BAW-larvae and 46.3-74.7% and 100% mortality on TSM-females with the compounds, respectively. However, the median lethal times of the compounds for the pests were calculated as 2.96- and 3.31-fold more than that of the brine shrimps' tests, respectively. Furthermore, the cost of the experiments was reasonably lower than that of the insect screening assays. So, the use of the *Artemia* screening test in the preliminary assays was recognized fit with the main toxicity experiments.

Key words: *Artemia* screening test, silver nanoparticles, emamectin benzoate, indoxacarb, bioassay

P-42-STU

NAD+ involvement in the virulence of *Pseudomonas syringae* effector hopag1

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Pseudomonas syringae is a world-widely distributed bacterium destructive for many economically relevant plants such as crops and fruit trees. The success of *P. syringae* as a pathogen comes from a wide range of effectors transported to plant cells via type three secretion system. Testing the function of a particular effector may help with understanding molecular mechanisms of host-pathogen interactions, which in turn may be useful in developing new methods for plant protection. NAD+ role in plant immunity came into the spotlight recently. It was shown that NAD+-originated molecules are involved in immune signalling and moreover some effectors seemed to be able to manipulate host NAD+ reservoir. HopAG1, a *P. syringae* effector, causes expandend cell death while expressed in Nicotiana benthamiana. Our initial prediction indicated that it might possess ADP-ribosyltransferase (ART) domain. ARTs catalyse ADP-ribosylation - a post-translational attachment of ADP-ribose derived from a cleaved NAD+ molecule. Thus, HopAG1 might act either by affecting modification status of host proteome or unbalancing defence signalling dependent on NAD+-derived molecules. To study NAD+ involvement in HopAG1 functioning, we designed a set of effector variants with substitutions within the predicted NAD+ binding site. Subsequently, they were transiently expressed in N. benthamiana. A substitution of the residue potentially involved in NAD+ positioning led to delayed cell death development, comparing to the wild-type HopAG1. These observations suggest that NAD+ binding seems to be essential for the function of the effector. The work was supported by National Science Centre (grant no. 2018/31/D/NZ3/03296).

Key words: *Pseudomonas syringae*, HopAG1, ADP-ribosyltransferase, nicotinamide adenine dinucleotide

P-43

Importance of crop wild relatives as potential source for resistance to biotic stress factors in plant breeding

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Crop wild relatives, can named as close or distant relative species of cultivated plants. They are plants with wild characteristics, which are closely related to a cultivated plant, whose geographical origins date back to the regions known as Vavilov's plant origin centers. It is either the wild ancestor of the cultivated plant or a closely related taxon. Generally these are; important in that they have high adaptability, resistance to environmental pressures, diseases and pests. Wild relatives as plant genetic resources are the biological basis of plant breeding. Agricultural diversity and wild genetic resources should be used more effectively to sustain the current level of food production and to solve future problems. Since the varieties in current use are often inadequate in many genes, especially biotic stress factors (diseases, pests) and also abiotic stress factors (cold, drought, salt, etc.). Because of that breeders constantly search for new sources of genetic materials. This is due to their potential content desirable traits which withstand adverse impacts of climate change, increasing scarcity of nutrients, water and other inputs, and new pests and diseases. Genes from wild plants have also provided cultivars with resistance against pests and diseases and improved tolerance to abiotic stresses. For instance the wild species have been utilized to date for 39% diseases, 17% pests as plant genetic resources in the improvement of varieties with new features is indisputably known. In anutshell they are used as genitor in plant breeding program. This review is based on reports to explain the importance crop wild relatives as source for resistance to biotic stress factors in plant breedıng of reviewing scientific literature.

Key words: Crop wild relatives, biotic stress factors, plant breeding

P-44-STU

Use of plant viruses and VLPs in vaccine production

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Vaccination, which is one of the most beneficial medical applications, has a long history, and since the first study, different methods and types have been developed. Classification based on functions includes vaccines against infectious diseases, cancer, and autoimmune diseases. Recombinant technologies are one of the many approaches used to produce them with advancing technology. Viruses and VLPs (Virus-Like Particles) have advantages for vaccine construction. Especially plant viruses and VLPs have properties that facilitate the construction of vaccines and their working mechanisms in organisms, so they can be used as a vector. This review summarizes vaccine studies based on plant viruses and VLPs.

Key words: Plant viruses, virus-like particles, vaccine production, recombinant technologies, immune response

P-45-STU

Emerging fungal threat for cotton production in Türkiye

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Cotton (*Gossypium hirsutum* L.) is one of the most widely grown cash crop in Türkiye. It plays a key role not only for the textile industry but also for the agricultural economy in Türkiye. Türkiye ranked as the 7th largest cotton supplier with approximately 825.000 tons; conversely, it is the 5th biggest demander behind China, India, Pakistan and Bangladesh in the world (National Cotton Consortium, 2021). The annual cotton consumption of the textile and clothing industries has reached 1 million 930 thousand tons depending on the developments in the global markets in 2021 in Türkiye (National Cotton Consortium). Only 38% (738000 metric tons) of this need could be met by domestic production, and the remaining 62% (1 million191 thousand 761 thousand tons) was provided with imports. The economic value of these imports is about 2.412 billion US$. This gap can be closed by producing more crops from limited fields because the cotton production area reached a maximum level in Türkiye. It is known that two main factors cause crop loss and yield loss. These are biotic and abiotic stresses. Although extreme changes in abiotic stresses, such as temperature *etc*. was not seen, average cotton yield drastically dropped in different cotton regions, especially Sanliurfa in 2019. No experts could explain exact reason/s, and it is still a mystery. Some cotton growers have faced problems such as leaf and stem desiccation, boll rot and plant death. To understand the main reason for the problem, we conducted surveys and collected plant samples throughout Sanlıurfa. Our first observation demonstrated that the main reason for the desiccation and boll rot results from a fungal pathogen that does not belong to the genera of *Fusarium*, *Verticillium*, *Rhizoctonia*, *Macrophomina*, *Aspergillus* and *Alternaria*. Now we have several strong clues that biotic factors, especially fungus, might seriously threaten cotton production. It is interesting that there have been 1427 records on diseases caused by fungus on cotton around the world (Farr and Rossman, 2022). These records have resulted from about 358 different fungus species. However, approximately only 6 different fungus, such as *Fusarium Oxysporum*, *Rhizoctonia solani etc*. cause diseases on cotton in Türkiye. There is a long way to go in the field of fungal diseases in cotton plants, which are widely grown in many regions of Türkiye and have many hosts in the world.

Key words: *Gossypium hirsutum*, cotton, plant pathogen, fungus species

P-46

Field Screening of anthracnose resistance in watermelon breeding lines under Bursa-Türkiye conditions

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Anthracnose, caused by the fungal pathogen *Colletotrichum orbiculare* (Berk. & Mont.) Arx syn. lagenaria, is one of the most important diseases of watermelon worldwide including Türkiye. The disease occurs under frequent warm temperatures (20 to 32°C), rainy conditions, and high humidity favors the spread of spores and spore germination. Symptoms associated with anthracnose are black to brown irregular spots found on the leaves, oval tan lesions on the stem, and brown sunken lesions on fruits. Until now, three races of the anthracnose fungus are of concern to watermelon production. It was reported that all genotypes were susceptible to race 2. The most effective way to combat the disease, which causes significant yiedl losses, is to develop resistant varieties. The development of parent lines is a must. It is reported that the most effective method is testing under field conditions, while recurrent testing is carried out during the seedling period as parent lines being developed. From this point of view, the aim of this study was to determine the Anthracnose resistance of watermelon lines with different backgrounds in natural conditions. In the study, 132 watermelon lines were scored in terms of Anthracnose in field conditions and the findings were evaluated. Two observations were made 40 days apart and evaluated on a 0-4 scale. According to the findings, 24 genotypes were determined between scale 1-2, and 100 between scale 3-5 in the first observation, while in the second observation 16 genotypes were determined between scale 1-2 that can be deemed resistant. According to the findings, in the second observation, it was determined that 16 genotypes of watermelon, which are between the scale of 1-2, can be used in watermelon Anthracnose tolerance breeding.

Key words: Watermelon, anthracnose resistance, breeding, field screening

P-47

Determination of disease resistance using molecular markers among tomato breeding lines from diverse origin

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Tomato is one of the most important vegetables produced in the world. China, USA and Türkiye are among the important producers. Diseases and pests are one of the most important problems in tomato. Breeding for disease resistance has been an important objective in tomato improvement. When preparing new breeding programs, genetic materials from different backgrounds are needed. However, the genes required for resistance to diseases and pests may vary according to the tomato production regions. In order to obtain the desired resistance in breeding programs, it is important to know pest / pathogen races and pressure. The study aimed to determine the distribution of disease and pest resistance of important lines developed from tomato varieties produced in Türkiye, USA and Jordan. In the materials selected from Türkiye in 2014, disease resistance other than Verticillium was rarely found, while Sw-5 and Ph3 genes were found in 2017 and 2019. On the other hand, it was determined that the majority of genetic materials originating from USA and Jordan had Ve, FF (I2), Mi1-2, Pto, Tm-2, Ty-3, Ph3 and SW-5 genes. The findings show that regional pest and pathogen races are not the same and developing disease and pest resistant varieties for different production regions requires pyramiding of disease resistance genes into commercial cultivars.

Key words: Tomato, disease resistance, molecular markers

P-48

In vitro analysis of the antagonistic effects of beneficial endophytic bacteria isolated from olive leaves against *Phytophthora infestans* and *Monilinia laxa*

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Plants all have a range of microbiota whose effects span a continuum from beneficial to pathogenic. Increasingly, endophytes (microbiota found in plant tissues) are being seen as potentially useful symbionts for providing disease suppression or abiotic stress tolerance. Beneficial endophytic bacteria are functional in protecting plants from the effects of various stressors and harmful pathogens and can increase yields in agricultural products. Commonly used approache to identify beneficial endophytic bacteria by default include plate competition assays and co-grafting on plant substrates in the laboratory. Endophytic bacteria isolated from olive leaves and flora show diversity in the Mediterranean geography where olive production is common. There have not been many studies on the diversity of microbiota of local olive varieties in Türkiye. After species determination and purification in vitro culture of endophytic bacteria isolated from local varieties grown in Izmir and its region, antagonistic activity analyzes were performed on *Phytophthora infestans* and *Moniliana Laxa.* In addition, the antagonistic activities of secondary metabolites of bacteria were tested by in vitro experiments and the most effective inhibition rate was measured as 90% for endophytic bacteria and 80% for secondary metabolite administration. Detailed information will be given in the poster presentation.

Key words: Endophytic bacteria, *Phytophthora infestans*, *Moniliana laxa*, antigonistic effects.

P-49-STU

Comparison of 3D protein structures of fungal effector candidates with defined effectors

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Effector proteins are secretory proteins that alter the structure of the host cell, interfere plant defenses or modify the physiology of plant cells. Identifying these proteins secreted by phytopathogens is important for developing molecular defense strategies for plants. Many effector candidates were determined with omics technologies, functional analysis of a small number of candidates was performed with functional genomic methods such as transgene and gene silencing methods. Bioinformatics tools have been developed to predict effector candidates with similar structure and sequence homology based on effectors identified by various methods. However, certainty about the accuracy of the effector candidates determined by these criteria is not sufficient. In this study, the 3D protein structure predictions of the seven effector candidates determined by the proteomic method were compared with the 3D structure of the AvrSr35 protein identified in the stem rust. The short protein chain structure of an effector candidate was found to be similar to AvrSr35. It is thought that the discovery of information on the use of 3D protein structure in the determination of effector candidates will pave the way for the effective use of bioinformatics tools in the identification of new effector candidates.

Key words: Fungal pathogens, effectors, 3D protein structure, bioinformatics

P-50-STU

RNAi mediated functional analysis of wheat yellow rust (*Puccinia striiformis* f. sp. *tritici*) effector candidate gene

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Yellow rust disease caused by *P. striiformis* is one of the most important biotic stress in global wheat production. Epidemics or even pandemics may occur by new aggressive races. The effectors are most important virulence factor of the phytopathogens. Identification of the effector genes is the best strategy to control the disease. In this study, we aimed to funtional confirmation of the candidate effector (PGTG_11681T0) which identified in our previous proteomics study by Host Induced Gene Silencing (HIGS) Therefore, it was determined whether these candidate effectors are true effectors and their role in the virulence of the pathogens. The wheat variety Morocco, susceptible to yellow rust disease, was used for plant material and *Warrior* and *Yr27* aggressive Pst races were used for pathogens. BSMV vectors were used for RNAi-mediated gene silencing. For HIGS of the candidate, 450 bp gene fragments of the PGTG_11681T0 was cloned to the BSMV gamma vector as sense and antisense orientations. Two leaf stage seedlings were inoculated by BSMV. The same seedlings were inoculated by Pst races at 10 dpi of BSMV. Infected leaves were visualised by microscobe for examination of the urediospor growth and development and qRT-PCR analysis were done from same samples to reveal of the PGTG_11681T0 expression level at 5 dpi. In addition, the same seedlings were observed for Pst infection type at 12 dpi. In conclusion, the functional analysis and confirmation of the candidate effector gene were tried to revealed by using the HIGS method.

Key words: *Puccinia Striiformis* f. sp. *tritici*, host induced gene silencing, candidate effector, BSMV, RNAi, yellow rust

P-51-STU

Spider venoms: Exploring their potential as bioinsecticides

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Bioinsecticides are potentially safer alternatives to chemical insecticides. Many studies have shown that spider venoms could be used as effective alternatives that could replace the chemical insecticides. Spider venoms are complex cocktails of various compounds, including salts, small organic molecules, peptides, and proteins. They target voltage-gated potassium (KV), calcium (CaV), or sodium (NaV) channels, partially or completely blocking these channels that are important for signal transmission, leading to paralysis of their prey. Insecticidal spider peptides have unique features, such as small size, resistance to proteolysis, and strong affinities for cell receptors. Such peptides are the primary components of spider venom, and some species produce venom with more than 1000 unique peptides, weighing 2-8 kDa. Most of the major components of spider venom are small, disulfide-rich peptides. Their small size and disulfide-rich nature lead to high stability and long-lasting biological activity, which are significant advantages compared to many other bioinsecticides. These peptides affect different systems in insects compared to chemical insecticides. Recombinant production of these peptides with fusion proteins, in addition to chemical synthesis, is a promising approach for their mass production.

Key words: Bioinsecticide, spider venom peptide

P-52-STU

A Novel approach to control stored product pests: RNA interference

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Control of stored product pests is mainly based on use of fumigants and/or residual insecticides. It has been well documented that major insect pest species of stored products developed resistance to such pesticides as a result of the continuous and improper use. Therefore, there is a need for environmentally friendly and more effective pest control strategies in the management of insect pests in pre- and postharvest situations in crop production. One of the promising alternative is based on use of a molecular approach, the RNA interference (RNAi), which refers to inhibiting the expression of specifically targeted genes. The use of RNAi technology is aimed to reduce both insect damage and population growth by silencing the target gene regions specific to the pest. In studies, double-stranded RNA (dsRNA) can be administered to targeted insects through diet or topical application. In the management of stored products insects, dsRNAs can be used as species-specific insecticides by silencing the essential gene which ultimately leads to reduced fitness or mortality. The approach is indeed quite promising for the control of beetles. This review discusses the possibilities of using gene-silencing techniques to manage stored products pests.

Key words: RNAi, stored product pests, RNA interference, dsRNA

P-53-STU

Mechanism of phosphine resistance in stored product pests

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Stored products, especially cereals, nuts, dried fruits, and other processed food products, have been disinfected with fumigants for decades. After the banning of methyl bromide due to its damage to the stratospheric ozone layer, phosphine gas (PH3) use as a fumigant in postharvest storage has also increased. Continuous and improper use of phosphine has led to resistance development in various major insect species worldwide. Insect resistance is described as the adaptation developed by the target pest to make its survival possible at the recommended dose of an insecticide that could be toxic to the rest of the individuals in a normal (susceptible) population. In the recent years, many studies have been increasingly carried out to understand the molecular background of phosphine resistance. Identifying these resistance mechanisms in insects and transferring this knowledge into the resistance management strategies is very important to tackle the problems arising from pest resistance, as well as human-environmental health concerns and economic issues. This review aims to review the studies on phosphine resistance developed by stored product pests.

Key words: Phosphine resistance, stored product pests, management

INDEX OF AUTHORS

E

F

G

H

I

J

INDEX OF AUTHORS

P

R

S

T

INDEX OF AUTHORS

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