



**International Workshop  
The Fruit Microbiome:  
A New Frontier**



**September 9 - 13, 2019.  
The National Conference Center  
Leesburg, Virginia, USA**

**Program and Book of Abstracts**

# Acknowledgment of sponsors:



United States – Israel  
Binational Agricultural Research and Development  
Fund (BARD)



United States Department of Agriculture  
Agricultural Research Service (USDA-ARS)  
Office of International Research Programs (OIRP)  
Office of Technology Transfer (OTT)



Agricultural Research Organization (ARO)  
The Volcani Center

# Content

---

<b>Sponsors</b>	<b>2</b>
<b>Program</b>	<b>4</b>
<b>Invited Abstracts</b>	<b>9</b>
<b>Poster Abstracts</b>	<b>36</b>
<b>Bios of Invited Speakers</b>	<b>45</b>
<b>List of participants</b>	<b>56</b>



**Workshop on  
The Fruit Microbiome: A New Frontier  
9-13 September 2019**

*National Conference Center, Leesburg, VA, US*

## **Scientific Program**

**Monday Sept. 9**

**Morning and afternoon:**

Arrival, registration and accomodation

**Evening:**

**(18:30-19:30) Dinner**

**(20:00-21:30) Welcome Reception**

Welcome the organizers of the Workshop

**Michael Wisniewski and Samir Droby**–

Welcome from BARD

**Prof. Yoram Kapulnik** - *Executive Director of BARD*

Welcome from USDA-ARS

**Dariusz Swietlik** - *Director Northeastern Area - USDA-ARS*

**Tracy Leskey** - *Director and Research Leader - USDA-ARS, Appalachian Fruit Research .*

## Tuesday Sept. 10

### Morning Session:

(08:00-08:30) Registration and Poster set up

(08:30-08:45) Opening and introduction

### **The Microbiome in Plant Health and Disease**

(Chair: Michael Wisniewski)

(8:45-9:30) **Sharon Doty**, *College of the Environment, Dept. of Microbiology University of Washington, Seattle, WA, USA*

Symbiotic–plant microbiome and its overall importance in plant health

(9:30-10:15) **Gabriele Berg**, *Institute of Environmental Biotechnology, Graz University of Technology, Graz, Austria*

Exploring the plant microbiome for managing pathogens and resistances

(10:15-10:45) **Coffee break**

(10:45-11:30) **Steven Lindow**, *College of Natural Resources Ecology of Plant-Associated Microorganisms, University of California, Berkeley, CA, US*

Assembly of epiphytic bacterial communities on plants and their interactions with the plant host

(11:30-12:15) **Colin Jackson**, *Department of Biology, University of Mississippi, MS, US*  
The role of the microbiome in the holobiont

(12:15-13:30) **Lunch break**

### Afternoon Session:

### **A The Rhizosphere, Phylloplane and Carposphere Microbiome**

(Chair: Samir Droby)

(13:30-14:15) **Mark Mazzola**, *USDA-ARS, Physiology and Pathology of Tree Fruits Research: Wenatchee, WA*

Manipulation of the orchard soil microbiome: Implications for soil-borne disease suppression and apple production

(14:15-15:00) **Jenny Kao-Kniffin**, *School of Integrative Plant Science, Cornell University, Ithaca, NY, US*

Ecological Assembly of Rhizosphere Microbiomes to Modify Plant Reproductive Traits

(15:00-15:30) **Coffee break**

(15:30-16:00) **Ahmed Abdelfattah**, *Department of Ecology, Environment and Plant Science  
Stockholm University, Stockholm, Sweden*  
The Inherited Microbiome of Oak

(16:00-16:30) **Michael Wisniewski**, *USDA-ARS, Appalachian fruit Research Station,  
Kearneysville, WV, US*  
Exploring the apple microbiome

(16:30-17:30) **Discussion Session**  
**Steven Lindow** and **Gabriele Berg** – moderators

### Wednesday Sept. 11

#### Morning Session:

**Bioinformatic analysis of microbial communities: composition and function**  
(Chair: Adam Rivers and Justin Shaffer)

(08:30-09:15) **Adam Rivers**, *USDA-ARS, Genomics and Bioinformatics Research Unit,  
Gainesville, FL, US*  
Microbiome data are compositional: What does that mean and how do we deal with it?

(09:15-10:00) **Adi Doron-Faigenboim**, *Plant Sciences, Vegetable and Field Crops  
ARO, The Volcani Center, Rishon LeZion, Israel, Rishon LeZion, Israel*  
Bioinformatic approaches for metagenomics data analysis

(10:00-10:30) **Coffee break**

(10:30-11:15) **Shiri Freilich**, *Plant Sciences, Vegetable and Field Crops, Newe-Ya'ar  
Research Center, Agricultural Research Organization, Ramat Yishay, Israel*  
Computational approaches for deciphering the functions of microbial communities

(11:15 – 12:00) **Justin Shaffer**, *Knight Lab, Department of Pediatrics, School of  
Medicine University of California, San Diego, La Jolla, CA, USA*  
Novel insights into plant microbial ecology revealed through use of consistent protocols  
and meta-analyses

(12:00-13:30) **Lunch break**

#### Afternoon Session:

**Bioinformatic analysis of microbial communities: composition and function-  
continued**

(13:30-14:15) **Tal Luzzatto-Knaan**, *Department of Marine Biology, Leon H. Charney  
School of Marine Sciences, University of Haifa, Israel*  
Harnessing metabolomics in microbiome studies

## **Plant Microbiome Research in relation to food quality and safety**

(Chair: Gabriele Berg)

(14:15-15:00) **Andrea Ottesen**, *U.S. Food and Drug Administration*

*Silver Spring, MD, US*

Microbiome Research in the Office of Regulatory Science

(15:00-15:30) **Coffee Break**

(15:30-16:15) **Dumitru Macarisin**, *U.S. Food and Drug Administration*,

*Silver Spring, MD, US*

Incidence and persistence of *Listeria monocytogenes* is associated with environment microbiota in tree fruit processing facilities

(16:15-16:45) **Edward Sionov**, *Department of Food Quality and Safety, ARO, The Volcani Center, Rishon LeZion, Israel*

Exploring grains microbiome during storage and its use for biocontrol of mycotoxigenic fungi

(16:45-17:15) **Silvana Vero**, *Facultad de Química – UdeLaR Cátedra de Microbiología, Montevideo, Uruguay*

Exploring the microbiome involved in the control of mycotoxigenic fungi in sorghum silage

(17:15-17:45) **Discussion Session**

**Adam Rivers** and **Andrea Ottesen** – moderators

**Thursday Sept. 12**

### **Morning Session**

#### **Industry Perspective on Plant Microbiome Research and Future Directions**

(Chair: Sharon Doty)

(08:30–09:15) **Barry Knight**, *Indigo Agriculture, Head of Indigo Research Partners, Boston, MA, US*

Developing and Commercializing Microbial Products for Farmers

(9:15 – 10:00) **Natalie Breakfield**, *Director, Molecular Biology, NewLeaf Symbiotics, BRDG Park, St. Louis, MO, USA*

Utilizing M-trophs for sustainable agriculture

(10:00-10:30) **Coffee break**

#### **Practical Applications of Microbiome Research for managing pre and postharvest pathogens**

(Chair: Mark Mazzola)

(10:30-11:00) **Susan Whitehead**, *Department of Biological Sciences, Virginia Tech, Blacksburg, VA, US*

Pest management impacts on the apple microbiome and downstream consequences for fruit quality and cider production

(11:00-11:30) **Samir Droby**, *Dept. Postharvest Science, ARO, the Volcani Center, Rishon LeZion, Israel*

Utilizing the fruit microbiome for biocontrol of postharvest diseases

(11:30-12:00) **Davide Spadaro**, *Dept. Agricultural, Forestry and Food Sciences, (DISAFA AGROINNOVA - Centre of Competence, University of Torino, Italy*

Towards metagenomics-based diagnostics to detect and prevent plant pathogens

(12:00-13:30) **Lunch Break**

### *Afternoon Session*

#### **Practical Applications of Microbiome Research for managing pre and postharvest pathogens- *continued***

(Chair Susan Whitehead)

(13:30-14:00) **Leonardo Schena**, *Department of Agriculture, Mediterranea University, Reggio Calabria, Italy*

Amplicon metagenomics to identify and detect fungal and oomycete plant pathogens: potentialities and shortcomings

(14:00-14:30) **Noam Alkan**, *Dept. Postharvest Science, ARO, the Volcani Center, Rishon LeZion, Israel*

Endophytic microbiome of fruit stem-end and its relation to development postharvest decay

(14:30-15:00) **Haissam Jijakli**, *Integrated and Urban Plant Pathology Laboratory Liège University, Gembloux Agro-Bio Tech, Gembloux, Belgium*

Sampling standardization and metagenomic analysis of epiphytic apple microbiome focusing on biocontrol taxonomy and functions

(15:00-15:30) **Coffee Break**

(15:15-16:00) Flash presentations – posters presenters will be given 5 min to highlight their research

(16:00-17:00) **Discussion Session**

**Michael Wisniewski and Samir Droby**- Moderators

Manipulating fruit microbiome for managing pathogens – Is it feasible?

(19:30-21:30) **Banquet**

**Friday Sept. 13**

**(07:00-08:30) Breakfast**

**Departure** – checkout by noon

## Posters:

**P1: Identification of helper strains from apple fruit epiphytic microbiome to increase *P. anomala* strain K efficacy against *B. cinerea* on postharvest apples**

Abdoul Razack Sare, M. Haïssam Jijakli, Sébastien Massart

**P2: Effect of pack-house treatments on the microbiome of citrus fruit**

Ajay Kumar<sup>1</sup>, V. Yeka Zhimo<sup>1</sup>, Antonio Biasi<sup>1</sup>, Ginat Rafael<sup>1</sup>, Oleg Feygenberg<sup>1</sup>, Shoshana Salim<sup>1</sup>, Michael Wisniewski<sup>2</sup>, Samir Droby<sup>1</sup>

**P3: Analysis of three methods for the concentration of genetic material in bacterial and fungal communities on apple surfaces**

Alexis M. Hamilton and Faith J. Critzer

**P4: Changes in the epiphytic microbiota of apple fruit during storage following the application of the yeast, *Metschnikowia fructicola***

Antonio Biasi<sup>1</sup>, V. Yeka Zhimo<sup>1</sup>, Ginat Rafael<sup>1</sup>, Ajay Kumar<sup>1</sup>, Oleg Feygenberg<sup>1</sup>, Shoshana Salim<sup>1</sup>, Michael Wisniewski<sup>2</sup>, Samir Droby<sup>1</sup>

**P5: High-throughput sequencing gives new insights on dates microbiome: the influence of developmental stage, tissue and growing season.**

Ahmed Abdelfattah<sup>1</sup>, Yaara Danino<sup>2</sup>, Edoardo Piombo<sup>3</sup>, Ginat Raphael<sup>2</sup>, Oleg Feygenberg<sup>2</sup>, Erik Burchard, Michael Wisniewski<sup>4</sup>, Samir Droby<sup>2</sup>

**P6: Apple microbiome response to hot water treatment and the potential of biological control**

Birgit Wassermann, Peter Kusstatscher, Henry Müller\*, Gabriele Berg

**P7: Comparative transcriptomic analysis of the interaction between *Penicillium expansum* and apple fruit during early stages of infection**

Kaili Wang <sup>a</sup>, Xiangfeng Zheng <sup>c</sup>, Xiaoyun Zhang <sup>a</sup>, Lina Zhao <sup>a</sup>, Qiya Yang <sup>a</sup>, Nana A. S. Boateng <sup>a</sup>, Joseph Ahima <sup>a</sup>, Hongyin Zhang <sup>a,\*</sup>, Jia Liu <sup>b</sup>

**P8: Exploring the functional capacity of seed meal-structured microbiomes in the control of apple replant disease**

Tracey Somera, Shiri Freilich, Mark Mazzola

**P9: Microbial consortium for the control of postharvest pathogens of soft berries**

V. Yeka Zhimo<sup>1</sup>, Antonio Biasi<sup>1</sup>, Ajay Kumar<sup>1</sup>, Ginat Rafael<sup>1</sup>, Oleg Feygenberg<sup>1</sup>, Shoshana Salim<sup>1</sup>, Michael Wisniewski<sup>2</sup>, Samir Droby<sup>1</sup>

# ABSTRACTS

## Oral Presentations

### **The Symbiotic–Plant Microbiome and Its Overall Importance in Plant Health**

Sharon L. Doty, Shyam L. Kandel, Pierre M. Joubert, Andrea Firrincieli, Zareen Khan, Andrew W. Sher, Hyungmin Rho, and Patricia Okubara

Just as the human microbiome has proven to be an important factor for our health, the plant microbiome may be an essential aspect of health for plants. The early successional pioneer tree species, poplar (*Populus sp.*) and willow (*Salix sp.*), colonize newly available primary substrates of sand and cobble. Lacking the nutrients found in soils, these plants associate with nitrogen-fixing (diazotrophic) endophytes that can supply this essential macronutrient. Many of the endophyte strains also solubilize phosphate, potentially making this macronutrient more bioavailable. Not only do the microbes improve growth of this important bioenergy plant species, they also increased growth, health, and yields of an exceptionally broad range of plant species, including rice, maize, tomato, pepper, apple, strawberries, ryegrasses, and Douglas-fir. Recently, field trials with some of the strains demonstrated increased yields with reduced fertilizer requirements. Under drought conditions, the endophytes promoted host plant survival, reduced host stress responses, and increased water use efficiency in controlled greenhouse studies. Some endophyte strains also have strong antimicrobial activities, inhibiting the growth of several major soil-borne plant pathogens including *Rhizoctonia solani*, *Pythium ultimum*, *Fusarium culmorum*, and *Gaeumannomyces graminis*. Mechanistic studies with one of the bacterial strains indicated that occidiofungin was largely responsible for the antimicrobial activity against *R. solani*. With the need to substantially and sustainably improve production to meet the needs of a growing human population, and with the increased impacts of climate change, the implications of plant-microbe symbioses for agriculture are profound.

## Exploring the plant microbiome for managing pathogens and resistances

Gabriele Berg, Peter Kusstacher, Birgit Wassermann, Tomislav Cernava, and Henry Müller  
Institute of Environmental Biotechnology, Graz University of Technology, Petersgasse 12,  
8010 Graz, Austria

The plant microbiome is crucial for growth and health (1). Intense agriculture and overuse of chemicals leads to biodiversity loss and resistant pathogens, which are difficult or impossible to suppress but cause enormous yield losses. The plant microbiome will be the key to the second green revolution because it can provide solutions for sustainable agriculture (1). To manage or exploit the plant microbiome require a deep understanding of the composition and function. Soil type, climate, geography, plant genotype and development stage were identified as main drivers of the plant microbiota (1). According to that, the post-harvest microbiome has a specific composition and function, which will be exemplarily shown for apples and sugar beets (2,3). Postharvest food decay, which is one major issue for today's food loss along the supply chain, corresponds with as significant microbiome shift. By conducting a detailed assessment of temporal microbiome changes during the storage of sugar beets, distinct indicator species for health and disease were identified (2). The insights generated in this study provide a novel basis to improve current or develop next-generation postharvest management techniques by tracking disease indicators during storage (2). In addition to monitoring, the microbiome can be managed indirectly by changing abiotic parameters or directly by microbial treatments or transplants. Here, combined approaches are often promising. For example, applying a combined approach of hot water treatment and a biological control consortium consisting of *Pantoea vagans* 14E4, *Bacillus amyloliquefaciens* 14C9 and *Pseudomonas paralactis* 6F3, were proven to be efficient in reducing both postharvest pathogens in apples (4). Altogether, microbial diversity is crucial for managing microbial diversity, pathogens and corresponding resistances (5).

### References

1. Berg *et al.* (2017). *FEMS Microbiology Ecology* 93(5).
2. Kusstacher *et al.* (2018). *Microbiome* 7(1).
3. Wassermann *et al.* (2019) *Frontiers in Microbiology*.
4. Wassermann *et al.* (2019) *under revision*.
5. Mahnert *et al.* (2019) *Nature Communication* 10(1).

## **Molecular Approaches to Study Microbial Ecology on Plant Surfaces**

### **Assembly of epiphytic bacterial communities on plants and their interactions with the plant host**

Steven Lindow

Department of Plant and Microbial Biology, University of California, Berkeley, Berkeley, CA USA

Aerial plant surfaces often harbor large epiphytic bacterial populations, ranging in size from  $10^4$  to  $10^7$  cells/cm<sup>2</sup>. The size and composition of these communities however are determined by both small-scale interactions of bacteria with each other and with their plant host that determine growth and survival, as well as large-scale features such as the proximity and abundance of other plant species that contribute immigrant inoculum. The maximum population size of epiphytic bacteria is limited by Carbon availability on the plant surface and differs among plant species due to the differing amounts of exudates. These Carbon sources and therefore sites of bacterial colonization on plants are spatially heterogeneous, with the majority of bacteria residing in localized sites harboring relatively large, mixed species cellular aggregates. Cell density-dependent behaviors, often modulated by so-called quorum sensing signal molecules facilitate preferential survival of bacteria at such sites during stressful desiccation conditions. Bacteria also modify the local environment on plant surfaces by their production of hygroscopic biosurfactants that make liquid water more available. Many bacteria also produce compounds such as 3-indole acetic acid (IAA) that apparently facilitate the plant conversion of sucrose to fructose, thus facilitating the growth of epiphytes that typically can consume such monosaccharides at the relatively low concentrations made available by exhibition from plants, but which cannot consume disaccharides at such low concentrations. Bacterial IAA production by epiphytes, however, is associated with altered plant development, such as the induction of fruit russeting. The composition of epiphytic bacterial communities is only moderately plant species-specific, apparently driven by yet to be determined morphological and chemical features of plant surfaces. Epiphytic bacteria readily escape from the surface of plants and strongly influence the composition of airborne bacteria nearby. As such, such airborne bacteria are a primary source of immigrant bacteria for the establishment of epiphytic communities on leaves, flowers, and fruit that typically harbor few or no resident bacteria early in their development. Because of the differing amounts and types of surrounding vegetation present during the development of new tissues of a given plant species, the composition and size of epiphytic communities on that plant species is very context-dependent, and can be strongly influenced by management practices that influence the agro-ecological context of a given crop plant.

## **The role of the microbiome in the holobiont**

Colin R. Jackson

*Department of Biology, University of Mississippi, University, MS. USA*

The concept of the holobiont, that the biological unit of organization thought of as an organism is really a metaorganism consisting of the host and all of its associated microorganisms is becoming more prevalent in microbial ecology, although controversy over the concept remains. While more often applied to animals, the holobiont idea is increasingly being applied to plants, and implies a co-evolutionary path between plants and their microbiota. Plant-associated bacteria are likely involved in host stress tolerance, growth promotion, nutrient acquisition and disease resistance, all of which would increase holobiont survival and fitness. However, beyond pathogen resistance and its applications to biocontrol, questions remain about how these concepts apply to parts of a plant post-harvest. Can harvested fruit and its microbiota still be viewed as a holobiont, even when no longer connected to the parent plant? How does the holobiont concept consider the dramatic changes that fruit undergoes during ripening and eventually senescence? These and other concepts relating to the role of the microbiome in plants and especially fruit will be discussed.

## **Manipulation of the orchard soil microbiome: Implications for soil-borne disease suppression and apple production**

Mark Mazzola, Tracey Somera, Christopher Van Horn, Rachel Leisso, Shiri Freilich  
*U.S. Department of Agriculture-Agricultural Research Service, Wenatchee, WA, USA;*  
*Agricultural Research Organization, The Volcani Center, Newe Ya'ar Research Center,*  
*Israel.*

Interventions targeted to manipulation of the soil/rhizosphere microbiome is a tool commonly employed to suppress activity of soil-borne pathogens. Such strategies often utilize an undirected approach, such as soil fumigation, or directed approaches that take advantage of host and non-host resistance (crop rotation) to a specific pathogen. The biologically multifaceted phenomenon termed apple replant disease is resistant to extended suppression, with soil fumigation generally providing a temporally limited (<1-year) period of disease control. This research program has sought to direct assembly of the soil/rhizosphere microbiome in a manner that provides initial soil-borne disease control while also limiting subsequent pathogen re-infestation of the orchard soil system. We have employed various strategies to attain this goal including pre-plant application of defined soil amendments and exploitation of rootstock genotypes to amplify or recruit specific microbial consortia to the rhizosphere. Sustained suppression of multiple soil-borne pathogens in response to Brassicaceae seed meal amendment was found to rely upon transformation of the indigenous soil microbiome. The dominant microbial elements contributing to disease suppression differed in a target pathogen-dependent manner with multiple functional modes of action inferred. Apple rootstock genotype also influenced composition of the rhizosphere and endophytic microbiome, and was associated with differences in the root exudate metabolome. Field trials demonstrated persistent (multi-year) changes to the rhizosphere microbiome and associated suppression of soil-borne pathogens in response to seed meal treatments. Non-target benefit, including suppressed inoculum of post-harvest pathogens, may also be realized. Our findings suggest that plant rhizosphere and amendment-based engineering of the soil microbiome may yield more resilient and productive orchard systems than that attained in response to pre-plant soil fumigation.

## **Ecological Assembly of Rhizosphere Microbiomes to Modify Plant Reproductive Traits**

Jenny Kao-Kniffin, Cornell University

Abstract: Soil microorganisms such as those found in the rhizosphere have a tremendous influence on different aspects of their host's biology, yet they are often overlooked in plant biology studies. In a series of experiments on directed evolution of the rhizosphere microbiome, we aimed to develop microbial communities associated with enhanced seed yield in rapidly cycling *Brassica rapa* and altered flowering time in *Arabidopsis thaliana* using a multi-generation experimental evolution system. Microbiomes were collected from the rhizosphere soil of a subset of plants to be used as inoculants for the subsequent planting generation. After multiple generations of selection for modified plant traits, the composition and function of the rhizosphere microbiome shifted away from the control microbiomes. The microbiomes assembled from a specific trait selection pressure showed the ability to alter the plant traits of novel plant host genotypes or species. The results of the experiments suggest that directed evolution of rhizosphere microbiomes impact the plasticity of flower and seed phenotypes, which could play an important role in commercial plant production systems.

## The inherited microbiome of oak

Ahmed Abdelfattah<sup>1</sup>, Michael Wisniewski<sup>2</sup>, and Ayco Tack<sup>1</sup>

<sup>1</sup> Department of Ecology, Environment, and Plant sciences, Stockholm University, Sweden

<sup>2</sup> U.S. Department of Agriculture—Agricultural Research Service (USDA-ARS), USA.

Plants, with no exception thus far, are associated with many microorganisms that live endo and/or epiphytically. These communities, also referred to as the plant microbiome, have been increasingly shown to play a crucial role in plant's health and productivity. While factors such as environment have an important impact on the plant microbiome and are considered one of its main sources, plant genotype was shown to be the main determinant of the microbial community composition. The hologenome theory of evolution suggests, in one of its four generalizations, that microorganisms are transmitted between generations. However, for plants, this principle was based transmission via vegetative reproduction or extreme symbionts that are transmitted by cytoplasmic inheritance e.g. chloroplast or other microorganisms that are transmitted to seeds from the environment. In this work we try to test the hypothesis that the plant microbiome is, at least partially, transmitted between generations by sexual reproduction via seeds. We also investigate their transmission route i.e. from seed's to seedling's phyllosphere and roots. To this aim we developed and used a state-of-the-art apparatus for growing common oak, as model species, in a germ-free environment while separating belowground (root system) and aboveground (phyllosphere) tissues. We used amplicon sequencing of the fungal ITS2 rDNA to identify the fungal communities present in acorns (embryos and pericarps) and oak seedlings (roots and phyllosphere). Our results shows that despite the harsh surface-sterilization of acorns and their growth in aseptic conditions, embryos, pericarps, leaves, and roots were colonized by a wide range of fungal taxa which differed greatly in their composition according to the tested tissue. In terms of similarity, embryos and leaves were more similar in their composition, whereas roots and pericarps had distinct communities. Nonetheless, the majority of the fungal community detected in acorns were also present in leaves, roots, or both. Interestingly, we observed although at a low relative abundance, a group of an unidentified AMF from the phyla Glomeromycota, which appeared to be present only in embryos and roots of oak seedlings. Results of this work may help explain the continuity of the plant microbiome between generations and increase our understanding of the role of these microbes during the early stages of the plant's life.

## **Exploring the Apple Microbiome**

Michael Wisniewski and Samir Droby

*U.S. Department of Agriculture – Agricultural Research Service (USDA-ARS), Kearneysville, WV USA, Agricultural Research Organization (ARO), The Volcani Center, Department of Postharvest Science, Bet Dagan, Israel*

As the human population of the world continues to increase, the challenge of providing enough food will also grow, especially as the climate begins to warm, episodes of erratic weather increase, and high-quality, arable land is lost to development. Serious questions have arisen regarding the ability of plant breeding to keep up with the demand for increased productivity. Within that scenario, the use of beneficial microbial consortia has been proposed as a way to maintain or increase plant productivity in stressful environments, offering the ability of plants to maintain or increase their growth in unfavorable environmental conditions, and increasing disease resistance. The recognition of the intimate relationship between organisms and their resident microbiota (both epiphytic and endophytic) has grown resulting in concepts such as the metaorganism and the holobiont. New sequencing approaches have enabled researchers to explore the microbiome of organisms and investigate their function in an unprecedented manner. Developing microbial consortia to increase plant productivity, however, represents only part of their potential use. Preserving food in a safe and effective manner represents another approach that can be used to provide enough food for a hungry world. Over the past few years, we have begun to explore the microbiome of apple in order to better understand apple biology within the context of the metaorganism concept and in hopes of developing new ways to prevent postharvest losses due to disease but perhaps also to physiological disorders (e.g., physiological scald). Thus far, we have been able to document spatial differences in the microbial composition of harvested fruit where calyx, peel, stem, and wounded tissues all exhibit distinct differences in beta-diversity. We are also in the process of determining if and to what extent a core microbiome of apple can be defined by sampling field-harvested “Royal Gala” fruit from several orchards throughout the world. Distinct genotypic (cultivar) differences in the composition of the endophytic microbiota of apple stems has also been documented. Lastly, the effect of postharvest handling practices (washing, waxing, and cold storage) on the microbiota of apple fruit has been examined. Future studies will move beyond compositional analyses into trying to analyze the functional role of specific microbiota and how developing fruit and the host microbiome effect each other.

## **Microbiome data are compositional: What does that mean and how do we deal with it?**

Adam R. Rivers. PhD  
Computational Biologist  
USDA-ARS Genomics and Bioinformatics Research Unit

Microbiome data are compositional. DNA sequencing is a process that samples an arbitrary number of reads from a much larger pool of DNA. This means that each taxon/gene detected has an effect on every other taxon/gene and the total number of reads only affects the accuracy of our estimates. This has profound implications that require a shift in the way we think about our data. The total number of reads assigned to a taxon or gene does not directly correspond to the number of copies in the sample. Dividing by the total does not solve this. The compositional nature means that many commonly used microbiome methods are inappropriate, including common methods of sub-setting data for bar plots, distance methods like Bray-Curtis, standard ordination and many covariance networks. Fortunately, the field of Compositional Data Analysis (CoDa) has developed a number of methods applicable to microbiome data and new microbiome specific analysis packages using these methods are available to analyze the data correctly. Doing this requires us to change our methods, and in some cases the way we formulate our research questions. This talk explains the problem, how compositional data use log ratios to solve it and how to replace conventional methods with statistically appropriate compositional methods.

## **Bioinformatics approaches for metagenomics data analysis**

Adi Doron-Faigenboim

*Plant Sciences, Vegetable and Field Crops ARO, The Volcani Center, Rishon LeZion, Israel*

Rishon LeZion 7528809, Israel

[adif@volcani.agri.gov.il](mailto:adif@volcani.agri.gov.il)

Next-generation sequencing technologies and computational biology allow characterization of the structure of microbial communities using metagenomic approaches. Amplicon sequencing of the 16S ribosomal RNA (rRNA), 18s rRNA or the Internal Transcribed Spacer genes (ITS) are a well-established method for taxonomic composition. An alternative approach to the amplicon sequencing method is whole genome shotgun sequencing (WGS) that randomly sequencing overlapping regions of a genome. The major advantages of the WGS method are that the taxa can be more accurately defined at the level of the species. A pipeline of the metagenome analysis includes: assemble the overlaps sequences to contigs, predict putative genes on that contigs, classifying genes by aligning them to public databases such as the non-redundant protein sequences of the National Center for Biological Information database (NCBI) and sequences in KEGG pathways database (Kyoto Encyclopedia of Genes and Genomes), analyze the biodiversity of the samples. Here, we review the computational pipeline and software that are used in microbiome analysis.

Detoxification of mycotoxins by yeast biocontrol agents – biochemical and molecular mechanisms.

## **Computational approaches for deciphering the functions of microbial communities**

Shiri Freilich, Maria Vetcos, Assaf Malik, Shlomit Medina, Edoardo Piombo, Matan Cohen, Maya Ofek-Lalzar, Adi Faiganbion-Doron Mark Mazzola

*U.S. Department of Agriculture-Agricultural Research Service, Wenatchee, WA, USA;  
Agricultural Research Organization, The Volcani Center, Newe Ya'ar Research Center,  
Israel.*

Soil-borne disease have, in many cases, efficient and environmentally friendly amendment-based solutions. Success of such amendment-based treatments to stimulate a microbiome-mediated disease control strategy is determined by the introduction of accessible metabolites that are beneficial to organisms functional in disease control or deleterious to organisms contributing to disease progression. Metagenomic surveys allow exploring the significance of shifts in community structure through comparing the functional potential of different samples. In my talk, I will present the application of network approaches for finding environmental friendly solutions for soil borne diseases, based on the analyses of metagenomics data from healthy vs. symptomatic apple orchards following effective and non-effective soil amendment treatments. Such integration of metagenomics data aims at laying foundations for the educated design of sustainable solutions for suppressing soil-borne disease symptoms through substrate mediated recruitment of disease-suppressive microbiomes in cropping systems.

## **Novel insights into plant microbial ecology revealed through use of consistent protocols and meta-analyses**

Justin P. Shaffer

Postdoctoral Fellow

Department of Pediatrics, School of Medicine, University of California, San Diego, La Jolla, CA 92093

[jpshaffer@ucsd.edu](mailto:jpshaffer@ucsd.edu)

Our growing understanding of microbial community ecology has benefited greatly from the adoption of novel protocols that allow for reproducible, multiplexed sequencing of hundreds-if-not-thousands of samples, economically viable even outside of medical fields. In particular, studies of plants using such methods have revealed a diversity of microbial associates not observed using more traditional, culture-based techniques – which have implications for promoting plant health and sustainability. Still, much work remains with respect to confidently comparing results across studies, in large part due to the great number of analytical pipelines and tools used to analyze microbial community sequence data. Each research group has their favorite methods – often justifiably so. However, to bootstrap our knowledge of plant-microbe interactions as such to reveal novel insights into their ecology, alongside the adoption of universal sequencing protocol, a widely accepted analytical framework is needed – one that allows for streamlined meta-analyses of all reasonably comparable data available. Here, we demonstrate the utility of such a framework across a subset of plant microbial datasets, highlighting emergent findings from both re-analysis of individual studies using a single analysis pipeline, as well as from a meta-analysis across all studies.

## **Harnessing metabolomics in microbiome studies**

Tal Luzzatto-Knaan

Natural products, are small molecules produced by an organism and have various biological roles in nature. Some serve as regulators of cellular processes, some as communication signals and some as defensive molecules that may be utilized in agriculture, biotechnology and medicine. Metabolomics is an emerging field targeting to explore the unique chemical profile characterizing a biological sample. This talk demonstrates a metabolomic approach using orthogonal mass spectrometry to study natural products involved in microbial interactions and large-scale collections of microbial environmental samples. The ability to explore the spatial and temporal metabolomic patterns enable the discovery of new biological functions as well as novel compounds.

## **Microbiome Research in the Office of Regulatory Science**

Andrea Ottesen

U.S. Food and Drug Administration, CFSAN FDA, Silver Spring, MD, USA

Culture-independent next-generation sequencing technologies have fueled a renaissance in our understanding of what it means to be human. Targeted and target-independent metagenomic data have been used to describe microbial ecologies from soils to clouds and from body surfaces (skin) to internal processes (gut). Even the human immune system can no longer be understood without also considering a 1,000 fold more abundant complement of microbial genes compared to host genes. This paradigm shift has also occurred in our understanding of the foods we consume and the complex microbial ecologies along the farm-to-fork continuum. These ecologies are important both for food safety (exposure to pathogens) and for issues of nutrition, allergy, and immunology. Despite the emphasis on “purity” in the Pure Food and Drug Act of 1906, which led to the creation of the Food and Drug Agency, the Act was written at a time when the word “purity” completely excluded microbes. It is now understood that almost every food (except, potentially, highly processed foods) has a bacterial, fungal, viral, and potentially archaeal component to its “naive” (pure) state. Food science finds itself at a new and exciting interface of microbiology, nutrition, and immunology. We are reevaluating nutritional sciences, using a more comprehensive inventory of the prebiotic and probiotic potential of foods. Dr. Ottesen will discuss laboratory and bioinformatic approaches used at the Center for Food Safety and Applied Nutrition of the FDA to track pathogens, characterize food microbiomes and identify plant species used in foods and dietary supplements.

## **Incidence and persistence of *Listeria monocytogenes* is associated with environment microbiota in tree fruit processing facilities**

Dumitru Macarisin<sup>1</sup>, Xiaoqing Tan<sup>2</sup>, Yi Chen<sup>1</sup>, Luke LaBorde<sup>2</sup>, Jasna Kovac<sup>2</sup>

<sup>1</sup> Center for Food Safety and Applied Nutrition, Food and Drug Administration, College Park, MD 20740, USA

<sup>2</sup> Department of Food Science, The Pennsylvania State University, University Park, PA 16802, USA

The implication of three fruits in recalls and outbreaks of human illnesses, due to contamination by foodborne pathogens, has been on the rise over the last decade. The outbreaks caused by *Listeria monocytogenes* have been particularly puzzling, because the implicated tree fruit commodities (apple and stone fruit) do not support growth of this pathogen. The sources and routes of apple and stone fruit contamination by *L. monocytogenes* remained unknown. This lecture will deliver novel findings on the occurrence and persistence of *L. monocytogenes* in tree fruit packing environments, as well as the effect of conventional postharvest practices on the long-term survival of this pathogen in whole apples. It will also provide an insight in build environmental microbiomes of tree fruit packing facilities and their association with occurrence and persistence of the foodborne pathogen, *L. monocytogenes*.

## Exploring grains microbiome during storage and its use for biocontrol of mycotoxigenic fungi

Edward Sionov<sup>1</sup>, Manoj Kumar Solanki<sup>1</sup>, Ahmed Abdelfatah<sup>2</sup>, Michael Wisniewski<sup>3</sup>, Samir Droby<sup>1</sup>

<sup>1</sup>*Agricultural Research Organization (ARO), The Volcani Center, Institute of Postharvest and Food Sciences, Rishon LeZion, Israel*, <sup>2</sup>*Department of Ecology, Environment and Plant Sciences Stockholm University, Stockholm, Sweden*, and <sup>3</sup>*U.S. Department of Agriculture – Agricultural Research Service (USDA-ARS), Kearneysville, WV USA*,

Mycotoxins are low-molecular weight natural products produced as secondary metabolites by toxigenic filamentous fungi that contaminate food, the food chain, and represent a risk to human and animal health. The major mycotoxins that occur in food and agricultural commodities are produced by *Fusarium* (deoxynivalenol, trichothecenes, fumonisins and zearalenone), *Alternaria* (alternariol, altenuene, tenuazonic acid), *Aspergillus* and/or *Penicillium* (aflatoxins, ochratoxin A, patulin). Mycotoxins have been shown to be the number one threat amongst food and feed contaminants regarding chronic toxicity. Moreover, the presence of mycotoxins in agricultural products is also an economic concern. A quarter of the world's crops are estimated to be contaminated to some extent with mycotoxins.

Under certain storage conditions, fungi can cause spoilage in stored crop seeds, decreasing crop value, or produce mycotoxins that have a direct effect on human health. Protecting stored wheat grain from fungal spoilage is an essential part of their production. Wheat associated microorganisms can have beneficial effects on the stored grain's health. Understanding the composition and role of stored wheat grain microbiota is crucial toward agricultural practices that are less dependent on chemical fungicides, which has known negative effects on the environment and human health. High-throughput amplicon sequencing of the bacterial 16S rRNA gene and fungal internal transcribed spacer (ITS) region was used to analyze the wheat grain microbiome at different times over a 6 months period of storage. Results of the present study indicate that microbiome of stored wheat grains was strongly affected by phosphine fumigation (one of the most effective methods to eliminate insects in stored commodities), which changed the structure of the microbial community leading to shifts in species composition toward mycotoxigenic strains.

A number of bacterial and yeasts isolates, which were cultured from wheat grains and assessed for their antifungal activity, presented antagonistic properties against a variety of mycotoxigenic fungal pathogens. A better understanding of the complex interactions within the microbial communities of stored grains will assist in the development of novel biocontrol strategies to overcome mycotoxin contamination.

## **Exploring the microbiome involved in the control of mycotoxigenic fungi in sorghum silage**

Mariana Gonda, Gabriela Garmendia, Caterina Rufo, Michael Wisniewski, Samir Droby, Silvana Vero

*Área Microbiología, Departamento de Biociencias, Facultad de Química, Universidad de la República, Montevideo 11800, Uruguay, U.S. Department of Agriculture – Agricultural Research Service (USDA-ARS), Kearneysville, WV USA, Agricultural Research Organization (ARO), The Volcani Center, Department of Postharvest Science, Bet Dagan, Israel*

The capacity of microorganisms from water kefir (WK) to control *Aspergillus flavus* growth during the aerobic phase of ensiled sorghum grains was determined. Sorghum inoculated with *A. flavus* was treated with filter-sterilized and non-sterilized water kefir, ensiled, and incubated 7 days at 25 °C. *A. flavus* growth was quantified by qPCR after incubation. Mold growth was inhibited in the presence of water kefir while no inhibition was observed when filter-sterilized water kefir was applied, demonstrating the relevant role of the microorganisms in the kefir water in the biocontrol process. Fungal and bacterial diversity in treated sorghum mini-silos was analyzed by high-throughput sequencing. Firmicutes was the predominant bacterial phyla and *Lactobacillus* represented the most abundant genus, while Ascomycota was the predominant fungal phyla with *Saccharomyces* and *Pichia* as the major genera. Bacterial and yeast counts before and after incubation indicated that the microbial community obtained from WK was able to grow in the sorghum mini-silos in the presence of *A. flavus*. Results of the present work indicate that the use of a mixed inoculum of microorganisms present in WK may represent an alternative management practice to avoid the growth of *A. flavus* in ensiled sorghum grains and the concomitant contamination with aflatoxins.

## **Developing and Commercializing Microbial Products for Farmers**

Barry Knight, Head of Indigo Research Partners, Indigo Agriculture, Memphis, TN

Indigo Agriculture improves grower profitability, environmental sustainability, and consumer health through the use of natural microbiology and digital technologies. Utilizing beneficial plant microbes and agronomic insights, Indigo works with growers to sustainably produce high quality harvests. The company then connects growers and buyers directly to bring these harvests to market. Working across the supply chain, Indigo is furthering its mission of harnessing nature to help farmers sustainably feed the planet.

Inspired by insights from the human microbiome, Indigo was founded in 2014 with the hypothesis that naturally occurring microbes living inside a plant (endophytes) are vital to its health. With sophisticated sequencing techniques, Indigo has assembled a world-class database of genomic information from these microbes. Potentially beneficial microbes are identified and tested in the lab, greenhouse, field, and, finally, on farms through a program called Indigo Research Partners. Through this network of over 75 large and influential growers, Indigo has instrumented fields across the US, Argentina, and Australia to gather over a trillion data points each day and test hundreds of agricultural technologies. The ultimate ambition of Indigo Research Partners is to enable data-based agronomic and financial decision making, while accelerating the adoption of innovative technologies.

## Utilizing M-trophs for sustainable agriculture

Natalie Breakfield

*NewLeaf Symbiotics, Saint Louis, MO*

Pink-pigmented facultative methylotrophs in the genera *Methylobacterium* and *Methylorubrum* (M-trophs) are highly abundant members of the plant microbiome. NewLeaf Symbiotics is harnessing the power of these beneficial bacteria to improve yield and strengthen plants under field conditions. We are optimizing genotypic and phenotypic data in our Prescriptive Biologics Knowledgebase™ (PBK). Our focus on M-trophs has enabled us to use comparative genomics to make initial predictions of which M-trophs will perform best for a given condition and crop. These predictions are then tested in the field, and these data are used to improve our processes. Our pipeline has led to the introduction of our first four products under our Terrasym™ brand.

## **Pest management impacts on the apple microbiome and downstream consequences for fruit quality and cider production**

Susan Whitehead, *Department of Biological Sciences, Virginia Tech, Blacksburg, VA, USA*

Increasing the sustainable production of healthy food will depend on integrative approaches to manage not only crops themselves, but the entire phytobiome, including plants and their associated microbes. Our understanding of these communities is burgeoning, in large part due to new technologies that enable rapid characterization of microbial communities. However, few studies have examined microbial communities occurring in and on fruits, despite the importance of fruits as the edible commodity for many crops. Fruit microbes likely interact with major insect pests and pathogens and affect fruit quality traits that can directly impact both the nutritional and economic value of our food. Using apples as a model system, our research aims to uncover how: 1) organic and conventional pest management practices shape microbial communities surrounding fruits, 2) microbial communities, in turn, affect fruit quality traits that determine market and nutritional value and, 3) microbial communities and fruit quality traits affect hard cider production, currently the fastest growing segment of the American beverage industry. Our new USDA-funded research brings together a multi-disciplinary team with expertise in plant interactions and chemical ecology, microbial ecology and bioinformatics, and food science and cider production. Our specific objectives are to: 1) Characterize variation in apple microbiomes among 20 organic and conventional apple orchards and use generalized joint attribute modeling to understand relationships among pest management, fruit microbiomes, fruit quality, and pest/pathogen resistance, 2) Establish an orchard that will allow us to experimentally determine the effects of specific pest management practices on fruit microbiomes and the effects of specific microbial taxa on fruit quality and pest resistance, and 3) Determine how fruit interactions with microbes and associated changes in fruit quality affect the sensory and phytochemical properties of hard cider. This talk will provide an overview of our planned research as well as preliminary data on the impacts of pest management on the fruit-associated microbiome. Considering the economic value of apples and their iconic image as both health-promoting fruits and symbols of American culture, our research program can simultaneously improve our fundamental understanding of agroecosystems, provide new direction for applied technology in microbiome management, and engage students and the general public in the importance of ecological interactions in shaping our food systems.

## Utilizing the fruit microbiome for biocontrol of postharvest diseases

Samir Droby<sup>1</sup> and Michael Wisniewski<sup>2</sup>

<sup>1</sup>*Department of Postharvest Science, Agricultural Research Organization (ARO), the Volcani Center, Bet Dagan, Israel*

<sup>2</sup>*Appalachian Fruit Research Station, USDA-ARS, Kearneysville, WV, USA*

Harvested fruits and vegetables are dynamic systems with complex interactions between microbial communities and their fruit hosts. The role and function of the microbiome in fruit physiology, quality, and disease resistance before and after harvest are largely unknown. The complexity of fruit microbiome was demonstrated in recent studies performed on different types of fruit tissues as well as the effect of various pre and postharvest treatments. The approach of using a single antagonist for biocontrol of postharvest diseases should be re-examined taking into consideration the dynamics and plasticity of the complexity of the microbiome of harvested commodities. Although several biocontrol products, based on single antagonist have been developed, their efficacy under commercial conditions has been inconsistent and fallen short of industry requirements. Thus, a more comprehensive understanding of the dynamics and function of the fruit microbiome is needed to design better biocontrol systems.

In a recent effort to characterize the postharvest fruit microbiome, a global effort was used to identify the existence of a core microbiome that could be utilized to select a consortium of microorganisms for postharvest biocontrol of fruit diseases. Such a consortium may provide distinct advantages in terms phenotypes/functions, such as optimal colonization of surface wounds and utilization of available nutrients, enhanced ability to induce resistance, microbes that can colonize intact surfaces and/or special niches, production of secondary metabolites, proteases, and fungal cell-wall-degrading enzymes, etc. Another approach that is being examined is the application of genome-wide modeling to provide information that could be used to establish and sustain beneficial microbial communities on fruit surfaces. Characterization and analysis of microbial networks are being used to predict the beneficial effects of specific microbial genera or species and design ways to specifically manipulate their population through the use of nutrient amendments.

## **Towards metagenomics-based diagnostics to detect and prevent plant pathogens**

Davide Spadaro<sup>1,2</sup>, Edoardo Piombo<sup>1,2</sup>

<sup>1</sup>*Department of Agricultural, Forestry and Food Sciences (DISAFA), University of Torino, Grugliasco, Italy;* <sup>2</sup>*Centre of competence for the innovation in the agro-environmental sector (AGROINNOVA), University of Torino, Grugliasco, Italy*

Plant diseases are a major cause of food loss worldwide, contributing to losses in agricultural productivity ranging from 20% to 40%. These losses are either direct or indirect, resulting from a disruption of food quality and safety, and they have profound effects on food chains. In such a context, reliable diagnostic methods are needed to identify risks to plant health and promptly and efficiently administer plant protection products.

Current molecular diagnostic techniques, usually based on PCR, are very sensitive, specific and accurate. Some, especially those based on LAMP, are also very portable and allow for in the field molecular detection of plant pathogens, but they are always limited to detecting one or very few pathogens with each analysis. A completely non-targeted approach would provide an unbiased, holistic view of all the organisms (pathogenic or otherwise) in the sample of interest and would be of significant value in finding new and emerging pathogens, as well as for finding and identifying organisms that are unexpectedly present in a sample. A potential solution for surveillance in this type of material is a non-targeted approach based on High throughput Sequencing (HTS). Metabarcoding and shotgun metagenomics provide a useful tool for identifying at the same time a high number of possible pathogens in plants or seeds, but their application is still rare in the diagnostic field, except for shotgun metagenomics-based detection of viruses. Metabarcoding-based analyses are cheaper than shotgun metagenomics, they require less storage space, as well as less computational power, and they are easier to deal with from a bioinformatics point of view. However, the choice of the primers heavily influences the outcome, and for some genera, especially fungal ones, their resolution does not go beyond the genus-level. Shotgun metagenomics suffers no PCR-derived biases and allows for the analysis of the whole genome of pathogens, but it is expensive and can perform poorly when there is high biodiversity, many related strains are present and/or organism distribution is very uneven. The quality of databases is another central point to consider when applying any of these techniques for diagnostic purposes.

We consider the applicability of metagenomics in plant diseases diagnostics, discussing the limitations and applications of each technique. Problems that the scientific community needs to solve to enable the implementation of this tool are identified, and the interaction of metagenomics with other approaches, such as sampling of the airborne inoculum, is explored.

## **Amplicon metagenomics to identify and detect fungal and oomycete plant pathogens: potentialities and shortcomings**

Leonardo Schena, Ahmed Abdelfattah

Dipartimento di Agraria, Università Mediterranea di Reggio Calabria, Italy; Department of Ecology, Environment and Plant Sciences, Stockholm University, Stockholm, Sweden

Amplicon metagenomics and second-generation high-throughput sequencing (HTS) methods represents a powerful tool to investigate the microbial communities from any kind of sample and matrix and to understand ecology and functioning of microorganisms. These methods also have great potential applications in plant pathology to investigate etiology, epidemiology, and biology of diseases as well as to protect plants from new pathogen introduction through effective plant biosecurity programs. They have the potential to be applied in broad surveys to simultaneously detect multiple pathogens including those still unknown to the scientific community that escape all other currently available detection methods. However, applications in plant pathology are still limited, mainly because currently available methods accurately identify microorganisms at the genus and at higher taxonomic levels, but generally fails in identifying species and/or subspecies. This limit is extremely important because phylogenetically related taxa may have a completely different behavior, for instance in term of pathogenicity or biocontrol efficacy. Possible strategies to improve the level of discrimination include the phylogenetic analysis of related HTS sequences along with validated panels of reference sequences, the identification and validation of alternative barcode genes and primers, and the simultaneous analysis of two or more barcode genes. Third-generation sequencing methods also have the potentiality of greatly improving the molecular identification of organisms by enabling the analysis of longer barcode genes and/or the PCR-free sequencing of genomes, but their high sequencing errors rate still limits their application. Potentialities and shortcomings of different strategies will be analyzed.

## **Endophytic microbiome of mango-stem-end and its relation to development of postharvest decay**

Noam Alkan, Ortal Galsurker, Sonia Diskin, Dalia Maurer, Oleg Feygenberg  
Department of Postharvest Science, ARO, Volcani Center, Rishon LeZion, Israel.

Stem-end rots (SER) develop in ripe fruits and cause significant losses. SERs are caused by pathogenic fungi that endophytically colonize the vascular-stem-tubes during fruit development in the orchard and remain quiescent until fruit ripening. When the fruit ripens, the fungi switch to necrotrophic colonization of fruit parenchyma, causing SER. Since fruit stem-end is also colonized by non-pathogenic fungi, yeast, and bacteria, we hypothesized that the variance of the microorganism community or the occurrence of endophytic-fungal-pathogens in the microbiome will determine the incidence of postharvest decay and specifically SER in mango fruit. Characterization of the endophytic-microbiome-dynamics in the stem-end tissue of mango fruit in various conditions showed that tolerant fruit restricted the pathogenic-fungi occurrence and usually had a higher variance of the endophytic-microbiome. One example showed that fruits subjected to sunlight in the orchard accumulated anthocyanins and red-peel-color and were more tolerant to SER. Those red and tolerant fruits contained less Pleosporaceae (*Alternaria*) the most abundant fungal-pathogen and had higher microbial variance in their stem-end than green mango fruits from the same tree. Another example showed that harvesting mango fruits with their stem-end resulted in less postharvest decay, the fungal community in both treatments of harvesting with or without stem was similar before harvest, but the occurrence of endophytic-pathogenic-fungi in the microbiome increased during long storage in fruits without a stem. Similarly, during storage, the fruits ripen and become more susceptible, in parallel, the fruit stem-end microbiome changes and contain more fungal-pathogens. Soon before the development of SER, the increased amount of fungi was correlated with the increase in abundance of chitin degrading Chitinophagaceae bacteria. Collectively, our results show that pre and post-harvest treatments/conditions could modify the microbiome to a less pathogenic-community with higher microbial-variance in the fruit-stem-end, these changes were associated with reducing postharvest SERs and with higher tolerance of the fruit to biotic and abiotic stresses.

## Sampling standardization and metagenomic analysis of epiphytic apple microbiome focusing on biocontrol taxonomy and functions

M. Haïssam Jijakli, A. R. Sare, S. Massart

*Integrated and Urban Plant Pathology Lab, Gembloux Agro bio tech, Passage des Déportés, 2, 5030 Gembloux, Belgium*

The epiphytic plant microbial communities living at the surface of fruit have been the source of most current biocontrol agents (BCAs) and can influence fruit quality during storage. Their taxonomical and functional analysis is then crucial and has been boosted by the exponential evolution of High Throughput Sequencing (HTS) technologies. Some studies were recently published on such plant communities and more particularly on apple fruits<sup>1,2</sup>. However, the publications currently use diverse protocols, making their comparison difficult while the full potential of microbiome analyses can only be achieved if scientific results can be shared and compared with limited bias. The need for standardization of the different steps in plant-microbiome studies is therefore a recurrent theme amongst research groups and microbiota harvesting is the first step that can introduce biases using HTS.

During the first phase of our study, the microbiota of the apple fruit carposphere was harvested by four successive washes of whole apples of the commercial Golden Delicious cultivar with four different washing methods. Our results indicate that the washing method strongly influences the quantity of microorganisms harvested and that 4 successive washes can increase the concentration of microorganisms recovered up to 3 times. However, when analysing the microbial composition, the washing method seemed to have little impact, even though the pool of 4 successive washes allowed the harvest of more microbial diversity and reduced the inter sample variability.

The second objective of this study was to characterise the bacterial and fungal communities residing on the surface of *Pinova* cultivar apples at the taxonomical and functional levels by using a shotgun metagenomics approach. *Pinova* Apples from an organically managed orchard bearing no symptom of disease development were sampled in an orchard at harvest, and their epiphytic microbiota was isolated with one washing. After DNA extraction, 14.1 Gbases of raw sequences were generated by HTS. These sequences were annotated following two pipelines in parallel: (i) they were individually analysed by the MG-RAST server, and (ii) they were de novo assembled into contigs and the contigs were annotated by the IMG server.

Our results showed a very high fungal and bacterial diversity, with a higher proportion of fungal sequences (79.0%) than bacterial sequences (13.8%). Considering the genera including beneficial fungi and bacteria identified on *Pinova*, a high relative proportion of epiphytic yeasts were identified. *Filobasidiella* was the most abundant genus, followed by *Talaromyces*, *Bacillus*, *Candida*, and *Saccharomyces*. In total, 21 genera including apple-beneficial microorganisms were detected.

The functional analysis highlighted sixty-five biocontrol genes in the apple metagenome. For example, a total of 31 genes linked to mycoparasitism, plant resistance, and secondary metabolite production were found to be carried by BCA species, mostly *F. neoformans*.

1. S. Droby and M. Wisniewski (2018). The fruit microbiome: A new frontier for postharvest biocontrol and postharvest biology. *Postharvest Biology and Technology*, 140, 107-112.
2. D. Angeli, A. R. Sare, M. H. Jijakli, I. Pertot, S. Massart (2019). Insights gained from metagenomic shotgun sequencing of apple fruit epiphytic microbiota. *Postharvest Biology and Technology*, 153, 96-106.

## Poster Presentations

### **Identification of helper strains from apple fruit epiphytic microbiome to increase *P. anomala* strain K efficacy against *B. cinerea* on postharvest apples**

Abdoul Razack Sare, M. Haïssam Jijakli, Sébastien Massart

*Integrated and Urban Plant Pathology Lab, Gembloux Agro bio tech, Passage des Déportés, 2, 5030 Gembloux, Belgium*

Apple fruit epiphytic microbiota has been the source of the majority of biocontrol agents (BCAs) and can influence the fruit quality during storage. However, the use of BCA in commercial application is limited by low or non-reliable efficacies in comparison to chemical fungicides. Indeed, once applied on the fruit surface, a BCA faces a complex microbiota where ecological interactions (parasitism, mutualism, commensalism) occur, thus affecting its efficacy. To address this concern, Massart et al. (2015) suggested the use of microbiota to improve BCA efficacy by the selection of helper strains. Apple fruit samples of fifteen varieties grown in four disease management practices (DMP) (never treated, light organic, organic and conventional) were collected in Belgium. Their epiphytic microbiota were harvested and their efficacy to raise the biocontrol of *Pichia anomala* strain K against *Botrytis cinerea* were tested. Amplicon (V3-V4 region of 16s rRNA gene and ITS1 region) high throughput sequencing allowed to decipher the bacterial and fungal populations of the microbiota. Results of the taxonomic profiling reveal significant differential abundances of microorganisms (FDR-p < 0.05), influenced by DMP (ADONIS test  $p < 0,05$ ). The core microbiota (OTUs shared in 90% of our samples), showed a diversified profile including 60 bacterial OTUs and 26 fungal OTUs at genera level. Results of the biological assay disclosed that apple microbiota can either raise up to 100%, or reduce at 17% the biocontrol of the strain K against *B. cinerea*. Co-clustering analysis of the correlation between the biological assays and the amplicon sequencing, have help to detect 81 interesting genera being isolated for their ability to significantly raise the efficacy of strain K.

## Effect of pack-house treatments on the microbiome of citrus fruit

Ajay Kumar<sup>1</sup>, V. Yeka Zhimo<sup>1</sup>, Antonio Biasi<sup>1</sup>, Ginat Rafael<sup>1</sup>, Oleg Feygenberg<sup>1</sup>, Shoshana Salim<sup>1</sup>, Michael Wisniewski<sup>2</sup>, Samir Droby<sup>1</sup>

<sup>1</sup>Dept. Postharvest Science, ARO, The Volcani Center, P.O. Box 15159, Rishon, Lezion 7505101, Israel,

<sup>2</sup>Appalachian Fruit Research Station, USDA-ARS, Kearneysville WV, US

The most serious postharvest decays of citrus fruit are caused by *Penicillium digitatum*, *P. italicum* and *Geotrichum candidum* var. *citri-aurantii*. Currently, decay by these organisms is principally controlled by the application of chemical fungicides in the packhouse within 24 to 48 hours after harvest. Packhouse treatments include a series of steps carried out after harvest: drenching of the fruit with chemicals upon arrival to the packhouse, washing and initial disinfection, immersion of fruit in heated solutions of fungicides, and coating fruit with wax containing fungicides. The purpose of these treatments is primarily to reduce the inoculum load of the pathogens, eradicate existing infections, and protect fruit against future infections. At present, there is little information on the effect of postharvest treatments on the naturally-occurring microbiota of citrus fruit.

The present study was designed to provide information on potential alterations in the fruit microbiome of harvested citrus due to the application of commercial packhouse treatments. Mandarin fruit (cv. OR) was sampled at different stages of postharvest processing: arrival from the orchard, after drench with TBZ and chlorine, after washing and disinfection, after hot water bath with Imazalil, and after application of wax containing Imazalil and TBZ. Fruit peel samples (peel strips, at 1 mm depth and 10 cm width) were collected in triplicate with each replicate containing a pool of peel tissue from five fruits. DNA was extracted, amplified with 16s and ITS primers to generate amplicons that were sequenced using an Illumina miSeq platform. Results revealed significant differences in the microbiome of mandarin fruit following each treatment at the packhouse. Untreated fruit, sampled immediately after harvest, had the greatest bacterial and fungal diversity. Treatments on the packing line significantly reduced the microbial loads and diversity. Bacterial diversity prior to processing was similar to the diversity found after drenching with TBZ and chlorine, while the microbial community remaining on the fruit surface after a hot water bath with Imazalil and after the application of wax containing Imazalil and TBZ were similar to each other. A similar trend was found in the case of fungal communities, i.e., the level of diversity and overall composition prior to processing was closer to drenched fruit, while the composition after hot water treatment was similar to the waxed fruits. The surface microbiome of fruit following washing and disinfection, however were very different from each other according to Bray-Curtis analysis.

## **Analysis of three methods for the concentration of genetic material in bacterial and fungal communities on apple surfaces**

Alexis M. Hamilton and Faith J. Critzer

*School of Food Science, Irrigated Agriculture Research and Extension Center,  
Washington State University, Prosser, WA, USA*

The controlled atmosphere cold storage environment used in apple storage is designed to delay fruit ripening and decay; however, some fungal species survive in this environment and grow on the apple surface, causing rot. *Penicillium expansum* and *Botrytis cinerea*, the causative agents of blue and gray molds, respectively, cause the majority of rot-associated losses. As these organisms decay the fruit surface, it may leave the fruit at increased risk of colonization by saprophytic foodborne pathogens like *Listeria monocytogenes*. Although decaying fruit is not consumed, it does contact zone 1 food contact surfaces and other apples during the storage and packing environments which could promote transfer of foodborne pathogens. Since these organisms are likely present in low concentrations, it is necessary to utilize a sensitive concentration and extraction method for detecting them. The objective of this study was to identify a reproducible method to concentrate and analyze fungal and bacterial DNA from fresh apple surfaces. Microbial species were collected from apple surfaces using one of three methods: 1) a 25-milligram (mg) sample of excised surface material, 2) swabbing of a five-centimeter by five-centimeter area of the apple surface, or 3) submersion in a 250-milliliter (ml) 1X Tris-EDTA (TE) buffer solution. The buffer solution was sonicated for 5 minutes, separated into 25-ml aliquots, and centrifuged at 4,000 x g for 20 minutes. The supernatant was discarded, the pellet resuspended in 1 ml 1X TE, and all sub-samples were pooled back together prior to a final centrifugation. The supernatant was discarded, and the pellet resuspended in 250  $\mu$ l 1X TE. DNA was extracted from all samples using a ZymoBIOMICS DNA/RNA Miniprep Kit and quantified using a Qubit 4 Fluorometer (Thermo Fisher Scientific, Waltham, MA). Collection methods isolated significantly different quantities (pg/ $\mu$ l) of DNA from apple surfaces (one-way ANOVA,  $F_{2,24} = 17.83$ ,  $p < 0.0001$ ). Specifically, the surface excision method ( $662 \pm 46$ ) derived significantly higher quantities of DNA than either the sonication ( $25 \pm 4$ ) or surface swab ( $<1 \pm 0.000$ ) methods (one-sample  $t$ -test,  $t_{24} = 2.06$ ,  $p < 0.0001$ ). Surface excision methods provide the greatest opportunity for isolating low concentrations of microbial species from fresh apple surfaces. Genetic sequencing of these isolates would provide insight into changes in apple microbiome throughout controlled atmosphere storage.

## Changes in the epiphytic microbiota of apple fruit during storage following the application of the yeast, *Metschnikowia fructicola*

Antonio Biasi<sup>1</sup>, V. Yeka Zhimo<sup>1</sup>, Ginat Rafael<sup>1</sup>, Ajay Kumar<sup>1</sup>, Oleg Feygenberg<sup>1</sup>, Shoshana Salim<sup>1</sup>, Michael Wisniewski<sup>2</sup>, Samir Droby<sup>1</sup>

<sup>1</sup>Dept. Postharvest Science, ARO, The Volcani Center, P.O. Box 15159, Rishon, Lezion 7505101, Israel

<sup>2</sup>Appalachian Fruit Research Station, USDA-ARS, Kearneysville WV, US

The yeast *Metschnikowia fructicola* was developed as a commercial biological control product against postharvest diseases of fruits and vegetables. Its efficacy has been tested on a wide variety of crops, including citrus, apple, stone fruit, grapes, strawberries, sweet potatoes, carrots, and peppers. Although extensive knowledge about the efficacy and mode of action of this antagonist is available, the interaction of *M. fructicola* with the native microbiome of fruit has not been investigated. The aim of the present study was to provide a comprehensive description of the changes occurring in epiphytic microbiota of apple fruit (cv. Pink Lady, *Malus pumila*) during storage following the application of *M. fructicola*.

Fruit was harvested in November 2018 and immediately treated by dipping the fruit in cell suspension of *M. fructicola* ( $10^8$ CFU/ml for 30 sec). Fruits were air-dried at 20 °C for 2 hours and then stored at 1 °C. Fruit surfaces were swabbed with sterile cotton applicators at 2 weeks intervals for up to 8 weeks of storage. Cotton swabs were submerged in PBS solution and subjected to strong agitation followed by sonication in a water bath. The solution was centrifuged at 7000 rpm for 45 minutes and the resulting pellet was used to characterize the culturable bacterial and fungal communities, as well as for extracting DNA for metabarcoding. Results of the molecular identification of culturable isolates indicated that there was no significant differences in the number of filamentous fungal species between the control, non-treated and treated fruits, with the genera *Cladosporium* and *Penicillium* being the most predominant. Interestingly, the control had a higher diversity of yeasts than treated samples, most likely due to the introduction of a high population of *M. fructicola* to treated fruits. *Bacillus* was the most common bacterial genus observed. High-throughput amplicon sequencing revealed significant differences in the diversity of bacterial OTUs (16s amplicons) in samples treated with *M. fructicola* and also exhibited distinct clustering in the PCoA analysis. The results demonstrate that the application of a biocontrol agent has a marked effect on the native, epiphytic microbiota of fruit. Alterations in microbial communities may play a major role in the biocontrol of postharvest fruit pathogens.

## High-throughput sequencing gives new insights on dates microbiome: the influence of developmental stage, tissue and growing season

Ahmed Abdelfattah<sup>1</sup>, Yaara Danino<sup>2</sup>, Edoardo Piombo<sup>3</sup>, Ginat Raphael<sup>2</sup>, Oleg Feygenberg<sup>2</sup>, Michael Wisniewski<sup>4</sup>, Samir Droby<sup>2</sup>

<sup>1</sup>*Department of Ecology, Environment and Plant Sciences, Stockholm University, Stockholm, Sweden*

<sup>2</sup>*Dept. Postharvest Science, Agricultural Research Organization (ARO), The Volcani Center, Bet Dagan, Israel*

<sup>3</sup>*Department of Agricultural, Forestry and Food Sciences (DISAFA), University of Torino, Grugliasco, Italy*

<sup>4</sup>*U.S. Department of Agriculture – Agricultural Research Service (USDA-ARS), Kearneysville, WV USA*

Date is considered one of the most important food crops in many African and Middle Eastern countries due to its health promoting properties and nutritional value. The fruit serves as a source of several minerals, vitamins, carbohydrates and fibers, and it is consumed on a regular basis as a primary food. In this work, we investigated the changes in the fungal communities and analysed the differences between the populations residing in the pulp and the peel of Medjool cultivar. Our results showed that Ascomycota was the dominant phylum, accounting for 79% of the total fungal community, followed by Basidiomycota, Mucoromycota, Chytridiomycota and Glomeromycota. *Penicillium*, *Mycosphaerella*, *Aspergillus* and *Alternaria* were the most abundant genera, with a diverse distribution among the considered time points and tissues. *Penicillium* was more present in the pulp at the green developmental stage (Kimri), while *Aspergillus* was more frequent in the peel at the brown developmental stage (Tamar), and the highest abundance of *Alternaria* was detected at the start of the development, at the Hanabauk stage. Regarding the yeast community, we observed that *Candida* remained stable up until the yellow stage (Khalal), with a sudden growth in the brown one (Tamar), while the important biocontrol genus *Metschnikowia* showed no significant differences among the considered situations.

This work constitutes the most complete analysis to date on the microbiome of *Phoenix dactylifera* fruits, revealing changes in microbiome composition induced by different factors. In particular, this study was able to identify the time points and tissues in which the main pathogen genera on dates have maximum abundance, producing useful information for controlling diseases on this food crop.

## **Apple microbiome response to hot water treatment and the potential of biological control**

Birgit Wassermann, Peter Kusstatscher, Henry Müller\*, Gabriele Berg

*Graz University of Technology, Institute of Environmental Biotechnology, Petersgasse 12, 8010 Graz, Austria*

\* Presenting author

Postharvest food decay is one major issue for today's food loss along the supply chain. Hot water treatment (HWT), a sustainable method to reduce pathogen-induced postharvest fruit decay, has been proven to be effective on a variety of crops. However, the microbiome response to HWT is still unknown and the role of postharvest microbiota for fruit quality is largely unexplored. In a combined approach of metabarcoding analysis and real time qPCR, bacterial and fungal dynamics during storage were assessed on an industrial scale. Small scale storage experiments were conducted combining HWT and a biological control consortium to investigate the effect on fruit decay caused by *Neofabraea* species and *Penicillium expansum*. Overall, HWT was highly effective in reducing rot symptoms on the industrial scale, while the efficiency was rather due to induced plant response than due to alterations of the microbiome; the fungal microbiota was only slightly, and the bacterial community insignificantly affected by HWT. Pathogen infection, however, significantly decreased the bacterial and fungal diversity; almost 90% of the total fungal community was composed by co-occurring storage pathogens *N. alba* and *P. expansum*. Additionally, the prokaryote to eukaryote ratio, almost balanced in apples before storage, was shifted to 0.6% bacteria and 99.4% fungi in diseased apples, albeit the total bacterial abundance was stable across all samples. Healthy stored apples shared 18 bacterial and 4 fungal taxa that were not found in diseased apples, therefore defining a health-related postharvest microbiome. Small-scale storage experiments, applying a combined approach of HWT and a biological control consortium, were proven to be efficient in reducing both postharvest pathogens. The present study is the first providing deeper insights into the microbiome changes induced by currently in-use HWT on industrial scale and provides evidence of a combined process with biological control consortia.

## Comparative transcriptomic analysis of the interaction between *Penicillium expansum* and apple fruit during early stages of infection

Kaili Wang <sup>a</sup>, Xiangfeng Zheng <sup>c</sup>, Xiaoyun Zhang <sup>a</sup>, Lina Zhao <sup>a</sup>, Qiya Yang <sup>a</sup>, Nana A. S. Boateng <sup>a</sup>, Joseph Ahima <sup>a</sup>, Hongyin Zhang <sup>a,\*</sup>, Jia Liu <sup>b,\*</sup>

<sup>a</sup> School of Food and Biological Engineering, Jiangsu University, Zhenjiang 212013, Jiangsu, China

<sup>b</sup> College of Forestry & Life Science/Institute of Special Plants, Chongqing University of Arts and Sciences, Yongchuan, Chongqing 402160, China

<sup>c</sup> School of Food Science and Engineering, Yangzhou University, Yangzhou 225009, Jiangsu, China

Blue mold, caused by *Penicillium expansum*, is an important postharvest disease of apple, and can result in significant economic losses. The present study investigated the interaction between *P. expansum* and wounded apple fruit tissues during the early stages of the infection. Spores of *P. expansum* became activated at one hour post-inoculation (hpi), exhibited swelling at 3 hpi, and germ tubes entered into apple tissues at 6 hpi. RNA-seq was performed on samples of *P. expansum* and apple fruit tissue collected at 1, 3, and 6 hpi. The main DEGs that were identified in *P. expansum* were related to interaction, contained cell wall degradation enzymes, anti-oxidative stress, pH regulation, and effectors. Apple tissues responded to the presence of *P. expansum* by first activating PAMP-triggered immunity (PTI) at 1hpi, then both effector-triggered immunity (ETI) and PTI at 3 hpi. This research provides new information on the interaction between *P. expansum* and apple fruit tissue at an early stage of the infection process.

## **Exploring the functional capacity of seed meal-structured microbiomes in the control of apple replant disease**

Tracey Somera, Shiri Freilich, Mark Mazzola

*U.S. Department of Agriculture – Agricultural Research Service (USDA-ARS), Wenatchee, WA USA, Agricultural Research Organization (ARO), and The Volcani Center, Institute of Plant Sciences, Ramat Yishay, Israel, and U.S. Department of Agriculture – Agricultural Research Service (USDA-ARS), Wenatchee, WA USA*

When grown in soils amended with Brassicaceae seed meal, the apple rhizosphere supports a specialized microbiome which can promote suppression of apple replant disease (ARD) pathogens through various modes of action. Combining seed meal treatments with specific rootstock genotypes known to possess ARD tolerance is also integral to optimizing the disease-suppressing potential of the rhizosphere microbiome. To date, the combined effects of seed meal x rootstock genotype on rhizobiome composition have been described in several different soil types (i.e. orchard locations), yet the functional significance of these community shifts remains poorly characterized. In this experiment, amplicon sequencing of the ITS and 16S ribosomal RNA gene was used to characterize seed-meal induced changes in rhizosphere fungal and bacterial communities, respectively, from a tolerant (G.210) and susceptible (M.26) apple rootstock. To explore the functional potential of these systems in more depth, we conducted a literature review and used our own data in a comparative assessment of microbial community structure across 3 different soil types in which seed meal amendment used in concert with specific apple rootstocks provided effective control of ARD. We show that seed meal-induced shifts in microbial community composition vary with soil type, yet similar functional capabilities, which may enable “effective” disease control and/or promote plant productivity, are consistently reflected in dominant taxa. The present study is part of a larger effort to better understand metabolic functions in the rhizobiome of seed meal-structured disease control systems, and future work will further assess functional-oriented interpretations of rhizobiome composition using metagenomic data.

## **Microbial consortium for the control of postharvest pathogens of soft berries**

V. Yeka Zhimo<sup>1</sup>, Antonio Biasi<sup>1</sup>, Ajay Kumar<sup>1</sup>, Ginat Rafael<sup>1</sup>, Oleg Feygenberg<sup>1</sup>, Shoshana Salim<sup>1</sup>, Michael Wisniewski<sup>2</sup>, Samir Droby<sup>1</sup>

<sup>1</sup>Dept. Postharvest Science, ARO, The Volcani Center, P.O. Box 15159, Rishon, Lezion 7505101, Israel

<sup>2</sup>Appalachian Fruit Research Station, USDA-ARS, Kearneysville WV, US

Numerous microbial antagonists (yeasts and bacteria) of postharvest pathogens have been identified, some of which have reached advanced levels of development and commercialization. Early investigations of potential biocontrol agents adopted the same strategy used for finding biocontrol agents against foliar and soil-borne diseases where the isolation and screening program was designed to identify single potent antagonists. This approach, however, neglected the fact that the introduced antagonist was not the only "player" present on the harvested commodity. Consequently, their success remains limited due to inconsistency and variability in the efficacy of the product under commercial conditions. To overcome the shortcomings of existing biocontrol strategies, a microbial consortium consisting of probiotic bacteria and yeasts that are capable of exhibiting more robust and consistent biocontrol efficacy against a wide range of postharvest pathogens was evaluated. Biocontrol efficacy was tested against the development of postharvest rots of soft berries using near harvest application. The microbial components of the consortium successfully colonized fruit surface and significantly reduced postharvest fungal decay incidence and severity in strawberries and raspberries. Based on our results, microbial consortia prove to be an ideal candidate to be used in the management of postharvest decay of soft berries which are highly perishable and also where postharvest fungicidal applications are not practical.

## Bios of Invited Speakers

### Ahmed Abdelfattah



Dr. Ahmed Abdelfattah is a researcher at Stockholm University and a former postdoc at Mediterranean University of Reggio Calabria. He received his doctoral degree in 2016 from Palermo University, in Agro-forestry sciences. During his PhD and previous postdoctoral fellowship he gained extensive knowledge in microbial ecology, plant pathology, and microbiome research. His research was one of the earliest studies to decipher the microbiome of fruit crops, such as olive, orange, tangerine, strawberries, grapes, and apples. At his current affiliation, he is focused on understanding how plant-associated microbes are transmitted between generations and how climate change may influence their community composition. Dr. Abdelfattah was recently awarded the Marie Curie fellowship, a prestigious grant funded by the European Commission, to continue his work on the apple microbiome with Prof. Gabriele Berg at Graz University of Technology [www.applebiome.com](http://www.applebiome.com).

### Gabriele Berg



Gabriele Berg studied biology and biotechnology at the universities in Rostock and Greifswald obtained her Ph.D. in 1995 in microbiology from Rostock University (Germany). In 2003, she got a Heisenberg grant from the DFG (Deutsche Forschungsgemeinschaft), and in 2005 she became a full professor in environmental biotechnology at Graz University of Technology (Austria). Her interests are focused on microbiome research and translation of the results into new biotechnological concepts for health issues. Results have published in more than 200 peer-reviewed papers and in several patents. She received numerous awards, e.g. Science2Business Award Austria, “ÖGUT Umweltpreis” (2011) and Fast Forward Award Styria (2015). According to Clarivate Analytics, she belongs to the most influential researchers world-wide (top 1, for the category Cross Fields in 2018).

### Natalie Breakfield



Natalie Breakfield is Molecular Biology Director at New Leaf Symbiotics in Saint Louis, Missouri, USA. In this role, she oversees the isolation, sequencing, and initial phenotyping of *Methylobacterium* and *Methylorubrum* spp. (M-troph) isolates. She works with other teams to advance the most promising candidates through NewLeaf’s product pipeline. NewLeaf is focused on discovering how M-trophs benefit plants across a large variety of field conditions, and currently has two bio-complement products on the market: Terrasym401 for soy and Terrasym402 for peanut. Dr. Breakfield obtained her Ph.D. from Duke University and was a postdoctoral fellow at University of North Carolina - Chapel Hill. She is a member of the board of directors of the International Alliance for Phytobiomes Research (Phytobiomes Alliance).

### Sharon Doty



Doty received a B.S. degree in Genetics from the University of California, Davis. Her Ph.D. research in the Microbiology Dept. at the University of Washington (UW) was on *Agrobacterium* plant signal perception and responses, and her postdoctoral research was in plant biochemistry, developing plants with improved capacity to remove environmental pollutants. She is currently a Professor in the UW School of Environmental and Forest Sciences (SEFS) and an Adjunct Professor with the UW Microbiology Department. Her research focus is on the importance of the plant microbiome for plant growth, nutrient acquisition, and tolerance to both abiotic (drought, heat, pollutants, salt) and biotic (pathogens) stresses. Through her outreach and teaching, Doty emphasizes the ability of natural plant-microbe partnerships to address environmental challenges including agricultural chemical run-off, climate change, and pollution. Prof. Doty serves on the executive teams of the International Symbiosis Society and the International Poplar Commission, and is an associate editor for *Frontiers in Microbiology*.

### Adi Doron-Faigenboim



Undergraduate studies on Biology and computer Science followed by masters and PhD degrees in Cell research and immunology. Joint the ARO, the Volcani Center in 2011 to establish a bioinformatics unit with the aim of assisting scientists advance their research with bioinformatics methodologies. The unit provides data analysis services, consultation and training to scientists. Main areas of expertise include the analysis of experiments which use genomic technologies (e.g. Next Generation Sequencing). Main activity is NGS analyses of RNA-seq for differential expression, whole genome (WGS) for variant calling (SNPs and Indels), and Metagenomics.

### Samir Droby



Prof. Samir Droby is a senior research scientist at the Department of Postharvest Sciences, ARO, the Volcani Center and Professor of Plant Pathology and postharvest Sciences at the Division of Biochemistry and Food Science at the Robert H. Smith Faculty of Agriculture Food and Environment, The Hebrew University of Jerusalem. His research expertise include developing biological and natural based control strategies for postharvest diseases, microbiome of harvested fruit and its use to study microbial networks fruit surfaces, mode of action of yeast biocontrol agents, Pathogenicity mechanisms of *Penicillium* species on citrus and apple fruit and resistance mechanisms of fruits against postharvest pathogens. Prof. Droby published more than 150 articles in peer-reviewed journal, 25 review articles and 25 book chapters on various topics on postharvest pathology.

### **Shiri Freilich**



Graduate and masters studies in Tel Aviv University in life and plant sciences. Completed her PhD studies in Bioinformatics in Cambridge University, UK. Joined the Agricultural research Organization (ARO) in Newe Yaar research Center in 2012 to work on systems biology in ecology and agriculture. Her research aims at harnessing microbial function for the service of ecology & agriculture through the educated design of communities. To this end, she applies and develops computational models for predicting and understanding the networks of interactions formed within microbial communities by analyzing meta/genomics data.

Using the tools we can delineate trophic dependencies, exchanges, competitive and cooperative interactions within natural microbial communities and use simulations for predicting potential routes for the optimization of predefined functions. The research in the group focuses on the activity of microbial communities in agricultural soil and is targeted for harnessing genomic approaches towards promoting sustainable solutions in agriculture practice. Research projects include promoting enhanced degradation of herbicides in soil. Deciphering microbial functions in amendment-based solutions for soil-borne disease suppression. Delineating tri-trophic networks between crop plants, sap-feeding pests and their microbial symbionts.

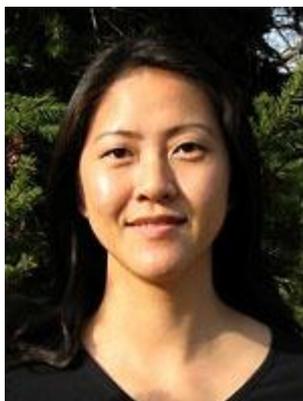
### **Colin Jackson**



Dr. Colin Jackson is in the Department of Biology at the University of Mississippi and has been working in the area of microbial ecology and diversity for almost 25 years. His research examines the structure and function of the microbiomes of organisms, both plants and animals, and also that of natural environments. Plant microbiome work in his lab has primarily focused on the phyllosphere, examining spatial and temporal patterns in the bacterial phyllosphere community. Other areas of interest include the importance of the plant microbiome in plants of nutritional and medicinal importance. Dr. Jackson's current research is exploring how host genetic and phylogenetic

diversity interact with the microbiome to form a functional holobiont.

### **Jenny Kao-Kniffin**



Jenny Kao-Kniffin [pronunciation: GAOW-nif-IN] is an Associate Professor at Cornell University's School of Integrative Plant Science. She received her Ph.D. from the University of Wisconsin-Madison in Land Resources, with a specialization in Ecosystem Microbiology. She then served as a Postdoctoral Research Fellow with the National Science Foundation (NSF) investigating landscape-scale patterns of microbial composition near Barrow, Alaska. Dr. Kao-Kniffin is passionate about studying the biological component of soils, and its intricate relationship with plants. The research subjects range from crops and model plant species to invasive plants and weeds in agricultural and natural ecosystems, with a major focus on microbiome assembly, modification, and resilience impacting plant traits.

## Barry Knight



As Head of Indigo Research Partners, Barry oversees the world's largest agriculture laboratory. Prior to joining Indigo, Barry held senior positions in agricultural companies as CEO of Cresco Ag, CCO of Pinnacle Ag Holdings, and President of Jimmy Sanders. At Sanders, company sales grew by three-fold over four years while increasing its EBITDA by 4X. This successful growth led to the shareholders' desire to sell the company to Apollo Global Management. Before Sanders, Barry led Monsanto's sales in the coastal region of the US with over \$1 billion in sales of seed, chemistry and biotech traits. Barry entered the agriculture industry through the USDA before spending time working for American Cyanamid. Barry received a B.S. degree in Agronomy from Oklahoma

State University and a M.S. degree in Agronomy specializing in plant breeding from Mississippi State University. Barry was selected as Alumni Fellow at Mississippi State in 2011 and serves on the Scientific Advisory Board for the Vice President of Research and Development and on the School of Agriculture's Advisory Committee.

## Steven Lindow



Assembly of epiphytic bacterial communities on plants and their interactions with the plant host. The Lindow lab focuses on the ecology and management of plant-associated bacteria with a focus on both epiphytic and endophytic bacteria. A thrust of the lab has been on identification of traits that confer fitness and stress tolerance of bacteria on leaf surfaces and their regulation. The contribution of intra- and inter-species chemical communication that mediates expression of cell density-dependent traits in both *Pseudomonas syringae* and *Xylella fastidiosa* are

being addressed with the aim of modifying their behaviors to achieve plant disease control. The benefit to bacteria of their production of factors such as plant hormones such as 3-indole acetic acid, biosurfactants, and other extracellular products to the colonization of plants and of the effect of these compounds on plant is also being investigated. The emigration of bacteria from, and immigration of bacteria to plants, via airborne transport is being studied to better understand processes determining the context-dependent assembly of epiphytic communities on plant surfaces.

## Tal Luzzatto-Knaan



Completed her undergraduate studies in Biotechnology and Environmental Sciences at Tel-Hai Academic College. Earned her Masters in Biotechnology and Ph.D in Biochemistry, Food Science and Nutrition at the Hebrew University of Jerusalem and Volcani center (ARO), studying the role of secondary metabolites in plant-pathogen interactions. As a BARD post-doctoral fellow at UCSD she gained her expertise in mass spectrometry-based metabolomics, by developing tools for studying microbial chemistry and natural products discovery. Joint the department of Marine Biology at the University of Haifa, where she uses metabolomic approaches to explore the spatial and temporal patterns of natural products in marine photosynthetic microorganisms.

## Dumitru Macarisin



Dr. Dumitru Macarisin is a Research Microbiologist in the Division of Microbiology, in the Center for Food Safety and Applied Nutrition, Food and Drug Administration (FDA), at College Park in Maryland, U.S. Dr. Macarisin is FDA subject matter expert for *Listeria monocytogenes* in and he also leads the Agency's development and implementation of research projects related to microbial safety of fresh fruits and vegetables. Dr. Macarisin earned his Ph.D. in Plant Physiology and Biochemistry in 2003 and pursued further postdoctoral research in the Agricultural Research Organization - Volcani Center, Israel followed by an 8-year research tenure with the Agricultural Research Service-United States Department of Agriculture. He conducted extensive research in postharvest pathology and biocontrol, plant stress response, produce safety, and microbiology. Dr. Macarisin came to the FDA in 2013 and his primary research interests are to identify the mechanisms of fresh fruit contamination and environmental reservoirs of foodborne pathogens and develop mitigation strategies to improve good agricultural practices in the prevention of produce recalls and foodborne outbreaks. Dr. Macarisin represents the FDA nationally and internationally on critical food safety issues. He has been furnishing recommendations on preventive controls, environmental monitoring and the improvements of quality controls to other governmental agencies and food industries.

## Mark Mazzola



Mark Mazzola is a Research Plant Pathologist with the USDA-Agricultural Research Service Tree Fruit Research laboratory in Wenatchee, Washington. He serves as a faculty member in the Department of Plant Pathology at Washington State University, as well as Professor in the Department of Plant Pathology at Stellenbosch University, South Africa. Dr. Mazzola leads a team which seeks to effectively engineer structure and function of the indigenous soil, rhizosphere and endophytic microbiome through utilization of differentially selective host genotypes and biologically active organic residue soil inputs. The overall goal of this program is the formulation of effective and ecologically sound systems for soil-borne disease suppression in orchard ecosystems.

## Justin Shaffer



Presentation title: Plant microbial ecology: developing a framework for meta-analyses and other comparative studies.

Bio: I am a broadly trained plant and microbial ecologist with expertise in lichenology, mycology, and community ecology. My research interests are centered on plant-microbe interactions, particularly those involving fungi, and seek to elucidate the roles of such microbes in driving community-wide patterns, such as those influencing host fitness, and/or impacting ecosystem services. Currently, I am exploring deep parallels in environmental and host-associated microbial community ecology using large scale, multi-omics and meta-analytical approaches, in part by working with the American Gut Project, Global FoodOmics, and the Earth Microbiome Project.

## Leonardo Schena



Leonardo Schena, is associated professor of Plant Pathology at the Department of Agriculture of the Mediterranean University of Reggio Calabria, Italy, since 2007. From November 2000 to February 2007 he was a free researcher at the Department of Plant Protection and Applied Microbiology (DPPAM) of the University of Bari, Italy, with an interruption of 18 months (March 2004-September 2005) during which he was Research Scientist at the Scottish Crop Research Institute, United Kingdom, having been awarded a Marie Curie Intra-European Fellowship. Previously he was a PhD student at the DPPAM (January 1998-October 2000) and research fellow (January-December 1997) at the Department of Postharvest Science, The Volcani Center, Israel. He has published more than 90 peer-reviewed journal articles and several books chapters. Current research mainly focuses on the microbiota of important crops such as olive,

citrus, strawberries, grape, wheat, and apples, to understand structure and function of the microbiome. He also used amplicon metagenomics approaches to investigate the aetiology of plant diseases and evaluate the impact of environmental conditions, management practices, and host genotype on the plant microbiome. He documented how external factors such as olive fruit fly infestations may cause imbalanced fungal communities in the olive carposphere. Other research lines include the evaluation and use of alternative control methods against diseases of fruit and vegetables and the development of quantitative molecular detection methods for bio-control agents and fungal and bacteria plant pathogens. The European and Mediterranean Plant Protection Organization (EPPO) currently use some of the developed methods in official diagnostic protocols. A special focus of his career has been given to study Oomycetes species. He contributed to resolve inter- and intra-specific phylogenetic correlations among *Phytophthora* species and discovered and characterized new *Phytophthora* hybrids and species as well as a related genus named *Nothophytophthora*. He also was a pioneer in the development and application of an amplicon metagenomics approach based on genus specific primers to detect *Phytophthora* species.

### Edward Sionov



**Edward Sionov** is a research scientist at the Agricultural Research Organization (The Volcani Center), Israel. His research combines molecular biology and analytical chemistry approaches to study mechanisms and environmental conditions associated with development of mycotoxigenic fungi and the production of mycotoxins in agricultural commodities, raw and processed food and feed. His lab has great expertise in molecular biology studies, analyses of the fungal secondary metabolites and mycotoxins regulation.

### Davide Spadaro



**Davide Spadaro** is Associate Professor of Plant Pathology at the University of Torino and Researcher at AGROINNOVA. He was Visiting Professor at the Thammasat University of Bangkok (Thailand), Visiting Scientist at the University of Edinburgh (UK), Research fellow at the University of Lleida – IRTA (Spain) and at the University of Bonn (Germany). He is member of the Teaching Committee of the Ph.D. School in Biological Sciences and Applied Biotechnologies of the University of Torino. He is Secretary of the Subject Matter Committee Postharvest of the International Society of Plant Pathology. He is member of the Council of the Italian Society of Plant Pathology. Member of the Accademy of Agriculture of Torino. He is author of 11 book chapters and 4 patents. His 106 papers on international Journals have been cited over 2,200 times, his H-index is 25 (Scopus). He worked on several European and national projects. His research topics spans from the mechanisms of postharvest biocontrol to the use of essential oils and thermotherapy in postharvest, from the prevention and control of mycotoxins to the development of diagnostic tools for plant pathogens.

## Silvana Vero



Dr. Silvana Vero is Associate Professor in the Department of BioSciences at Universidad de la República, Montevideo, Uruguay. She is a Chemist and completed a Ph.D. in Chemistry at the same University. She got a post-doctoral position in Food Microbiology at Universidad de Córdoba, Spain. Her research focuses on the biology and biotechnological applications of fungi. In particular, some of her projects have focused on biological control of postharvest diseases using cold adapted yeast and also on the control of mycotoxigenic molds in grains. She is now working with food fermented products like kefir, studying the microbial consortia and looking for applications of those microorganisms in preserving food and feed products. She has also worked in the analysis of microbiome in sea waters from Antarctica.

## Michael Wisniewski



Dr. Michael Wisniewski is a Lead Scientist in the USDA-ARS and is located at the Appalachian Fruit Research Station, Kearneysville, WV. He has conducted research in postharvest pathology, postharvest biological control, and cold hardiness of fruit crops for over 30 years. He has published well over 200 peer-reviewed publications and more than 30 book chapters. He holds several patents and was elected a Fellow of the American Society of Horticultural Science and an Honorary Life Time Member of the Canadian Society of Plant Pathology. As a recipient of numerous U.S. – Israel Binational Agricultural and Research Development (BARD) grants, he has collaborated with Dr. Samir Droby for many years on topics related to postharvest pathology and biological control. Together, they have sponsored several international workshops on topics related to postharvest and founded the ISHS working group on Postharvest Pathology. His research was the first to document the ability of yeast to parasitize higher fungi and he and his colleagues developed the first genetic marker for postharvest disease resistance to *P. expansum* in the progenitor apple species, *Malus sieversii*.

## Susan Whitehead



Dr. Susan Whitehead is an Assistant Professor in the Department of Biological Sciences at Virginia Tech. Previously, she completed a B.A. in Biology at Oberlin College, a Ph.D. in Ecology and Evolutionary Biology at the University of Colorado at Boulder, and post-doctoral studies in Applied Chemical Ecology at Cornell University. Her research focuses on the evolutionary ecology of interactions between plants and other organisms. In particular, most of her projects have focused on plant secondary chemistry and its fundamental role in shaping complex interaction webs among plants, herbivores, pathogens, microbial partners, pollinators, and seed dispersers. Dr. Whitehead's research is grounded in field-based studies that span tropical and temperate forests as well as agricultural systems. She is currently spearheading a large USDA-funded project focused on the apple microbiome. The project examines how different pre-harvest pest management practices impact the apple microbiome, and how the microbiome, in turn, impacts fruit chemistry, pest resistance, and fruit quality for specialty uses such as hard cider.



Dr. Noam Alkan, Research Group Leader, ARO-Volcani Center, Israel

I graduated from The Hebrew University in plant pathology and microbiology. My Ph.D. studies focused on postharvest pathology under the supervision of professor Dov Prusky. My post-doctorate at Weizmann institute under the supervision of Prof. Robert Fluhr focused on fruit pathogens interaction at the genomic and transcriptomic level. From 2013, I am a group leader at Volcani Research Center. My group focuses on subtropical fruit physiology and pathology, which include mango stem-end microbiome and fruit-fungal interactions. On those subjects we managed to enhance fruit quality, yield and reduce postharvest decay by various means. Another part of my lab study induced resistance and activation of phenylpropanoid pathway in order to enhance fruit tolerance to pathogens and chilling. Additionally, we also work on the induction of cold tolerance in subtropical fruits for enabling cold-quarantine.

## Haïssam Jijakli



Professor in Plant Pathology, Haïssam Jijakli has been working for 28 years on the development of biocontrol methods based on micro-organisms and their derivatives to protect plants against pathogens and weeds. He participated or coordinated more than 40 projects with Belgian and foreign partners and produced more than 400 scientific publications (including 130 peer-reviewed articles). He also authored 7 patents and created 4 spin-off companies, one being involved in the development of a biopesticide based on a yeast against postharvest diseases of fruits. That yeast, *Candida oleophila* strain O is now registered in the EU and the US under the name of NEXY. Another recent spin-off is dedicated to the development of herbicides based on essential oils. Thanks to these results and fruitful collaborations, his laboratory internationally recognized for its research on biocontrol using fundamental and practical approaches.



Microbiome Research in the Office of Regulatory Science, CFSAN FDA

Dr. Ottesen uses metagenomic approaches to better understand phytobiomes and important food microbiomes. Her research focus has been on the description of microbiota along the farm to fork continuum to identify environments and conditions that may correlate with an increased risk of introducing pathogens to the food supply. Her research also contributes data to support the evolution of good agricultural practices (GAPs) and improved Food Safety Modernization Act (FSMA) regulatory policy. She is currently coordinating the implementation of MetaGenomeTrakr as part of the GenomeTrakr program. MetaGenomeTrakr is focused at pathogen source tracking but also on the description of the microbiota of all American food for a wider range of food quality and nutrition metrics that may be microbiome dependent.

## List of Participants

<u>Name</u>	<u>Affiliation</u>	<u>E-Mail</u>
Abdelfattah, Ahmed	Department of Ecology, Environment, and Plant Sciences, Stockholm University, Sweden	<a href="mailto:ahmed.abdelfattah@su.se">ahmed.abdelfattah@su.se</a>
Alkan, Noam	ARO, The Volcani Center, Rishon LeZion, Israel	<a href="mailto:noamal@volcani.agri.gov.il">noamal@volcani.agri.gov.il</a>
Berg, Gabriela	Graz University of Technology, Graz, Austria	<a href="mailto:gabriele.berg@tugraz.at">gabriele.berg@tugraz.at</a>
Biasi, Antonio	ARO, The Volcani Center, Rishon LeZion, Israel	<a href="mailto:antoniobiasi84@gmail.com">antoniobiasi84@gmail.com</a>
Breakfield, Natalie	NewLeaf Symbiotics, BRDG Park, St. Louis, MO, USA	<a href="mailto:nbreakfield@newleafsym.com">nbreakfield@newleafsym.com</a>
Burchard, Erik	USDA-ARS, Kearneysville, WV	<a href="mailto:erik.burchard@ars.usda.gov">erik.burchard@ars.usda.gov</a>
Doty, Sharon	University of Washington, Seattle, WA, USA	<a href="mailto:sldoty@uw.edu">sldoty@uw.edu</a>
Droby, Samir	ARO, The Volcani Center, Rishon LeZion, Israel	<a href="mailto:samird@volcani.agri.gov.il">samird@volcani.agri.gov.il</a>
Fagenboim, Adi	ARO, The Volcani Center, Rishon LeZion, Israel	<a href="mailto:adif@volcani.agri.gov.il">adif@volcani.agri.gov.il</a>
Feygenberg, Oleg	ARO, The Volcani Center, Rishon LeZion, Israel	<a href="mailto:fgboleq@volcani.agri.gov.il">fgboleq@volcani.agri.gov.il</a>
Freilich, Shiri	Newe-Ya'ar Research Center, ARO, Ramat Yishay, Israel	<a href="mailto:shiri.freilich@gmail.com">shiri.freilich@gmail.com</a>
Gerstaedt, Christian	Graz University of Technology, Graz, Austria	<a href="mailto:office@biotenz.at">office@biotenz.at</a>
Guilli, El	Institut National de la Recherche Agronomique (INRA) URPPP; CRRA-Kenitra. El Menzeh.BP : 293 Kenitra 14 000	<a href="mailto:mguilli@yahoo.com">mguilli@yahoo.com</a>
Hamilotn, Alexis	Washington State University, Prosser, WA, U	<a href="mailto:alexis.hamilton@wsu.edu">alexis.hamilton@wsu.edu</a>
Hanrahan, Ines	Washington Tree Fruit Research Commission, WA	<a href="mailto:hanrahan@treefruitresearch.com">hanrahan@treefruitresearch.com</a>
Jackson, Colin	Department of Biology, University of Mississippi, MS	<a href="mailto:cjackson@olemiss.edu">cjackson@olemiss.edu</a>
Jijakli, Haissam	Gembloux Agro Bio Tech, Gembloux, Belgium	<a href="mailto:mh.jijakli@uliege.be">mh.jijakli@uliege.be</a>
Kao-Kniffin, Jenny	Cornell University, Ithaca, NY	<a href="mailto:jtk57@cornell.edu">jtk57@cornell.edu</a>
Kapulnik, Yoram	Director, BARD, Rishon LeZion, Israel	<a href="mailto:kapulnik@bard-isus.com">kapulnik@bard-isus.com</a>
Knight, Barry	Indigo Agriculture, Memphis, TN	<a href="mailto:bknight@indigoag.com">bknight@indigoag.com</a>
Lindow, Steven	University of California Berkeley, Berkeley, CA	<a href="mailto:icelab@socrates.berkeley.edu">icelab@socrates.berkeley.edu</a>
Liu, Jia	Chongqing University, Chongqing, China	<a href="mailto:liu.jia1983@hotmail.com">liu.jia1983@hotmail.com</a>
Luzzato-Knaan, Tal	School of Marine Sciences, University of Haifa, Israel	<a href="mailto:tal.luzzatto@mail.huji.ac.il">tal.luzzatto@mail.huji.ac.il</a>

Macarisin, Dumitru	Food and Drug Administration, College Park, MD	<a href="mailto:Dumitru.Macarisin@fda.hhs.gov">Dumitru.Macarisin@fda.hhs.gov</a>
Maurer, Dalia	ARO, The Volcani Center, Rishon LeZion, Israel	<a href="mailto:daliam@agri.gov.il">daliam@agri.gov.il</a>
Mazzola, Mark	USDA-ARS, Wenatchee, WA USA	<a href="mailto:mark.mazzola@usda.gov">mark.mazzola@usda.gov</a>
Meakam, Victoria	Virginia Tech Blacksburg, VA	<a href="mailto:vmeakem@vt.edu">vmeakem@vt.edu</a>
Muller, Henry	Graz University of Technology, Graz, Austria	<a href="mailto:henry.mueller@tugraz.at">henry.mueller@tugraz.at</a>
Oliveira, Samara	Clemson University, Clemson, SC	<a href="mailto:solivei@g.clemson.edu">solivei@g.clemson.edu</a>
Piombo, Edward	University of Torino, Grugliasco, Italy	<a href="mailto:edoardo.piombo@unito.it">edoardo.piombo@unito.it</a>
Otteson, Andrea	U.S. Food and Drug Administration, Silver Spring, MD	<a href="mailto:Andrea.Ottesen@fda.hhs.gov">Andrea.Ottesen@fda.hhs.gov</a>
Rivers, Adam	Computational Biologist USDA-ARS Genomics and Bioinformatics Research Unit	<a href="mailto:adam.rivers@usda.gov">adam.rivers@usda.gov</a>
Sare, Abdoul	Gembloux Agro Bio Tech, Gembloux, Belgium	<a href="mailto:abdoulrazack.sare@uliege.be">abdoulrazack.sare@uliege.be</a>
Schena, Leonardo	Università Mediterranea di Reggio Calabria, Italy;	<a href="mailto:lschena@unirc.it">lschena@unirc.it</a>
Shaffer, Justin	University of California, San Diego, La Jolla, CA, US	<a href="mailto:jpshaffer@UCSD.EDU">jpshaffer@UCSD.EDU</a>
Sionov, Edward	ARO, The Volcani Center, Rishon LeZion, Israel	<a href="mailto:edwardsio@volcani.agri.gov.il">edwardsio@volcani.agri.gov.il</a>
Somera, Tracy	USDA-ARS. Wenatchee, WA USA	<a href="mailto:tracey.somera@usda.gov">tracey.somera@usda.gov</a>
Spadaro, Davide	University of Torino, Grugliasco, Italy	<a href="mailto:davide.spadaro@unito.it">davide.spadaro@unito.it</a>
Torres, Rosario	IRTA, Lleida, Spain	<a href="mailto:Rosario.Torres@irta.cat">Rosario.Torres@irta.cat</a>
Vero, Silvana	University of the Republic, Montevideo, Uruguay	<a href="mailto:sverom@gmail.com">sverom@gmail.com</a>
Vetcos, Maria	Newe-Ya'ar Research Center, ARO, Ramat Yishay, Israel	<a href="mailto:mariavetcos@gmail.com">mariavetcos@gmail.com</a>
Whitehead, Susan	Virginia Tech Blacksburg, VA	<a href="mailto:swhitehead@vt.edu">swhitehead@vt.edu</a>
Wisniewski, Michael	USDA-ARS, Kearneysville, WV	<a href="mailto:wwisniewski@gmail.com">wwisniewski@gmail.com</a>
Zhang, Hongyin	Jiangsu University, Zhenjiang 212013, Jiangsu, China	<a href="mailto:zhanghongyin126@126.com">zhanghongyin126@126.com</a>
Zhimo, Yeka	ARO, The Volcani Center, Rishon LeZion, Israel	<a href="mailto:yekaz@volcani.agri.gov.il">yekaz@volcani.agri.gov.il</a>
Zhu, Yanmin	USDA-ARS, Wenatchee, WA USA	<a href="mailto:yanmin.zhu@usda.gov">yanmin.zhu@usda.gov</a>