Phytobiomes: From Microbes to Plant Ecosystems

Scientific Organizers:
Jan E. Leach
Kellye A. Eversole
Jonathan A. Eisen
Gwyn Beattie

Part of the Keystone Symposia Global Health Series

November 8–12, 2016

Hilton Santa Fe Historic Plaza Hotel
Santa Fe, New Mexico, USA

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on Molecular and Cellular Biology
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Note-taking pages available after page 60.

#KSphytobiome

Visit **www.keystonesymposia.org/16S2** to view the conference program online.

Unless otherwise noted, the information in this book is current as of **October 17, 2016**. If you registered after this date, your name is included in an online list accessed from attendees' Keystone Symposia accounts.

Please be advised that no video equipment, cameras, audio equipment or any other type of recording device will be allowed in the conference room or poster sessions. Full conference policies are on page 4.

KEYSTONE SYMPOSIA™
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info@keystonesymposia.org | www.keystonesymposia.org

Welcome

Dear Conference Participant,

I am delighted that you have chosen to join us for this Keystone Symposia conference. Over the next few days, we hope that you will be stimulated by new data, new ideas, and new connections with fellow scientists. In last year's attendee surveys, 82% of participants said that they learned something new that will change the direction of their research. We hope that you will experience a similar "Eureka" moment, too!

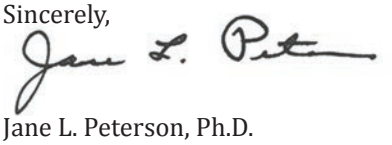
In 2016-2017, we will convene a record number of conferences – ten – outside North America, including our first sets of joint meetings abroad, in both Denmark and Ireland. We are also embarking on a two-year special celebration of diversity – in particular, to recognize the contributions that women scientists and those from underrepresented (UR) ethnic backgrounds make to the life sciences. One of our goals is to improve the numbers of UR and female scientists on the podium at each meeting. Our goal over the next two years is to increase the number of women on our programs by one percentage point per year to 32% of those speaking, the equivalent of the percent of women in assistant to full professor positions in academia. The percent of women giving short talks is already 40%+ of speakers, about the same as the ratio of women scientists in our audience. Even after we accomplish our goals, we will continue to strive to increase the number of women on our programs.

Increasing the number of UR scientists on our programs and at our meetings is more difficult. We have assembled an effective Diversity Advisory Committee that is helping us identify UR speakers. While our scholarships, travel awards and Fellows Program (see pages 17-18 for more information) do a good job of increasing overall participation, it is more challenging to increase the number of UR scientists speaking at the podium. We intend to increase this number by at least one percentage point annually to 4% of the total, and UR short talk speakers from 6.5% currently to 7.5% of the total. As with our global expansion, we will continually assess the progress of our efforts.

Keystone Symposia is a 501(c)(3) nonprofit organization. This means that we supplement registration fees with industry, foundation, government and individual donations and grants, enabling us to keep the registration fees as reasonable as possible, as well as to award scholarships and travel awards to deserving graduate students, postdoctoral fellows and early-career investigators. We are extremely grateful for this support.

We look forward to your feedback in the survey you will receive when the conference concludes, or by sending me an email.

Sincerely,



Jane L. Peterson, Ph.D.
President and Chief Executive Officer, Keystone Symposia
janep@keystonesymposia.org

Maximimizing Your Experience

The conference program has been designed around our mission: to accelerate life science discovery by providing a forum to present top-quality science, foster new collaborations and help prepare the next generation of life scientists.

Poster Abstract Sessions

Poster sessions play host to some of the most dynamic interactions that take place at our conferences and are not to be missed. Abstracts are numbered by session: abstracts presented during Poster Session 1 are numbered in the 1000s, Poster Session 2 in the 2000s, etc. Scientific organizers have selected short talks for plenary sessions and sometimes workshops from submitted poster abstracts. These oral poster abstract presentations may or may not fall on the same day as the presenter's poster session.

If you are a presenter, please check the index to find your abstract number; poster abstracts can be viewed on your Keystone Symposia online account and on the dedicated meeting mobile app. Speaker abstracts are also available on these two platforms, as well as after the program in this printed book in chronological order. To make the most of the formal poster sessions, we encourage you to preview posters during the time slots marked for informal poster abstract viewing.

Enjoying the Location

Please be aware of your environment as you plan your free time. If at a high-altitude conference, we urge you to rest on your first day and drink plenty of water. Check the bulletin board for group outings and other activities and discounts that Keystone Symposia and venue staff may have arranged.

Meals

The meals included in your registration vary by site. Check the program for meals marked "On Your Own" and plan accordingly. Meals listed with a time and place are provided as part of your registration. Some attendees choose to make a meal out of the evening social hour. Please note that alcohol and entertainment are not funded by registration fees or US government grants. Funding for this expense is generously provided by other supporters of Keystone Symposia.

Dear Colleague,

I am very pleased to send you greetings as the newly elected Chair of the Board of Keystone Symposia. Following eight highly effective years in this role, Dr. Juleen Zierath of the Karolinska Institutet stepped down in June 2016 at the conclusion of her scheduled term. She has kindly agreed to remain on the Board for an additional year as Chair of the Keystone Scientific Advisory Board. Assisting her in this endeavor will be newly appointed Deputy Chair of the Scientific Advisory Board, Dr. Margaret ("Peggy") Goodell of Baylor College of Medicine.

As Chair of the Scientific Advisory Board (SAB) for the past four years, I have witnessed firsthand the hard work and dedication of the Keystone Symposia staff, SAB members, Programming Consultants, and organizers who have put this conference together. Planning for this meeting started more than two years ago, in the autumn of 2014. At that time, review committees proposed the 2016-2017 conference topics, including some topics suggested through our online submission process (www.keystonesymposia.org/submitconcept). The Scientific Advisory Board then met in January and June 2015 to finalize these topics and propose scientific organizers. The location and speakers were identified in the summer of 2015.

The scientific organizers who put together this conference serve entirely in a volunteer capacity. Neither they nor the speakers receive an honorarium. We are very grateful for their tireless efforts. It is a reflection of the high quality of Keystone Symposia conferences that the world's top scientists make time and effort in their busy schedules to speak in the Keystone Symposia conferences.

And of course, we are grateful to you, the conference participants, for your interest in the exciting science that emerges from our meetings. Without your engagement and support, none of this would be possible. Thank you for choosing to share this time with us.

Sincerely,

Gary J. Nabel, M.D., Ph.D.
Chair, Keystone Symposia Board of Directors
Chief Scientific Officer, Sanofi

Meeting Books and Online Resources

Digital Meeting Book from Your Account

You may download a PDF of the meeting book from your Account on our secure website beginning seven days before the meeting and for up to 90 days afterwards. Your Account page also contains other useful content such as printable invoices and invitation letters, your profile with mail/email preferences, and much more. If you have questions about accessing your Account, don't hesitate to ask one of our on-site staff at the registration desk. If you find you prefer the digital format of the book, feel free to return this printed book to the registration desk.

Social Media Networks

Join us on the following social media platforms to stay informed, interact with other participants, and post your own photos, videos and text about your conference experience:

We Want Your Feedback!

Please be sure to give us your feedback by completing the survey that will be emailed to you at the conclusion of the meeting, as well as the briefer one on the mobile app. Your input is very valuable to us as we plan future conferences.

Keystone Symposia Mobile App

Our mobile app can be used on phones, tablets and laptops. Create an EventMobi account within the app to personalize your participant profile: upload a photo; add biographical information; take notes; and save a customized personal agenda for the week. Scan the QR code to the right to get the app from the Internet at **apps.eventmobi.com/ks.**

The app is available via:

Keystone Symposia Policies

Harassment Policy

Keystone Symposia is committed to maintaining a positive and respectful environment at its conferences and other events. We expect participants in our events to engage in constructive and professional discussion, in which all are valued for their scientific contributions and work. We value diversity, and desire that no participant should be subjected to harassment while involved in our events.

For purposes of this policy, harassment means unwelcome and offensive comments or behavior directed to the participant's sex, race, color, national origin, religion, sexual orientation or gender identity, disability or other status protected under applicable law. Harassment can include, for example, unwelcome attention, comments or jokes that focus on gender differences or sexual topics and that distract from the professional topics under discussion, unwelcome advances or requests for dates or sexual activities, and the use of language or images that demean or degrade persons of particular gender, racial, ethnic, religious or national identity.

To this end, we expect all participants to support these values and to avoid harassment of others participating in our conferences and other events. We expect all attendees to assist in ensuring that Keystone Symposia events are free from harassment of any kind, including reporting any instances of harassment directly to Dr. Jane Peterson, CEO, at **janep@keystonesymposia.org** and/or Dr. David Woodland, CSO, at **davidw@keystonesymposia.org**. Anyone who has experienced harassment, or who has witnessed such behavior, should notify one of the above persons as soon as possible.

Persons who act contrary to these values and expectations may be warned or asked to leave the event in which the behavior occurred, may be excluded from access to Keystone Symposia conferences and/or other events, and/or may be subject to other disciplinary or corrective action, at the discretion of Keystone Symposia.

Privacy Policy

Keystone Symposia is committed to protecting the privacy of its website visitors and meeting attendees. Keystone Symposia collects personal information when individuals register for our meetings and upon a visitor's request to subscribe to newsletters and meeting announcements (both print and online). Information that our visitors and attendees provide or that is derived from internal website tracking is not sold, rented or shared with any third-party individual or organization. Once on our mailing lists, individuals always have the option of unsubscribing so that they no longer receive all or certain types of our communications.

By participating in a Keystone Symposia meeting, attendees acknowledge that their name and photograph may be published in a limited fashion in materials produced by Keystone Symposia. For example, to make the meeting a more valuable experience for all involved, attendee names and institutions are listed on our website in a secure section accessible only by attendees of the same meeting. Attendee names and institutions are also pre-populated in our secure mobile app, but attendees decide for themselves whether to enter further information in the app.

Attendee names and contact information are also listed in the meeting book. Except in the meeting book in this fashion, we will not disclose attendee contact information, even to other attendees. Photographs of meeting interactions taken by Keystone Symposia may occasionally be used in our marketing literature.

For our full privacy policy, please visit **www.keystonesymposia.org/privacy**.

If you have any further questions or comments about our privacy policy, please send your feedback to **info@keystonesymposia.org**.

Meeting Room Policy

No video equipment, cameras, audio equipment or any other type of recording device will be allowed in the meeting rooms or poster sessions. Occasionally, Keystone Symposia may use such devices for its own publicity purposes. While we do not prohibit laptop computers, cell phones and PDAs, they must not be used for recording and should be operated in "silent" mode out of consideration for speakers and other conference attendees.

Attendees will be required to wear name badges for access to meeting sessions. Due to problems we have encountered at some meetings, we will be performing random badge checks. Attendees without badges will be turned away from the session.

Please note that spouses traveling with registered conference attendees are not permitted inside the sessions unless they pay the registration fee. However, they are welcome to attend evening receptions. They may attend breakfasts upon payment of a nominal daily fee.

Media and Communications Policy

Keystone Symposia recognizes that presenters of scientific data may have reasons for not wanting early results reported to the general public prior to peer review. We also recognize, however, that raising society's level of science knowledge and awareness is essential for appropriate scientific input into public policy and decision-making by political leaders, which is in everyone's best interest. We therefore encourage and will try to facilitate interactions between the scientists attending our conferences and the media. We ask both to be understanding when considering each other's objectives and the overarching goal of raising science literacy worldwide.

If approached with sufficient advance notice, Keystone Symposia can provide assistance to journalists to contact our speakers and abstract authors directly. We can prearrange interviews with specific meeting organizers, speakers, authors or Keystone Symposia staff.

We ask that all writers attending a Keystone Symposia conference gain approval from a speaker or poster presenter prior to quoting or publishing that individual's scientific results. This policy applies whether you are a professional writer/journalist or a non-journalist blogging about the conference or otherwise sharing information among a group of individuals.

Audio, still photo and video recording by any device (e.g., cameras, laptops, PDAs, cell phones, watches) is strictly prohibited during the sessions, unless in certain circumstances when prior permission must be obtained from Keystone Symposia. Photographs taken by Keystone Symposia may be available on request.

Keystone Symposia welcomes members of the scientific and general media at our meetings. Due to the costs of providing meals and other facilities, payment of the regular registration fee is required. Keystone Symposia may be able to give some consideration to journalists from nonprofit organizations, as well as to journalists who wish to attend the meeting for just one day. Such inquiries and arrangements should be made in advance.

Keystone Symposia does not require our presenters to submit papers, nor do we record or transcribe our sessions. Speaker abstracts are available in the meeting book provided to each registrant. Meeting books are available after the meeting to non-attendees for a nominal fee.

Keystone Symposia provides a venue for scientists to come together and share their ideas with each other in a relaxed setting. While we wish to accommodate members of the press, we ask that all members of the media respect our mission and the freedom we allow our scientists to discuss their work in a protected and informal environment.

If you have questions about this policy, contact Yvonne Psaila, Director of Marketing and Communications, **yvonnep@keystonesymposia.org**, **1.970.262.2676**.

Policy for Displaying Literature at Keystone Symposia Meetings

Keystone Symposia provides financial and in-kind donors with the ability to display a limited amount of literature or small promotional items on a table near the registration desk at Keystone Symposia meetings. Financial donors at certain levels can also insert literature into delegate bags at the specific meeting(s) they have chosen to support. Literature placed by organizations that are not current supporters will be removed until the meeting participant who placed it can be contacted.

Please contact the following Keystone Symposia staff if you are interested in displaying literature at our meetings and becoming a donor:

Financial support (e.g., corporations, foundations):	**Sarah Lavicka**, Assistant Director of Development **1.970.262.2690**; **sarahl@keystonesymposia.org**
In-kind support (e.g., publishers, societies/associations, conference organizers):	**Yvonne Psaila**, Director of Marketing and Communications **1.970.262.2676**; **yvonnep@keystonesymposia.org**

Nonprofit, academic and government institutions may post a flyer about grant and job opportunities or upcoming events of interest on the bulletin board in the registration area, and job postings can also be placed on the meeting mobile app. Please see a Keystone Symposia on-site representative if you need help with this or have questions while at the conference.

Phytobiomes: From Microbes to Plant Ecosystems

Scientific Organizers:
Jan E. Leach
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November 8–12, 2016
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Plants grow in association with complex communities of organisms. Phytobiomes encompass all of the organisms and all aspects of the environment that influence or are influenced by plants. Due to the diverse and dynamic processes carried out by biome members, phytobiomes have an important role in the sustained health and productivity of plants and plant ecosystems. Advances in systems biology approaches as well as supporting technologies, such as high-throughput sequencing, computational biology and many '-omics' technologies, are enabling exploration of the functional networks and activities of the component communities that comprise phytobiomes. These research technologies in the lab are being paralleled by next-generation precision agriculture technologies in the field, creating unprecedented opportunities for translation of phytobiomes knowledge into practice. Our fundamental knowledge of phytobiomes is vital to ensuring sustained global food security in the face of increasing global population and threats to crop productivity due to climate change as well as water, land and nutrient constraints. Advancing a systems-level understanding of phytobiomes and translating this knowledge into practice will require interactions across a spectrum of disciplines. This conference brings together a broad and international community of scientists in the public and private sector to collectively advance this newly-emerging field.

*Schedule may have changed since this book was prepared. Visit **www.keystonesymposia.org/16S2** and the conference mobile app at **apps.eventmobi.com/ks** for the most up-to-date program. Hashtag for this meeting: **#KSphytobiome***

Program (current as of October 17, 2016)

TUESDAY, NOVEMBER 8

16:00–20:00	Promenade	Arrival and Registration
18:00–20:00	Promenade	Welcome Mixer

WEDNESDAY, NOVEMBER 9

07:30–08:30	Pecos/Canyon	Breakfast
08:30–09:30	**Mesa A-B**	**Welcome and Keynote Address** ***Jan E. Leach**, Colorado State University, USA **Pamela C. Ronald**, University of California, Davis, USA *A Microbially Derived Tyrosine Sulfated Peptide Mimics a Plant Peptide Hormone*
09:30–12:00	**Mesa A-B**	**Phytobiome Community Assembly and Functions** ***Jan E. Leach**, Colorado State University, USA **Janet K. Jansson**, DOE Pacific Northwest National Laboratory, USA *Deciphering Soil Microbiomes using Multi-Omics* Coffee Break **Julia A. Vorholt**, ETH Zürich, Switzerland *The Leaf Microbiota: Responses to and Impacts on Plants* **Gabriel Castrillo**, University of North Carolina at Chapel Hill, USA *Designing Microbial Synthetic Communities for Controllable Outputs* **Angela D. Kent**, University of Illinois at Urbana-Champaign, USA (1032) *Short Talk: Selecting for Sustainability: Plant Genotype Shapes Microbial Functional Groups* **Natália de Brito Damasceno**, State University of Campinas, Brazil (1012) *Short Talk: Mapping the Colonization of a Synthetic Microbial Community Inoculum in Different Plant Models* On Own for Lunch
12:00–13:00	Mesa C	Poster Setup
13:00–22:00	Mesa C	Poster Viewing

*Full talk speaker abstracts can be viewed in chronological order beginning on page 27. Short talk speaker abstracts can be found on your Keystone Symposia online account or on the meeting mobile app at **apps.eventmobi.com/ks** (abstract number is shown in parentheses in the program above).*

WEDNESDAY, NOVEMBER 9 (continued)

14:30–16:30 **Mesa A-B**

Workshop 1

***Alejandra I. Huerta**, Colorado State University, USA
Collin Michael Timm, University of Tennessee, USA (2019)
Model Communities to Study Mechanisms of Phytobiome Function
Eric Kemen, Max Planck Institute for Plant Breeding Research, Germany (1031)
Dynamics in Shaping the Leaf Microbiome
Matthew Bakker, US Department of Agriculture, Agricultural Research Service, USA (1004)
Amplicon Sequencing Reveals Dominance of Cultivation-Resistant Oomycetes, and Fungal Community Dynamics in Roots of an Herbicide-Terminated Cereal Rye Cover Crop
Rachel D. Capouya, Ohio State University, USA (1009)
Fungal Endophyte Community Analysis of Green Coffee Beans: A Comparison Across Growing Regions and Qualities
Paloma Durán, Max Planck Institute for Plant Breeding Research, Germany (1014)
Dissecting the Multispecies Interaction Network at the Arabidopsis Root-Soil Interface
Rumakanta Sapkota, Aarhus University, Denmark (2013)
Cropping History Shapes Soil Fungal, Oomycete and Nematode Communities of Arable Soil
Emily Luna, Colorado State University, USA (2004)
Insect-Bacteria-Plant Interactions: Bacteria Associated with Russian Wheat Aphid (Diuraphis noxia) Enhance Aphid Virulence to Wheat
Amanda Rosier, University of Delaware, USA (2012)
Interspecies Interactions in the Rhizosphere May Influence the Functions of Plant Growth Promoting Rhizobacteria

16:30–17:00 Promenade Coffee Available

17:00–19:00 **Mesa A-B**

Signaling within the Phytobiome

***Jonathan A. Eisen**, University of California, Davis, USA
Steven Lindow, University of California, Berkeley, USA
Aggregation of Phyllosphere Inhabitants Facilitate Cell-Cell Signaling and Community Assembly
Choong-Min Ryu, Korean Research Institute of Bioscience and Biotechnology, South Korea
Bacterial Volatiles and Plant Health
Gwyn Beattie, Iowa State University, USA
Environmental Signals Directing Phytobiome Responses
Stephen Philip Cohen, Colorado State University, USA (1010)
Short Talk: Transcriptomic Analysis Reveals Key Genetic Responses Involved in the Rice Response to Simultaneous Abiotic (High Temperature) and Biotic (Bacterial Blight) Stresses

19:00–20:00 Pecos/Canyon Social Hour with Lite Bites

19:30–22:00 **Mesa C**

Poster Session 1

Poster sessions provide exciting opportunities for engagement between all levels of investigators. Abstracts beginning with the number 1 are featured during this poster session.

THURSDAY, NOVEMBER 10

07:30–08:30 Pecos/Canyon Breakfast

08:30–11:45 Mesa A-B

Multi-Trophic Interactions in the Phytobiome

***Steven Lindow**, University of California, Berkeley, USA
Elizabeth Arnold, University of Arizona, USA
Leveraging Endophyte Biodiversity Data for Discovery of New Fungal Symbionts of Plants
Marilyn J. Roossinck, Pennsylvania State University, USA
Viruses in the Phytobiome: Abundance and Ecological Roles

Coffee Break

Ana Pineda, NIOO-KNAW, Netherlands
Impact of Rhizosphere Microbes on Plant-Insect Interactions
Takema Fukatsu, National Institute of Advanced Industrial Science and Technology, Japan
Symbiotic Bacteria Underpinning Insect-Plant Interactions
Daniel Jacobson, Oak Ridge National Laboratory, USA (1026)
Short Talk: GWAVA – Genome-Wide Association Viriome/Microbiome Analysis
Posy Busby, Oregon State University, USA (1007)
Short Talk: Plant Disease Modification by Fungal Leaf Endophytes Depends on Tri-trophic Interactions in the Populus Phytobiome

On Own for Lunch

13:15–14:45 Mesa A-B

Virtual Keystone Symposia Global Webcast on "The Genome Editing Revolution: Translating Genome Editing Technologies into Human Therapies"

14:45–15:30 Mesa A-B

Workshop 2: International Phytobiomes Alliance Overview

*__Kellye A. Eversole__, Eversole Associates, USA
Susan Huse, Indigo, USA
Natalie W. Breakfield, NewLeaf Symbiotics, USA
Chris J. Grandlic, Monsanto, USA
Kelly D. Craven, Samuel Roberts Noble Foundation, USA
Steven Lindow, University of California, Berkeley, USA
Carolyn Anne Young, Samuel Roberts Noble Foundation, USA
Daniel P. Schachtman, University of Nebraska, USA
Varghese Thomas, Bayer, USA

16:30–17:00 Promenade Coffee Available

17:00–19:00 Mesa A-B

Imaging and Modeling of the Phytobiome

***Janet K. Jansson**, DOE Pacific Northwest National Laboratory, USA
Elizabeth Shank, University of North Carolina at Chapel Hill, USA
Visualizing Metabolic Exchange among Plant and Soil Microbiomes
Jonathan A. Eisen, University of California, Davis, USA
Phylogenomic and Metagenomic Approaches to the Study of Phytobiomes
Tiina Roose, University of Southampton, UK
Multiscale Modeling of Plant-Soil Interaction
Joseph Evan Spraker, University of Wisconsin-Madison, USA (2017)
Short Talk: Fusarium Fujikuroi Chlamydospore Development and Secondary Metabolite Production is Induced by Ralstonia Solanacearum Lipopeptide

THURSDAY, NOVEMBER 10 (continued)

19:00–20:00	Pecos/Canyon	Social Hour with Lite Bites

FRIDAY, NOVEMBER 11

07:30–08:30	Pecos/Canyon	Breakfast
08:30–11:45	**Mesa A-B**	**Phytobiome Engineering** ***Andrew Jones**, Colorado State University, USA **Paul M. Schulze-Lefert**, Max Planck Institute for Plant Breeding Research, Germany *Exploring Root Microbiota Functions by Synthetic Communities and Germ-Free Plants* **Michael S. Strano**, Massachusetts Institute of Technology, USA *The Emergence of Plant Nanobionics* Coffee Break **Stephan C. Schuster**, Nanyang Technological University, Singapore *Phytobiomes Constitute an Innate Part of the Air Microbiome* **Ian Kaplan**, Purdue University, USA (1030) *Plant-Soil Feedbacks on Crop Management via the Rhizosphere Microbiome* **Kimberly Allen**, NewLeaf Symbiotics, USA (1028) *Short Talk: Application of Methylobacteria in the Agro-Ecosystem* **Molly Cadle-Davidson**, Advanced Biological Marketing, Inc, USA (1008) *Short Talk: Leveraging the Phytobiome and the Promise of Biologicals in Agriculture* On Own for Lunch
11:45–13:00	Mesa C	Poster Setup
13:00–22:00	Mesa C	Poster Viewing
16:30–17:00	Promenade	Coffee Available
17:00–19:00	**Mesa A-B**	**Phytobiomes in Data-Driven Crop Production** ***Kellye A. Eversole**, Eversole Associates, USA **Angela Sessitsch**, Austrian Institute of Technology GmbH, Austria *Endophytic Colonization from Roots to Seeds: Ecology and How Plants Can Benefit* **Adriana Hemerly**, Instituto de Bioquímica Médica Leopoldo de Meis, Brazil *Association with Beneficial Endophytes: A Perspective from the Plant Side* **John Fulton**, Ohio State University, USA *Ag Data Coalition: Advancing Agriculture* **Joshua R. Herr**, University of Nebraska, Lincoln, USA (1024) *Short Talk: Surveying the Plant Microbiome through Plant Genome Sequencing Project Data Mining*
19:00–20:00	Pecos/Canyon	Social Hour with Lite Bites
19:30–22:00	**Mesa C**	**Poster Session 2** *Poster sessions provide exciting opportunities for engagement between all levels of investigators. Abstracts beginning with the number 2 are featured during this poster session.*

Program (current as of October 17, 2016)

SATURDAY, NOVEMBER 12

07:30–08:30	Pecos/Canyon	Breakfast
08:30–11:30	**Mesa A-B**	**Applications Toward Sustainability** ***Angela Sessitsch**, Austrian Institute of Technology GmbH, Austria **Geoffrey von Maltzahn,** Indigo Agriculture, USA *The Role of Endophytes in the Evolution of Agriculture* **Luiz de Araújo**, University of São Paulo, Brazil *Endophytic Methylobacterium spp: Diversity and Molecular Interaction with the Host Plant* Coffee Break **Matthew Wallenstein**, Colorado State University, USA *Can Microbial Biostimulants Enhance Agricultural Efficiency and Productivity? Promise, Perils and Possibilities* **Antonio Gonzalez-Rodriguez**, Universidad Nacional Autónoma de México, Mexico (1022) *Short Talk: Variation in Ecoenzyme Activity and Nutrient Concentration in Soil and Litter Across a Gradient of Oak Species Richness in Mexico* **Harsh Bais**, University of Delaware, USA (1003) *Short Talk: Functional Microbiome: Belowground Solutions for Aboveground Problems*
		On Own for Lunch
14:30–16:30	**Mesa A-B**	**Workshop 3: International Phytobiomes Alliance Standards Meeting**
16:30–17:00	Promenade	Coffee Available
17:00–18:45	**Mesa A-B**	**Phytobiomes and the Vision for Tomorrow's Agriculture** ***Gwyn Beattie**, Iowa State University, USA **Kellye A. Eversole**, Eversole Associates, USA *Translating Phytobiomes Knowledge* **Andrew Jones**, Colorado State University, USA *Linking Climate and Weather Scenarios to Crop and Economic Models* **Jan E. Leach**, Colorado State University, USA *Future Directions for Phytobiomes Research and Translation*
18:45–19:00	**Mesa A-B**	**Meeting Wrap-Up: Outcomes and Future Directions**
20:00–21:00	Promenade/Mesa Ballroom	Social Hour with Lite Bites
20:00–23:00	Mesa Ballroom	Entertainment

SUNDAY, NOVEMBER 13

Departure

Thank you…

…to all our donors supporting this meeting. Their generosity and dedication to the mission of collaborative science distinguish them as valuable members of the Keystone Symposia community.

This conference is part of the ***Keystone Symposia Global Health Series****, supported by the* ***Bill & Melinda Gates Foundation****.*

We appreciate the in-kind advertising/marketing support of:

Phytobiomes **journal,**
published by The American Phytopathological Society

Scholarship and Travel Award Recognition

Congratulations

The following participants were awarded financial aid to attend this meeting. Be sure to stop by their poster sessions to see the abstracts that earned their merit-based support. Poster numbers are listed in parentheses, with the first digit indicating the corresponding poster session. Visit ***keystonesymposia.org/financialaid*** *for more information on Keystone Symposia's scholarship and travel award opportunities.*

The following scholarship recipients are funded by:

Keystone Symposia Future of Science Fund*

Rachel D. Capouya, Ohio State University, USA (1009)

Rumakanta Sapkota, Aarhus University, Denmark (2013)

Keystone Symposia Global Health Travel Award Recipients

Made possible by funding from the Bill & Melinda Gates Foundation

Adefoyeke Olufunmilayo Aduramigba-Modupe, University of Ibadan, Nigeria (1034)

Cecile Annie Ewane, University of Yaoundé, Cameroon (1017)

Amit K. Jaiswal, Hebrew University, Israel (1027)

Bunmi Olasanmi, University of Ibadan, Nigeria (2028)

Conference Assistant

We would like to thank our conference assistant for contributing to this meeting. This individual assists the scientific organizers and Keystone Symposia's onsite staff throughout the meeting and compiles a meeting summary for submission to our government financial supporters.

Alejandra I. Huerta, Colorado State University, USA (1025)

*To learn more about the Keystone Symposia Future of Science Fund, see page 25 or visit **keystonesymposia.org/FSF**; ( ) = abstract number

Meet the Scientific Organizers

Jan E. Leach, Ph.D. is a University Distinguished Professor and Associate Dean for Research in the College of Agriculture at Colorado State University. She is a plant pathologist who studies how plants defend themselves from pathogens. Her focus is on understanding the molecular mechanisms of plant disease susceptibility and resistance.

Dr. Leach is a Fellow and a past President of the American Phytopathological Society (APS). She is a Fellow of the American Association for the Advancement of Science (AAAS) and a Fellow of the American Academy of Microbiology. In 2016, Dr. Leach was named Non-Resident Fellow in the Plant Biology Division of the Noble Foundation. She serves as a member of the Global Rice Partnership Science Oversight Committee. For more than 16 years, she has served on the APS Public Policy Board, where she led the development of the *Phytobiomes Initiative*, a systems-level approach to improving crop productivity.

Kellye A. Eversole, has been President of Eversole Associates, a US agricultural science and technology consulting firm since 1991 (www.eversoleassociates.com). An expert in sequencing technologies and strategies, she has led the development of genome sequences for several crop and livestock species and still serves as the executive director of the International Wheat Genome Sequencing Consortium. She helped develop the Phytobiomes Roadmap and currently leads the International Alliance for Phytobiomes Research, a public-private consortium (www.phytobiomesalliance.org). She was elected a Fellow of the American Association for the Advancement of Science in 2013. Passionate about innovation for societal benefits, Kellye mentors entrepreneurs from emerging economies who are launching S&T-based businesses. She has been involved actively in various aspects of the agricultural industry since her childhood and co-owns a farm in southwestern Oklahoma.
Twitter: @EversoleAssoc, @phytobiomes.

Jonathan A. Eisen, Ph.D. is a Professor at the University of California, Davis with appointments in the Genome Center, the Department of Evolution and Ecology and the Department of Medical Microbiology and Immunology. His current research focuses on the evolution, ecology and function of communities of microbes and how the microbes interact with each other and with hosts. Most of his work involves the use of high-throughput DNA sequencing methods to characterize microbes and then the use and development of computational methods to analyze this type of data.

Prior to moving to UC Davis, he was on the faculty of The Institute for Genomic Research (TIGR) and held an Adjunct appointment at the Johns Hopkins University. He earned his Ph.D. in Biological Sciences from Stanford University and his A.B. in Biology from Harvard College. Dr. Eisen was elected to the American Academy of Microbiology in 2012.

In addition to his research Dr. Eisen is heavily involved in science communication and open science activities and is an active and award-winning blogger (e.g., http://phylogenomics.blogspot.com and http://microbe.net) and microblogger (e.g., Twitter @phylogenomics).

Gwyn Beattie, Ph.D. is currently the Robert Earle Buchanan Distinguished Professor of Bacteriology in the Department of Plant Pathology and Microbiology at Iowa State University. Her teaching and research are focused on the genomics and ecology of plant-associated bacteria, with current projects on the influence of microbial communities on plant water use efficiency and the factors enabling bacterial pathogens to use light and environmental stress signals to colonize leaves. She is a member of the American Society for Microbiology and The American Phytopathological Society (APS), the APS Public Policy Board Chair, and a co-author of the *Phytobiomes Roadmap* (www.phytobiomes.org).

Keystone Symposia on Molecular and Cellular Biology

About Keystone Symposia

Keystone Symposia on Molecular and Cellular Biology is a 501(c)(3) nonprofit organization headquartered in Silverthorne, Colorado, USA that convenes open, peer-reviewed conferences across a broad range of the life sciences. Our mission is to accelerate life science discovery by providing a forum to present top-quality science, foster new collaborations and help prepare the next generation of life scientists. Approximately 50–60 conferences take place each year. More than half the symposia are held in mountain venues across the American and Canadian West, with the remainder primarily in North American cities and various global locations. We have now convened conferences on five continents: Africa, Asia, Australia, Europe and North America. The first in South America was held in Ouro Preto, Brazil in May 2013.

Keystone Symposia receives revenue from two sources: registration fees (approximately 65-70%) and generous support from corporations, foundations, government entities and individuals (approximately 30-35%). This support provides funding for scholarships as well as speaker travel expenses (subsidies are based on economy-rate travel and no honoraria are paid), allowing registration fees to be kept as low as possible. Many speakers forego expense reimbursement to provide more funds for scholarships.

Under the direction of Chief Executive Officer Jane Peterson, Chief Scientific Officer David Woodland and an advisory Board of Directors, a staff of approximately 45 full-time, part-time or seasonal employees handles all aspects of administration, meeting management/logistics, attendee services, fundraising and marketing.

How Keystone Symposia Conferences Are Programmed

All Keystone Symposia conferences are developed through a rigorous peer-review system that involves the coordinated efforts of a Scientific Advisory Board (SAB) comprised of more than 90 leading scientists from academia, industry and government worldwide, as well as approximately 500 programming consultants who provide additional expertise in specific scientific areas.

Meeting development starts more than two years in advance through teleconference and online discussion forums involving SAB members and study group programming consultants. This process generates information on trending scientific areas and new meeting ideas. The SAB then convenes in Keystone, Colorado in January and uses the study group-generated information to identify conference topics, suggest potential scientific organizers, make recommendations regarding meeting content and identify meetings that could be held jointly. Based on the recommendations of the SAB, Keystone Symposia staff solicits conference organizers and helps them prepare programs for peer review.

The SAB meets again in June to review all submitted meeting proposals, recommend whether proposals should be accepted and provide constructive feedback to organizers.

Keystone Symposia's History

Founded in 1972 in Los Angeles as the ICN-UCLA Symposium on Molecular Biology by Professor C. Fred Fox, the organization evolved into UCLA Symposia before relocating to Silverthorne, Colorado in 1990. At that time we became a free-standing division of a nonprofit called The Keystone Center and were renamed Keystone Symposia on Molecular and Cellular Biology. We separated from The Keystone Center and became an entirely independent nonprofit in a phased transition beginning in 1995 and ending in 1997.

Attendees at the first Keystone Symposia meeting in Squaw Valley in 1972.

Notable Milestones

1972: Keystone Symposia was founded as the ICN-UCLA Symposium on Molecular Biology and held an initial conference on membrane research in Squaw Valley, California, March 13-17, 1972.

1984: Keystone Symposia convened the first-ever open, international meeting on AIDS in 1984, which was widely credited with catalyzing a consensus that AIDS was caused by a retrovirus now known as the Human Immunodeficiency Virus.

1990: Under the chairmanship of Dr. Pedro Cuatracasas (then President of the Parke Davis Research Laboratories) followed by Professor Ralph Bradshaw (then at the University of California, Irvine), Keystone Symposia relocated to Silverthorne, Colorado, became a division of The Keystone Center and was renamed Keystone Symposia on Molecular and Cellular Biology.

1995: Under the Board leadership of Professor Dennis Cunningham of the University of California, Irvine, Keystone Symposia began a phased transition to separate from The Keystone Center.

1997: Under the chairmanship of Professor Edward A. Dennis of the University of California, San Diego, this separation was completed and Keystone Symposia became a completely independent nonprofit 501(c)(3) organization.

(continued on next page)

2001: We held our first conference outside of the US in Canada ("Hematopoiesis" in Whistler, British Columbia, Canada) and also launched our formal diversity initiatives, supported first by a grant from the David and Lucile Packard Foundation and later by another from the Alfred P. Sloan Foundation.

2003: Dr. James W. Aiken assumed the new position of Chief Executive Officer.

2005: Keystone Symposia's first conference in Asia convened ("Stem Cells, Senescence and Cancer" in Singapore).

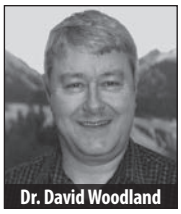
2006: We held our first conference in Europe ("Multi-Protein Complexes Involved in Cell Regulation" in Cambridge, UK) and also launched the Keystone Symposia Global Health Series, supported by the Bill & Melinda Gates Foundation, which also funds Global Health Travel Awards to enable developing-country investigators to attend meetings in this Series.

2007: Keystone Symposia's first conference in Africa and the first Global Health Series meeting convened ("Challenges of Global Vaccine Development" in Cape Town, South Africa).

2009: We organized our first conference in Australia ("Telomere Biology and DNA Repair" in Ashmore).

2010: Keystone Symposia received a five-year, US$1.37 million MARC (Minority Access to Research Careers) grant from the National Institute of General Medical Sciences of the US National Institutes of Health to help fund expanding diversity initiatives.

2011: Dr. David L. Woodland ("Woody") joined Keystone Symposia as Chief Scientific Officer.


Dr. David Woodland

2013: Keystone Symposia convened its first conference in South America ("The Innate Immune Response in the Pathogenesis of Infectious Disease" in Ouro Preto, Brazil).

2014: Keystone Symposia appointed a new President and Chief Executive Officer, Dr. Jane L. Peterson, upon the retirement of Dr. James W. Aiken. Dr. Peterson took up the position effective April 14, 2014.


Dr. Jane Peterson

The SAB also reviews the entire meeting portfolio to determine whether any additional meetings need to be "fast-tracked" to fill gaps in the portfolio. While the key focus of the SAB is the quality of the scientific content, considerable attention is paid to speaker diversity in the programs, including gender, stage of career, ethnicity, affiliation, geographical distribution and speaker return rate. In addition, efforts are made to ensure appropriate representation of basic, clinical and industry research in the programs, depending on the scientific topic. Organizers submit revised meeting programs by September and October, allowing Keystone Symposia staff to start inviting speakers well over a year in advance of the conference season.

To ensure the best-quality science unencumbered by commercial interests, Keystone Symposia does not accept any requests to speak on the programs. Similarly, corporate sponsors do not receive speaking slots and are not given preference when organizers invite speakers. Even in cases where nonprofit foundations and publishers sponsor sessions or speakers, the organizers always select the associated speakers and topics.

Like the SAB members and study group programming consultants, scientific organizers serve in an entirely volunteer capacity with only their economy-rate travel, lodging and registration expenses paid. Organizers fine-tune their programs and select speakers, using guidelines from Keystone Symposia to encourage fresh and diverse participation. A number of slots in each session are left open for late-breaking developments to be later filled by short talks that the organizers select from submitted abstracts.

Keystone Symposia chooses conference venues that are able to accommodate the expected number of participants, provide cost-effective facilities and offer an atmosphere conducive to information exchange and informal networking. Keystone Symposia staff negotiate discounted lodging rates, and every attempt is made to select sites that are environmentally conscientious.

Keystone Symposia Diversity Initiatives

Keystone Symposia strives to engage conference attendees with many different experiences and backgrounds – e.g., different research interests and work environments, career stages and cultures. Diverse experiences and backgrounds provide the lens through which we discern and conceive of research questions. By including a rich variety of perspectives, we ensure that the best research questions and problem-solving approaches are represented at the conferences.

We are dedicated to increasing the number of scientists from designated underrepresented backgrounds and female scientists as organizers, speakers and attendees. Scholarships and highly interactive poster sessions encourage the participation of students and postdoctoral fellows, who typically account for 40% of attendees each year. The Keystone Symposia Global Health Travel

(continued on next page)

Keystone Symposia on Molecular and Cellular Biology

Awards make possible the participation of investigators from developing countries in meetings of the Keystone Symposia Global Health Series.

Through a range of initiatives in diversity, we actively promote participation of UR (underrepresented) investigators. Overseen by our Director of Diversity in Life Science Programs, (DLSP) with input from scientists, and science policy makers, on the Diversity Advisory Committee, these initiatives include:

Scholarships – We encourage UR trainees to apply for scholarships which provide $1,200 for graduate students and postdoctoral fellows to attend a Keystone Symposia conference. Submission of an abstract is required and selection is based on the quality of the abstract. Visit **www.keystonesymposia.org/scholarships**.

ABRCMS Scholarships – Each year during the Annual Biomedical Research Conference for Minority Students (ABRCMS), managed by the American Society for Microbiology, Keystone Symposia awards scholarships to two students at the graduate and/or postdoctoral research level who are presenting research or mentoring early career UR trainees at the conference. Visit **www.keystonesymposia.org/ABRCMS**.

Early-Career Investigator Travel Awards – We award up to $1,200 for UR scientists who are assistant professors or industry scientists at equivalent levels with US citizenship or permanent residency to attend a Keystone Symposia meeting. The application requires the candidate to identify a specific question he/she is researching which might be addressed by attending a particular meeting. It also requires a commitment to mentoring a student (undergraduate, graduate, postdoc) from an underrepresented background in a laboratory around career development and positioning issues for a minimum of one year. These competitive Awards are made possible by Biogen and Burroughs Wellcome Fund. Applications are reviewed and ranked by meeting organizers. Visit **www.keystonesymposia.org/EarlyCareerAward**.

Keystone Symposia Fellows Program – Keystone Symposia accepts on average ten early-career UR scientists annually who are committed to a research career and to enhancing diversity in the life sciences by increasing participation of designated UR scientist populations. The Keystone Symposia Fellows Program provides an opportunity to engage in the Keystone Symposia program development process and gain insight into the inner workings of the life science community. Fellows interact at the highest levels with renowned scientists, engaging via teleconferences and face-to-face participation in the meetings of our Scientific Advisory Board and onsite Fellows Circle at the June SAB meeting. Visit **www.keystonesymposia.org/Fellows** to learn more, apply or read about past and current Fellows. The application deadline for the 2018 Fellows Program is **March 15, 2017.**

Peer-to-Peer Program – Participants from UR backgrounds are emailed information on the DLSP prior to their attendance at a Keystone Symposia conference. The DLSP director also provides first-time UR attendees with a link to a Google Hangout conducted by Fellows on "What to Expect at a Keystone Symposia conference." If Keystone Symposia Fellow(s) are in attendance the Fellow(s) serve as DLSP ambassadors to UR first-time attendees and their names and contact information are sent in advance of the conference to establish communication. This provides an opportunity to share research backgrounds and have names and faces to connect with throughout the conference. Attendees who have self-identified as being members of a federally designated UR population will be sent these advanced email notifications.

Biogen Mentoring Program – Keystone Symposia collaborates with Biogen in offering formal mentoring sessions to scientists from UR backgrounds at selected Keystone Symposia meetings. These sessions are facilitated by scientists from Biogen.

Strategic and Deliberate Outreach – Keystone Symposia's DLSP Director presents information and attends national diversity conferences such as ABRCMS, Understanding Interventions, The Leadership Alliance National Symposium (LANS), SACNAS (Society for the Advancement of Chicanos and Native Americans in Science) Annual Conference, and other molecular and cellular biology conferences for diversity trainees at universities and medical schools nationwide. Ongoing collaborations to promote early-career investigator development and diversity enhancement include work with Brown University, Harvard Medical School, The Leadership Alliance, The Endocrine Society, Biogen, Novartis Institutes for BioMedical Research, the Society for Neuroscience (SfN), and the National Institutes of Health (NIH) National Research Mentoring Network (NRMN).

*For more information on Keystone Symposia's Diversity in Life Science Programs, please visit **www.keystonesymposia.org/diversity**.*

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*If you are interested in supporting these Programs, please contact Irelene Ricks, Director of Diversity in Life Science Programs, at **irelener@keystonesymposia.org.***

Thank you

To fulfill our nonprofit scientific mission, Keystone Symposia relies on significant financial commitment from government, foundation and industry donors as well as generous support from individuals. Gifts to the discretionary Directors' Fund ensure Keystone Symposia's ability to provide sufficient program support for meetings on a greater variety of scientific topics than would be possible if gifts were restricted to specific meetings in each case. All contributions are vital to the fulfillment of our mission — catalyzing collaborations to accelerate discoveries and helping to prepare and position the next generation of leading life scientists.

To all of our faithful supporters:
Thank you for your generous commitment to Keystone Symposia.

If your organization is interested in making a donation to Keystone Symposia, please contact our Development Office at ***development@keystonesymposia.org****. You can also visit* ***keystonesymposia.org/corporategiving*** *for more information.*

If you are interested in making a personal donation to the Future of Science Fund, please visit our secure individual donor platform at ***keystonesymposia.org/FSF****.*

To explore personal bequests and other planned gift vehicles, please contact our Development Office.

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Thank you…

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Top-tier donors making an ongoing, annual commitment of $100,000+. Their public championing of Keystone Symposia's cause provides inspirational leadership commitment to our shared scientific mission of catalyzing collaborations, accelerating discoveries, and preparing and positioning the next generation of leading life scientists.

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The generous support of our Partners, Patrons, Donors and Contributors makes possible the outstanding scientific quality of our meetings, and unsurpassed opportunities for interaction among attending scientists.

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Thank you…

Support for Keystone Symposia Diversity in Life Science Programs

We are grateful for this valuable support directed at increasing the participation of underrepresented scientists among meeting leaders and attendees, thereby enhancing diversity in the life science research community. Read more about our Diversity in Life Science programs on page 17.

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US Federal Grant Funding

Keystone Symposia truly appreciates the support received from various institutes of the National Institutes of Health. This support primarily funds scholarships for graduate students and postdoctoral fellows to attend our conferences. US federal grant support for the 2016–2017 meeting series was generously provided by:

National Institute on Aging (NIA)
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These generous alumni of previous meetings and others with a passion for ensuring a future of scientific discovery that benefits humankind have made gifts during the last 12 months to support the Keystone Symposia Future of Science Fund. Through their generosity, we are able to provide scholarships and travel awards to the next generation of biomedical and life scientists, whose education and careers are enhanced by the opportunity to attend meetings and interact with the world's leading senior scientists.

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The Future of Science Fund is a way, through outright or estate gifts, to provide educational program or scholarship support to help fulfill Keystone Symposia's mission of catalyzing collaborations to accelerate discovery and of preparing and positioning the next generation of leading life scientists. Gifts to the Future of Science Fund can be designated to support:

- Competitive-based scholarships for students and postdoctoral fellows
- General conference program support

For more information on the Future of Science Fund or to make a gift, please visit **keystonesymposia.org/FSF** or contact Rosie Stermer at **rosies@keystonesymposia.org**.

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Ronald

A Microbially Derived Tyrosine Sulfated Peptide Mimics a Plant Peptide Hormone

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Plant and animal pathogens have developed diverse mechanisms to manipulate host biological processes. One intriguing strategy employed by biotrophic pathogens, which require a living host for infection, is the production of molecules that mimic host growth promoting factors. The biotrophic pathogen *Xanthomonas oryzae pv. oryzae(Xoo)* produces a sulfated peptide named RaxX, which shares similarity to peptides in the PSY (plant peptide containing sulfated tyrosine) family. Alignment of RaxX and PSY sequences reveals a 13 amino acid region of high similarity. A synthetic sulfated RaxX derivative comprising these 13 residues, RaxX13-sY, induces root growth in Arabidopsis and rice in a manner similar to that triggered by PSYs. Analyses of multiple RaxX peptides identified residues that are required for activation of immunity mediated by the rice XA21 receptor but that are not essential for root growth induced by PSY. These findings suggest that RaxX serves as a molecular mimic of PSY peptides and that XA21 has evolved the ability to recognize and respond specifically to the microbial form of the peptide.

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Jansson

Deciphering Soil Microbiomes Using Multi-Omics

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Soil microbial communities (microbiomes) play several key ecosystem services, including cycling of carbon and other nutrients and support of plant growth. Despite their essential role for life on our planet, the specific roles carried out by individual members of soil microbiomes has been challenging to dissect, due to the high complexity and high microbial diversity of soil ecosystems. To meet this challenge we have been applying a suite of omics tools to uncover both the phylogenetic representation and the functional properties of soil microbes in complex soil microbiomes. Most of our studies are based on the analysis of soil metagenomes that subsequently serve as a scaffold for understanding gene expression data (metatranscriptomes and metaproteomes). Deep soil metagenome sequencing has now developed to the point that it is possible to bin near complete and complete genomes from soil microbial communities; the majority of which represent novel species that have never been isolated or studied in the laboratory. We used metagenomics to study the impact of different land management practices on soil microbial community compositions and functions. The first study was a comparison of long-term cultivated soil metagenomes to those from native prairie, across a 3 state transect of the United States Great Prairie. The findings demonstrated shifts in community structure with land management; including shifts in microbes and processes involved in the nitrogen cycle. We specifically focused on one of the sites, Kansas native prairie, to develop our omics pipeline. The soil was incubated with nutrients (glycine) or with water addition and studied using a multi-omics approach. This enabled us to determine which microbes were active and what genes were expressed in the various treatments. We also developed an assembly and binning pipeline to bin genomes from the soil. By mapping the metatranscriptome reads we were able to determine which of the genome bins represented microbes that were active at the time of sampling. In a second study we studied soil metagenomes obtained from soils undergoing different land management practices at a long-term field station at Rothamsted, UK. The treatments included long-term bare fallow, long-term cultivation and undisturbed grassland plots. These comparisons allowed us to dissect the relative contributions of cultivation on the soil microbiome. Importantly, the bare fallow treatment, without any influence of plants, enabled us to determine the long-term influence of plant inputs on the soil microbiome.

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Vorholt

The Leaf Microbiota: Responses to and Impacts on Plants

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The aerial parts of the plants, which are dominated by leaves, represent one of the largest terrestrial habitats for microorganisms. This habitat, called the phyllosphere, is occupied by a diverse community of microorganisms, which is important for plant health and growth. Most of the phyllosphere inhabitants are not well investigated; however, there is a growing interest to study commensal bacteria to elucidate their interactions with the plants, among each other and to learn how they withstand the hostile conditions of their habitat. A predominance of Proteobacteria, Actinobacteria and Bacteroidetes living in the phyllosphere of numerous plants has been revealed, while metagenomics and metaproteomics approaches gave insights into the general bacterial adaptation strategies to the phyllosphere. Recently, we conducted large-scale experiments to isolate *Arabidopsis thaliana* leaf bacteria as pure cultures. Individual plants as well as individual leaves were sampled at different European sites to determine their core leaf community and to establish a reference strain collection using flow cytometry and dilution series plating. After identifying approximately 3,000 isolates using a high-throughput DNA sequencing-based method we selected more than 200 representative strains belonging to 52 genera of the major phyllosphere phyla covering the majority of the culture-independent taxonomic diversity. Draft genomes of all selected isolates were generated. Recolonization experiments using synthetic communities in a gnotobiotic model system showed reproducible colonization patterns and represents a valuable starting point to identify mechanisms of community formation and function. Examination of plant responses to its microbiota revealed that the plant reacts differently to members of its natural phyllosphere microbiota. A subset of commensals increase expression of defense-related genes and thereby may contribute to plant health and performance.

Castrillo

Designing Microbial Synthetic Communities for Controllable Outputs

Gabriel Castrillo
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Root-associated microbes can help plants to cope with nutrient stresses. This has inspired interest in designing synthetic microbial consortia for agricultural development. Here, we used the response to phosphate starvation (PSR) as a model system to investigate bacterial effects on phosphate accumulation in plants. We demonstrate that binary plant-bacterium interactions provide predictive information for the design of bacterial synthetic communities with a controllable plant output. We show that the accumulation of Pi, the end-point marker of plant PSR, is driven by the composition of root-associated bacterial communities. Using shoot Pi accumulation data from a small number of synthetic communities, we successfully applied and validated a comprehensive mathematical model for predicting shoot Pi content as a function of microbiome composition.

Lindow

Aggregation of Phyllosphere Inhabitants Facilitate Cell-Cell Signaling and Community Assembly

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Aerial plant surfaces often support large population sizes (> 10^6 cells/cm^2) of a variety of bacterial colonists. The large majority of these colonists occur in relatively large cellular assemblages, apparently driven by localized abundance of limiting carbon resources and more conducive environmental conditions at such sites. The production of so-called quorum sensing signal molecules such as acyl homoserine lactones and various unsaturated fatty acids is common in these communities, and the frequent absence of free water that would dissipate such signals maximizes the opportunities for interspecific interactions among community members. Since many plant pathogenic bacteria modulate expression of virulence factors and control behaviors needed for epiphytic colonization via such signal molecules, the incidence of plant disease can be strongly influenced by the composition of the microbial communities on that plant part. Plants also can detect bacterial signal molecules and often respond by inducing host defenses. Bacterial growth and survival is strongly favored in cellular aggregates, which also are sites of preferential recruitment of immigrant inoculum. Emigration of bacteria from plants is quite efficient and thus the abundance and composition of microbes in air near plants is strongly influenced by the amount and type of vegetation nearby. Phyllosphere microbial communities thus are assembled from a metacommunity contributed and shared by nearby plants in a process that likely involves microhabitat modification at sites of microbial aggregation by initial plant colonists. Leaf surface microbial communities therefore are quite context-dependent and can be managed either by direct inoculation or by changing the agroecological context in which crops are grown.

Ryu

Bacterial Volatiles and Plant Health

Choong-Min Ryu
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In the phytobiome world, microbial metabolic activity includes the secretion of diverse infochemicals that influence interspecific plant and microbes. Previously the metabolites have been utilized upon improving plant health. Certain plant growth-promoting rhizobacteria (PGPR) elicit induced systemic resistance (ISR) and plant growth promotion in the absence of physical contact with plants *via* bacterial volatile compound (BVC) emissions. In this presentation, I review the recent progress made by research into the interactions between PGPR and BVC, focusing on BVC emission by PGPR strains in plants. Particular attention will be given to the mechanisms by which these bacterial species elicit ISR. We provide an overview of recent progress in the elucidation of PGPR BVC interactions from studies utilizing transcriptome, metabolome and proteome analyses. By monitoring defense gene expression patterns, performing 2-dimensional electrophoresis, and studying defense signaling null mutants, salicylic acid and ethylene were found to be key players in plant signaling pathways involved in the ISR response. BVCs also confer induced systemic tolerance to abiotic stresses, such as drought and heavy metals. The current analytical approaches for PGPR volatiles profiling is also provided with needed future developments. Furthermore, to assess potential utilization of PGPR volatiles for crop plants, volatile suspensions were applied to crops like pepper and cucumber and were found to be effective at protecting plants against plant pathogens and insect pests in the field. Taken together, these studies provide further insights into the biological and ecological potential of BVCs for enhancing plant self-immunity and/or adaptation to biotic and abiotic stresses in modern agriculture.

Beattie

Environmental Signals Directing Phytobiome Responses

Gwyn Beattie
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Systems knowledge of phytobiomes requires understanding how environmental signals impact the behavior and interactions among organisms. For example, water availability influences plant-pathogen relations, plant susceptibility to disease, and pathogen survival strategies. Plant-associated microbes have increasingly been recognized for their ability to enhance plant drought stress tolerance by mechanisms such as enhancing root growth and water uptake. We have characterized the impact of soil water deficits on belowground microbial communities during successive growth cycles under water-limited and water-rich conditions. Our studies highlighted the potential for plants to enrich for beneficial microbial communities based on the increased plant water use efficiency during the late growth cycles. Moreover, they suggested that bacterial exposure to drought-induced changes in plants (e.g., ROS, hormone or metabolite changes) impact community composition more strongly than bacterial exposure directly to water deficits; this was evidenced by the greater impact of water limitation on bacterial communities within roots than in the ectorhizosphere or bulk soil. Although we identified bacterial and fungal genera that were favored specifically during plant growth under drought, our results indicate that a mechanistic understanding of this environment-plant-microbe nexus could help in optimizing the use of microbials for plant drought protection.

We have also explored light as a cue that influences the behavior of plant-associated bacteria. Whereas plants exploit light signals for defense against pathogens, our studies have demonstrated that at least one bacterial pathogen exploits light signals for plant colonization, which may enable it to evade circadian-based plant defenses. Far-red light is enriched in plant tissues due to the absorption of red and blue light and is conducted over long distances through stems and roots. We discovered a much stronger response of our foliar pathogen to far-red than to red light, supporting the possibility that this pathogen and other microbes can exploit far-red light gradients as spatial and temporal cues within plant tissues.

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Arnold

This abstract was not available at the time of printing.

Roossinck

Viruses in the Phytobiome: Abundance and Ecological Roles

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We are analyzing plant viruses in a biodiversity hotspot in northwestern Costa Rica with about 10,000 species of native plants, and a low diversity natural area in the United States: the Tallgrass Prairie Preserve. We find many viruses that are distantly related to known viruses, an equal or greater number of completely unknown viruses, and a few known viruses. Persistent viruses are the most common, and appear to have very long relationships with their hosts with nearly 100% rates of vertical transmission. Acute viruses are found in each study site, some with wide-spread infections. Mixed infections are also common. In Costa Rica we have found a massive invasion of a plant pathogenic virus, *Zucchini yellow mosaic virus*, that appears to be from spillover events from adjacent agricultural areas. The virus does not cause any detectable disease in native plants, which may be dead-end hosts. There is some evidence of spill-back into crops, however these viruses are attenuated in the disease symptoms that they induce.

A common assumption is that emerging viruses invade humans and their domesticated plants and animals from wild relatives; however, little has been done to look at how "domestic" viruses affect wildlife. These studies suggest that wild plants may be equipped to tolerate viruses acquired from domestic hosts, and perhaps change them to less virulent forms. In addition, there is little evidence that viruses evolve towards increased virulence. Implications for agriculture will be discussed.

Pineda

Impact of Rhizosphere Microbes on Plant-Insect Interactions

Ana Pineda
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Plant roots are colonized by an extremely high number of microorganisms in a similar way to the human intestinal tract. In the last decade, evidence is accumulating that rhizosphere microbes confer plants an extended phenotype that enhances plant growth, tolerance to abiotic stresses and resistance to their biotic attackers. From all those attackers, I am especially interested on how rhizosphere microbes affect insects aboveground at several trophic levels, i.e., both herbivores and their natural enemies. The underlying mechanisms of these interactions are fascinating, and go from molecular changes in the plant to synthesis of chemical metabolites, changes that can have strong ecological consequences. In the end, rhizosphere microbes have plant-mediated effects on the performance and the behaviour of aboveground insect communities. Despite the strong advances that this field has experienced in the last years, the astonishing diversity of microbes that colonize plants is constantly opening new questions on their impact on plant-insect interactions. We need to move from working with single strains to evaluate full microbiomes, and to understand what the role is those single strains play in the microbiome network. Understanding how microbiomes affect plant-insect interactions in natural ecological systems may give us new insights on how to apply microbiomes on ecologically intensive agroecosystems. Here I will discuss how plant-soil feedbacks, a long-standing concept of soil ecology, can help us to manage the soil microbiome to enhance the control of insect pests.

Fukatsu

Symbiotic Bacteria Underpinning Insect-Plant Interactions

Takema Fukatsu
National Institute of Advanced Industrial Science and Technology (AIST), Japan

Diverse insects and other organisms are associated with symbiotic microbes, which entail a variety of ecological and evolutionary consequences. In particular, plant-sucking insects of the order Hemiptera, which embrace a large number of agricultural pest species, are highly dependent on their microbial partners and possess well-developed symbiotic systems in their specialized tissues, cells or gut regions. Since plant sap is generally deficient in proteins, vitamins and other nutrients, the insects require symbiont-provisioned essential amino acids, B vitamins and other nutrients for their growth and survival.

In addition to the nutritional provisioning, such microbial symbionts play substantial roles in plant adaptation, pest status, insecticide resistance, and other plant- and agriculture-related traits of their insect hosts. Here I overview our recent findings as to how microbial symbionts are involved in insect-plant interactions in the agro-ecosystem.

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Shank

Visualizing Metabolic Exchange among Plant and Soil Microbiomes

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In nature, bacteria are rarely found in isolation; they are most often surrounded by other microorganisms. We are interested in how microbes within these complex microbial communities alter their physiology and development in response to metabolites secreted by their microbial neighbors. To explore this question we are studying the coculture interactions of bacteria isolated from two plant systems that represent topologically distinct, naturally occurring small ecosystems: the roots of *Arabidopsis thaliana* and the pitfall traps of *Sarracenia* carnivorous pitcher plants. We are dissecting the cooperative, competitive, and metabolic interactions between the members of these plant-associated microbial communities using a combination of coculture, fluorescent reporter bioassays, and imaging mass spectrometry. In addition, we are developing transparent soil microcosms to directly visualize how these bacteria use secreted chemical cues to spatially interact in native-like microenvironments. Exploring these microbial interactions both *in vitro* and *in planta* will allow us to explore the molecular mechanisms that underlie them and discover their role in microbiome ecology.

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Eisen

Phylogenomic and Metagenomic Approaches to the Study of Phytobiomes

Jonathan A. Eisen
University of California, Davis, CA, USA

High throughput sequencing and computational analysis of the resulting data has become a powerful tool for characterizing the evolution, ecology and function of communities of organisms, especially microbes. However such approaches have some major constraints that limit their utility. I will discuss how integrated "phylogenomic" approaches can improve the utility of such sequence data in the context of phytobiome studies. I will focus in partiuclar on examples from new studies of the communities associated with seagrasses. Examples will include the value of reference genomes of cultured isolates, co-evolutionary studies of hosts and associated microbiomes, generation of reference databases of functional and phylogenetic marker genes, and biogeographic analysis of key taxa and communities.

Roose

Multiscale Modeling of Plant-Soil Interaction

Tiina Roose
Bioengineering Sciences Research Group, University of Southampton, UK

In this talk I will describe a state of the art image based model of the soil-root interactions, i.e., a quantitative, model of the rhizosphere based on fundamental scientific laws. This will be realised by a combination of innovative, data rich fusion of structural imaging methods, integration of experimental efforts to both support and challenge modelling capabilities at the scale of underpinning bio-physical processes, and application of mathematically sound homogenisation/scale-up techniques to translate knowledge from rhizosphere to field scale. The specific science question I will address with these techniques is how to translate this knowledge from the single root scale to root system, field and ecosystem scale in order to predict how the climate change, different soil management strategies and plant breeding will influence the soil fertility.

Schulze-Lefert

Exploring Root Microbiota Functions by Synthetic Communities and Germ-Free Plants

Stephane Hacquard, Paloma Duran, Rafal Zgadzaj, Ruben Garrido-Oter, Stijn Spaepen, Thorsten Thiergart, Ryohei Nakano, Masayoshi Hashimoto, Amine Hassani and Paul Schulze-Lefert
Department of Plant Microbe Interactions, Max Planck Institute for Plant Breeding Research, Cologne, Germany

We established *Arabidopsis* leaf- and root-derived microbiota culture collections representing the majority of bacterial species that are reproducibly detectable by culture-independent community sequencing. Using defined bacterial communities and a gnotobiotic *Arabidopsis* plant system we have shown that the isolates form assemblies resembling natural microbiota on their cognate host organs, but are also capable of ectopic leaf or root colonization (Bai *et al*., *Nature* 2015).

We have now extended this work and established a culture collection of root-derived fungal and oomycete endophytes from healthy Arabidopsis plants grown in natural soil. I will present results of microbiota reconstitution experiments in which we examined the impact of synthetic microbial communities consisting either of a single or combinations of microbial classes on plant growth. Our findings suggest that the bacterial microbiota plays an important role in protecting the host against soil-borne fungi and oomycetes.

Strano

The Emergence of Plant Nanobionics

Michael S. Strano
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Our laboratory at MIT has been interested in exploring the relatively new interface between living plants and non-biological nanostructures to impart the former with new and enhanced functions, which we call Plant Nanobionics. We demonstrate that the introduction of particular nanoparticles such as poly (acrylic acid) nanoceria (PAA-NC) and their corresponding nanotube complexes (SWNT-NC) into isolated chloroplasts can yield chloroplasts that are more stable to reactive oxygen species ex vivo[1,2], possess enhanced solar conversion efficiencies, are able to produce glucose, and allow real-time information exchange via embedded nanosensors for free radicals. Specifically, superoxide concentration can be suppressed 59% by assembling PAA-NC inside chloroplasts. SWNT-NC promote photoactivity 3.1 times above controls while PAA-NC extend glucose production from 0.5 to 88 hours[2]. SWNT chloroplast complexes also allow fluorescent reporting of nitric oxide generation. We further investigate the transport and localization of nanoparticles into plant cells (protoplasts) and organelles (chloroplasts) and show that strongly cationic or anionic nanoparticles (| zeta potential | > 30 mV) are able to penetrate and remain kinetically trapped within chloroplasts. A generalized Lipid Exchange Envelope Penetration (LEEP) mechanism[3] for nanoparticle localization within living plants was developed with excellent predictive capabilities on what particle sizes and types will localize within plant tissue, and should be a valuable tool for plant nanobionic engineering. Lastly, progress toward photonic plants and those capable of sensing[4], IR communication, and groundwater monitoring in real time will be described. Plant Nanobionics has potential to create new technology using wild-type, living plants as the starting platform.

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Schuster

Phytobiomes Constitute an Innate Part of the Air Microbiome

Akira Uchida, Enzo Acerbi, Caroline Chénard, Elena Gusareva, James Nicholas Ian Houghton, Dana Meyer Miller, Daniela Moses, Rikky Wenang Purbojati, Megan Elise Clare, Cassie Elizabeth Heinle, Sandra Kolundžija, Anthony Wong, Nicolas Gaultier, Balakrishnan Nair Vasantha Premkrishnan, Deepa Nikappil Sudarsana Panicker, Michelle Koh Yanqing, Phung Wen Jia, Viacheslav Ryukhko, Federico Lauro, Yehuda Cohen, Hie Lim Kim, Ana Carolina Martins Junqueira, and Stephan C. Schuster
Nanyang Technological University, Singapore

Microbial communities inhabiting terrestrial and aquatic ecosystems have long been studied. With the onset of metagenomics, the degree of diversity and abundance of these communities have become apparent, even on a global scale. In contrast, the atmosphere, despite its enormous planetary volume, has largely been neglected as a habitat for microbial communities, despite providing means of transport with an intercontinental range. We have studied the occurrence of airborne microbial organisms in the tropical climate of Singapore and found robust and persistent assemblages, both on an intra-day and a month-to-month time scales. Plant-associated bacteria and fungi were found to be the major constituent of the air microbiome, in addition to DNA derived from plants and insects. Besides conducting in-depth metagenomics studies that identified the diversity and abundance of airborne organisms, we have sequenced and assembled "100 genomes from air" using single molecule real-time sequencing (SMRT). These genome data, together with organismal and habitat information, are stored in a "DNAir database", which largely extends the organismal range of public databases and also includes previously uncultivatable organisms.

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Kaplan

Plant-Soil Feedbacks on Crop Management via the Rhizosphere Microbiome

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Plants imprint distinct signatures on the rhizosphere microbiome, resulting in species-specific effects on the belowground microbial community. These soil legacies are perhaps most apparent in agriculture. Indeed, among the earliest agricultural advancements—dating back >2,000 years—was the development of rotations to disrupt phytopathogenic microorganisms that accumulate in soil when the same crop is repeatedly cultivated. However, high intensity production systems with no rotation are still relatively common. Although techniques such as soil fumigation and steam sterilization are used, these broad-spectrum, non-selective biocides also eliminate beneficial microbes that promote crop health. Further, plant domestication has disrupted the ability of crops to cultivate symbiotic associations in the rhizosphere that enhance growth and protection against attackers. In this work, we study the consequences of domestication and plant-soil feedbacks on tomato grown in high intensity rotations for plant performance and vulnerability to aboveground insect pests. Using a pool of 36 tomato lines (30 crop cultivars, 6 wild ancestors), we show that tomato has strong negative feedbacks (ca. 30% reduction) on seed germination and seedling growth when growing in tomato vs. non-tomato soil. Interestingly, the magnitude of this feedback strongly varied at both an intra-specific level (i.e., among crop cultivars) and between wild vs. cultivated species. Certain lines had little to no feedback after one round of soil conditioning. Feedback strength was highly correlated with several components of the rhizosphere microbiome, including total living microbial biomass, gram-positive bacteria, and arbuscular mycorrhizal fungi. These data demonstrate that plant-soil feedbacks, and their impact on soil microbes, can be manipulated to optimize crop management in high intensity production systems.

Sessitsch

Endophytic Colonization from Roots to Seeds: Ecology and How Plants Can Benefit

Angela Sessitsch*, Birgit Mitter, Carolina Escobar-Rodríguez, Nikolaus Pfaffenbichler, Stéphane Compant, Livio Antonielli, Friederike Trognitz
AIT Austrian Institute of Technology, Health & Environment Department, Bioresources Unit, Tulln, Austria

Plants are associated with highly complex microbiomes. The rhizosphere is a hot spot of microbial diversity and activity due to the availability of root exudates, which serve as nutrients. Several rhizosphere colonizers may also enter roots and colonize as endopyhtes intercellular spaces and xylem vessels. Once established within roots, endophytes may systemically colonize other plant tissues such as stems, leaves and even reproductive organs. Working with different plant species such as rice, maize and the model plant *Setaria viridis,* we have found highly tissue-specific microbial communities indicating high sensitivity and response to the distinct physiological conditions encountered in different plant tissues. Of particular interest are seed endophytes. They show rather low complexity, but represent important members of the next generation plant and may be highly important for early plant establishment. By analysing microbiomes associated with different tissues of *Setaria viridis* and *S. pumila* collected at different locations in Austria we revealed information regarding the origin and ecology of seed-associated microbiota.

We further addressed the question how seed endophyte communities can be manipulated and developed an approach to integrate a strain of interest into seed with the aim to establish in next generation plants. For this approach we chose the model endophyte strain *Paraburkholderia phytofirmans* PsJN. This strain is able to efficiently colonize different plant tissues, promote plant growth and enhance plant tolerance to drought stress. We will show results using this strain from lab to field including genome and transcriptome analysis as well as seed microbiome manipulation and field application.

Hemerly

Association with Beneficial Endophytes: A Perspective from the Plant Side

Thais L.G. Carvalho, Helkin G.F. Ballesteros, José Paulo M. Filho, Pablo Hardoim; João Luis Mendes, Matheus Atella, Thayssa M.D. Fernandes, Paulo C. G. Ferreira and Adriana S. Hemerly
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An important biotechnological challenge of this century is to develop tools to apply for a sustainable agriculture that would increase productivity using less fertilizers, pesticides, water and cultivated area. The associations that occur between sugarcane and other grasses with nitrogen-fixing endophytic bacteria have raised a large interest in their use in agriculture, in view of the positive effects on root development, and the increase in biomass and productivity.

In Brazil, BNF plays a fundamental role in sugarcane cultivation by reduction of the use of nitrogen fertilizers, making Brazilian sugarcane culture more competitive in global markets. Inoculants of associative and endohytic diazotrophic bacteria had been shown to lead to positive results on sugarcane yields, which are dependent on the plant genotype and soil conditions.

Our group has been studying plant genes involved in the establishment of a beneficial type of association with nitrogen-fixing bacteria, aiming to assist in the development of more responsive cultivars to inoculants of beneficial diazotrophs. An integrated differential transcriptome was generated by Illumina RNA sequencing and it provided an overview of sugarcane metabolism, growth and development controlled by nitrogen, water and endophytic nitrogen-fixing bacteria during a successful association. All together, the data suggest that an important control of the efficiency of the association is already set in the early stages of plant-bacterium recognition, when specific plant genotypes sense the environment and regulate several plant signaling pathways involved in microorganism recognition and plant defense.

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Fulton

This abstract was not available at the time of printing.

von Maltzahn

This abstract was not available at the time of printing.

de Araújo

This abstract was not available at the time of printing.

Wallenstein

Can Microbial Biostimulants Enhance Agricultural Efficiency and Productivity? Promise, Perils and Possibilities

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Plants co-evolved with microbes, and plants that supported beneficial microbiomes likely increased their fitness. Healthy microbiomes enable nutrient acquisition, provide pathogen resistance, and modulate plant stress responses. However, the green revolution overlooked these positive interactions, often replacing biology with chemistry. The depression of positive plant-microbiome interactions in modern agriculture likely contributes to low nutrient use efficiency and high pathogen pressure.

The opportunity to harness the microbiome to improve the sustainability and efficiency of agriculture has been validated by significant recent investments. However, a long history of ineffective microbial biostimulants has resulted in entrenched skepticism.

I posit that most biostimulants have been ineffective in practice because they ignore fundamental ecological interactions. I will propose an ecological framework for effective biostimulants, with supporting evidence from recent studies. Finally, I will speculate on the future role of biostimulants in agriculture.

Eversole

Embracing the Complexity of Phytobiomes and the Vision for Crop Production

Kellye A. Eversole
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To meet the demands of a global human population expected to exceed 9.6 billion by 2055, crop productivity in sustainable agricultural systems must improve considerably in the face of a steadily changing climate and increased biotic and abiotic stressors. Traditional agricultural sciences have relied mostly on research within individual disciplines and linear, reductionist approaches for crop improvement. While significant advancements have been made in developing and characterizing genetic and genomic resources for crops and in understanding plant and soil microbiomes, we still have a very limited understanding of genotype by environment by management (GxExM) interactions that determine productivity, sustainability, quality, and the ability to withstand biotic and abiotic stressors. Embracing complexity and the non-linear organization and regulation of biological systems would enable a paradigm shift in breeding and crop production by allowing us to move towards a holistic, systems level approach that integrates a wide range of disciplines (e.g., geophysics, biology, agronomy, physiology, genomics, genetics, breeding, physics, pattern recognition, feedback loops, modeling, and engineering) and knowledge about crop phytobiomes (i.e., plants, their associated macro- and micro-organisms, and the geophysical environment of distinct geographical sites). By focusing on the phytobiome, we will be able to elucidate, quantify, model, predict, act, manipulate, and prevent and ultimately prescribe the cropping systems, methods, and management practices most suited for a particular farm, grassland, or forest. To ensure progress towards this vision, the new International Alliance for Phytobiomes Research, an industry-academic consortium, has been created.

Jones

Linking Climate and Weather Scenarios to Crop and Economic Models

Andrew S. Jones
Colorado State University, Fort Collins, CO, USA

Improved understanding of systems-level Phytobiome community interactions and enhanced predictive capabilities for field-based farm management are needed to advance food security and sustain a growing global population. The geophysical environment includes interactions, sensitivities, feedbacks, and constraints with respect to weather, climatic trends and events, and interdisciplinary linkages between biological aerosols, hydrology, soils, and atmospheric properties. This talk presents a vision for linking big data and data analytics of climate and weather scenarios to crop and economic models. This is essential if the Phytobiome community is to explore, integrate, optimize, and apply knowledge advances within all system components, including process-level studies of interactions among components. Implicit in these approaches is the need for interdisciplinary interactions. The talk will highlight global outreach capabilities for enhancement of in-field interactions/integration critical to Phytobiomes from a weather and climate perspective to ensure plant, soil, human and global health, including sustainable and productive agricultural systems and universal access to a safe food supply.

Leach

Future Directions for Phytobiomes Research and Translation

Jan E. Leach
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Fundamental knowledge of phytobiomes is crucial to ensuring sustained global food security. Due to conceptual and technological advances in 'omics sciences, systems biology, microbial ecology, data science and precision crop management systems we are now poised to comprehensively characterize and understand phytobiomes. This presentation will open discussions of key future research areas to close knowledge gaps, such as fundamental studies of phytobiome components, interactions, dynamics, and functions; the generation of integrated systems-based models for phytobiome analysis and prediction; and the development of practical phytobiome-based crop management strategies. To achieve a truly systems level understanding of the interactions within and between phytobiomes components, and how to translate that information to predictive rather than reactive agricultural practices, will require collaboration across disciplines and national boundaries in ways that integrate efforts of public and private sector scientists, engineers, crop producers, extension, and agribusiness professionals at unprecedented levels.

Poster Session 1

Wednesday, November 9 | 19:30-22:00
Location: Mesa C

Presenter	Poster #	Abstract Title
Aduramigba-Modupe, Adefoyeke	1034	Management of Stalk Rot Disease of *Sorghum bicolor* (L.) Moench. caused by *Fusarium verticilloides* using Plant Growth Promoting Rhizobacteria (PGPR)
Armanhi, Jaderson	1002	Construction and annotation of a community-based culture collection representing the sugarcane core microbiome
Bais, Harsh	1003	Functional microbiome: Belowground solutions for aboveground problems
Bakker, Matthew	1004	Amplicon sequencing reveals dominance of cultivation-resistant oomycetes, and fungal community dynamics in roots of an herbicide-terminated cereal rye cover crop
Barret, Matthieu	1005	Diversity and dynamics of seed-associated microbial assemblages
Brown, Shawn	1006	Host genotype and environmental effects on disease-modifying endophytes of Populus
Busby, Posy	1007	Plant disease modification by fungal leaf endophytes depends on tri-trophic interactions in the Populus phytobiome
Cadle-Davidson, Molly	1008	Leveraging the Phytobiome and the promise of biologicals in agriculture
Capouya, Rachel	1009	Fungal endophyte community analysis of green coffee beans: a comparison across growing regions and qualities
Chicoine, Tayler	1035	Variation in Microbial Communities and Nitrogen Transformation Rates among Switchgrass Varieties
Cohen, Stephen	1010	Transcriptomic analysis reveals key genetic responses involved in the rice response to simultaneous abiotic (high temperature) and biotic (bacterial blight) stresses
Coleman-Derr, Devin	1011	The Effect of Drought on the Sorghum Microbiome
Copeland, Julia	1036	The effect of tillage and crop rotation on the soil community of experimental wheat fields
Damasceno, Natália	1012	Mapping the colonization of a synthetic microbial community inoculum in different plant models
Dijkstra, Paul	1013	From Taxon-Specific Responses To Whole System Carbon Cycling In The Root Microbiome
Durán, Paloma	1014	Dissecting the multispecies interaction network at the Arabidopsis root-soil interface
Dykes, Gretchen	1015	Microbial Activity Spurred By Silicon Amendment Addition Alters the Biogeochemical Cycling of Arsenic, Iron, and Methane in Flooded Rice Paddies
Escobar Rodriguez, Carolina	1016	Seed-Associated Microbiota: Composition, Drivers and Transmission Routes employing the Model Plant *Setaria viridis* L
Ewane, Cecile Annie	1017	Physiological state of banana fruit: biotic and abiotic pre-harvest factors affect the appearance and the severity of crown rot disease
Favela, Alonso	1019	Consequences of Domestication on the Maize Microbiome
Finkel, Omri	1037	A plant-microbiome mesocosm for studying the mechanisms of plant microbiome assembly and maintenance
Fitzpatrick, Connor	1020	The root microbiome and plant-soil feedback

Poster Session 1

Wednesday, November 9 | 19:30-22:00
Location: Mesa C

Presenter	Poster #	Abstract Title
Ginnan, Nichole	1021	Uncovering the Role of the Citrus Microbiome in Pathogen Tolerant Phenotype
Gonzalez-Rodriguez, Antonio	1022	Variation in ecoenzyme activity and nutrient concentration in soil and litter across a gradient of oak species richness in Mexico
Grandlic, Chris	1023	Biologicals in Agriculture: Discovery and Testing at Scale
Herr, Joshua	1024	Surveying the plant microbiome through plant genome sequencing project data mining
Huerta, Alejandra	1025	Exception to the norm: Rice Resistance Locus Xo1 is Triggered by Inactive TAL Effectors
Jacobson, Daniel	1026	GWAVA – Genome-Wide Association Viriome/Microbiome Analysis
Jaiswal, Amit	1027	Linking the Belowground Microbial Composition, Diversity and Activity to Soilborne Disease Suppression and Growth Promotion of Tomato Amended with Biochar
Jansson, Christer	1038	The integrated Plant-Atmosphere-Soil Systems (iPASS) Initiative
Jimenez, Desmond	1028	Application of Methylobacteria in the Agro-Ecosystem
Kaplan, Ian	1030	Plant-soil feedbacks on crop management via the rhizosphere microbiome
Kemen, Eric	1031	Dynamics in shaping the leaf microbiome
Kent, Angela	1032	Selecting for sustainability: Plant genotype shapes microbial functional groups
Kostka, Joel	1033	The *Sphagnum* phytobiome: new insights from an ancient plant lineage

Poster Session 2

Friday, November 11 | 19:30-22:00
Location: Mesa C

Presenter	Poster #	Abstract Title
Lee, Jidam	2027	Analysis of the rhizosphere microbiome of tomato cultivars that are resistant or susceptible to bacterial wilt
Lee, Yong-Hwan	2002	EPSS Ring: Switching Fungal Lifestyles among Endophyte–Pathogen–Saprotroph-Symbiont as a Circle
Luna, Emily	2004	Insect-Bacteria-Plant Interactions: Bacteria Associated with Russian Wheat Aphid (*Diuraphis noxia*) Enhance Aphid Virulence to Wheat
Micallef, Shirley	2005	Response of Cucumber and Tomato Microbiomes to Rainfall
Morsy, Mustafa	2006	Bio-Boom: Integration of Fungal Endophytes for Improved Crops
Mougel, Christophe	2007	*Brassica napus* holobiont and bioagressor interactions : do soil microbiote diversity modulate the interactions?
Nicolaisen, Mogens	2032	The mycobiome of cereals
Olasanmi, Bunmi	2028	Effect of storage environment and period on viability of breadnut (*Artocarpus camansi* Blanco) seeds
Parker, Jane	2008	Exploring the ecological significance of a polymorphic *Resistance* gene cluster in a *wild Arabidopsis* thaliana population
Posch, John	2009	Exploring the disease caused by a soil-borne fungus on soybean in the presence of other pests
Randall, Jennifer	2010	*Carya illinoinensis* and the associated phytobiome
Robeson, Kalen	2011	Transcriptional Activity of a Lake Erie Microcystis Bloom
Rosier, Amanda	2012	Interspecies interactions in the rhizosphere may influence the functions of plant growth promoting rhizobacteria
Sapkota, Rumakanta	2013	Cropping history shapes soil fungal, oomycete and nematode communities of arable soil
Schadt, Christopher	2014	The microbiome landscape of *Populus* trees from the soil to the canopy
Schuster, Stephan	2029	Phytobiomes constitute an innate part of the air microbiome
Sharon, Amir	2015	Reflection of the host genetics in endophytes composition and diversity
Simmons, Tuesday	2033	Elucidating the role of Actinobacteria in drought-stressed cereals
Souza, Rafael	2016	Unraveling the cross-talk between microbiome and bioenergy crop sugarcane
Spraker, Joseph	2017	*Fusarium fujikuroi* chlamydospore development and secondary metabolite production is induced by *Ralstonia solanacearum* lipopeptide
Sword, Gregory	2018	Exploiting fungal microbiomes for plant stress resistance and improved yields in cultivated cotton
Timm, Collin	2019	Model communities to study mechanisms of phytobiome function
Trail, Frances	2020	Comparative analysis of wheat, corn, and soy crop-associated microbes across four field management strategies
Tringe, Susannah	2021	Drivers of plant microbial community composition
Wagner, Maggie	2022	Effects of host genotype and secondary chemistry on foliar microbiomes in a wild relative of Arabidopsis
Wall, Hollie	2023	Mycoremediation Progress: From Laboratory Culture to Field Application

Poster Session 2

Friday, November 11 | 19:30-22:00
Location: Mesa C

Presenter	Poster #	Abstract Title
Wallace, Jason	2024	The Effect of Host Genetics on the Maize Leaf Microbiome across 270 Diverse Inbred Lines
Washburne, Alex	2030	Phylogenetic factorization of microbiome data
Xia, Ye	2025	Community study of culturable bacterial endophytes of switchgrass (*Panicum virgatum* L.) and their effects on plant growth
Zgadzaj, Rafal	2026	Root nodule symbiosis in *Lotus japonicus* drives the establishment of distinctive root-associated bacterial communities
Zhang, Yunzeng	2031	Huanglongbing causes downward spiral in microbiome-host interaction

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Translational Vaccinology for Global Health (S1)
Organizers: Christopher L. Karp, Gagandeep Kang and Rino Rappuoli
Oct 25–29, 2016 | Park Plaza Riverbank | London | United Kingdom

Phytobiomes: From Microbes to Plant Ecosystems (S2)
Organizers: Jan E. Leach, Kellye A. Eversole, Jonathan A. Eisen and Gwyn Beattie
Nov 8–12, 2016 | Hilton Santa Fe Historic Plaza Hotel | Santa Fe, New Mexico | USA

Hemorrhagic Fever Viruses (S3)
Organizers: William E. Dowling and Thomas W. Geisbert
Dec 4–8, 2016 | Hilton Santa Fe Historic Plaza Hotel | Santa Fe, New Mexico | USA

Cellular Stress Responses and Infectious Agents (S4)
Organizers: Margo A. Brinton, Sandra K. Weller and Beth Levine
Dec 4–8, 2016 | Eldorado Hotel & Spa | Santa Fe, New Mexico | USA

Cell Plasticity within the Tumor Microenvironment (A1)
Organizers: Sergei Grivennikov, Florian R. Greten and Mikala Egeblad
Jan 8–12, 2017 | Big Sky Resort | Big Sky, Montana | USA

Precision Genome Engineering (A2)
Organizers: J. Keith Joung, Emmanuelle Charpentier and Olivier Danos
Jan 8–12, 2017 | Beaver Run Resort | Breckenridge, Colorado | USA

Transcriptional and Epigenetic Control in Stem Cells (J1)
Organizers: Konrad Hochedlinger, Kathrin Plath and Marius Wernig
joint with
Neurogenesis during Development and in the Adult Brain (J2)
Organizers: Alysson R. Muotri, Kinichi Nakashima and Xinyu Zhao
Jan 8–12, 2017 | Resort at Squaw Creek | Olympic Valley, California | USA

TGF-ß in Immunity, Inflammation and Cancer (A3)
Organizers: Wanjun Chen, Joanne E. Konkel and Richard A. Flavell
Jan 9–13, 2017 | Sagebrush Inn & Suites | Taos, New Mexico | USA

Mitochondria Communication (A4)
Organizers: Jared Rutter, Cole M. Haynes and Marcia C. Haigis
Jan 14–18, 2017 | Sagebrush Inn & Suites | Taos, New Mexico | USA

New Developments in Our Basic Understanding of Tuberculosis (A5)
Organizers: Samuel M. Behar and Valerie Mizrahi
Jan 14–18, 2017 | Fairmont Hotel Vancouver | Vancouver, British Columbia | Canada

PI3K Pathways in Immunology, Growth Disorders and Cancer (A6)
Organizers: Leon O. Murphy, Klaus Okkenhaug and Sabina C. Cosulich
Jan 19–23, 2017 | Hilton Santa Fe Historic Plaza Hotel | Santa Fe, New Mexico | USA

Biobetters and Next-Generation Biologics:
Innovative Strategies for Optimally Effective Therapies (A7)
Organizers: Cherié L. Butts, Amy S. Rosenberg, Amy D. Klion and Sachdev S. Sidhu
Jan 22–26, 2017 | Snowbird Resort | Snowbird, Utah | USA

Diabetes (J3)
Organizers: Jiandie Lin, Clay F. Semenkovich and Rohit N. Kulkarni
joint with
Obesity and Adipose Tissue Biology (J4)
Organizers: Marc L. Reitman, Ruth E. Gimeno and Jan Nedergaard
Jan 22–26, 2017 | Keystone Resort | Keystone, Colorado | USA

Omics Strategies to Study the Proteome (A8)
Organizers: Alan Saghatelian, Chuan He and Ileana M. Cristea
Jan 29–Feb 2, 2017 | Beaver Run Resort | Breckenridge, Colorado | USA

Epigenetics and Human Disease:
Progress from Mechanisms to Therapeutics (A9)
Organizers: Johnathan R. Whetstine, Jessica K. Tyler and Rab K. Prinjha
Jan 29–Feb 2, 2017 | Sheraton Seattle Hotel | Seattle, Washington | USA

Hematopoiesis (B1)
Organizers: Catriona H.M. Jamieson, Andreas Trumpp and Paul S. Frenette
Jan 31–Feb 4, 2017 | Fairmont Banff Springs | Banff, Alberta | Canada

Noncoding RNAs: From Disease to Targeted Therapeutics (J5)
Organizers: Kevin V. Morris, Archa Fox and Paloma Hoban Giangrande
joint with
Protein-RNA Interactions: Scale, Mechanisms, Structure and Function of Coding and Noncoding RNPs (J6)
Organizers: Gene W. Yeo, Jernej Ule, Karla Neugebauer and Melissa J. Moore
Feb 5–9, 2017 | Fairmont Banff Springs | Banff, Alberta | Canada

Inflammation-Driven Cancer: Mechanisms to Therapy (J7)
Organizers: Fiona M. Powrie, Michael Karin and Alberto Mantovani
joint with
Microbiome in Health and Disease (J8)
Organizers: Julie A. Segre, Ramnik Xavier and William Michael Dunne
Feb 5–9, 2017 | Keystone Resort | Keystone, Colorado | USA

Autophagy Network Integration in Health and Disease (B2)
Organizers: Ivan Dikic, Katja Simon and J. Wade Harper
Feb 12–16, 2017 | Copper Mountain Resort | Copper Mountain, Colorado | USA

Asthma: From Pathway Biology to Precision Therapeutics (B3)
Organizers: Clare M. Lloyd, John V. Fahy and Sally Wenzel-Morganroth
Feb 12–16, 2017 | Keystone Resort | Keystone, Colorado | USA

Viral Immunity: Mechanisms and Consequences (B4)
Organizers: Akiko Iwasaki, Daniel B. Stetson and E. John Wherry
Feb 19–23, 2017 | Hilton Santa Fe Historic Plaza Hotel | Santa Fe, New Mexico | USA

Malaria: From Innovation to Eradication (B5)
Organizers: Marcel Tanner, Sarah K. Volkman, Marcus V.G. Lacerda and Salim Abdulla
Feb 19–23, 2017 | Speke Resort & Conference Centre | Kampala | Uganda

Lipidomics and Bioactive Lipids in Metabolism and Disease (B6)
Organizers: Alfred H. Merrill, Walter Allen Shaw, Sarah Spiegel and Michael J.O.Wakelam
Feb 26–Mar 2, 2017 | Granlibakken Tahoe | Tahoe City, California | USA

Bile Acid Receptors as Signal Integrators in Liver and Metabolism (C1)
Organizers: Luciano Adorini, Kristina Schoonjans and Scott L. Friedman
Mar 3–7, 2017 | Hyatt Regency Monterey | Monterey, California | USA

Rare and Undiagnosed Diseases:
Discovery and Models of Precision Therapy (C2)
Organizers: William A. Gahl and Christoph Klein
Mar 5–8, 2017 | Fairmont Copley Plaza | Boston, Massachusetts | USA

mRNA Processing and Human Disease (C3)
Organizers: James L. Manley, Siddhartha Mukherjee and Gideon Dreyfuss
Mar 5–8, 2017 | Sagebrush Inn & Suites | Taos, New Mexico | USA

Synapses and Circuits: Formation, Function and Dysfunction (X1)
Organizers: Tony Koleske, Yimin Zou, Kristin Scott and A. Kimberley McAllister
joint with
Connectomics (X2)
Organizers: Olaf Sporns, Danielle Bassett and Jeremy Freeman
Mar 5–8, 2017 | Eldorado Hotel & Spa | Santa Fe, New Mexico | USA

*Dates, locations and details are subject to possible change. Please visit us online at **www.keystonesymposia.org** or join our various mailing lists or online networks for updates.*

Kinases: Next-Generation Insights and Approaches (C4)
Organizers: Reid M. Huber, John Kuriyan and Ruth H. Palmer
Mar 5–9, 2017 | Beaver Run Resort | Breckenridge, Colorado | USA

Tumor Metabolism: Mechanisms and Targets (X3)
Organizers: Brendan D. Manning, Kathryn E. Wellen and Reuben J. Shaw
joint with
Adaptations to Hypoxia in Physiology and Disease (X4)
Organizers: M. Celeste Simon, Amato J. Giaccia and Randall S. Johnson
Mar 5–9, 2017 | Whistler Conference Centre | Whistler, British Columbia | Canada

Engineered Cells and Tissues as Platforms for Discovery and Therapy (K1)
Organizers: Laura E. Niklason, Milica Radisic and Nenad Bursac
Mar 9–12, 2017 | Fairmont Copley Plaza | Boston, Massachusetts | USA

Frontiers of NMR in Life Sciences (C5)
Organizers: Kurt Wüthrich, Michael Sattler and Stephen W. Fesik
Mar 12–16, 2017 | Keystone Resort | Keystone, Colorado | USA

Sex and Gender Factors Affecting Metabolic Homeostasis, Diabetes and Obesity (C6)
Organizers: Franck Mauvais-Jarvis, Deborah Clegg and Arthur P. Arnold
Mar 19–22, 2017 | Granlibakken Tahoe | Tahoe City, California | USA

Cancer Immunology and Immunotherapy: Taking a Place in Mainstream Oncology (C7)
Organizers: Robert D. Schreiber, James P. Allison, Philip D. Greenberg and Glenn Dranoff
Mar 19–23, 2017 | Fairmont Chateau Whistler | Whistler, British Columbia | Canada

Pattern Recognition Signaling: From Innate Immunity to Inflammatory Disease (X5)
Organizers: Thirumala-Devi Kanneganti, Vishva M. Dixit and Mohamed Lamkanfi
joint with
Type I Interferon: Friend and Foe Alike (X6)
Organizers: Alan Sher, Virginia Pascual, Adolfo García-Sastre and Anne O'Garra
Mar 19–23, 2017 | Fairmont Banff Springs | Banff, Alberta | Canada

Injury, Inflammation and Fibrosis (C8)
Organizers: Tatiana Kisseleva, Michael Karin and Andrew M. Tager
Mar 26–30, 2017 | Snowbird Resort | Snowbird, Utah | USA

HIV Vaccines (C9)
Organizers: Andrew B. Ward, Penny L. Moore and Robin Shattock
Mar 26–30, 2017 | Sheraton Steamboat Resort | Steamboat Springs, Colorado | USA

Immune Regulation in Autoimmunity and Cancer (D1)
Organizers: David A. Hafler, Vijay K. Kuchroo and Jane L. Grogan
Mar 26–30, 2017 | Whistler Conference Centre | Whistler, British Columbia | Canada

Molecular Mechanisms of Heart Development (X7)
Organizers: Benoit G. Bruneau, Brian L. Black and Margaret E. Buckingham
joint with
RNA-Based Approaches in Cardiovascular Disease (X8)
Organizers: Thomas Thum and Roger J. Hajjar
Mar 26–30, 2017 | Keystone Resort | Keystone, Colorado | USA

Genomic Instability and DNA Repair (Z1)
Organizers: Julia Promisel Cooper, Marco F. Foiani and Geneviève Almouzni
joint with
DNA Replication and Recombination (Z2)
Organizers: John F.X. Diffley, Anja Groth and Scott Keeney
Apr 2–6, 2017 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

B Cells and T Follicular Helper Cells: Controlling Long-Lived Immunity (D2)
Organizers: Stuart G. Tangye, Ignacio Sanz and Hai Qi
Apr 23–27, 2017 | Whistler Conference Centre | Whistler, British Columbia | Canada

Mononuclear Phagocytes in Health, Immune Defense and Disease (D3)
Organizers: Steffen Jung and Miriam Merad
Apr 30–May 4, 2017 | Hyatt Regency Austin | Austin, Texas | USA

Modeling Viral Infections and Immunity (E1)
Organizers: Alan S. Perelson, Rob J. De Boer and Phillip D. Hodgkin
May 1–4, 2017 | Stanley Hotel | Estes Park, Colorado | USA

Angiogenesis and Vascular Disease (Z3)
Organizers: M. Luisa Iruela-Arispe, Timothy T. Hla and Courtney Griffin
joint with
Mitochondria, Metabolism and Heart (Z4)
Organizers: Junichi Sadoshima, Toren Finkel and Åsa B. Gustafsson
May 8–12, 2017 | Eldorado Hotel & Spa | Santa Fe, New Mexico | USA

Neuronal Control of Appetite, Metabolism and Weight (Z5)
Organizers: Lora K. Heisler and Scott M. Sternson
joint with
Gastrointestinal Control of Metabolism (Z6)
Organizers: Randy J. Seeley, Matthias H. Tschöp and Fiona M. Gribble
May 9–13, 2017 | Tivoli Hotel and Congress Center | Copenhagen | Denmark

Aging and Mechanisms of Aging-Related Disease (E2)
Organizers: Kazuo Tsubota, Shin-ichiro Imai, Matt Kaeberlein and Joan Mannick
May 15–19, 2017 | Pacifico Yokohama | Yokohama | Japan

Single Cell Omics (E3)
Organizers: Sarah Teichmann, Evan W. Newell and William J. Greenleaf
May 26–30, 2017 | Clarion Hotel Sign | Stockholm | Sweden

Integrating Metabolism and Immunity (E4)
Organizers: Hongbo Chi, Erika L. Pearce, Richard A. Flavell and Luke A.J. O'Neill
joint with
Cell Death and Inflammation (K2)
Organizers: Seamus J. Martin and John Silke
May 29–June 2 | Royal Society Dublin | Dublin | Ireland

Neuroinflammation: Concepts, Characteristics, Consequences (E5)
Organizers: Richard M. Ransohoff, Christopher K. Glass and V. Hugh Perry
Jun 19–23, 2017 | Keystone Resort | Keystone, Colorado | USA

*Conference dates are listed with the first date typically being that of afternoon registration and an evening welcome mixer, and the last day when organized sessions conclude, usually in the evening with a closing plenary session followed by food and entertainment. However, some program formats vary. Please check our website for program specifics for each individual meeting. You can view each program directly by entering **www.keystonesymposia.org** and then / and the alpha-numeric program code (e.g., **www.keystonesymposia/17A1**).*

2017–2018 Keystone Symposia Conference Topics

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Advances in Neurodegenerative Diseases Research and Therapy

Aging, Inflammation and Immunity

Antibodies as Drugs: Translating Molecules into Treatments

Antimicrobials and Resistance: Opportunities and Challenges

Atherosclerosis: Lessons Learned and Concepts Challenged

B Cells

Bioenergetics and Metabolic Disease

Cancer Epigenetics: New Mechanisms, New Therapies

Cancer Immunotherapy: Combinations

Cell Death, Inflammation and Adaptation to Tissue Stress

Chromatin Architecture and Chromosome Organization

Cryo-EM from Cells to Molecules:
Multi-Scale Visualization of Biological Systems

DNA and RNA Methylation

Emerging Cellular Therapies: T Cells and Beyond

Emerging Technologies in Vaccine Discovery and Development

Endoderm Development and Disease:
Cross-Organ Comparison and Interplay

Exosomes/Microvesicles:
Heterogeneity, Biogenesis, Function and Therapeutic Developments

Frontiers in Islet Biology and Diabetes

Frontiers of Serotonin Beyond the Brain

Gene Control in Development and Disease

GPCR Structure and Function:
Taking GPCR Drug Development and Discovery to the Next Level

Heart Failure: Crossing the Translational Divide

HIV and Co-Infections: Pathogenesis, Inflammation and Persistence

Immunological Memory: Innate, Adaptive and Beyond

Intrinsic Defenses and Counterdefenses

iPSCs, a Decade of Progress and Beyond

Lymphocytes and their Roles in Cancer

Manipulation of the Gut Microbiota for Metabolic Health

Maternal-Fetal Cross Talk: Harmony vs. Conflict

Microbiome, Host Resistance and Diseases

Mitochondrial Biology

Mobile Genetic Elements and Genome Plasticity

Myeloid Cells

Natural Products and Synthetic Biology: Parts and Pathways

New Frontiers in Neuroinflammation:
What Happens When CNS and Periphery Meet?

Noncoding RNAs: Form, Function Physiology

Novel Aspects of Bone Biology

One Million Genomes: From Discovery to Health

Organ Crosstalk in Obesity and NAFLD

Organs- and Tissues-on-Chips

Phosphoinositide Biology: New Therapeutic Targets Beyond Class I PI3K

Plant Signaling: Molecular Pathways and Network Integration

Precision Genome Editing with Programmable Nucleases

Precision Medicine in Cancer

Progress and Pathways Toward an Effective HIV Vaccine

Pushing the Limits to Healthspan and Longevity

Regenerative Biology and Applications:
Cell Differentiation, Tissue Organization and Biomedical Engineering

Regulation and Dysregulation of Innate Immunity in Disease

Selective Autophagy

State of the Brain:
Genetic Dissection of Brain Circuits and Behavior in Health and Disease

T Cell Dysfunction, Cancer and Infection

The Resolution of Inflammation in Health and Disease

Therapeutic Targeting of Hypoxia-Sensitive Pathways

Translational Chemical Biology

Translational Systems Immunology

Tuberculosis:
Translating Scientific Findings for Clinical and Public Health Impact

Tumor Metabolism

Ubiquitin Signaling

Uncomplicating Diabetes:
Reducing the Burden of Diabetes-Related End-Organ Injury

Vascular Biology and Human Diseases:
From Molecular Pathways to Novel Therapeutics

Vectors, Pathogens and Diseases:
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