Plant Abiotic Stress and Sustainable Agriculture: Translating Basic Understanding to Food Production

Scientific Organizers:
Julia Bailey-Serres and **Mike Hasegawa**

Sponsored by:
Monsanto Company

January 17–22, 2013
Sagebrush Inn and Conference Center
Taos, New Mexico, USA

KEYSTONE SYMPOSIA™
on Molecular and Cellular Biology
Accelerating Life Science Discovery

a 501(c)(3) nonprofit educational organization
www.keystonesymposia.org

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Visit **keystonesymposia.org/13A6** to view the meeting program online.

Twitter hashtag for this meeting: **#KSplant**

Unless otherwise noted, the information in this book is current as of **December 18, 2012**. Participants registering after this date are listed on **page 75**.

Please be advised that no video equipment, cameras, audio equipment or any other type of recording device will be allowed in the meeting room or poster sessions. Full meeting policies are on page 70.

KEYSTONE SYMPOSIA™
on Molecular and Cellular Biology
Accelerating Life Science Discovery

Keystone Symposia is a 501(c)(3) nonprofit organization directed and supported by the scientific community.

info@keystonesymposia.org — www.keystonesymposia.org

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Welcome

Dear Keystone Symposia Meeting Attendee,

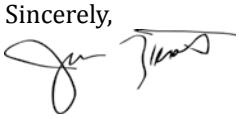
As Chair of the Board of Keystone Symposia, I am pleased to welcome you to the meeting on *Plant Abiotic Stress and Sustainable Agriculture: Translating Basic Understanding to Food Production*. The organization and I value your participation and appreciate your taking the time out of your busy schedule to join us in beautiful Taos, New Mexico. We think you'll be glad you did.

Face-to-face conferences represent enormous value for participants that "virtual" communications simply can't replicate. The lively debate at the poster sessions, the audience Q&A following a stimulating lecture, the informal discussions during the free time and the resulting collaborations – all cultivated my own enthusiasm, research directions, and development as a scientist.

Keystone Symposia conferences have earned a reputation for their top-quality science and collegial atmospheres where cross-disciplinary, collaborative thinking are the order of the day. In my position as Chair of the Board of this now-40-year-old nonprofit, I am honored to work alongside the other Board members to help guide the organization so that this reputation continues and grows. Challenges such as globalization and ensuring participation from both academia and industry are some of the other issues that are foremost concerns of the Board. With the day-to-day leadership of President Jim Aiken and Chief Scientific Officer David ("Woody") Woodland, the organization is in extremely capable hands.

Whether this is your first Keystone Symposia meeting or your tenth, we look forward to welcoming you again in the future, and to hearing your feedback.

Sincerely,



Juleen R. Zierath, Ph.D.
Professor of Molecular Medicine and Surgery, Karolinska Institutet
Chair of the Board, Keystone Symposia

Dear Meeting Participants,

Thank you for choosing to attend. Our highest priority is to provide the most stimulating meeting programs and environment for sharing data, generating ideas, starting collaborations, and maybe launching life-long collegial relationships. In spite of the continuing worldwide economic troubles which may affect some scientists' ability to attend, we are gratified that many do continue to engage in this vital face-to-face debate of the scientific challenges facing the world.

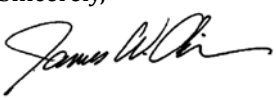
Our meeting participation is also becoming more global in reach. In 2012, participants came from 88 countries, including 19 African, 8 South American, and 25 Asian countries. Ten years ago, the year before I joined Keystone Symposia, participants came from 58 countries. During those ten years, the number of participants from the USA increased by about 5%, while non-USA participation increased by 65%. Last year, 43% of all attendees came from outside the USA. These simple numbers just hint at the intricacy of the present era of science globalization. We will continue to expand our global programs; this year we will be holding our first conference in South America (Ouro Preto, Brazil).

Dr. David Woodland is completing his first year as Chief Scientific Officer. Woody has moved quickly to ensure the continuing high quality of the conferences. Quality in programming is highly dependent on feedback from attendees, so please be generous with comments, either good or bad. The CSO, Scientific Advisory Board, and Scientific Organizers integrate feedback to generate a portfolio of annual meetings that we hope will energize the scientific community.

We greatly value the financial support of corporations, foundations, governments and individuals. Keystone Symposia does not have an endowment, so this continuing diverse base of support on an annual basis is vital. Through generous donations, we are able to defer some of the expenses of many deserving early-career scientists and also offset many of the costs we would otherwise have to pass on to attendees.

I hope that your experience at this conference is valuable and memorable and that you will spread the word to others who might benefit from what you learn.

Sincerely,



James W. Aiken, Ph.D.
President and Chief Executive Officer, Keystone Symposia

Meeting Format

The conference program has been designed around Keystone Symposia's 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 have been 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; your abstract will appear in the corresponding poster abstract section of the book. (*Note: Plenary session speakers are numbered in the hundreds: day one speakers are the 100s, day two speakers are the 200s, etc. Speaker abstracts are located before the poster abstracts in this book.*) 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 activities. If you are at a high-altitude meeting, 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 nightly "Lite Bites."

Abstract Books and Online Resources

With the anticipation that digital delivery of conference materials will eventually supplant print, Keystone Symposia staff is working to provide you with multi-platform access to all conference information. If you find you prefer the digital formats, feel free to return this printed abstract book to the registration desk.

In further efforts to cut back on waste, we have also replaced the notepads provided in the past with extra note-taking pages in the back of this book. Our staff has also been working hard to consolidate the abstract book to reduce the total number of pages. We anticipate this will save roughly 400,000 sheets of paper this meeting season!

Digital Abstract Book from Your Account

You may download a PDF of this book from your Account on our secure website. The full book is available on registration day. An updated version will be available at the close of the meeting with any last-minute registrants listed in an updated participant list and will remain available for 30 days after the meeting. 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.

Keystone Symposia Mobile App

We are excited to announce our new mobile app for phones and tablets, which is also available as a website on laptops. If you have not already done so, please download the app by scanning the QR code or visiting **www.eventmobi.com/agri13a6**. Creating an EventMobi account within the app will also allow you to personalize your participant profile by uploading a photo and adding biography information, as well as save a customized personal agenda for the week.

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:

Facebook – facebook.com/KeystoneSymposia
LinkedIn – linkd.in/Ox70RJ
Twitter – twitter.com/KeystoneSymp (Twitter hashtag for this meeting: **#KSplant**)
YouTube – youtube.com/KeystoneSymposia

Download the meeting app!

We Welcome 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. Your input is very valuable to us as we plan future meetings.

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Visit **keystonesymposia.org/13A6** to view the meeting program online. The program on the following pages is current as of December 11, 2012.

Twitter hashtag for this meeting:
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The world must immediately increase global crop production to meet the food, fiber and biofuel demands of our growing population. This challenge is complicated by a decline in arable farmland due to human occupancy and soil degradation. Crop production is also compromised by an increased occurrence of severe weather events due to global climate change. To meet human needs, major crops must be rapidly modified to ensure productivity in extreme environments. A major target is the improvement of tolerance to abiotic stresses including extremes in water availability and temperature, as well as soil contamination by salts, phosphate and heavy metals. Allied with abiotic stress tolerance is the need to improve crop yields in nutrient-poor soils. Genetic diversity for stress tolerance and nutrient acquisition exists within some crop species. The molecular genetic basis of this diversity is being identified and harnessed into cultivars by marker-assisted breeding. The use of functional genomics to dissect abiotic stress sensing and signaling networks and the downstream adjustments in metabolism and development can provide additional solutions for crop improvement through genetic engineering, while the emergence of deep-sequencing promises to permit rapid exploration of abiotic tolerance mechanisms of non-crop plants. Finally, the efforts to precisely define abiotic stress tolerance mechanisms can aid the effective pyramiding of multiple tolerances in a single plant. This Keystone Symposia conference will highlight progress in the dissection of the molecular basis of abiotic stress tolerance and the practices that enable rapid translation of abiotic stress tolerance to the farmer's field.

THURSDAY, JANUARY 17

16:00–20:00 Chamisa Lobby — Arrival and Registration

FRIDAY, JANUARY 18

07:00–08:00 Los Vaqueros — Breakfast

08:00–09:00 Chamisa Ballroom 1 — **Welcome and Keynote Address**

***Mike Hasegawa**, Purdue University, USA
Marc Van Montagu, Ghent University, Belgium (0101)
30 years of Transgenic Plants: Discover, Innovate, Communicate

09:00–11:15 Chamisa Ballroom 1 — **Harnessing Genetic Diversity to Improve Crop Stress Tolerance**

Mark Tester, University of Adelaide, Australia (0102)
Harnessing Diversity for Salt and Drought Tolerance in Cereals

Chamisa Lobby — Coffee Break

Julia Bailey-Serres, University of California, Riverside, USA (0103)
Flooding Survival Strategies
Sigrid Heuer, International Rice Research Institute, Philippines (0104)
A Novel Rice Protein Kinase, OsPSTOL1, Confers Tolerance of Phosphorus Deficiency by Enhancing Root Growth
Matthew H. Siebers, University of Illinois at Urbana-Champaign, USA (2021)
Short Talk: Heatwaves in a Warming World: The Effects of an Extended, Extreme Climate Event under Elevated CO_2

11:15–13:00 Chamisa Ballroom 2 — Poster Setup

On Own for Lunch and Recreation

13:00–22:00 Chamisa Ballroom 2 — Poster Viewing

16:30–17:00 Chamisa Lobby — Coffee Available

17:00–19:00 Chamisa Ballroom 1 — **Extremes in Water Availability: From Genes to Field**

***Susan von Caemmerer**, Australian National University, Australia
L.A.C.J. Rens Voesenek, Utrecht University, Netherlands (0105)
Submergence Coping Mechanisms in Wild Species
Andy Pereira, University of Arkansas, USA (0106)
Enhancing Photosynthesis for Increasing Yield and Abiotic Stress Resistance in Rice
Michael L. Nuccio, Syngenta Biotechnology, Inc., USA (0107)
Improvement of Drought Tolerance in Crops
Stephen H. Howell, Iowa State University, USA (1024)
Short Talk: Binding Protein Is a Switch that Regulates the ER Stress Sensor/Transducer, bZIP28, in Response to Environmental Stress

19:00–20:00 Chamisa Ballroom 2 — Social Hour with Lite Bites

19:30–22:00 Chamisa Ballroom 2 — **Poster Session 1**

Poster sessions provide exciting opportunities for engagement between all levels of investigators. Pages 44–52 contain the abstracts featured at this evening's poster session (abstract numbers 1001–1033).

SATURDAY, JANUARY 19

07:00–08:00	Los Vaqueros	Breakfast
08:00–11:00	**Chamisa Ballroom 1**	**Understanding and Improving Water Use Efficiency** ***Dirk Inzé**, VIB–Ghent University, Belgium **Michael V. Mickelbart**, Purdue University, USA (0201) *Physiological and Genetic Basis of Water Use Efficiency* **Alistair M. Hetherington**, University of Bristol, UK (0202) *Environmental Regulation of Stomatal Dynamics*
	Chamisa Lobby	Coffee Break **Dominique Bergmann**, Stanford University, USA (0203) *Stomatal Pattern: Developmental Regulation and Functional Consequences in Representative Monocot and Dicot Species* **Hilde Nelissen**, VIB–Ghent University, Belgium (2011) *Short Talk: The Effect of Drought on the Growth Processes in the Maize Leaf* **Biswa R. Acharya**, Pennsylvania State University, USA (1002) *Short Talk: Protein Interaction Network in Arabidopsis Guard Cell ABA Signaling: A Systems Biology Approach* **Julian I. Schroeder**, University of California, San Diego, USA (2016) *Short Talk: Molecular Mechanisms Mediating CO2 Control of Transpiration and Stomatal Development*
		On Own for Lunch and Recreation
16:30–17:00	Chamisa Lobby	Coffee Available
17:00–19:15	**Chamisa Ballroom 1**	**Stress Sensing, Signaling and Response Networks** ***Julian I. Schroeder**, University of California, San Diego, USA **Sean Cutler**, University of California, Riverside, USA (0204) *Structure and Function of ABA Receptors* **Dongdong Kong**, University of Maryland, USA (1028) *Short Talk: Arabidopsis Glutamate Receptor Homologs Regulate Ca^{2+} Homeostasis and Signaling* **Jörg Kudla**, Universität Münster, Germany (1029) *Short Talk: Functions of the Ca^{2+} Decoding CBL-CIPK Signaling Network in Mediating and Enhancing Abiotic Stress Responses* **Jian-Kang Zhu**, Purdue University, USA (0205) *Plant Abiotic Stress Sensing and Signaling* **Ron Mittler**, University of North Texas, USA (0206) *Dissecting the Rapid Systemic Signaling Pathway of Plants*
19:15–20:00	Chamisa Ballroom 2	Social Hour with Lite Bites

*Session Chair; ( ) = abstract number

SUNDAY, JANUARY 20

07:00–08:00 Los Vaqueros — Breakfast

08:00–11:00 Chamisa Ballroom 1 — **Roots and their Environment**

***Sigrid Heuer**, International Rice Research Institute, Philippines
Luis Herrera-Estrella, Cinvestav, Mexico (0301)
A Novel Fertilization and Weed Control System Based on Transgenic Plants Able to Metabolize Phosphite
Leon V. Kochian, ARS, US Department of Agriculture, Cornell University, USA (0302)
Elucidating the Molecular and Biochemical Basis for Crop Aluminum Tolerance to Improve Cereal Production on Acid Soils

Chamisa Lobby — Coffee Break

Mary Lou Guerinot, Dartmouth College, USA (0303)
From the Soil to the Seed: Metal Homeostasis in Plants
Maria J. Harrison, Boyce Thompson Institute for Plant Research, USA (0304)
Phosphate Acquisition through Symbiosis with Arbuscular Mycorrhizal Fungi
Aaron P. Smith, Louisiana State University, USA (2022)
Short Talk: Dissecting the Roles of Nucleosome Occupancy and H2A.Z Abundance in Modulating Responses to P- and/or Fe-Deficiency in Rice

11:00–13:00 Chamisa Ballroom 2 — Poster Setup

On Own for Lunch and Recreation

13:00–22:00 Chamisa Ballroom 2 — Poster Viewing

16:30–17:00 Chamisa Lobby — Coffee Available

17:00–19:00 Chamisa Ballroom 1 — **Stress Systems Biology to Genetic Variation**

***Alistair Hetherington**, University of Bristol, UK
Jerzy Paszkowski, University of Geneva, Switzerland (0305)
Epigenetics Regulation of Abiotic Stress Responses
Philip N. Benfey, Duke University, USA (0306)
The Genetic Basis of Root System Architecture Traits
Dirk Inzé, VIB–Ghent University, Belgium (0307)
The Impact of Stress on Growth and Development
Claudia Jonak, Gregor Mendel Institute of Molecular Plant Biology, Austria (1027)
Short Talk: The RNA-Directed DNA Methylation Pathway Regulates the Temperature Stress Response

19:00–20:00 Chamisa Ballroom 2 — Social Hour with Lite Bites

19:30–22:00 Chamisa Ballroom 2 — **Poster Session 2**

Poster sessions provide exciting opportunities for engagement between all levels of investigators. Pages 53–60 contain the abstracts featured at this evening's poster session (abstract numbers 2001–2029).

MONDAY, JANUARY 21

07:00–08:00	Los Vaqueros	Breakfast
08:00–11:00	**Chamisa Ballroom 1**	**Challenges and Solutions in the Field** ***Mark Tester**, University of Adelaide, Australia **Donald E. Nelson**, Monsanto Company, USA (0401) *Advances in Abiotic Stress Tolerance in Key Crops* **Mitch R. Tuinstra**, Purdue University, USA (0402) *Prospects for Adapting Maize to Drought and High-Temperature Stress*
	Chamisa Lobby	Coffee Break **Richard A. James**, CSIRO, Australia (0403) *Development and Evaluation of Salt-Tolerant Wheat* **Katharina Bräutigam**, University of Toronto, Canada (1007) *Short Talk: Genetic and Epigenetic Impacts on the Poplar Drought Response* **Amandeep Mittal**, Texas Tech University, USA (2005) *Short Talk: Field Testing of Transgenic Cotton Expressing Arabidopsis ABA Insensitive5 (ABI5) and B3-Domain Related to ABI3/VIVIPAROUS1 (RAV) Transcription Factors*
		On Own for Lunch and Recreation
16:30–17:00	Chamisa Lobby	Coffee Available
17:00–19:00	**Chamisa Ballroom 1**	**Global Climate Change: CO_2 and Temperature** ***Julia Bailey-Serres**, University of California, Riverside, USA **Jian Hua**, Cornell University, USA *Talk Title to be Determined* **Lisa Ainsworth**, ARS, US Department of Agriculture and University of Illinois at Urbana-Champaign, USA (0405) *Maximizing Soybean Production in a High-CO_2 World* **Sharon B. Gray**, University of Illinois at Urbana-Champaign, USA (1021) *Short Talk: Elevated Atmospheric CO_2 Alters Root Depth Distribution, Enhancing Abscisic Acid Signaling and Stomatal Closure under Drought in Field-Grown Soybean* **Susan von Caemmerer**, Australian National University, Australia (0406) *Impacts of Elevated CO_2 on Photosynthesis and Other Processes*
19:00–20:00	Chamisa Ballroom 2	Social Hour with Lite Bites
20:00–23:00	Chamisa Ballroom 2	Entertainment

TUESDAY, JANUARY 22: DEPARTURE

*Session Chair; ( ) = abstract number

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 meeting is sponsored by:

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Additional gifts for this meeting provided by:

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Syngenta Biotechnology, Inc.

Directors' Fund (contributors listed on page 15)

In-kind speaker support from:

Monsanto Company

Syngenta Biotechnology, Inc.

In-kind marketing/advertising support from:

Wiley-Blackwell – ***The Plant Journal*** and ***Plant, Cell & Environment***

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.*

Keystone Symposia Future of Science Fund* Scholarship Recipients

Biswa R. Acharya, Pennsylvania State University, USA (1002)

Nobuhiro Suzuki, University of North Texas, USA (2024)

*To learn more about the Keystone Symposia Future of Science Fund, see page 21 or visit **keystonesymposia.org/FSF**; ( ) = abstract number

Julia Bailey-Serres is a Professor of Genetics in the Department of Botany and Plant Sciences and the Center for Plant Cell Biology at the University of California, Riverside. A graduate of the University of Utah, with a Ph.D. from Edinburgh University, she was a postdoctoral researcher at UC Berkeley with Michael Freeling. She has been a member of the faculty at UC Riverside since 1990, where she is now a full professor. Her recognitions include the USDA National Research Initiative Discovery Award for Outstanding Agricultural Research to Enhance Submergence Tolerance in Rice in 2008, fellow of the American Association for the Advancement of Science and fellow of the American Society of Plant Biologists. She is an Associate Editor of *Plant Physiology* and Secretary of the American Society of Plant Biologists. As Director of the NSF ChemGen IGERT program at UC Riverside, she established practices that foster cross-disciplinary training of plant scientists.

Dr. Bailey-Serres' research group studies the sensing, signaling and acclimation responses to low oxygen stress in plants. Her multi-disciplinary approach combines genetic, molecular, biochemical and bioinformatic technologies and has significant implications for agricultural and global food challenges. She has received international attention for her group's dissection of the mechanistic role of the SUB1A gene in conferring submergence tolerance in rice. Her accomplishments also include the pioneering of methods for profiling the "translatomes" of discrete cell-types of plants and identification of a homeostatic sensor of oxygen deprivation in plants. She is currently director of the Center for Plant Cell Biology at UC Riverside.

Mike Hasegawa is a distinguished professor in the HLA Department at Purdue University. He is a graduate of the University of California, Riverside, from the laboratory of Toshio Murashige. Mike joined the faculty at Purdue in 1977. His initial research was on plant morphogenesis and genetic transformation, and now focuses on plant responses to abiotic stresses. Accomplishments include identification and characterization of PR-5 protein osmotin, HKT1 as a salt tolerance determinant, and sumoylation as a post-translational modification process in stress signaling. He is a fellow of the American Association for the Advancement of Science and an ISI Most Highly Cited Researcher. He is/has been on the editorial board for *Plant Cell, Tissue and Organ Culture, Plant Physiology, Plant and Cell Physiology* and *Plant Journal*.

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 will be 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 James Aiken, Chief Scientific Officer David Woodland and an advisory Board of Directors, a staff of approximately 40 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 70 leading scientists from academia, industry and government worldwide, more than 100 programming consultants and the Keystone Symposia staff.

Meeting development starts more than two years in advance through teleconference and online discussion forums involving SAB members and ad-hoc 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 online-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 staff also receives 12-15 additional organizer-initiated proposals during this time.

The SAB meets again in June to review all submitted meeting proposals (both solicited and unsolicited), recommend whether proposals should be accepted or rejected and provide constructive

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 first Dr. Pedro Cuatracasas, President of the Parke Davis Research Laboratories, and then Professor Ralph Bradshaw, 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 will convene its first conference in South America ("The Innate Immune Response in the Pathogenesis of Infectious Disease" in Ouro Preto, Brazil).

Did You Know? Ralph Bradshaw is writing a book on the history of Keystone Symposia.

To share your stories and photos relating to past Keystone Symposia meetings, please email ***marketing@keystonesymposia.org****.*

feedback to organizers to improve programs. 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 and geographical distribution. Particular attention is also given to reducing the number of repeating speakers if a similar conference has recently been held. Finally, 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 ad-hoc programming consultants, scientific organizers serve in an entirely volunteer capacity with only their 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

(continued on next page)

Keystone Symposia Diversity Initiatives (continued)

attendees each year. The Keystone Symposia Global Health Travel 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 underrepresented minority (URM) investigators. Overseen by our Director of Diversity in Life Science Programs, with input from scientists on the Diversity Advisory Committee, these initiatives include:

Underrepresented Minority Scholarships – We award up to $1,200 for URM graduate students and postdoctoral fellows of US citizenship or permanent residency to attend a Keystone Symposia conference. Submission of an abstract is required. These competitive Scholarships are made possible in part by Keystone Symposia's NIH MARC grant and Keystone Symposia funds. Applications are reviewed by meeting organizers. Visit **keystonesymposia.org/URMScholarship** to learn more.

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 presenting research at the conference.

Early-Career Investigator Travel Awards – We award up to $1,800 to scientists from underrepresented backgrounds 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 research problem which might be addressed by attending a particular meeting, and a commitment to mentoring a URM student (undergraduate, graduate, postdoc) in a laboratory around career development and positioning issues for a minimum of one year. These competitive Awards are made possible by Keystone Symposia's NIH MARC grant and Biogen Idec. Applications are reviewed by meeting organizers. Visit **keystonesymposia.org/EarlyCareerAward** to learn more.

Keystone Symposia Fellows Program – Keystone Symposia accepts on average five early-career scientists annually who are committed to diversity in the life sciences and 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 Fellows Circle. This program is funded by Keystone Symposia's NIH MARC grant. Visit **keystonesymposia.org/Fellows** to learn more, apply, or read about past and current Fellows.

Peer-to-Peer Program – Participants from underrepresented backgrounds are invited by email before a conference begins to meet with each other at a specified time and place during the conference to share research backgrounds and have names and faces to connect with throughout the conference.

Scholars Program – Every year, undergraduates at the University of New Mexico–Taos, a minority-serving institution, are able to participate in a unique program funded by Novartis Institutes for BioMedical Research that allows them to attend Keystone Symposia conferences held in Taos while completing an intensive tutorial-style reading and discussion undergraduate course.

Strategic Outreach – Keystone Symposia's Director of Diversity in Life Science Programs, Chief Scientific Officer and other staff members present at conferences such as ABRCMS, Understanding Interventions Conference, The Leadership Alliance National Symposium, SACNAS (Society for the Advancement of Chicanos and Native Americans in Science) Annual Conference and at molecular and cellular biology conferences, universities and medical schools nationwide. Ongoing collaborations to promote early-career investigator development and diversity enhancement include work with Brown University, Harvard University, The Leadership Alliance, The Endocrine Society, Biogen Idec, Novartis Institutes for BioMedical Research and the American Physician Scientist Association (APSA).

Our Director of Diversity in Life Science Programs, ***Laina King, Ph.D.****, welcomes your input and can be reached at* ***lainak@keystonesymposia.org*** *or* ***1.970.262.1230 ext. 137****.*

If you are interested in supporting these Programs, please contact Dr. Laina King or Dr. Christopher Atwood, Director of Development, at ***chrisatwood@keystonesymposia.org*** *or* ***1.970.262.1230 ext. 124****.*

To learn more about Keystone Symposia's Diversity in Life Science Program initiatives and their evolution, visit ***keystonesymposia.org/diversity*** *and* ***keystonesymposia.org/timeline****.*

To find out ways you can help foster diversity in the life sciences, visit ***keystonesymposia.org/diversityhelp****.*

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We are grateful for this valuable support directed at increasing the participation of underrepresented minority 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 15.

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Keystone Symposia truly appreciates the support received from various institutes of the National Institutes of Health and from the National Science Foundation. This support primarily funds scholarships for graduate students and postdoctoral fellows to attend our conferences. US federal grant support for specific conferences is listed per meeting, as available, within the "Gifts and Grants" pages following the Future Science Fund donor listings.

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- 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, visit keystonesymposia.org/FSF.

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Visit **opm.gov/cfc** to learn more on the federal website.

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0101: Van Montagu

30 years of Transgenic Plants: Discover, Innovate, Communicate

Marc Van Montagu
Institute Plant Biotechnology Outreach (IPBO), Gent University, Belgium

The first transgenic plants expressing a foreign gene (Kanamycine resistance) were presented at the Miami Winter Symposium 1983. This new technology is at the base of the tremendous progress in plant science, but only some innovations in agriculture and much confusion around the social and economic value of these applications.

Today, the major challenge for plant science is how to integrate the fast growing fundamental research and the more empirical knowledge built up by plant breeders and agronomists. Another important challenge is how to communicate to society the importance of this research.

Trying to find out the molecular base of crown gall induction by the ubiquitous soil bacterium Agrobacterium tumefacians, we stumbled on the finding that this cell proliferation was induced through a natural event of gene engineering. This observation brought a lot of interesting information on plant bacteria interactions. It also led to the development of a universal gene transfer method for plants. The availability of such a genome modification technology made plant molecular genetics and developmental biology possible. The wealth of data that became available in the last decennia, should be transformed into knowledge on the molecular mechanisms that evolved and were selected during the evolution of today's plants. The powerful "omics" technologies, the emerging understanding of epigenetics and the progress in IT, guarantee us that such knowledge creation will continue at an accelerated speed.

Parallel with this fundamental progress in basic research, an innovative applied research developed which resulted in the construction of crop plants with new agronomical beneficial traits, the now called "GM-Crops". For the scientists, the economic advantages and the benefit for environment were so obvious that they proceeded rapidly with constructing a variety of food/feed and industrial crops as well as transgenic trees. By not communicating with society on the importance of this technology, plant scientists alienated themselves from the public at large. Organized disinformation created a lot of fear of transgenic crops, often extending to general fear of science applications. This attitude, particularly in Europe, made that the possible innovations remained blocked for more than 15 years.

The action of Non Governmental Organizations against GM-Crops also resulted in a complex series of extremely expensive regulatory processes. This price tag makes that no SME or none of the developing countries can afford to commercialize their own GM crops, leaving a monopoly to six major multinationals. Some of the emerging countries like Brazil, China and India did develop novel GM-crops but large scale production is not always evident.

Meanwhile the ever increasing world population, the necessity to replace fossil oil and coal by renewable plant derived raw materials for the chemical industry and the climate instability confront us with the need for a more intensive but sustainable agriculture. This year the UN declared at the Rio+20 meeting that our goals for the coming decennium should be to stop hunger, stop poverty and stop deforestation. Will scientists be able to develop in due time the novel crops needed and obtain their global commercialization?

Results presented at this meeting stress the potential of the research tools. If the public sector scientists would also collaborate in communicating their results to society, stressing that there is no danger to health of humans or animals and surely not for the environment, then there is hope that the ban on GM-crops can be lifted. If the political will is there to fight for the Rio+20 goals, then plant R&D should be able to construct the performing GM-crops requested.

Literature:
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0102: Tester

Harnessing Diversity for Salt and Drought Tolerance in Cereals

Mark Tester
Australian Centre for Plant Functional Genomics; The Plant Accelerator, Australian Plant Phenomics Facility; and School of Agriculture, Food and Wine, University of Adelaide, Australia

Genetics and genomics are powerful tools for gene discovery. In this talk, forward genetic approaches for discovery of genes related to salinity tolerance in wheat and barley will be described, and used as an example for approaches to drought tolerance research.

Increasingly efficient transgenic technologies are generating large numbers of GM crop plants. However, gene expression often needs to be manipulated in more targeted ways by, for example, activating genes in only specific cells or at specific times. Using salinity as an example, it will be shown how gene over-expression in specific cells in the root can increase salinity tolerance, including in rice.

The genotyping of mapping and mutant populations is now highly efficient. However, the ability to quantitatively phenotype these populations is now commonly limiting forward progress in plant science. The increasing power of digital imaging and computational technologies offers the opportunity to relieve this phenotyping bottleneck. The Plant Accelerator™ is a 4500 m^2 growth facility which provides -omic-scale phenotyping of large populations of plants. New genetic loci for components of salinity tolerance discovered using this exciting new approach will be presented.

The application of these technologies provides opportunities to significantly increase abiotic stress tolerance of crops, and thus contribute to increasing agricultural production in many regions.

0103: Bailey-Serres

Flooding Survival Strategies

Julia Bailey-Serres
Center for Plant Cell Biology, Department of Botany and Plant Sciences, University of California Riverside, USA

Extremes in water availability – droughts and floods – have increased in frequency and intensity over the past fifty years throughout the world. Presently, over 35% of the world's rice acreage is flood prone and much is in regions characterized as food insecure. To help stabilize crop production in these areas it is essential to develop and adopt germplasm that is better able to endure abiotic assaults. One example of this is the introduction of new rice varieties that survive transient submergence events. This was made possible by the transfer of the genetic locus *SUBMERGENCE1* from a farmer's landrace to modern varieties by use of marker-assisted breeding. The molecular characterization of *SUB1A*, the determinant of submergence tolerance, has led to the recognition of members of the APETELA2/Ethylene Responsive Factor (ERF) group VII transcription factor family as pivotal regulators of flooding and low oxygen responses in plants. In *Arabidopsis thaliana,* the regulation of the abundance of group VII ERF proteins provides a homeostatic sensing mechanism of oxygen availability. These proteins are marked for degradation by a branch of the N-end rule pathway of targeted proteolysis under oxygen-replete conditions and become stabilized under oxygen deficient conditions. Their expression is necessary for induction of genes that enable energy-efficient anaerobic metabolism and low-oxygen stress survival. However, SUB1A appears to evade oxygen-regulated N-end rule destruction, playing its role in an effective flooding survival strategy prior to severe oxygen deprivation. Thought the evaluation of the gene networks regulated by group VII ERFs in rice and Arabidopsis, we have further resolved counterbalanced strategies that enable survival of transient floods.

Research funded by grants from the National Science Foundation (MCB-1021969, IOS-1121626) and the USDA National Institute of Food and Agriculture (2011-04015).

0104: Heuer

A Novel Rice Protein Kinase, OsPSTOL1, Confers Tolerance of Phosphorus Deficiency by Enhancing Root Growth

Sigrid Heuer[1], R Gamuyao[1], JH Chin[1], P Pesaresi[2], M Wissuwa[3]
[1]International Rice Research Institute (IRRI), Philippines; [2]Department of Bioscience, University of Milano, Italy; [3]Japan International Research Center for Agricultural Sciences (JIRCAS), Japan

Currently known rock phosphate reserves, the source of phosphorus (P) fertilizer, are estimated to last about another 300 years and P-fertilizer prices have almost tripled since 2005. In addition, P fixation is a widespread global problem since it renders P unavailable to plants and severely limits crop productivity and fertilizer efficiency. A major quantitative trait locus (QTL) for phosphorus-deficiency tolerance, *Phosphorus uptake 1* (*Pup1*), has been identified about a decade ago in the traditional *aus*-type rice variety Kasalath. The major tolerance gene has now been identified coding for a Ser/Thr protein kinase that is specific to Kasalath and other tolerant rice varieties but absent from intolerant genomes, including the Nipponbare reference genome. This novel protein kinase, named *Phosphorus Starvation Tolerance 1* (*OsPSTOL1*), is specifically expressed in root primordia and acts as an enhancer of root growth. The larger root system enables plants to forage nutrients from a larger soil area thereby enhancing uptake of P, and other nutrients. Expression of root-development and stress-related genes is altered in 35S::*OsPSTOL1* plants suggesting that this gene acts as an important upstream regulator. This is further supported by a germplasm survey using *Pup1*-specific molecular markers that revealed high conservation of *OsPSTOL1* in stress-adapted rice accessions. Analyses of breeding lines developed by marker-assisted backcrossing showed that the presence of *Pup1*/*OsPSTOL1* can significantly enhance yield under medium and severe P deficiency. Introgression of this gene into local rice varieties is expected to have a significant impact on food security, especially for poor farmers.

0105: Voesenek

Submergence Coping Mechanisms in Wild Species

L.A.C.J. Voesenek
Institute of Environmental Biology, Utrecht, the Netherlands

The area exposed to flooding is on a world scale more than 17 million km^2 per year; double the size of the USA. Due to global climate change the frequency and severity of floods increases. These floods negatively interfere with plant life as gas exchange between flooded plants and the atmosphere almost ceases and consequently plants are depleted in O_2 and CO_2. However, some plant species possess traits enabling them to cope with flooding stress. Naturally occurring flooding regimes have selected for two flood tolerance strategies: (i) 'escape' through vigorous shoot growth allowing snorkeling leaf tips to facilitate oxygen entry and diffusion to the almost anaerobic root tips, and (ii) 'quiescence' to endure long-term submergence by extremely slow rates of energy and carbohydrate consumption. The wetland species *Rumex palustris* escapes from complete submergence by elongation of petioles. This submergence-induced response is regulated via an ethylene-driven signaling network in which apoplastic acidification, expansin action and interactions between the hormones abscisic acid, auxin and gibberellin are crucial. *R. acetosa*, a species from rarely flooded field sites, lacks this escape response when submerged and endures flooding by conservation of carbohydrates and energy. The transcriptome of these two wild *Rumex* species during submergence was characterized using next generation RNA sequencing (NGS). The results confirm previously established processes and identified unknown players that facilitate emergence out of the flood water. *Arabidopsis thaliana* is relatively intolerant to flooding. In a screen with 86 natural *Arabidopsis* accessions for phenotypic variation in submergence tolerance the most tolerant accession (C24) had a median lethal time (LT_{50}) of 11.2 days, whereas the most intolerant accession (Cvi-0) had an LT_{50} of 4 days indicating large genetic variation. The transcriptomes of tolerant and intolerant accessions were characterized by means of NGS to identify genes that underpin submergence tolerance in *Arabidopsis*.

0106: Pereira

Enhancing Photosynthesis for Increasing Yield and Abiotic Stress Resistance in Rice

Madana Ambavaram[1], Arjun Krishnan[1], Utlwang Batlang[1], Ramegowda Venkategowda[2], Supratim Basu[2], Mangu Venkata[3], Rohit Joshi[3], Niranjan Baisakh[3], Andy Pereira[1,2]
[1]Virginia Bioinformatics Institute, Virginia Tech, VA; [2]CSES, University of Arkansas, Fayetteville, AR; [3]Louisiana State University Agricultural Center, LA

To dissect the complex traits of yield and drought stress resistance, and identify the network of genes and biological processes involved, we developed a regulatory association network in rice using genome-wide expression profiles of rice genes under several control and stress conditions. This network represents the association of each of 328 'specific' biological process/pathway to every transcription factor (TF) in the rice genome. We queried the network for the association of TFs to processes related to photosynthesis and carbohydrate metabolism, key biological processes affected by drought stress. A TF gene HYR was identified that is positively associated with photosynthetic carbon metabolism under non-stressed conditions and is upregulated by drought in vegetative and reproductive stages. HYR was overexpressed in multiple rice genotypes for functional analysis and the HYR lines analyzed for drought response and yield parameters. Morpho-physiological analysis of the rice HYR lines showed an increase in biomass, water use efficiency, root growth, photosynthesis, sugars, drought resistance and yield under normal and drought conditions. Gene expression profiles of HYR lines revealed that genes involved in photosynthesis, carbohydrate metabolism and cell cycle were significantly up-regulated. The results suggest a model of HYR function in rice where drought causes up-regulation of HYR and might have a specific role in regulating photosynthesis and carbohydrate metabolism under stress.

0107: Nuccio

Improvement of Drought Tolerance in Crops

Michael L. Nuccio, Jeff Wu, Yan Gao, Xi Chen, Hua-ping Zhou, Moez Meghji, L. Mark Lagrimini
Syngenta Biotechnology, Inc., 3054 E. Cornwallis Road, Research Triangle Park, North Carolina, 27709-2257 USA

Water deficit substantially reduces yield in cultivated maize (*Zea mays*), particularly when it occurs during the two-three week flowering period. Technology being developed to address this complex problem encompasses many disciplines including water management, field management, germplasm development and genetic engineering (GM). Many GM strategies that demonstrate measurable effects on plant response to water deficit also affect other aspects of plant development, including growth rates and top-end yield. One way to address this is to consider drought response part of the crop development cycle. An area of interest is modification of carbohydrate metabolism during early reproductive development. Our work in this area identified a way to reduce yield loss in maize subject to water deficit imposed at flowering. Greenhouse studies show the trait increases kernel set in plants exposed to water deficit, and in some cases well-irrigated plants. Data suggest this trait enables plants to develop more biomass, increasing kernel set. Extending the analysis to field environments under grower conditions shows the trait improves yield in plots subject water deficit during reproductive development, but has no negative impact on yield in well-irrigated plots. Progress to date will be discussed.

0201: Mickelbart

Physiological and Genetic Basis of Water Use Efficiency

Michael V. Mickelbart
Center for Environmental Stress Physiology, Purdue University, USA

Decreasing water supplies and changing rainfall patterns have prompted renewed interest in plant water use efficiency (WUE): the amount of carbon, biomass, or yield attained per unit of water required. In most documented cases, improvement in WUE appears to be related to the regulation of transpiration rather than an increase in carbon assimilation. The relationship between specific physiological factors (e.g., stomatal traits) and WUE in natural and domesticated populations is often weak, and breeding for WUE using physiological traits as screens has not resulted in significant improvement in crop WUE. However, genetic determinants for stomatal factors that have a large effect on transpiration rate have been identified in isogenic lines. In particular, regulators of the stomatal development pathway that act to modulate stomatal characteristics in response to environmental stimuli may be useful in biotechnology approaches to improving WUE and drought tolerance. GTL1, a transcription factor that functions as a node to integrate hyper-osmotic signaling into stomatal development changes through *SDD1* is one such regulator that we have characterized and utilized to demonstrate the possibility of improving WUE through reduced transpiration as a result of a lower stomatal density without a concomitant reduction in biomass production. Therefore, there is reason to believe that genetic manipulation of one to a few genes could result in improved crop plant WUE; however, the specific genetic targets are likely to be different in various cropping systems.

0202: Hetherington

Environmental Regulation of Stomatal Dynamics

Alistair M Hetherington
School of Biological Sciences, University of Bristol, Bristol, UK

Stomata are pores on the surfaces of leaves, surrounded by two guard cells, which regulate the uptake of carbon dioxide for photosynthesis and the concomitant loss of water vapour. The aperture of the stomatal pore is controlled by the turgor of the two guard cells. By integrating signals of internal plant status (such as hormones) and environmental cues (such as light intensity, atmospheric relative humidity (RH) and atmospheric carbon dioxide concentration) stomata "set" gas exchange to suit the prevailing environmental conditions. A complex intracellular signalling network is responsible for coupling signal perception to changes in stomatal aperture.

The presentation will cover three topics; the evolution of guard cell signalling; intracellular signalling during light-induced opening and the intracellular signalling pathways underlying elevated carbon dioxide, reduced RH and ABA-induced closure. Evidence will be presented supporting a role for triacylglycerol breakdown during light-induced stomatal opening and cytoskeletal involvement during stomatal closure.

0203: Bergmann

Stomatal Pattern: Developmental Regulation and Functional Consequences in Representative Monocot and Dicot Species

Dominique Bergmann[1,2], Graham Dow[1], On Sun Lau[1], Joe Berry[3], Emily Abrash[1], Juliana Matos[1] and Akhila Bettadapur[2]
[1],Department of Biology and [2] Howard Hughes Medical Institute, Stanford University, Stanford, CA 94305. [3] Carnegie Institution, Department of Global Ecology, Stanford, CA 94305

Stomata provide a framework to study the fundamental processes of plants at different organizational levels, from molecules and cells to whole plants and ecosystems. The collective activity of stomata drives global carbon and water cycles, but, simultaneously, plant production of stomata is regulated by the global environment. How do plants sense the environment, and how do they alter their stomatal development in response? We are investigating the regulatory connection between environmental inputs and the activities of core developmental regulators, among them the bHLH transcription factors like SPEECHLESS (SPCH). SPCH is a target of MAPK-mediated phosphoregulation, leading to the attractive hypothesis that SPCH may be the control point for many environmental inputs. Preliminary results indicate that mutations in certain phosphorylation sites render SPCH insensitive to changes in light, but not [CO2]. We are currently testing which elements of well-established light and hormone signaling pathway are involved in SPCH regulation. We are also using our ability to change stomatal numbers, arrangements and functions in Arabidopsis to test current models for stomatal function and experimentally ascertain whether these differences lead to changes in water use efficiency and drought tolerance under current and simulated climate change regimes. Finally, although the work in Arabidopsis has been informative, other plant groups have made striking innovations in stomatal morphology and pattern and I will discuss our latest work extending out to some of these other plant groups.

The work was funded by Stanford Bio-X and the Gordon and Betty Moore Foundation

0204: Cutler

Structure and Function of ABA Receptors

Sean Cutler[1], Masanori Okamoto[1], Francis Peterson[2], Brian Volkman[2] and Andrew Defries[1]
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[2]Dept. of Biochemistry, Medical College of Wisconsin, Milwaukee, WI 53226

Abscisic acid controls many of its cellular responses by binding to a family of soluble receptors called PYR/PYL/RCAR (*Pyrabactin Resistance 1 / PYR1-like / Regulatory Component of ABA Receptor*) proteins, which belong to the large START superfamily of ligand-binding proteins. When agonists bind to these receptors, contacts between a mobile gate loop and agonist stabilize gate closure, which allows the receptors to dock into and inhibit the active sites of clade A PP2Cs. The complex is further stabilized by a water-mediated contact between the PP2C's lock tryptophan residue and ABA's ring ketone. We previously described the synthetic ABA agonist pyrabactin, which selectively activates the seed ABA response pathway in Arabidopsis via activation of PYR1. Pyrabactin fails to elicit vegetative ABA responses, which suggests that a pan agonist (one that activates all ABA receptors) might be required for vegetative pathway activation. To examine this, we screened ~75,000 compounds for ABA agonists using plant and yeast-based receptor assays. Our efforts yielded a potent new agonist, quinabactin, which activates 5 of the 13 Arabidopsis ABA receptors with ABA-like potency. An x-ray structure of a PYL2-quinabactin-PP2C complex suggests that quinabactin's potency is conferred by its ability to engage the PP2C tryptophan lock, closely mimicking ABA's binding mode. Transcript profiling reveals that quinabactin's effects are nearly indistinguishable from exogenous ABA applications. Moreover, quinabactin applications trigger guard cell closure, suppress water loss and promote strong drought tolerance in Arabidopsis and *Glycine max*. Thus, activation of a restricted set of ABA receptors is sufficient to activate the vegetative ABA response pathway. The isolation of quinabactin demonstrates that ABA receptors can be "drugged" to elicit protection against drought stress.

0205: Zhu

Plant Abiotic Stress Sensing and Signaling

Jian-Kang Zhu
Department of Horticulture and Landscape Architecture, Purdue University, West Lafayette, IN 47907 West Lafayette, IN 47907, USA; Center for Plant Stress Biology, Shanghai Institute for Biological Sciences, Chinese Academy of Sciences, Shanghai 200032, China

An important part of plant stress biology is to understand how plant cells perceive water, salt, temperature and other abiotic stresses and transmit the stress signals to the cell nucleus to reprogram gene expression. Traditionally, it is thought that the stress signals are perceived at the cell surface and the signals are then transmitted to the nucleus. However, emerging evidence suggests that the stress signals may be perceived at many different cellular locations including various organelles and the signals must then be integrated to regulate nuclear gene expression and other cellular activities. I will present a model for this dispersed sensing of abiotic stress signals. I will also give an update of recent progresses in the sensing and signaling of abscisic acid and osmotic stress.

0206: Mittler

Dissecting the Rapid Systemic Signaling Pathway of Plants

Ron Mittler
University of North Texas

Reactive oxygen species (ROS) play a multitude of signaling roles in different organisms from bacteria to mammalian cells. We recently reported that a rapid, long-distance, auto-propagating, wave of ROS spreads within minutes from a local group of cells, subjected to abiotic stress, to the entire plant, and that this signal is essential for the activation of acclimation mechanisms in systemic tissues. A number of key questions related to the biological function of the ROS wave, its integration with ABA signaling, and its specificity and networking with other signaling pathways will be presented and discussed.

0301: Herrera-Estrella

A Novel Fertilization and Weed Control System Based on Transgenic Plants Able to Metabolize Phosphite

Damar López-Arredondo and Luis Herrera-Estrella
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Poor soil fertility and aggressive weeds pose major constraints to meeting the increasing demand for global food production. Starting with the green revolution in the 1960s, higher yields have been accompanied by a steady increase in the use of fertilizers and herbicides. Phosphorus (P) is a nutrient that limits crop yield in over 60 percent of the world's arable land. To increase plant productivity in soils with low P availability, several million tons of P fertilizer is applied every year to agricultural soils. However, by some estimates, world resources of inexpensive P may be depleted by 2080. Low Pi availability in the soil is mainly due to its high reactivity with soil components and rapid conversion by soil bacteria into organic forms that are not readily available for plant uptake. Due to both of these factors, as little as 20–30% of the Pi that is applied as fertilizer is actually used by cultivated plants. The inefficient utilization of Pi present in fertilizer is further aggravated by the competition of weeds with crops for soil resources. Because Pi cannot be substituted in plant nutrition, relatively little attention has been given to the use of other chemical forms of phosphorus to formulate effective and potentially less environmentally hazardous fertilizers. Phosphite, a reduced form of phosphorus, was proposed as a promising alternative fertilizer after the Second World War, owing to its distinct chemical and biochemical properties compared with orthophosphate, including higher solubility, lower reactivity with soil components and the inability of most microorganisms to use it as a phosphorus source. However, plants cannot metabolize phosphite, limiting its use as a fertilizer. In this paper I will report on the development of a novel fertilization and weed control system by engineering plants to metabolize phosphite. This was achieved by expressing a phosphite oxido/reductase that converts phosphite into Pi, in transgenic plants. When grown in soil that contains native microflora and fertilized with phoshite, engineered plants expressing the phosphite oxidoreductase achieve maximum productivity with 30 to 50% less P than that required to reach the same productivity using Pi as fertilizer. Since non-engineered plants are unable to use phosphite as a P source, when fertilized with phosphite the engineered plants easily outcompete weeds reducing or eliminating the need for herbicides to achieve maximum yield. In contrast to Pi that when released from contaminated rivers into the ocean promotes toxic algal blooms that kill aquatic organisms, phosphite should not cause these severe ecological problems since it cannot be used as a nutrient by algae. Thus these metabolically engineered plants allow the design of a dual fertilization and weed control system with both potentially important economical and ecological benefits.

0302: Kochian

Elucidating the Molecular and Biochemical Basis for Crop Aluminum Tolerance to Improve Cereal Production on Acid Soils

Leon Kochian[1], Jiping Liu[1], Jurandir Magalhaes[2], Miguel Pineros[1], Lyza Maron[1], Claudia Guimaraes[2], and Robert Schaffert[2]
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Aluminum (Al) toxicity is a major limiting factor both for food and bioenergy crops on acid soils that comprise up to 50% of the world's potentially arable lands. A large proportion of the acid soils occur in developing countries in the tropics and subtropics where food and energy security are the most tenuous. Also, there is a significant area of acid soils in the Southeastern U.S., which may be a useful region for the production of bioenergy sorghum. Because of the agronomic importance of crop Al toxicity, identifying the molecular determinants for Al tolerance has attracted significant interest from a number of laboratories around the world. We are now poised, based on recent discoveries by our labs and others, to develop the molecular and genetic resources required to address a worldwide agronomic problem that is only exceeded by drought stress with regards to abiotic limitations to bioenergy and food crop production.

In this talk, the isolation of the major sorghum Al tolerance gene, *SbMATE*, via high-resolution mapping has opened up new avenues for improving cereal acid soil tolerance. The role of this gene in controlling the wide range of Al tolerance in sorghum via regulation of *SbMATE* expression will be described. Furthermore, the combination of association genetics, genomics and protein biochemistry has shown us that other molecular determinants reside in the sorghum genome that help regulate both *SbMATE* expression and SbMATE protein function, resulting in greater levels of Al tolerance. This research is allowing us to assemble a molecular toolbox that is being used to translate these discoveries into more Al tolerant sorghum lines for production on acid soils both in Brazil and in developing countries in sub-Saharan Africa.

0303: Guerinot

From the Soil to the Seed: Metal Homeostasis in Plants

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More than 2 billion people are iron deficient because their plant-based diets are not a rich source of this essential nutrient. Clearly, we need to understand iron homeostasis in plants, both from the point of view of improving plant growth and crop yields as well as improving human nutrition. Despite progress in tracing how iron moves throughout the plant, we still do not fully understand how plants sense and respond to iron availability. Our goal is to identify and characterize the network of genes responsible for integrating information about iron status and orchestrating a coordinated response. To identify an iron sensor, we set up a genetic screen using an *IRT1* promoter-luciferase fusion construct. IRT1 is the major transporter responsible for iron uptake from the soil. One recessive mutant *uri* (upstream regulator of *IRT1*) displayed defects in induction of the reporter as well as the endogenous *IRT1*. As might be expected of a mutant that does not make the iron transporter, the *uri* mutant dies after germination in soil unless fed supplemental iron. Microarray analysis of the *uri* mutant revealed vast alterations in the expression of iron-deficiency regulated genes. *URI* itself encodes a bHLH transcription factor that is predicted to bind to a G-box, is expressed in all plant tissues and whose steady state mRNA levels do not change in response to iron deficiency.

Using ICP-MS (inductively coupled plasma-mass spectroscopy) for elemental profiling of EMS mutants, we have identified a line that accumulates iron due to constitutive expression of the iron-deficiency response genes, including *IRT1*. We have also been continuing our studies on localization of metals using synchrotron X-ray fluorescence spectroscopy, allowing us to understand the role of various genes in metal distribution.

This work has been funded by grants from NSF (IOS-0919941; DBI 0701119) and DOE (DE-FG02-06ER15809).

0304: Harrison

Phosphate Acquisition through Symbiosis with Arbuscular Mycorrhizal Fungi

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In natural ecosystems, most vascular flowering plants live in symbiosis with arbuscular mycorrhizal (AM) fungi. These mutually beneficial associations develop in the roots, where the fungus obtains carbon from the plant and delivers phosphate, nitrogen and other mineral nutrients to the roots. Development of the symbiosis is a complex process that requires the differentiation of both symbionts. The fungus grows into the root cortical cells where it undergoes terminal differentiation to form elaborately branched hyphae, called arbuscules. Differentiation of the fungal hyphae is coordinated with cellular differentiation of the root cortical cells which envelop the arbuscule in a new membrane called the periarbuscular membrane. Nutrient exchange occurs at the arbuscule/periarbuscular membrane interface; phosphate, released from the arbuscule, is transferred into the cortical cell by plant phosphate transporters in the periarbuscular membrane

Our research focuses on the molecular events that underlie development of the arbuscule/periarbuscular membrane and phosphate transport at this membrane interface. A combination of genomics coupled with reverse genetics has enabled us to identify components of the plant cellular program required for development of arbuscules and symbiotic phosphate transport. In *Medicago truncatula*, a novel protein, Vapyrin, plays a role in cellular remodeling to enable arbuscule development during AM symbiosis. Development of the periarbuscular membrane requires symbiosis-inducible components of the EXOCYST complex and regulation of arbuscule formation requires the action of DELLA proteins. A symbiosis-specific phosphate transporter MtPT4, plays a major role in the acquisition of phosphate delivered by the AM fungus and is also essential for maintenance of the symbiosis. Recent developments in these areas will be discussed.

The work was supported by grants from the U.S. National Science Foundation (IOS-0842720 and IOS-1127155).

0305: Paszkowski

Epigenetics Regulation of Abiotic Stress Responses

Jerzy Paszkowski
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Large proportions of eukaryotic genomes consist of epigenetically silenced transposable elements (TEs), predominantly retrotransposons. These are generally considered to be intra-chromosomal parasites. However, their periodical bursts of activity have influenced the organization of host genomes and contributed to beneficial traits. Remarkably, a number of what turned out to be transposon-generated phenotypic innovations were selected by humans during plant domestication and breeding. Therefore, TEs can be considered as an attractive endogenous source of genetic variation. I will discuss whether there are technical means to exploit this potential in a controlled fashion to induce genetic variation in responses to particular abiotic stress factors.

0306: Benfey

The Genetic Basis of Root System Architecture Traits

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Biology Department and Duke Center for Systems Biology, Duke University, HHMI and GrassRoots Biotechnology, Durham, NC USA

Root systems are high value targets for crop improvement due to their potential to boost or stabilize yields in saline, dry, and acid soils, improve disease resistance, and reduce the need for fertilizers. Root system architecture (RSA) describes the spatial organization of the root system, which is critical for its function in challenging environments. We have developed a semi-automated 3D imaging and phenotyping system to identify the genetic basis of root architecture. The integrated system combines hardware, imaging, software and analysis. We automatically reconstructed and phenotyped a well-studied rice mapping population identifying QTLs for RSA traits that control the extent, shape, distribution, and surface size of root networks. Apparent tradeoffs at some hotspots were consistent with genetic limitations on 'ideal' RSA phenotypes. We also used a novel multivariate-composite QTL approach to extract central RSA phenotypes and identify large effect QTLs that control multiple root traits. Thus, our approach can directly aid breeding efforts as well as identify important genes underlying environmentally robust QTLs.

0307: Inzé

The Impact of Stress on Growth and Development

Dirk Inze*
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Growth of plants and plant organs is orchestrated by complex molecular networks that integrates both intrinsic development signals encoded by the genome as well as a wide variety of environmental cues such as light, availability of water and minerals, temperature, e.a. Understanding the molecular composition and topology of these networks ultimately will accelerate advanced breeding and gene engineering for higher yielding crops. We have chosen leaves as a model organ to understand growth and size control mechanisms. As leaf growth is a quantitative trait, several (semi-) automated growth analysis platforms were developed to analyze leaf growth over time. Detailed cellular and molecular analysis of numerous *Arabidopsis* mutants revealed the existence of at least five mechanisms that contribute to final leaf size: i) the initial size of the leaf primordium; ii) cell cycle duration; iii) the developmental timing of the transition from cell division to cell expansion; iv) the timing of meristemoid division; and v) cell expansion. For each mechanism, multiple genes have been identified that when overexpressed or mutated enhance leaf organ size. For example, cell cycle duration appears to be controlled by the ANAPHASE PROMOTING COMPLEX, a multi-protein E3 ligase that is involved in mitosis. On the other hand the transition from cell division to cell expansion during leaf development is mediated by the gibberellic acid (GA) dependent activity of a chromatin remodeling complex. GA levels in the growth zones are regulated by the activity of two stress responsive transcription factors ERF5 and ERF6 and our experimental data show that these transcription factor have a pivotal role in regulation growth in response to the environment. Furthermore, GA also was shown to have an important function in mediating leaf growth in maize and by engineering GA metabolism maize leaves that have a 40% increase in length were obtained. We will discussed our current understanding of growth regulatory networks and how we can use this information to improve crop yield.

0401: Nelson

Advances in Abiotic Stress Tolerance in Key Crops

Donald Nelson
Monsanto Company

To help farmers mitigate some of the risk associated with drought, Monsanto has developed a drought-tolerant corn family termed DroughtGard Hybrids. These hybrids were developed using select germplasm and a drought-tolerant biotechnology trait. When used in combination with agronomic recommendations, plants are designed to enhance yield stability when water is limited. This presentation will focus on water use efficiency and how it may be addressed by an approach emphasizing all of agronomic practice, genetics, germplasm variation, and biotechnology. This systems approach is expected to be more effective than any one of the parts and will likely become a powerful tool for farmers in the Western Great Plains.

0402: Tuinstra

Prospects for Adapting Maize to Drought and High-Temperature Stress

Mitchell R. Tuinstra
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Climate modeling studies suggest that weather conditions characterized by higher day and night temperatures combined with increased variability in rainfall will become more common in future environments. Current advancements in plant breeding and biotechnology are contributing maize genetic technologies that enhance productivity under abiotic stress; however, future efforts must focus on integrating multiple climate adaptation traits to provide tolerance to a broad spectrum of adverse conditions.

Our analyses of drought stress tolerance in maize have focused on tolerance during the grain maturation stage of development. The ability for annual crop species to delay senescence or "stay-green" throughout the grain filling period has been associated with increased productivity. Germplasm characterization studies identified several large-effect genetic loci associated with functional stay-green under drought stress conditions. Analyses of introgression lines in near-isogenic hybrids indicated these genetic loci can substantially improve crop performance under late-season drought stress.

Heat stress tolerance is another important constraint to maize productivity. Researchers at CIMMYT and Purdue University are collaborating on research to study heat stress tolerance in temperate and tropical maize. Results from these experiments indicated that most temperate and tropical genotypes including B73, a temperate inbred line that serves as the reference genome of maize, are poorly adapted to high-temperature stresses. A few heat-tolerant genotypes were identified that display good adaptation and normal development under high-temperature stress. Very little is currently known about the biochemical and physiological mechanisms that contribute to heat stress tolerance of maize; however, genetic variation to improve crop productivity under these conditions is present in certain maize breeding populations.

This project was supported in part by AFRI Competitive Grant no. 2009-65114-05979 from the USDA NIFA.

0403: James

Development and Evaluation of Salt-Tolerant Wheat

Richard A James[1], Rana Munns[1], Stuart Roy[2,3], Mark Tester[2,3], Matthew Gilliham[3]
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Salinity limits crop yield in arid and semi-arid areas, due either to irrigation with water containing dissolved salts, rising water tables resulting from land clearing, or natural subsoil salinity. Sodium exclusion is a critical mechanism for salinity tolerance of cereals and considered important for the greater salt tolerance of bread wheat relative to durum wheat. Durum wheat lacks the Na^+-excluding locus *Kna1* which enables bread wheat to maintain lower leaf Na^+ and a greater K^+ to Na^+ ratio. A novel source of Na^+ exclusion, not present in either durum or bread wheat, was found in an ancestral wheat relative *Triticum monococcum*. Two genetic loci named *Nax1* and *Nax2* were identified and both were found to confer a reduced rate of Na^+ transport from roots to shoots. The *Nax1* and *Nax2* loci carry *TmHKT1;4-A2* and *TmHKT1;5-A* respectively, which are the candidate genes for this function. *TmHKT1;5-A* encodes a Na^+-selective transporter located on the plasma membrane of root cells surrounding xylem vessels, and so is ideally localised to withdraw Na^+ from the xylem.

Advanced breeding (near-isogenic) lines containing the *Nax* loci were developed and evaluated in controlled environment and on farmer's fields of varying salinity.

In the field on highly saline soils, *Nax2* (*TmHKT1;5-A)* reduced leaf Na^+ concentration three fold and improved grain yield by 25% compared to the recurrent parent without *TmHKT1;5-A*. *Nax1* (*TmHKT1;4-A2*) reduced leaf Na^+ concentration by 100 fold, yet yield declined by 5 – 10%, possibly due to compromised osmotic adjustment and turgor maintenance. Research is continuing on improving the salt tolerance of wheat by targeting tolerance to the osmotic stress caused by salinity.

This research was supported by the Australian Grain Research and Development Corporation (GRDC).

0404: Hua

This abstract was not available at the time of printing.

0405: Ainsworth

Maximizing Soybean Production in a High CO_2 World

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While the future crop growing environment is likely to be warmer and with more variable water available, the stimulation of C3 photosynthesis by elevated CO2 concentration provides a potential benefit of global climate change. However, experimental field studies suggest that C3 crops fall short of the theoretical maximum stimulation in yield when grown at elevated CO2. This may be because crops are not adapted to current atmospheric CO2 concentrations, much less future elevated CO2 concentrations, and lack the sink capacity to maximize the potential gain in carbon from greater photosynthetic rates. However, only a tiny fraction of available germplasm has been screened for CO2 response. At the SoyFACE experiment in central Illinois, over 20 genotypes of soybean (*Glycine max* Merr.) have been screened for CO2 responsiveness. On average, seed yield is stimulated by ~15%; however, genotypes with a range of responses from no stimulation in yield to 25% stimulation in yield have been identified. We investigated the photosynthetic basis for variation in CO2 response in two soybean lines in an effort to determine mechanisms for maximizing yield responses to elevated CO2. Changes in photosynthetic acclimation as well as changes in partitioning of carbon to seed biomass underpin variation in soybean yield responses to elevated CO2. These results will be discussed in combination with efforts to transgenically modify soybean to maximizing its production in a high CO2 world.

0406: von Caemmerer

Impacts of Elevated CO_2 on Photosynthesis and Other Processes

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A better understanding of leaf level gas exchange processes is important for understanding the impacts of elevated CO_2 on photosynthesis and its coordination with stomatal function. Mathematical models of leaf photosynthesis provide a mechanistic base for predicting and assessing changes in photosynthetic CO_2 fixation in different environments. However we lack a mechanistic understanding of how photosynthetic capacity and stomatal function are coordinated in responses to environmental perturbations such as increasing atmospheric CO_2 and/or temperature. We have used molecular technologies to study the regulation of C_3 and C_4 photosynthesis by generating a number of transgenic plants of *Nicotiana tabacum* (a C_3 species) and *Flaveria bidentis* (a C_4 species) where the photosynthetic metabolism has been impaired with RNA antisense constructs to various photosynthetic proteins. These molecular manipulations result in plants with a range of reductions in the amounts of the target protein, making this approach ideally suited to a quantitative analysis of photosynthetic processes and its coordination with stomatal function. Several examples will be presented that explore the relationship between photosynthetic rates and stomatal function at elevated CO_2 and temperature in C_3 and C_4 species.

1001 Volatiles involvement in bacterially induced drought stress tolerance in wheat

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The present study was conducted to improve the drought stress tolerance of wheat using Plant Growth Promoting Bacteria PGPB. Pre-treating wheat grains with well characterized PGPB strains allowed us to grow wheat without any water supply for 9 days. Moreover, significantly reproducible improved phenotypes were always recorded in bacterial treated seedlings. Plants are knows to emit volatile organic compounds VOC in response to several abiotic stresses. However, it's not clear if the interactions between PGPB and plant have any role in VOC emission due that, we aimed to explore that possibility through monitoring VOC emission. Stress impacts on plant were characterized through recording phenotypes, growth and photosynthesis parameters and VOC emission. Emission of several VOC related to monoterpenes class as well as, ethylene was detected from wheat leaves at different time points after stress application. We detected a significant increase in the emission of some monoterpenes especially benzaladyde, geranyl acetate and β- pinene from leaves after growing wheat for 5 days without water. Generally, bacterial treated drought stressed seedlings showed much lower VOC emission compared with their stressed counterparts. An Interesting, strong correlation between VOC emission and ethylene emission was observed in bacterial treated seedlings. In most cases, drought stress induced ethylene emission from leaves. In some cases, bacterial treated seedlings showed lower ethylene emission under drought stress condition. These results strongly support the strategy of using PGPB inoculation as an eco-friendly approach to control drought stress in wheat. Also, we showed that PGPB inoculation has involved in VOC emission and we suggest that the fine tuning in VOC emission could play an important role in stress tolerance mechanisms in plants.

1002 Protein Interaction Network in Arabidopsis Guard Cell ABA Signaling: A Systems Biology Approach

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Osmotic swelling and shrinking of guard cells in response to environmental signals, including drought, determines stomatal apertures. Drought causes accumulation of the hormone abscisic acid (ABA), which promotes stomatal closure and inhibits stomatal opening, thereby promoting plant water conservation. To improve molecular mechanisms of drought tolerance, it is essential to first understand the relationships between different components of the ABA signaling network. In this regard, systems biology approaches can aid in both synthesizing the network and evaluating the relative importance of different paths of signal propagation. We previously (Li et. al., PLoS Biol, 2006, 4(10): p. e312) constructed a dynamic and predictive model of the guard cell ABA signaling network which included ABA as the input and stomatal closure as the output, and encompassed more than 50 intervening signaling components. In the model, proteins adjacent to each other based on pharmacological or genetic study were separated by an intermediate node.
Experimental analysis of protein-protein interactions (PPIs) can identify direct interaction partners and place individual protein nodes in specific positions in signaling pathways. Accordingly, a major focus of the present work was to evaluate the inferred topology of our model, and to improve and extend the model by performing systematic protein-protein interaction (PPI) screens. Our PPI analyses based on yeast two-hybrid and BiFC methods have identified targets for key signaling proteins (e.g. protein kinases, phosphatases, G protein subunits), and in some cases have eliminated intermediate nodes. We also have evaluated interactions between protein nodes of our original model and recently discovered ABA receptors. An updated dynamic model of guard cell ABA signaling is being constructed using these data and results from mining the recent literature.

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1003 Functional characterization of the ABFs and CBFs in cotton (*Gossypium hirsutum*)

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Drought and protracted periods of extreme temperatures can necessitate high levels of irrigation to maintain a healthy cotton crop. These conditions cause abiotic stress leading to reduced fiber yield and quality. In response to these challenges, our goal is to characterize a suite of genes that play significant roles in regulating plant responses to abiotic stress, and use this knowledge to create novel germplasm resources that can be used to develop cotton varieties better able to withstand these conditions. Of the many gene families involved in the abiotic stress response, the ABA-responsive element binding factors (ABFs) and C-repeat binding factors (CBFs/DREBs) are of particular interest for their roles in a variety of abiotic stress responses, most notably, drought and temperature stress, respectively. In addition, members of these gene families have been shown to interact. Constitutive overexpression of Arabidopsis ABF3 in cotton was found to confer a high level of water deficit tolerance under controlled conditions, though this benefit was offset by delayed reproductive transition. Members of the endogenous cotton ABF and CBF gene families show distinct expression profiles with marked differences in responsiveness to both water deficit and temperature stress treatments and preliminary promoter screens have uncovered putative *cis*-acting elements linked to abiotic stress regulation. Though still in the early stages, we believe the functional characterization of select ABFs and CBFs in cotton can lead to the development of viable strategies for improvement of drought tolerance in plants.

This work was supported in part by the Ankur Seed Company Ltd. Nagpur, India.

1004 Growth and Survival of Some Trees as a Response to Saline Water irrigation in Saudi Arabia

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Saudi Arabia is an arid country with limited and non-renewable freshwater resources. Scarcity of irrigation supplies is one of the major factors limiting agricultural expansion. Greenhouse experiment was carried out to determine the effect of water salinity on the growth and survival of Acacia nilotica, Prosopis juliflora, Eucalyptus camaldulensis and Parkinsonia aculeate. Increasing soil salinity resulting from irrigation water salinity significantly decreased the growth and survival period of experimental trees. The survival period of Acacia nilotica and Prosopis juliflora was significantly more than Eucalyptus camaldulensis and Parkinsonia aculeate under all salinity levels. Prosopis juliflora tolerated soil salinity (EC_e) up to 39.5 dS m^{-1} and A. nilotica up to 44.9 (EC_e) when irrigated with water salinity of 12.80 dS m^{-1}; P. aculeate up to 29.26 (EC_e) when irrigated with water salinity of 6.45 dS m^{-1}; and E. camaldulensisup to 34.3 (EC_e) when irrigated with water salinity of 6.45 dS m^{-1}. The sequence in salt tolerance was found to be P. juliflora and A. nilotica > P. aculeate > E. camalduensis. Trees survival and proper establishment is possible if we provide a good management practices such as leaching requirement (at least 15%), proper selection of trees, right irrigation water salinity, and proper planting methods. The results suggested that the A. nilotica and P. juliflora should be cultivated as landscape trees for controlling desertification, establishing shelterbelts around cities, and in sand stabilization projects under arid environmental conditions.

1005 Natural variation of Maize physiology

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Maize has been domesticated over the past 10,000 years to become today a highly efficient crop alleviating a large part of human nutrition. Its genome sequence evidenced an abundant mosaic of transposable elements accountable of a highly plastic and dynamic genome. How this molecular plasticity is reflected at the physiological level is poorly known. In this study, we used a field grown set of 19 maize lines covering maize genetic natural diversity to evaluate the evolution of physiological traits and metabolic strategies. Analyses were performed at both vegetative and maturity stages and concerned maximal enzyme activities of carbon and nitrogen assimilation pathways, primary and secondary metabolite content, biomass and yield parameters. Variability analysis of these 187 traits evidenced a clear distinction between the development stages, high variability coefficients for some amino acid and phenylpropanoid content but consistent total carbon and nitrogen content and phosphoenolpyruvate carboxylase maximal activity across the lines. Physiological clustering of the genotypes according to all dataset or to selected variable type failed to produced clear groups (including according to maize origins), illustrating a wide and complex range of metabolic strategies. The large Maize natural variation at the genome level is therefore well translated at the metabolic dimension. Correlation studies between agronomic and physiological traits allowed identifying a number of unexpected metabolic pathways exhibiting high genetic variability across the lines and having a putative role in plant growth and yield.

1006 Using *Malus sieversii* Ledeb., the Wild Apple Progenitor of *Malus* x *domestica* Borkh., to Identify Genes Contributing to Water Use Efficiency and Potential Drought Resistance

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Dehydration is a feature of many abiotic stresses, but is more often an agricultural threat in its own right. Plants have evolved numerous mechanisms for coping with dehydration, including morphological, biochemical and molecular biological responses. These mechanisms are complex and involve various combinations of response mechanisms. In Kazakhstan, wild apples (*Malus sieversii* Ledeb.) have adapted to local habitats, including several xeric sites where rainfall is less than 250 mm annually. We have exploited this material to try to identify germplasm with enhanced water use and/or drought resistance. A common commercial cultivar, 'Royal Gala' was used as a standard for comparison. Two subpopulations of approximately 30 individuals representing >95% of the diversity of populations adapted to xeric sites 6 and 9 were analyzed for stable carbon isotope incorporation, leaf area and stomatal density, parameters commonly associated with screening for drought resistance and water use efficiency (WUE). Extremes were chosen from the site 6 material and used in an experiment to simulate a severe drought over a two-week period. Parallel seedlings of 'Royal Gala' were subjected to the same treatment. The results indicate that the most WUE lines tested were not significantly different from 'Royal Gala', but that the least WUE lines responded differently to the drought treatment.

1007 Genetic and epigenetic impacts on the poplar drought response

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Within an organism's lifetime, previous exposure to environment conditions shapes future responses. This is likely to be particularly important for trees, which must contend with fluctuating, frequently challenging, environmental conditions throughout their long lifetimes.
Here we study the persistent influence of past experiences on the capacity of trees to respond to a current stress, drought. Vegetatively propagated trees of the genus *Populus* from different geographic locations (i.e. genetically identical individuals with different clone histories) were studied. Analyses of transcriptome responses to drought under common garden conditions uncovered differences in transcript abundance patterns based on differences in geographic origin of poplar clones with identical genotypes. While classic fingerprinting confirmed genetic identity of the trees obtained from different locations, whole genome sequencing is currently under way to detect possible somatic mutations that might have arisen independently in different geographic locations. Differences in total DNA methylation based on differences in clone history were found to parallel differences in drought transcriptomes. A more detailed analysis by fingerprinting detected some loci with variable methylation patterns based on geographic location within the same genotype, while genotype-specific patterns were also detected.
These data provide insight into the interplay between genotype and the local environment, and hint that epigenetic mechanisms may add an additional layer of plasticity. Moreover, the data provide insights into long-standing applied questions related to the nursery source of poplar clones and how that impacts on future clone performance in plantations.

1008 New insights into the regulation of the stomatal red-light response

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Stomata regulate the uptake of CO_2 and the loss of water in leaves of higher plants. Plants that maximize their CO_2 uptake by opening the stomata are faced with an increased rate of transpiration, which is problematic especially under conditions of water limitation. Therefore, stomatal movement is tightly regulated to maximize the plant's water use efficiency. The guard cells, controlling stomatal opening, respond to a number of different environmental stimuli, such as water status and CO_2 concentration. The response of stomata to light follows two independent pathways: blue light is sensed by the photoreceptor phototropin. Red light also stimulates stomatal opening, but the underlying sensing mechanisms are unknown. In particular, the role of photosynthesis in the stomatal red-light response has been disputed for decades. Here we examined the hypothesis that red light is sensed by the redox state of the photosynthetic electron transport chain. Our hypothesis is prompted by the observation in the literature that the stomatal red-light response is suppressed when photosynthesis is impaired upstream of plastoquinone (PQ), but is unaffected or increases in strength when impaired downstream of PQ. PQ, a molecule shuttling electrons between photosystem II and the cytochrome b_6f complex, is already known to be involved in the regulation of protein phosphorylation and gene expression. The redox state of PQ (measured by chlorophyll a fluorescence as 1-qL) strongly correlates with stomatal conductance independent of experimental condition, such as red light intensity, O_2 and CO_2 concentration. In combination with knowledge gained from published work, this makes PQ a possible candidate as the mediator for the stomatal red-light response. A better understanding of stomatal regulation will help to improve the water use efficiency in crops.

1009 Phenotyping Salt Tolerance Responses in Cotton, Sorghum and Castor

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Sorghum, cotton and castor are three crops that essentially provide food, clothing, and fuel in many areas of the world. Sorghum is considered a feed grain cereal, while cotton is a high-value fiber crop and its seed is used for feed and oil. The oil extracted from castor seed is versatile and easy to use for the production of a number of products such as cosmetics, fluids, additives, biofuel, etc. Sorghum, cotton and castor grow well in warm and semi-arid climates. They have adapted well to harsh conditions over time. However, the toxicity effect from increasing levels of sodium chloride (NaCl) has become harmful to the plants. Other salts such as calcium, sulfate, bicarbonate, and magnesium impart a negative effect on plants as well, but NaCl is considered the most detrimental salt. Searching for ways to understand the effect of salinity, the objective of this research is to single out phenotypic responses to salinity stress in cotton, sorghum and castor.
By screening and evaluating the effects of salinity, three experiments were carried out and were conducted over-time and with different concentrations of NaCl. The seed of 12 sorghum bicolor (L.) cultivars were grown for 90 days in a saline soil media, while in the hydroponics, 290 cotton cultivars, G. hirsutum L. and 8 castor experimental cultivars were grown suspended in water for approximately 45 days. The saline solution was prepared by mixing 91.2 grams of sodium chloride in reverse osmotic (RO) water and added every 48 hours.
Experimental design for each study was a randomized block design with four replications.
The results showed different phenotypic responses in sorghum, cotton and castor to the saline treatments. The main differences observed were plant height, root biomass, tissue damage, flower delay, fruiting capabilities, seed number index, fiber development, boll size, and yield potential. In some cases some of the responses were analyzed using various microscopes.
Phenotypic responses to salinity stress should be considered when selecting cultivars that can thrive in saline soils and during the development of new germplasm resources.

1010 Functional analysis of *MtWXP1/2* genes in *Medicago truncatula*

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Water deficit is a critical issue for legume crop production. Under drought stress, it is beneficial for plants to have decreased water loss through transpiration to have a relatively restrictive water balance. *Medicago truncatula* has been developed into a model legume species. Previously, we indentified a novel ERF transcription factor from *M. truncatula*, named MtWXP1, which can increase wax production in alfalfa (Medicago sativa). Overexpression of the *MtWXP1* gene in alfalfa and white clover led to decreased water loss and enhanced drought tolerance. Overexpression of *MtWXP1* or its paralog *MtWXP2* also conferred drought tolerance in *Arabidopsis*. However, analysis of freezing tolerance at the whole plant level revealed that the *MtWXP1* plants had increased freezing tolerance while the *MtWXP2* plants were more sensitive to low temperature treatment. To elucidate mechanisms of MtWXP1/2 in stress response, we overexpressed *MtWXP1/2* in *M. truncatula* and obtained large numbers of transgenics. By utilizing the infrared thermal imaging technique, difference in leaf temperature between wild type and overexpression plants was detected. Leaves of overexpression plants showed a hot-leaf phenotype, which means lower water loss through transpiration; such plants tend to retain more water than the control. The transgenics that have very high levels of gene expression showed small leaves and dwarf phenotype. Because no *MtWXP1/2* mutants were identified from a large collection of Tnt1 retrotransposon tagged *M. truncatula* mutants, we also produced MtWXP1/2-SDRX repressor plants. Detailed molecular and biochemical analyses of the transgenic *M. truncatula* plants may allow us to better understand the functional mechanism and identification of downstream genes of MtWXP1/2.
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1011 Water stress on the camptothecin content in *Nothapodytes nimmoniana*

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Plant secondary metabolites are closed related the environmental stress.
The camptothecin is an alkaloid with antitumor activity and as precursor of antitumor drug. Most camptothecin was extracted from camptothecin-containing plants. The *Nothapodytes nimmoniana*, a tree original in Taiwan, is one of the plants with high content of camptothecin of the world; however, few researches concentrate on the environmental stress and the camptothecin content. In this research, we try to find out the effect of shading and water stress on the nitrogen metabolite and camptothecin content in *N. nimmoniana*.
In 2008, we choose three-year-old *N. nimmoniana* grown in Taipei, Taiwan. All shoots were cut off from the 37 cm in height above ground on before treatment. After the sprouted then two months of cultivation and one month of treatments were conducted. The treatments are water stress and shading. For water stress treatment, the plants were withheld water after one hour of leaf wilting. Then the plants were watered and a new drought cycle started. The shading treatment was processed with a black shade cloth that reduces 66% full sunlight.
In the biomass, the results showed that water stress and shading had no significant effect on the upper parts of plants; water stress results in increase the dry weight of root. Water stress resulted in decrease in the total nitrogen concentration of the leaf, and increase in nitrate concentration, proline concentration in the leaf and camptothecin concentration in the root. Shading has no effect on the total nitrogen concentration in all parts of plants and proline concentration in leaf; increase in the concentrations of the nitrate in all parts of plants and camptothecin in the trunk. In conclusion, the short water stress and shading treatment had increase the potential of nitrogen metabolite to camptothecin in *N. nimmoniana* and this could be a potential strategy for camptothecin production in *N. nimmoniana*.

1012 Dissection of heat tolerant mechanisms in maize

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As global warming becomes inevitable, the sustainability of agricultural production in US and worldwide faces serious threat from extreme weather conditions, such as drought and high temperature (heat stress). Heat and drought stresses occurred during maize growing season in the US High Plains in 2011 and in most maize growing area in 2012 caused significant reduction in grain yield and grain quality. While drought stress can be relieved through irrigation, little can be done with heat stress through crop management. More importantly, heat induced tissue injuries in the field are mostly irreversible. Therefore, the only feasible way to cope with temperature extremes in agriculture production is through genetic improvement to develop heat tolerant hybrid. Evaluation of genetic variation and identification of specific traits for heat tolerance/sensitivity in maize are primary and essential steps in the study of genetic mechanisms of heat tolerance and in developing heat tolerant hybrids. For the past two seasons, we have evaluated a selected number of maize germplasm panels for heat tolerance in Lubbock, TX, where hot and dry environments during the growing season are ideal for field phenotype evaluation. Maize inbred lines with contrasting heat tolerant phenotypes at different developmental stages have been selected to generate mapping populations. Preliminary genetic analysis revealed several independent traits that contribute to the variation in heat tolerance in field-grown maize. QTLs associated with heat tolerance were identified in 2 NAM RIL populations. The long term goals of this newly initiated research project are to 1) map major QTLs contributing to heat tolerance, 2) identify molecular markers for MAS of heat tolerant lines in breeding programs, and 3) study the genetic and molecular mechanisms that confer tolerance to high temperature in maize.

1013 Cyanobacterial gene *groEL$_2$*, targeted to the chloroplast, protects transgenic tobacco plants against abiotic stress stimulators

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GroEL- like proteins are heat shock proteins, highly conserved from bacteria to eukaryotes and their function as molecular chaperones is indispensable. In a transcriptomic and proteomic analysis of the response of *Synechocystis* PCC6803 to stress tolerance, *groEL$_2$* has been identified. Since *Synechocystis* is a progenitor of the present day chloroplast, enhancing plant tolerance to abiotic stress conditions by targeting the cyanobacterial chaperone *groEL$_2$*, to the chloroplast of *Nicotiana tabacum* L var. Xanthi, as a model system is an innovative and promising approach.
The *groEL$_2$* was cloned into the plant binary vector pCAMBIA 2300, with and without the chloroplast transit peptide (CTP) of the small subunit of the Rubisco complex from *Brassica juncea*. The CTP-*groEL$_2$* directs its translocation into the stroma of the chloroplast. In the present day a comparison has been made of the tobacco transgenic plants with and without targeting of *groEL$_2$* to the chloroplast for assessing the role of chaperone in the chloroplast in stress alleviation. The seedlings and leaf discs of T_2 transgenics were subjected to various stresses like osmotic, salinity and drought. Also, six week old, pot grown transgenic plants were subjected to water withholding and the plants were analyzed for photosynthetic efficiency and oxygen evolution. The chlorophyll and the proline contents were analyzed and the extent of lipid peroxidation was also assessed.
In all the above abiotic stresses, the CTP-*groEL$_2$* plants demonstrated significantly higher tolerance compare to the cytosolic- *groEL$_2$* transgenics and the non-transformed control plants. These studies demonstrate the importance of *groEL$_2$* as a chaperone in the chloroplast and a potential candidate in the manipulation of the abiotic stress tolerance in plants.

The work has been funded by University of Hyderabad.

1014 Pause-and-stop: The dynamic response of proliferating leaf cells to osmotic stress

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Drought is responsible for considerable yield losses in agriculture due to its detrimental effects on growth. Drought responses have been extensively studied, but mostly on the level of complete plants or mature tissues. However, stress responses were shown to be highly tissue- and developmental stage-specific, and growing tissues have developed unique mechanisms to respond to stress. Studying these mechanisms allows engineering of "bolder" crops with decreased stress-induced growth inhibition for temperate climates where stress is not severe enough to kill plants, as enhanced survival under severe stress is not a good indicator for growth performance under more mild stress [1].
Using the developing Arabidopsis leaf as a model to study the response of growing tissues to osmotic stress, we developed a framework which was coined the "pause-and-stop model", describing three phases in the response of growing leaves to stress [2]. The first phase involves an ethylene-induced reversible post-transcriptional arrest of the cell cycle through modulation of CDKA activity.
In a later phase this is followed by DELLA-dependent irreversible mitotic exit and earlier onset of endoreduplication, which surprisingly is not mediated by classical cell cycle inhibitors but by modulation of APC/C activity by DEL1/E2FE and UVI4 [3]. The third and final phase occurs late in leaf development, and entails partial recovery of cell number through activation of dispersed meristemoid cells, which generate more pavement cells while keeping the number of stomata low.
Within this framework, current research focuses on the connection of stress to DELLAs through ERF transcription factors, downstream targets of DELLAs, and the regulation of meristemoids under osmotic stress and drought conditions.

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1015 The role of gibberellin signalling in the response to drought

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The phytohormone gibberellin (GA) promotes and coordinates plant growth and development. In addition, there is accumulating evidence for a role for GA in the response to abiotic stress. Plants with reduced GA content or responsiveness show enhanced tolerance to several forms of abiotic stress, including cold and salinity. However, the physiological basis for this tolerance remains to be fully elucidated. Here, we are investigating the role of GA signalling in the response to drought using both *Arabidopsis* and wheat. For *Arabidopsis*, we have established a soil-based assay, imposing progressive soil drying on rosette-stage plants. Using quantitative RT-PCR, we monitored the expression of genes involved in GA metabolism and signalling in *Arabidopsis* rosettes during exposure to drought. The gene encoding GA 2-oxidase 1 (GA2ox1), an enzyme involved in GA inactivation, was most strongly up-regulated. The induction of *GA2ox1* coincided with a reduction in GA levels in the rosette, and correlated with the onset of rosette growth-restriction in drought-stressed plants. We are now testing whether a reduction in GA contributes to rosette growth restriction and/or stress tolerance under drought conditions using *Arabidopsis* lines with altered GA content or signalling.
In addition to work in *Arabidopsis*, similar experiments have been carried out with wheat. Transcript analysis has revealed up-regulation of specific *GA2ox* genes in the shoots of wheat seedlings exposed to progressive soil drying, in parallel with down-regulation of *GA2ox* genes in the roots. These results suggest that regulation of GA inactivation may be involved in controlling the partitioning of growth between shoots and roots during exposure to drought. This is now being investigated further with detailed growth analysis.

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1016 Yield and Ion relations of Alfalfa (*Medicago sativa* L.) in response to irrigation with saline waters

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Alfalfa is a major forage crop utilized in arid and semi arid regions under irrigation; these regions are commonly impacted by saline water and soils. Four commercial non-dormant, purported salt tolerant Alfalfa cultivars 'Salado', 'S&W8421s', 'S&W9720' and 'S&W9215' were grown in 24 outdoor sand tanks in Riverside CA, with irrigation water (sodium sulfate dominated) at EC: 3.1 (control), 7.2, 12.7, 18.4, 24.0 and 30 dS m^{-1}, imposed at planting date. We evaluated four replicates per treatment for yield, ion composition and physiological parameters. Forage yield of cultivars per harvest (relative to control; average from seven harvests) was significantly influenced by salinity above EC 12.7 dS m^{-1} except 'S&W 8421s' that showed reduction with EC above the control. There were no significant yield differences among cultivars at EC 7.2 and 12.7 dS m^{-1}. At EC 18.4 dS m^{-1} Salado had the highest yield and differed significantly from the rest. At 24 dS m^{-1} the yield decreased for all cultivars but Salado showed the least reduction. At EC 30 dS m^{-1} (highest level) there were no survivor plants. The photosynthetic rate (Pn), leaf transpiration rate (tr) and leaf stomatal conductance (gs) all showed a decrease with increasing EC. Potassium shoot concentrations decreased in all cultivars with increasing salinity. Chloride increased from the control to all other salinity levels and was lowest for Salado at elevated EC, but there were no significant differences among cultivars. Sodium shoot concentration increased in all cultivars with increasing salinity, however Salado maintained significantly lower concentrations at all salinity levels (up to 40 % less than the mean of the other cultivars at 18.4 dS m^{-1}). These results suggest that Na^+ exclusion is an important factor in determining alfalfa salt tolerance.

1017 Chemical genetics analysis of the Pi-starvation response in Arabidopsis

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We used a chemical genetics strategy to dissect the pathways involved in Pi homeostasis. Based on the expression of the PHT1.4::GUS-reporter gene, we screened for molecules that either mimic or suppress the low-Pi responses. We identified MC2 and MC11, two drugs mimicking phosphate starvation. Both stimulate the physiological (including modification of root architecture) and molecular markers associated with the phosphate starvation. Many of these traits are associated with Pi recovery or uptake mechanisms, and as a consequence both drugs promote overaccumulation of Pi.
In order to look for the target of the drug we have isolated two EMS mutants that are less sensitive to MC2. Interestingly, these mutants present striking physiological features (reduced Pi content and increased biomass) suggesting modification of Pi homeostasis.
For the second molecule, MC11 we identified the active moiety which turns out to accumulate in roots but not in shoot. Nevertheless, MC11 triggers responses associated to Pi starvation in this tissue by activation of Pi systemic response in plants.
AC6 inhibits the expression of the PHT1.4::GUS-reporter gene in seedlings grown on a low-Pi medium. This drug reduces the expression of the endogenous PHT1.4 as well as the others PHT1 genes. A transcriptomic analysis shown that AC6 represses many other genes normally induced by Pi-starvation. Interestingly, AC6 suppresses the root growth arrest imposed by low-Pi medium.
Remarkably, a structural analogue of MC2 inactive on high Pi medium, turns out to present similar properties of AC6 on a low Pi medium suggesting a molecular switch mechanisms for Pi sensing.

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1018 Association genetics of shoot ureide concentration

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Drought stress is considered to be a major constraint to the production and yield of soybean [Glycine *max* (L.) Merr.], the world's leading economic oilseed crop. One of the major benefits of legumes in agriculture is their capacity to symbiotically fix atmospheric nitrogen, thus reducing the need to use nitrogen fertilizers. In drought conditions, soybean not only suffers from reduced leaf area development and photosynthesis, but its symbiotic N2 fixation is also especially vulnerable. Tropical legumes such as soybean produce ureides, (allantoin and allantoate) the final products of N2 fixation that are exported from soybean nodules to shoot, where they are catabolized. Earlier experiments have shown that increases in shoot ureide concentrations are associated with inhibition of N2 fixation in nodules under water deficit stress conditions. A collection of 343 diverse soybean genotypes were separated into two broad clusters and three distinct sub-clusters with SNP markers. Analyses of phenotypic data were conducted to examine the relationship between genetic clustering and phenotypic responses at two distinct locations in two consecutive years (2009 and 2010). Mean ureide values among the clusters were statistically compared and revealed that one sub-group was significantly different from the other two groups. Although the ureide values were significantly different between the two locations in both years, results were consistent across years and locations. Our results indicate that identified SNP markers can be used to interrogate diverse germplasm for ureide dynamics and thus N2 fixation-based drought tolerance in soybean.

1019 A Multi-faceted Approach to Increasing Drought Tolerance in Maize

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The importance of drought tolerance in commodity crops was emphasized due to the severe drought that occurred in the US during the 2012 growing season. DuPont Pioneer is actively pursuing both native and transgenic approaches to improve drought tolerance in crops. Optimum® Aquamax™ is a new commercial maize product, launched in 2011, that delivers yield performance under drought, while providing top-end yield potential. The success of Optimum® Aquamax™ has shown that selective native trait breeding is an effective approach to deliver solutions for complex agronomic traits like drought. Transgenic approaches expand our ability to create drought tolerant maize products. We are actively employing a pipeline approach to identify and evaluate drought tolerance transgenes. Using managed stress environments, we have identified drought tolerance leads and assessed their transgenic effects on crop yield, physiology, and contributions to drought tolerance. We are evaluating multiple product concepts that relate to native and transgenic sources of genetic diversity to deliver yield stability and yield potential.

1020 Transcriptome analysis in the resurrection grass *Sporobolus stapfianus* in response to dehydration and rehydration

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Studying plant adaptations to tolerate dehydration is necessary to develop novel strategies for improving drought tolerance in sensitive crops. To investigate the dehydration tolerance mechanism in the resurrection grass species (*Sporobolus stapfianus*), we compared the mRNA expression profiling of leaf tissues using a *S. stapfianus* specific Nimblegen oligonucleotide based microarray at full hydration, during drying and after re-watering. A total of 4,751 transcripts were found to be significantly differentially expressed across the eight conditions. Dehydration resulted in a progressive decrease in the abundance of transcripts encoding proteins with functions related to photosynthetic metabolism. In contrast, transcript abundance increased for genes involved in biosynthesis of raffinose series sugars, lipid biosynthesis and turnover, and protection against oxidative stress. Other abundant groups of genes expressed in response to desiccation included LEA proteins, transporter proteins, and kinases and phosphatases. To effectively identify which genes play a central adaptive role in dehydration tolerance, we use the approach of sister group-comparison, by comparing gene expression with a desiccation sensitive sister species, *S. pyramidalis*. In addition, we will discuss the comparison of gene expression profiles with other desiccation tolerant plants and seeds to trace genes and gene networks through phylogenies to explore for conserved patterns that infer adaptive value. These ancestor-descendant comparisons will add to our understanding of the evolution of vegetative desiccation tolerance in plants. We are in the process of functionally testing over-expressing transgenic lines of the candidate genes in *Arabidopsis thaliana*.

1021 Elevated atmospheric CO_2 alters root depth distribution, enhancing abscisic acid signaling and stomatal closure under drought in field-grown soybean

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Rising atmospheric CO_2 concentrations and increasing frequency and severity of droughts will alter the environment for plant growth in the coming century and will challenge agricultural production. In models of future food supply and ecosystem function, it is currently predicted that elevated atmospheric CO_2 will reduce stomatal conductance and plant water use, leading to conservation of soil moisture and reduced drought stress. Additional carbohydrate availability under elevated CO_2 is also expected to increase root biomass. By these two mechanisms, elevated CO_2 is expected to more than compensate for the deleterious effects of drought on yield. Here, we present a 3-year dataset demonstrating that this prediction does not hold true for field-grown soybean as stress becomes more severe. We grew soybean (*Glycine max)* under ambient (390 ppm) or elevated (585 ppm) atmospheric CO_2 in combination with control or reduced precipitation in the field using Free Air CO_2 Enrichment (FACE) technology at the soyFACE facility in Champaign, IL in 2009-2011. Contrary to expectations, we found that elevated CO_2 conserved soil moisture only in control precipitation treatment and only during mild conditions. Elevated CO_2 never conserved soil moisture in reduced precipitation plots. During times of natural drought, the effect of elevated CO_2 on soil moisture was often reversed, with elevated CO_2 plants using more water than ambient CO_2 plants. Elevated CO_2 also increased root length density, but this effect occurred mainly in shallow soils with low soil moisture. Reduced precipitation also caused greater reductions in stomatal conductance in elevated CO_2 compared to ambient CO_2, associated with altered abscisic acid signaling in the xylem and at the leaf level. These data suggest that root responses to climate change are important in determining whole plant responses and should serve as a target for crop improvement in the coming century.

1022 Understanding the impact of cell walls on the plant abiotic stress response

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The cell wall is an integral element of a plant´s response to abiotic stress. Despite this involvement it is not well understood how changes in wall metabolism and structure are induced by water stress or how they affect the plant´s response to stress in turn. We have studied the response of Arabidopsis seedlings to cell wall damage (CWD) aiming to dissect the mode of action of the cell wall integrity maintenance mechanism. This mechanism monitors and maintains the functional integrity of the cell wall during exposure to abiotic and biotic stress by inducing changes in cell wall and cellular metabolism. Our previous results have shown that CWD induces ectopic lignin, callose, pectin and jasmonic acid production as well as redistribution of carbohydrates and inhibits photosynthetic activity. Genetic analysis suggested that both a turgor pressure sensitive and an independent signalling cascade mediate these effects. Here we will present the results of the functional characterization of these signalling cascades.

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1023 Approaches to improve plant abiotic stress tolerance

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The challenge facing agriculture is to secure the supply of food, feed and fuel in light of increasing world population, competition for arable land, water scarcity and climate change. Improving abiotic stress tolerance will be important to future gains in crop productivity. Despite the plethora of literature examples showing plants with increased "abiotic stress tolerance", the translation of such technologies into crops remains challenging. This presentation will give an overview on the current technology status and future perspectives in Bayer's abiotic stress R&D pipeline relating to enhanced energy use efficiency. It will highlight the benefits and needs of "translational research" to help translate findings from academic to applied research. Furthermore, it will show how collaborations with academic groups can benefit innovation through mode-of-action research and computational biology.

1024 BINDING PROTEIN is a switch that regulates the ER stress sensor/transducer, bZIP28, in response to environmental stress

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BINDING PROTEIN (BiP), a HSP70, is a major chaperone in the ER lumen. BiP binds to the C-terminal tail of the stress sensor/transducer, bZIP28, a membrane associated transcription factor, retaining it in the ER under unstressed conditions. In response to ER stress, BiP dissociates from bZIP28 allowing it to be mobilized from the ER to the Golgi where it is proteolytically processed and released to enter the nucleus. Under unstressed conditions, BiP binds to bZIP28 as it binds to other client proteins, through its nucleotide-regulated, substrate-binding domain. The dissociation of BiP from bZIP28 does not require bZIP28's mobilization to other organelles, because BiP dissociates even when the exit of bZIP28 from the ER or its release from the Golgi is blocked. BiP1 or BiP3 binds bZIP28, and when BiP1 is overexpressed it inhibits the mobilization of bZIP28 from the ER in response to stress. A truncated form of bZIP28, eliminating most the C-terminal tail to which BiP binds, is not retained in the ER under unstressed conditions, but constitutively relocates to the nucleus. BiP binding sites in the C-terminal tail of bZIP28 were identified in a phage display system. BiP was found to bind to intrinsically disordered regions on bZIP28's lumen-facing tail. Thus, the dissociation of BiP from the C-terminal tail of bZIP28 is a major switch that activates the organelle-to-organelle translocation of bZIP28 and triggers the unfolded protein response (UPR) in plants.

1025 Abiotic stress tolerance in 138 barley accessions tested in the future Nordic climate

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Climate change is progressing fast, why the development of high yielding cultivars suitable for the future growth environment is vital. We have screened 138 spring barley accessions in the RERAF phytotron under scenarios representing the climate in Northern Europe around year 2075. The abiotic factors; temperature, [CO_2] and [O_3] were constantly elevated in single factor treatments, and in a more realistic doublefactor treatment with temperature and [CO_2]. Temperature was elevated by 5°C to 24°/17°C (night/day), [CO_2] was doubled to 700 ppm and [O_3] was 100-150 ppb; as control was present Danish summer conditions (19°/12°C (night/day), 385 ppm [CO_2]. All climate scenarios were provided the same amount of water. The material screened included landraces, old and modern Northern cultivars in addition to lines from Nordic breeding companies. The +5°C treatment reduced the yield by about 50% in average and the elevated [CO_2] treatment increased yield by about 15%. No change was found when spring barley was grown under elevated [O_3]. In the doublefactor treatment, the yield stimulating effect of elevated [CO_2] was not able to counteract the reductions in yield caused by the +5°C, as the grain yield in the doublefactor treatment was reduced by about 30%. In general the reduced yield was caused by decrease in seed number and not amount of ears. The same trends were found for biomass as for yield, but the biomass was generally less affected than the yield. Accessions with static and dynamic yield stability were also identified. Based on the results an array of accessions has been selected to test in extreme event scenarios, where we e.g. explore the phenotypic and molecular response to a heat wave.

The research was funded by the 'Sustainable Primary Production in a Changing Climate' network under NordForsk, http://www.risoe.dtu.dk/nordforsk.aspx.

The RERAF phytotron, http://www.increase-infrastructure.eu/Experimental_sites/RERAF_DK.aspx

1026 Regulatory and Functional Changes in *SOS1* Contribute to the Extreme Salt Tolerance of *Eutrema salsugineum*

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Understanding how salt tolerant species have adapted to salinity will be critical for improving crop growth in saline soils. *Eutrema salsugineum* (Eutrema) is a salt-tolerant relative of the salt-sensitive model species *Arabidopsis thaliana* (Arabidopsis) and the agronomically important *Brassica* species. *SALT-OVERLY-SENSITIVE1* (*SOS1*) encodes a Na^+/H^+ antiporter that is required for growth in NaCl in both Arabidopsis and Eutrema. To determine whether evolutionary changes in *SOS1* have contributed to Eutrema's adaptation to salinity, we characterized *SOS1* regulation and function in the two species. When both genes are expressed under the control of their native promoters in the Arabidopsis *sos1-1* mutant, *EsSOS1* confers greater salt tolerance. To determine whether this was due to differences in *SOS1* regulation or function, we characterized the promoters and coding sequences from the two genes. When their promoters and coding sequences were exchanged, we found that the *EsSOS1* promoter confers greater salt tolerance in the *Atsos1-1* mutant than the *AtSOS1* promoter, regardless of the coding sequence. Analysis of *promoter:GFP* lines indicates that this result may be due to an expanded zone of root expression of the *EsSOS1* promoter compared to the *AtSOS1* promoter. Evolutionary analysis of the protein-coding sequences indicates that *SOS1* is under positive selection in Eutrema, supporting previous results showing that *EsSOS1* confers greater salt tolerance in yeast than *AtSOS1*. Analysis of *Atsos1-1* mutant plants complemented with *SOS1* from either cDNA or genomic DNA indicates an essential role for introns in regulating proper expression and/or stability of both the *AtSOS1* and *EsSOS1* transcripts. Together, these results suggest that changes in both the regulation and activity of *SOS1* contribute to the extreme salt tolerance of Eutrema.

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1027 The RNA-directed DNA methylation pathway regulates the temperature stress response

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Rapid and reversible modifications of the epigenetic status play an important role in the dynamic response of the genome to changing environmental conditions. To test for a mechanistic involvement of epigenetic regulation in heat stress responses, we analyzed the heat tolerance of mutants defective in DNA methylation, histone modifications, chromatin remodeling, or siRNA-based silencing pathways and found that the RNA-directed DNA methylation (RdDM) pathway, involved in siRNA biogenesis and in siRNA-mediated transcriptional gene silencing, is crucial for basal heat tolerance.
Subsequently, we studied the role of this epigenetic pathway in temperature-dependent regulation of global gene expression and found that the transcriptional response to temperature stress, at least partially, relies in a time-dependent manner on the integrity of the RNA-directed DNA methylation pathway. Detailed analysis of novel RdDM-regulated, stress-responsive loci identified several possible mechanisms of how transposons can control the expression of protein-coding genes during heat stress which we will present on this meeting.

1028 *Arabidopsis* Glutamate Receptor Homologs Regulate Ca^{2+} Homeostasis and Signaling

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Plasma membrane Ca^{2+} channels control cytosolic free Ca^{2+} concentration ($[Ca^{2+}]_i$) and play essential roles in diverse cellular processes. However, their molecular identity remains largely elusive in plants. Higher plants possess a family of proteins (GLR) that have been proposed to function as ligand-gated Ca^{2+} channels based on their structural similarity to animal ionotropic glutamate receptors, and little is known about their electrophysiological properties and cellular functions. Using Ca^{2+} imaging-based expression and patch-clamping analyses, we found that *Arabidopsis* GLR homologs form Ca^{2+}-permeable non-selective cation channels in the plasma membrane. Loss-of-function mutations in these *GLR* genes conferred low basal cytosolic Ca^{2+} levels as well as defects in multiple Ca^{2+}-regulated processes in plants. Our findings provide the direct *in vitro* and *in vivo* evidence that two GLRs form Ca^{2+} channels in the plasma membrane and govern $[Ca^{2+}]_i$ homeostasis.

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1029 Functions of the Ca^{2+} decoding CBL-CIPK signaling network in mediating and enhancing abiotic stress responses

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Calcium serves as a critical messenger in many adaptation and developmental processes including light and abiotic stress responses. Cellular calcium signals are detected and transmitted by sensor molecules such as calcium-binding proteins. In higher plants, calcineurin B-like (CBL) proteins and CBL-interacting protein kinases (CIPKs) represent important relays in calcium signaling during abiotic stress responses. In Arabidopsis, 10 CBL-type calcium sensor proteins form an interaction network with 26 CIPKs. The results of our investigation of the sub-cellular localization of all CBLs from Arabidopsis suggest that CBL/CIPK complexes can simultaneously decode distinct calcium signals emanating from different compartments. Preferential complex formation of individual CBLs with defined subsets of CIPKs appears to be one of the mechanisms generating the temporal and spatial specificity of calcium signals in plant cells.
Research during the past years has uncovered important roles of defined CBL-CIPK complexes in response to abiotic stresses like salt and drought stress and in regulating uptake of essential ions like potassium and nitrate. Moreover, several plasma membrane localized ion transporters and channels have been identified and characterized as targets of CBL-CIPK complexes.

Here we will report the identification of novel CBL-CIPK target proteins and will provide details how these calcium regulated signaling modules contribute to establishing abiotic stress tolerance. Examples will involve the regulation of stress induced ROS production by CBL-CIPK mediated modulation of NADPH oxidase activity. Moreover, we will present results of a combinatorial genetics transformation approach in which novel synthetic combinations of CBL and CIPK transgenes enhance plant's drought and salt tolerance.

1030 Vitamin E enriched Transgenic *Brassica juncea*: Sustainable Production Under Multiple Stress Conditions

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Alpha (α)-tocopherol, the biologically most active form of vitamin E, is a major antioxidant that bulwarks the cells against oxidative damage. It constitutes a small fraction of the total tocopherol pool in most oilseed crops. We generated transgenic (TR) *Brassica juncea* plants with ~6 fold higher α-tocopherol levels compared to the wild type (WT) plants by overexpressing γ-tocopherol methyl transferase. This enzyme catalyzes a rate limiting step in the α-tocopherol biosynthetic pathway. To better understand the roles of different tocopherol forms in plants we compared the performance of TR plants under conditions of abiotic stresses induced by NaCl (salinity), $CdCl_2$ (heavy metal) and mannitol (drought). This resulted in an increase in total tocopherol levels in both the WT and TR plants. Seed germination, shoot growth, and leaf disc senescence showed that TR *B. juncea* had enhanced tolerance to these stress and that induced by high temperature and methyl viologen. Damage caused by the induced stress was lower in TR plants compared to WT plants as assessed by their higher relative water content, lower MDA and H_2O_2 accumulation and lower electrolyte leakage. Lesser superoxide and H_2O_2 accumulation was observed in TR seedlings exposed to these stress. Enhanced levels of different antioxidant enzymes and molecules were present in TR plants when compared to WT plants under similar stress. Analysis of chlorophyll a fluorescence rise kinetics showed that there were differential effects of the applied stress on different sites of the photosynthetic machinery. These effects were found to be alleviated in TR plants. Thus, biofortification by metabolic engineering not only offers sustainable alternative to vitamin E supplementation for improvement of human health but also plays an important role in the alleviation of various environmental stress conditions in plants.

1031 Overexpression of Tea Gene *CsDFR* and *CsANR* in Transgenic Tobacco Induces Early Flowering & Confers Biotic and Aluminum Stress Tolerance

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Flavan-3-ols contribute significantly to flavonoid content of tea (*Camellia sinensis* L.). Dihydroflavonol 4-reductase (DFR) and anthocyanidin reductase (ANR) are known to be key regulatory enzymes of flavan-3-ols biosynthesis. In this study, we have generated the transgenic tobacco overexpressing individually tea genes *CsDFR* and *CsANR* to evaluate their influence on flavan-3-ols, antioxidant potential, biotic and aluminum stress tolerance.
The transgenic lines of *CsDFR* and *CsANR* produced early flowering and better seed yield. Root morphological/architectural features were also improved in *CsDFR* and *CsANR* overexpressing tobacco plants relative to control tobacco plants.
Flavan-3-ols such as catechin, epicatechin, epicatechingallate and epigallocatechin were found to be increased in transgenic lines. The free radical scavenging activity of *CsDFR* and *CsANR* transgenic lines was improved. Oxidative stress was observed to induce lesser cell death in transgenic lines compared to control tobacco plants. Transgenic tobacco overexpressing *CsDFR* and *CsANR* provided resistance against feeding by tobacco leaf cutworm *Spodoptera litura*. The transgenic lines of *CsDFR* and *CsANR* showed also improved root growth under toxic aluminum conditions. The results suggested that the overexpression of *CsDFR* and *CsANR* cDNA in tobacco may be positively involved in improving flavan-3-ols content and antioxidant potential. These attributes in transgenic tobacco ultimately lead to improve their growth, development, biotic and aluminum stress tolerance. This would provide protection to plants grown under adverse environmental conditions and prove to be an effective approach for sustainable agriculture.

This work was supported by grants from the Council of Scientific and Industrial Research (CSIR), Government of India under NMITLI program (TLP003).

1032 Molecular Responses of Maize to Submergence

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Little is known regarding the physiological and molecular responses of maize to transient submergence. In rice, group VII ethylene responsive transcription factors (G7ERFs) modulate antithetical strategies for submergence survival [Xu et al. 2006; Hattori et al. 2009]. The rice gene SUBMERGENCE1A (SUB1A) confers a quiescence strategy, whereas the SNORKEL1/2 genes confer an escape strategy. In Arabidopsis, G7ERFs are regulators of oxygen deprivation survival, a stress endured during flooding [Licausi et al., 2010; Hinz et al., 2010; Gibbs et al., 2011; Licausi et al., 2011]. Examination of the B73 maize reference genome identified 14 G7ERFs. Maize plants at the four-leaf stage were submerged for up to three days and monitoring of shoot mRNA levels by qRT-PCR confirmed the up-regulation of three genes that encode SUB1A-like ERF (*Sub1-like ERF* [Sbl]1-3), along with the low-oxygen marker gene *Alcohol Dehydrogenase1* (*Adh1*). Increased accumulation of *SBL1*, *SBL2*, *SBL3* and *ADH1* transcripts was also confirmed in submerged coleoptiles of pre-germinated maize seeds. The Arabidopsis G7ERFs are unstable in well-aerated tissue, as they are substrates of the N-end rule pathway of targeted proteolysis. The N-terminal cysteine of these proteins is necessary for their oxygen-mediated turnover [Gibbs et al., 2011; Licausi et al., 2011]. Oxygen-mediated turnover of G7ERFs can be recapitulated in a rabbit reticulocyte in vitro translation assay. Using this assay, we confirmed that maize G7ERFs are substrates of N-end rule degradation. Further investigation of the role of maize G7ERF family members is underway.
This research was supported by the US National Science Foundation grant MCB-1021969 and Pre-doctoral Fellowship DGE-0813967.

1033 The proteome response of *Hordeum spontaneum* to long-term salinity stress

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Hordeum spontaneum (wild barley) is a good gene source to improve salt tolerance in barley because it rapidly hybridizes and recombines with barley cultivars. Proteomics can assist in identifying proteins associated with a certain environmental or developmental signal. We employed a proteomic approach to understand the mechanisms of plant responses to salinity in a salt tolerant accession of *H. spontaneum*. At the 4-leaf stage, wild barley plants were exposed to 0 (control treatment) or 300 mM NaCl (salt treatment). The salt treatment lasted 3 weeks. Total proteins of leaf 4 were extracted and separated by two-dimensional gel electrophoresis. More than 500 protein spots were reproducibly detected. Of these, 29 spots showed significant differences between salt treatment and control. Using MALDI-TOF-TOF MS, we identified 29 cellular proteins, which represented 16 different proteins. These were classified into six categories and a group with unknown biological function. The proteins identified were involved in many different cellular functions. Three spots were identified as unknown proteins; searching in the NCBI database revealed that there was a 71% match with clathrin assembly protein putative [*Ricinus communis*], a 67% match with actin binding protein [*Zea mays*], and a 66% match with phosphatidylinositol kinase [*Arabidopsis thaliana*]. Other proteins identified included ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco), oxygen-evolving enhancer protein (OEE), photosystem II reaction center W protein (Psbw), ribosomal proteins, chloroplast RNA binding protein (ChRBP), superoxide dismutase (SOD), malate dehydrogenase (MDH), thioredoxin h (Trx), nucleoside diphosphate kinase (NDPK), profilin, translationally-controlled tumor protein (TCTP), polyamine oxidase (PAO) and universal stress protein family (USP).

2001 WITHDRAWN

2002 Leaf hydraulic conductance is maintained during drought in soybean

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As atmospheric greenhouse gas concentrations rise, climate change is causing more frequent extreme weather events, with the potential to challenge productivity in natural and agricultural ecosystems worldwide. In the Midwestern United States, drought events are projected to become more frequent as precipitation becomes more irregular. This could have a major impact on agricultural productivity in the US, where over 72 million acres are planted in soybean. Leaf hydraulics play a large role in both plant productivity and ecosystem hydrologic cycles, as up to 80% of resistance to water flow through the plant occurs in the leaves. However, the responses of leaf hydraulic conductance (K_{leaf}) to drought are not well understood. We hypothesized that K_{leaf} would decrease in drought-stressed soybean, accompanied by decreases in leaf water potential and transpiration. Drought was simulated in growth chambers and in the field by withholding water, and K_{leaf} was measured with the evaporative flux method. In experiments with both pot-grown and field-grown soybean, K_{leaf} did not change in drought-exposed plants, even as leaf water potential decreased. This suggests that leaf hydraulic pathways function to maintain stomatal conductance at the expense of leaf water status in soybean, rather than playing a protective role in leaf water status. The lack of hydraulic response to soil drying could help maintain productivity during periods of mild drought but may not offer enough protection from hydraulic failure during the types of intense droughts that soybean crops are likely to face in the coming decades.

2003 Analysis of *CBL10* Gene Duplication in Halophyte *Eutrema salsugineum*

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Soil salinity is one of the major abiotic stresses affecting agricultural productivity, limiting the growth and yield of most crop species which are unable to tolerate even modest levels of salinity (glycophytes). Genetic variability for salt tolerance exists with some plants (halophytes) adapted to environments with high salinity. Understanding mechanisms underlying halophyte adaptation will lead to effective strategies to improve crop salt tolerance.
The CALCINEURIN B-LIKE10 (CBL10) calcium sensor was identified as a component of salt signaling in the glycophyte *Arabidopsis thaliana* (Arabidopsis) based on hypersensitivity of the *cbl10* mutant (*Atcbl10*) to salt. AtCBL10 functions in a pathway with the SALT-OVERLY-SENSITIVE2 (SOS2) protein kinase to regulate the activity of the SOS1 Na^+/H^+ exchanger and reduce cellular sodium accumulation. *Eutrema salsugineum* (Eutrema), a halophytic relative of Arabidopsis, has two *CBL10*-like genes (*EsCBL10a* and *EsCBL10b*). To determine if *CBL10* gene duplication has contributed to Eutrema's greater salt tolerance, comparative functional analyses of the genes from the two organisms is underway. Like *AtCBL10*, *EsCBL10b* is expressed at a higher level in shoots than roots, while expression of *EsCBL10a* is expanded in roots. Expression of *EsCBL10a* or *EsCBL10b* with *AtSOS2* and *AtSOS1* in a salt-sensitive yeast strain indicates that *ECBL10b* confers greater salt tolerance than either *AtCBL10* or *EsCBL10a*. Analyses of Eutrema lines with reduced expression of the two *EsCBL10* genes individually and in combination, together with studies to determine the ability of these genes to complement the *Atcbl10* mutant salt-sensitive phenotype are underway. Results from these experiments will provide important insight into the functions of the two Eutrema genes and identify mechanisms that underlie their contribution to salt tolerance.

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2004 Elevated CO_2 induced transcriptional reprogramming of respiration and a stimulation of dark respiration as *Arabidopsis thaliana* leaves transition from sinks to sources

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A mechanistic understanding of respiration is critical to elucidating the relationship between increased atmospheric CO_2 concentration ($[CO_2]$) and plant function because this process provides the carbon skeletons and energy needed for growth and maintenance. Greater abundance of transcripts encoding the respiratory pathway (glycolysis, TCA cycle, mitochondrial electron transport) have been observed in mature Arabidopsis, rice and soybean leaves grown at elevated $[CO_2]$. This suggests transcriptional reprogramming of metabolism underpins greater rates of dark respiration and greater mitochondrial numbers in leaves of plants grown at elevated $[CO_2]$. In addition, within hours of mature Arabidopsis leaves being exposed to elevated $[CO_2]$, changes in gene expression in younger expanding leaves which were not exposed to the elevated $[CO_2]$ treatment have been observed, suggesting systemic signaling. This study tested the hypothesis that elevated $[CO_2]$ induces transcriptional reprogramming and stimulation of respiration throughout leaf development starting with the primordia and continuing through key phases of cell division and leaf expansion. Beginning in early leaf expansion, elevated CO_2 increased glucose concentration and caused transcriptional reprogramming of respiration. These effects occurred prior to detectable starch accumulation or treatment effects on sucrose concentration. Stimulation of dark respiration from elevated $[CO_2]$ was only distinguishable as leaves transitioned from rapidly expanding (sink) tissues without starch storage to mature (source) tissues that stored more starch in the elevated $[CO_2]$ treatment. Current analysis is examining the global transcriptional response to determine whether specific gene expression networks are altered by a constant stimulation of photosynthetic carbohydrate supply in elevated $[CO_2]$.

2005 Field testing of transgenic cotton expressing Arabidopsis ABA INSENSITIVE5 (ABI5) and B3-domain RELATED TO ABI3/VIVIPAROUS1 (RAV) transcription factors

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We conducted field trials for pro35S:ABI5 and pro35S:RAV transgenic cotton under the most extreme heat and drought conditions on record. AtRAV1 and RAV2 overexpression resulted in an average 9% increase in fiber length at higher nodes (10-12) and 5% increase at lower nodes (6-9) with improved fiber maturity and uniform fineness under both non-stressed and extreme abiotic stress conditions. Plant mapping in independent RAV overexpressing cotton lines showed that the higher nodes bear the maximum boll mass due to a one week delay in the onset of flowering and an increased duration of flowering (late cut-out), which correlated with lower transcript levels of *Flowering Locus T* (*GhFTL*). The yarn spun from RAV cotton lines showed improved tensile strength and uniformity under well watered conditions as well as deficit irrigation, whereas the wild type fiber from drought-stressed plants completely failed in this real world application. ABI5 transgenic cotton lines had ~6% higher gin turnout (% fiber in the boll). ABI5 and RAV cotton lines has bigger root mass, increased leaf area, delayed senescence, and lower stomatal conductance under deficit irrigation conditions leading to higher water use efficiency (WUE) throughout extended drought stress treatments, which we hypothesize resulted in photosynthate being channeled to sink tissues during flowering and fiber development. Taken together these value-added traits suggest a "less-stressed" phenotype and are consistent with studies showing RAVs function in reactive oxygen species (ROS) scavenging. We have evidence from greenhouse drought stress experiments that "stacking" ABI5 and RAV transgenic events provides a synergistic degree of drought avoidance than do single gene transgenics, substantiated by RNA blots showing reduced transcript abundances for *GhAdhA* and other stress-inducible marker genes, and increased expression of *Glutathione S Transferase and* other genes involved in ROS scavenging. We are testing the hypothesis that improved fiber qualities in these RAV cotton lines is due to altered ovule expression of *GhMYB25-Like*, *GhRESPONSIVE TO DROUGHT-Like1* and increased levels of peroxisome biogenesis genes *PEROXINs, COPINE/BONAZAI, and GA-Stimulated Transcript (GAST-Like)*. Drought avoidance and improved fiber traitsof RAV transgenics could benefit dryland cotton agriculture, a reality for sustainability in the arid southwest US.

2006 The Arabidopsis CALCINEURIN B-LIKE10 protein mediates flower development during plant growth in saline conditions

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By 2050, agricultural productivity must increase by 70% to feed the projected nine billion people worldwide. An increase of this magnitude will require cultivation of crops on marginal soils where build-up of salt (salinity) is a major challenge. Therefore, identifying the pathways that enable plant growth in salinity is a priority for plant biology. To identify genes involved in responses to salinity, a mutagenesis screen was performed in *Arabidopsis thaliana* to isolate mutants with altered salt sensitivity. Characterization of the proteins led to the identification of the Salt Overly Sensitive (SOS) pathway which functions to remove sodium from the cytoplasm preventing its toxic effect. In this pathway, perception of sodium triggers an influx in cytosolic calcium which is perceived by the SOS3 (roots) and CALCINEURIN B-LIKE10 (CBL10, leaves) calcium binding proteins, and leads to their interaction with and activation of the SOS2 protein kinase. SOS2 phosphorylates the SOS1 sodium-proton exchanger to transport sodium out of the cell. While previous research has focused on the pathways operating in leaves and roots, salinity also affects reproductive development. We show that, in addition to its role in leaves, the CBL10 calcium sensor protects flower development during growth in salinity, but does so independently of the SOS pathway. In flowers, successful fertilization requires the coordinated development of stamens and pistils. Stamens must elongate and dehisce to release pollen onto the stigma while the pistil prepares to receive the pollen and promote growth and targeting of the female gametophyte. Salinity disrupts these processes in the *cbl10* mutant; stamens are short and anthers do not dehisce and wild-type pollen tube growth is arrested in *cbl10* pistils.

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2007 WITHDRAWN

2008 Risk-taking plants: Anisohydric behavior as a stress-resistance trait

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Water scarcity is a critical limitation for agricultural systems. Two different water-management strategies have evolved in plants: isohydric and anisohydric. Isohydric plants maintain a constant midday leaf water status [i.e., relative water content (RWC) and water potential] by reducing stomatal conductance as necessary to limit transpiration. Anisohydric plants have more variable water statuses and keep their stomata open and photosynthetic rates high for longer periods, even in the presence of decreasing leaf RWC and water potential. This "risk-taking" strategy can be beneficial when water is abundant, as well as under moderately stressful conditions, however, not under intense drought conditions. Our study explored fundamental questions about the molecular, cellular and root-shoot mechanisms controlling these behaviors. We demonstrated the role that specific aquaporins (AQPs) play in plant water homeostasis by showing how they can make an isohydric tomato plant act in an anisohydric manner, resulting in significantly improved yields in field trials. Using tissue-specific (bundle sheath, mesophyll and guard cell) targeted artificial micro RNA (amiRNA), we were able to down-regulate the expression of the whole AQPIP1 subfamily. The results of this down-regulation support our hypothesis concerning the role of AQPs in the regulation of plant hydraulics, as well as our hypothesis that the leaf bundle sheath acts as an active hydraulic xylem-mesophyll barrier to control leaf water status.
Despite the large number of attempts to improve the abiotic stress tolerance of commercial crops, little progress has been made, emphasizing the complexity of the different traits involved.
A "calculated risk-taking" trait that could be introduced into plants to confer upon them the ability to engage in *dynamic* anisohydric-isohydric behavior regulated by environmental conditions and the plants' own developmental stage is discussed.

2009 Effect of Cd, As, Cu and NaCl on lettuce (*Lactuca sativa*) growth parameters

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In this work the response of lettuce **(***Lactuca sativa***)** to stress induced by several metals, As and NaCl was evaluated.

In the germination and growth assays Cd, Cu, Mn, Zn, As and NaCl (0, 5, 10, 25, 50, 100, 150, 250, 350 and 500 microM) was applied separately for assessing the germination rate and growth for 2 weeks. The germination rate was affected only by Cu, Zn and NaCl. Biomass and tolerance index were affected at the higher concentrations of all elements and NaCl.

In irrigation assays, solutions containing Cd, Cu, As and NaCl were applied separately. The number of leaves, biomass, dry matter content, chlorophyll content and mineral composition were determined. The application of Cd and NaCl led to a decrease in the number of leaves and in all experiments there was a significant reduction in biomass and chlorophyll in contaminated plants. The effect of the metals and NaCl on the uptake of other essential elements (Na, K, Mg, Zn, Mn, Fe, Cu and Ca) was also studied. The application of NaCl led to an increase in dry matter content and the plants were visibly affected. There was accumulation of all applied elements and of Na in all the plants growing in the contaminated medium, exceeding european legal limits for Cd and As, so their intake can be a hazard to human health.

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2010 *AtCYP710A1* gene-mediated stigmasterol production plays a role in imparting abiotic stress tolerance in *Arabidopsis thaliana* possibly by regulating membrane integrity

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Plasma membrane is one of the first parts of plant cell affected by abiotic stresses and hence maintenance of membrane integrity is one of the traits responsible for abiotic stress tolerance of plants. Membrane stability has been known to exhibit positive influence on various yield attributing physiological traits that condition plant responses to abiotic stresses such as water use efficiency and osmotic potential. Stigmasterol and sitosterol, important sterols present in Arabidopsis plants, are known to influence permeability and fluidity characteristics of plasma membrane and other organellar membranes. We had previously [Plant Physiology, 2012; 158, 1789-1802] demonstrated that *Atcyp710A1* gene, that catalyzes conversion of sitosterol into stigmasterol, plays a role in influencing plasma membrane permeability and thereby regulates leakage of cellular nutrients and water into apoplast. In the current study we demonstrate the relevance of this gene in imparting various abiotic stress tolerances in Arabidopsis. *Atcyp710a1* mutant plants exposed to low temperature stress showed reduction in biomass compared to wild-type plants at the end of stress period. Consistently, *AtCYP710A1* overexpressor plants exposed to low temperature showed higher biomass. Also, *Atcyp710a1* mutant plants showed up to 70% membrane leakage when exposed to high temperature stress whereas, wild-type plants showed only 50% leakage under stress. Further, the results pertaining to characterization of *Atcyp710a1* mutant and *AtCYP710A1* overexpressor plants for various other physiological and biochemical parameters will be presented. In addition to low and high temperature stress, we will also highlight the responses of *Atcyp710a1* mutant and *AtCYP710A1* overexpressor plants to various other abiotic stresses. Conclusively, our results showed that *Atcyp710A1* gene contribute in part to low temperature tolerance and thermotolerance.

2011 The effect of drought on the growth processes in the maize leaf

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One of the most fascinating open questions in biology is how organ and organism size is controlled. The maize leaf offers an excellent experimental system to study growth, due to the linear organization of cell division and expansion along its longitudinal axis: active cell divisions occur at the base of the leaf, and as the distance from the base increases cells will cease division and start expanding until they reach their mature cell size.
Recently, we found that bioactive gibberellins (GAs) peaked near the transition, and that the balance between GA biosynthesis and degradation determines the position of the transition. Additionally, we showed the functional importance of this transition for organ size since boosting GA biosynthesis in a GA20-oxidase overexpressing line and blocking GA production in the *dwarf3* biosynthetic mutant resulted in a shift of this transition and thus in the number of dividing cells, resulting in larger and smaller leaves, respectively.
Besides genetic perturbations, we found that a mild drought treatment reduces the growth of the fourth leaf by shifting the transition more basally, resulting in fewer dividing cells. The presented work will show how mild drought affects the transcriptome and hormonome specifically in the division, transition and expansion zone within the growth zone of the maize leaf. This analysis provides insights into the specific effects of drought on the different growth processes in the maize leaf and will allow to design novel strategies towards yield stability.

2012 Effects of Inorganic Fertilizer Applications on Yield Response under Salinity for Spinach (*Spinacia Oleracea*) and Celery Root (*Apium Graveolens)*

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Effects of Si and KNO_3 applications on plant yield parameters and chemical content of spinach and celery root were studied under the different salt levels. Silica has been reported to increase salt tolerance and nitrogen requirements are dependent on salinity.The experiment was conducted using a completely randomized factorial experimental design with 2 crops (spinach and celery root), 4 different EC levels (1, 4, 8 and 12 dS/m), 3 different Si applications (0, 2 and 4 mM) and 3 different KNO_3 applications (0, 20 and 40 mM) and 3 replications for a total of 216 pots. NaCl, $CaCl_2$ and $MgCl_2$ solutions were used as irrigation water to adjust the EC of soil. Silicon and potassium nitrate were applied to the pots before planting seeds. After a 90 day growing period, plants were harvested; vegetative parameters such as plant length, wet root weight and dry root weight as well as micro and micro nutrient contents were analyzed. At the end of the study, EC levels were compared, the highest plant dry weights were obtained from the 12 dS/m at 2mM Si treatment and 20 mM KNO_3 doses. Comparing to the control, there was a 6% increase in dry weight, 44% increase in chlorophyll content of spinach, and 24% increase in dry weight and 31% increase in chlorophyll content of celery root at EC 12 dS/m. An increase was seen in the content of Ca, K, Mg, Na, and Mn while there was a decrease in B, Fe and Cu of both spinach and celery root under the same level of EC (12 dS/m) with application of both Si and KNO_3. Increasing salinity stress causes a decrease in yield and yield parameters of both plants varied with Si and KNO_3 application with different apparent salinity tolerance. Addition of Si and KNO_3 to the soil provides some statistically important contribution to yield response under salinity.

2013 Control of gene expression mediated by epigenetic modulation of transposable elements in response to stress

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Water deficit is a condition in which the homeostasis of plants is abolished. Because the sedentary life of these organisms, different strategies to cope with this stressful condition have been selected along evolution. This response includes heritably gene expression modifications in the absence of changes in DNA sequence, formerly known as epigenetics. Some molecular analyses have shown that the regulation of the activation-inactivation of transposable elements (TE) is associated with epigenetic mechanisms suggesting that these genetic elements have played an essential role not only in plant adaptation but also in their adjustment to environmental stress (e.g. Naito K, et. al., *Nature*. 461: 1130-4, 2009; Ito H, et. al., *Nature*. 472:115-9, 2011). In this study, we asked whether the expression of water deficit responsive genes adjacent to TE is influenced by the TE epigenetically modulated expression and if this expression is altered by water deficit and other stressful conditions. Mutant phenotypes, gene expression patterns and other genomic and epigenetic approaches allowed us to identify candidate genes in *Arabidopsis thaliana*. The dependence of the expression of the identified genes from TE epigenetic modulation was experimentally tested under optimal and stress conditions. Results will be discussed.

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2014 WITHDRAWN

2015 Molecular characterization of cytochrome P450 reductase isoforms and monoxgenases in corroboration with tissue-specific chemoprofining and gene expression analysis in *Withania somnifera* (L.) Dunal: An Indian ginseng

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Withania somnifera (ashwagandha) is immensely reputed for its therapeutic importance since ancient times and is well documented in Ayurveda and Unani systems of medicine. Recent pharmacological findings have demonstrated its multifarious therapeutic potential particularly in various types of cancers and as an immunomodulator. Medicinal properties of *W. somnifera* are mainly attributed to C-26 and C-28 steroidal lactones called withanolides. Substantial pharmacological activity has been accredited to four main withanolides namely withanolide A (WS-1), withanone (WS-2) and withaferin A (WS-3), withanolide D (WS-D). Long gestation period between planting and harvesting for extraction from natural sources and chemical synthesis are time consuming and often result in low yield of metabolites. It is more important to identify the pathway genes involved in secondary metabolite biosynthesis and engineer them in heterologous microbial hosts for industrial up-scaling. In pursuance of intended targets, we successfully cloned two divergent isoforms of cytochrome P450 reductase (CPR1 & CPR2) and three P450 monoxygenases (CYP98, CYP76 & CYP710) from *W. somnifera*. These contain an open reading frame of 2058, 2142, 1536, 1547, 1506 bp encoding 685, 711, 511, 517 and 501 deduced amino acids respectively. All genes were cloned into pGEX4T-2 and transformed into *E.coli* BL21 (DE3) for heterologous expression and protein purification. Tissue-specific (leaf, stalk root, flower and berry) expression profiles of cloned genes were studied by quantitative real-time PCR. CPR1 transcript levels were prominent in roots while as CPR2, CYP98, CYP76, and CYP710 showed optimum expression in leaves. Least expression was observed in berries which presented undetectable levels of CYP98. Tissue-specific chemoprofiling was performed based on three key withanolides namely WS-1, WS-2 and WS-3 using High Performance Liquid Chromatography (HPLC).Leaf-specific higher transcript levels of cloned pathway genes corroborated well with accumulation of higher content of withanolides in leaves. Characterized genes belong to largest gene superfamily P450 monoxygenase which are mainly involved in various circuitries of secondary metabolite synthesis. P450 monoxygenases require cytochrome P450 reductase for the supply of electrons to catalyse the reaction. The prospection of these genes is a key requisite for intended pathway engineering.

2016 Molecular Mechanisms Mediating CO2 Control of Transpiration and Stomatal Development

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The continuing rise in atmospheric CO2 causes two distinct gas exchange responses: closing of stomatal pores and down-regulation of stomatal development. Although these responses globally affect CO2 influx into plants, transpiration, water use efficiency and leaf heat stress, the CO2 signal transduction mechanisms have remained largely unknown. We have recently characterized CO2-binding carbonic anhydrases, the SLAC1 anion channel, a protein kinase and calcium signaling mechanisms that are essential for triggering and transducing rapid CO2-induced stomatal closure (Hu et al., 2010 *Nature Cell Biol.* ; Young et al., 2006 *PNAS*; Vahisalu et al., 2008 *Nature*; Negi et al., 2008 *Nature*; Xue et al., 2011 *EMBO J.*). New genetic loci and mechanisms that mediate CO2-induced stomatal closure will be presented. However, how CO2 is perceived for CO2 down-regulation of the stomatal development machinery is not known. Currently one mutant, *hic*_ENREF_1, has been reported that impairs CO2-control of stomatal development (Gray et al., 2000 *Nature*). In recent research we have identified three mutants that give rise to a mechanistic framework for CO_2 input into the stomatal development machinery. These mechanisms also regulate CO2-dependent plant gas exchange. The results of these analyses and phenotypes of genes that mediate CO2-control of stomatal development will be presented along with a model for CO2 signaling input to the stomatal guard cell differentiation machinery.

2017 WITHDRAWN

2018 Defining the role of epicuticular leaf wax in heat tolerance in wheat in a TAM 111 X TAM 112 RIL population

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High temperature and drought are major constraints to wheat production. Collectively or individually heat and drought are the primary constraints to yield in wheat on a global basis. However, there are certain genotypes that tolerate high heat and drought through various adaptations such as high leaf wax content, leaf rolling and efficient root structure. We hypothesize that high leaf wax content is directly correlated to heat and drought tolerance in wheat in terms of yield and quality stability. For this study, a RIL population derived from TAM 111 and TAM 112 were grown in controlled greenhouse and multiple field locations. In the greenhouse at 10 days after pollination (DAP) plants were subjected to a three-day 38°C/18°C day/night heat stress treatment. Both in greenhouse and field flag leaf and glumes were sampled at 10 DAP for wax analysis. The samples collected for wax content, canopy temperature (CT), yield and other quality components are being analyzed for co-association between quantitative trait loci (QTL) regulating these phenotypic traits. This will help to determine the influence of leaf wax on the maintenance of yield performance during heat and drought stress.

2019 Molecular investigations of thermo periodic inhibition of stem elongation in petunia plants

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The growth hormone gibberellin (GA) has been suggested as the mediator of temperature effects on plant growth. In *Pisum sativum* reduced levels of GAs under temperature drop were regulated by transcriptional stimulation of GA deactivation gene G*A2-oxidase*.
In our study we investigated the thermo periodic inhibition of stem elongation in ornamental plant *Petunia x hybrida* by using a combination of light and temperature (drop) strategy. Four Petunia varieties ('Famous Red Fire', 'Famous Blue', 'Famous Electric Purple' and 'Famous White') were treated with 12h light during the day time (06-18h) and during the night time (22-02h) at an averaged daytime temperature of 20°C. The drop took place in combination with the night time exposure (22-02h). This temperature strategy was compared with a control without drop/light and the same averaged day time temperature, and duration of exposure (06-22h).
Expression levels of four different *GA2ox* genes, *PhGA2ox-1*, *-2*, *-3* and *-4*, were investigated in the shoot apex of treated Petunia varieties. To correlate the *PhGA2ox1* and *-2* mRNA levels with internodes length, expression were quantitatively analysed by qRT-PCR. *PhGA2ox-1* and *-2* expression in 'Famous Red Fire' and 'Famous Electric Purple' increased 3 hours after temperature drop (20°C to 6°C) in addition with night time exposure and decreased after the drop treatment at 20°C in darkness.
Expression levels of *PhGA2ox-1* and *-2* in the shoot apex of 'Famous Red Fire' and 'Famous Electric Purple' could be correlated with internodes length of both varieties.

2020 The splicing factor SHINY2 is a repressor for stress-inducible gene repression

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Gene regulation is central for plant adaptation to environments. Many plant genes are maintained at inactive state while poised for transcription for rapid response to environmental stresses. How these stress-inducible genes are repressed at normal growth conditions is still not well understood. Here we report the identification of a repressor protein named SHINY2 that is also important for mRNA splicing. The *shiny2* (*shi2*) mutant was isolated from a forward genetic screening for mutations causing elevated expression of the luciferase reporter gene driven by a stress-inducible promoter. *shi2* mutant is more sensitive to ABA in seed germination, exhibits inhibited growth at low temperature, and is hypersensitive to LiCl when compared to the wild type. Map-based cloning of *shi2* identified a mutation in a gene encoding a DEAD box RNA helicase. SHI2 shows high sequence similarity with the yeast splicing factor PRP5 and plays a role in mRNA splicing in Arabidopsis. SHI2 is a nuclear localized protein and contains an activation domain at its C-terminus. 5' capping and polyadenylation site selection of the luciferase transgene are affected by the *shi2* mutation, suggesting that, in addition to mRNA splicing, SHI2 is also involved in other co-transcriptional processes. We propose that SHI2 is a component within a repressor complex stalling at the stress-inducible promoter for gene repression while poised for transcription at normal growth conditions. This repressor complex may include essential components for both transcription and co-transcriptional processes and readily becomes an active transcription complex upon stress treatments.

2021 Heatwaves in a warming world: the effects of an extended, extreme climate event under elevated CO_2

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In 2010 Russia and Eastern Europe experienced a month long heatwave that caused a 40 percent decrease in wheat yields and redrew the maps of temperature records. In 2011 the south east United States experienced 47 days above 37° C which lead to an estimated 5 billion dollar loss. In 2012 Illinois experienced the second hottest July in state history. Nine of the ten warmest years have occurred in the 21st and the IPCC predicts an increase in the number, magnitude and length of extreme heat events in the next century. Along with rising temperatures, the concentration of CO_2 in the atmosphere has been increasing. Elevated CO_2 in the atmosphere lowers plant water usage and stimulates productivity in C_3 crops. By increasing soil moisture reserves and inhibiting the rate of photorespiration, elevated CO_2 may ameliorate yield losses due to heatwaves.
Using F.A.C.E. technology and IR heaters at the Soy FACE research site (Savoy Il, USA) we grew soy beans (*Glycine Max*) under standard agronomic practices and applied an extended heatwave to plants grown under ambient (385 ppm) and elevated (590 ppm) CO_2. The heatwave was two days longer than a usual extreme climate event in central Illinois. Canopy temperatures were elevated 6° C above ambient for five days. The experiment was a split-plot (n=4) design. Two heatwaves were applied during 2012, first to plants in vegetative development (V6), then later to separate plots in reproductive development (R5).
Results from previous heatwave experiments at Soy FACE under ambient CO_2 show yield losses of 10 percent when heatwaves occur at critical developmental stages. To determine the effects elevated CO_2 on heatwaves we measured: leaf level fluorescence and gas exchange, soil moisture, sugar metabolism, yield and ANPP. Preliminary results show that after the first heatwave, there was a 21 percent decrease in biomass in plants grown under ambient CO_2 and a 1 percent increase in biomass in plants grown in elevated CO_2.
USDA

2022 Dissecting the roles of nucleosome occupancy and histone H2A.Z abundance in modulating responses to phosphorus- and/or iron-deficiency in rice

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Phosphorus (P) and iron (Fe) are major limiters of crop productivity due to their low availability in most soils. Large inputs of P fertilizer are required to sustain crop yields world-wide, and because P is mined from non-renewable sources, its depletion is imminent. Fe-deficiency is common in aerobic soils, whereas Fe toxicity afflicts rice grown under flooded conditions. Plants respond to fluctuating P and Fe levels via complex transcriptional regulatory networks. Although chromatin structure plays a major role in controlling gene expression, the chromatin-level mechanisms involved in regulating nutrient homeostasis have not been investigated. We are using genome-wide approaches to identify chromatin-level mechanisms that regulate the uptake, assimilation, and utilization of P and Fe in rice. Illumina sequencing of mono-nucleosomal DNA has revealed genome-wide changes in nucleosome occupancy linked to P- and/or Fe-deficiency. In addition, physiological and gene expression analyses of *Actin Related Protein 6* (*ARP6*)-RNA interference rice lines have shown differential responses to P- and/or Fe-deficiency. ARP6 is a key component of the SWR1 complex, which exchanges canonical histone H2A with the H2A.Z histone variant. Correlations between nucleosome occupancy and H2A.Z abundance, and their possible roles in nutrient homeostasis will be presented. The identification of chromatin-level mechanisms that modulate P- and/or Fe-deficiency responses will provide opportunities for developing crops with improved nutrient use-efficiency, significantly improving global agriculture.

Funding is provided by a Plant Genome Research Program grant from the National Science Foundation (IOS- 1127051).

2023 Genetic basis of salt tolerance in beach morning glory (*Ipomoea imperati*), a wild relative of sweet potato (*Ipomoea batatas*)

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A major limitation affecting the growth and yield of important crops worldwide is the crops' sensitivity to harsh environments, including high salinity in soil. Many crop wild relatives are tolerant to environmental extremes and represent an important genetic reservoir that can be used to improve crop performance in harsh environments. Beach morning glory (*Ipomoea imperati*), a wild relative of sweet potato (*Ipomoea batatas*), can endure low nutrient levels with high concentration of salt. In this study, we initiated transcriptome comparison of beach morning glory plant in salt-treated conditions with an untreated control to identify salt-response genes. This is a foundation study for developing salt tolerant sweet-potato cultivar in the near future.

2024 Dissecting heat stress response signals in plants

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Heat stress can have a detrimental effect on yield production worldwide, causing devastating economical and societal impacts. Elucidating the mechanisms underlying the heat stress response of plant is therefore a high priority for scientific research, and could lead to the development of crops with enhanced tolerance to heat stress. We have revealed different mechanisms of heat stress responses that might function in different tissues or stages in Arabidopsis. The multiprotein bridging factor 1c (MBF1c) was shown to be a key regulator of thermotolerance that functions upstream to SA, ethylene and trehalose signaling in vegetative stage. We further suggested that MBF1c regulates heat stress response of plants by functioning as a transcription factor. Our current research has also uncovered mechanism of systemic acquired acclimation of plants to heat stress. This acclimatory response requires reactive oxygen species (ROS)-dependent long-distance systemic signaling mediated by the respiratory burst oxidase homolog D (RBOHD) protein, an NADPH oxidase located at the plasma membrane. In addition, signals that protect reproductive tissues against heat stress were shown to be induced in plants lacking the cytosolic ROS scavenging enzyme, ascorbate peroxidase 2 (APX2). This heat stress response signal activated by the disruption of APX2 is stage or tissue specific. Such diversity in mechanisms of heat stress responses might be attributed to differences in coordination of signals generated at different cellular compartments.

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2025 Industrial By-products: Stress Factors or Nutrients?

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The reduction of fertilizer's portion has become essential in the crop production by now. One of the reasons for that is during other industrial activities such as by-products are produced in high quality in which the necessary nutrients for plants can be found in a big amount. Besides the high fertilizer prices the use of produced wastes is economically reasonable. Finally, the other reason for the reduction of fertilizer use is that the inappropriate use of the fertilizers may cause environmental pollution. During the different industrial and production procedures and probably during everyday use some by-products and wastes are generated which have high micro- and macro element content and they do not endanger the environment. They should not be handled as wastes but rather as nutrient amendments.
The aim of our work was to examine six industrial by-products (sewage sludge, lime sludge, grinding sludge, flue-gas, extruded poppy-heads) in order to determine whether the examined by-products can be potentially used for the nutrition of plants. The dry matter accumulation, relative chlorophyll contents of the plants, as well as the absolute quantities of photosynthetic pigments, the concentrations of various elements in the shoots and roots were measured. Moreover, the number of chloroplasts and ultra-structural changes of chloroplasts also were examined. Maize (*Zea mays* L. cv. Norma) and sunflower (*Helinathus annuus* L. cv. Arena) were used in the experiments. Our experiments show, that the treatments with flue gas, sewage-sludge compost, grinding sludge and extruded poppy heads make changes in the number of chloroplasts in the mesophyll cells. It is proved, that the treatment with flue gas caused changes in the ultra-structure, and membrane structure of chloroplasts. Synergism was proved between the Fe and Al in my experiments that force us for further investigations on the field of membrane transporters regarding the two ions.
We have come to the conclusion that all of the examined by-products can be used in the nutrition supply of plants, but it is essential to determine the concentrations of application accurately for field use.

2026 WITHDRAWN

2027 The submergence tolerance gene, *SUB1A*, delays leaf senescence under prolonged darkness through hormonal regulation in rice

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Environmental stress poses a significant limitation to agricultural production worldwide. Stresses such as submergence, drought, and constant darkness can prematurely induce leaf senescence, an age-dependent process in plants. Leaf senescence results in chloroplast breakdown, reduced photosynthetic activity triggering catabolism of energy reserves, and induction of senescence-associated genes. Studies were conducted to evaluate the influence of the submergence tolerance regulator, *SUB1A*, during leaf senescence in response to prolonged darkness in rice (*Oryza sativa* L.) by use of near-isogenic and transgenic lines. qRT-PCR analysis indicated that *SUB1A* mRNA increased in response to dark stress. Physiological analysis revealed that conditional and over-expression of *SUB1A* contributes to maintenance of chlorophyll and carbohydrate reserves in photosynthetic tissue, resulting in enhanced recovery from dark stress. *SUB1A* genotypes also displayed faster recovery of photosynthetic activity upon light re-exposure, and restricted transcript accumulation of representative senescence-associated genes. Additionally, overexpression of *SUB1A* limited responsiveness to the senescence-regulatory hormones jasmonate and salicylic acid at physiological and molecular levels. Measurement of ethylene evolution revealed that ethylene enhanced senescence stimulated by darkness and jasmonate. Delayed senescence in *SUB1A* genotypes was correlated with their reduced ethylene accumulation in darkness. These findings reveal that *SUB1A* contributes to dark-induced responses by limiting: chlorophyll and carbohydrate catabolism, accumulation of senescence-associated gene transcripts, and responsiveness to senescence promoting hormones. We propose that the postponement of dark-induced senescence by *SUB1A* contributes to submergence tolerance.

This research was supported by grants from NSF (IOS-1121626) and USDA-NIFA-AFRI (2011-04015) awarded to Julia Bailey-Serres and Takeshi Fukao.

2028 A quartet of *Arabidopsis* AREB/ABF transcription factors play pivotal roles in gene expression via ABRE *cis*-elements in ABA signaling involved in drought stress tolerance

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Osmotic stress such as drought and high salinity induces accumulation of abscisic acid (ABA) in plant cells, resulting in expression of a myriad of genes that function in the stress tolerance. In the promoter regions of such ABA-inducible genes, conserved *cis*-elements, designated ABRE, control gene expression via bZIP-type AREB/ABF transcription factors. We have previously shown that AREB1, AREB2, and ABF3 play key roles in ABA signaling under drought conditions, however, it remains unclear whether ABRE-dependent gene expression is exclusively regulated by the three AREB/ABFs during the vegetative stage. To address this question, we examined whether ABF1, which is in the same phylogenetic clade of the three AREB/ABFs, is involved in ABA signaling in response to drought stress by comparative analyses between the *areb1 areb2 abf3 abf1* quadruple and the *areb1 areb2 abf3* triple mutants. Microarray analysis showed that expression of dehydration- and ABA-inducible genes, which harbor one or more ABREs in their promoters, was more impaired in the quadruple mutant than in the triple mutant. Compared with the triple mutant, the quadruple mutant displayed reduced tolerance to drought stress and sensitivity to ABA with respect to primary root growth. Thus, these results indicate that the core quartet of AREB/ABFs have pivotal roles in the ABRE-dependent gene expression in ABA signaling involved in drought stress tolerance.

This work was supported in part by the Science and Technology Research Partnership for Sustainable Development (SATREPS) of the Japan Science and Technology Agency/Japan International Cooperation Agency.

2029 Creating drought-, heat-, and salt-tolerant cotton

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Drought, heat, and salt are major environmental factors that limit agricultural productivity in the world, particularly in the semiarid land of America's Southwest. These stresses are becoming more serious issues for agriculture in the Southwestern USA as climate change predictions foresee increased temperature and rainfall variability in these areas in the future. To sustain agriculture in these areas and in areas of similar nature in the rest of the world, we must deveop drought-, heat-, and salt-tolerant crops. Based on previous works in our and others' laboratories, we plan to introduce several genes into cotton to improve stress tolerance. Among the the genes that we will introduce into cotton, *IPT* encodes an isopentenyltransferase that plays a key role in cytokinin biosynthesis and regulated over-expression of *IPT* leads to increased drought tolerance in transgenic plants. *AVP1* encodes a vacuolar pyrophosphatase and overexpression of *AVP1* increases both salt- and drought-tolerance in transgenic plants. *OsSIZ1* encodes a SUMO E3 ligase in rice and plays an important role in heat/drought tolerance. A modified Rubisco activase was previously shown to increase the thermotolerance of photosynthesis in transgenic plants. The drought genes, *IPT* and *AVP1,* are fused to the heat genes *OsSIZ1* and *RCA* respectively, and the four constructs are being introduced into Arabidopsis. After sucessful demonstration in Arabidopsis, these four constructs will be introduced into cotton for field analysis. Cotton is the primary source of natural fiber that underpins many global economies, and the successful demonstration of this work in cotton will have a major impact on sustaining US cotton production in the future.

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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.

Harassment Policy

Keystone Symposia is committed to maintaining a positive and respectful environment at its meetings. To this end, we ask and expect attendees to assist in ensuring that the meetings are free of harassment, sexual or otherwise, including reporting any instances of improper conduct to us. Keystone Symposia expects attendees to conform their conduct at these meetings to the policies and procedures of their employing institution or company. If we learn of improper conduct by an attendee, we will take appropriate action, including reporting such conduct to the attendee's employing institution or company and barring the attendee from participation in our meetings.

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 the mobile app that is publicized only to meeting attendees, but attendees decide for themselves whether to enter further information in the app.

Attendee names and contact information are also listed in the meeting Abstract Book. Except in the Abstract 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 **keystonesymposia.org/privacy**.

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

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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 Abstract Book provided to each registrant. Abstract 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**.

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Pulmonary Vascular Disease and Right Ventricular Dysfunction: Current Concepts and Future Therapies (S1)
Organizers: Georg Hansmann, Stephen L. Archer and Margaret R. MacLean
Sep 10–15 | Portola Hotel & Spa | Monterey, California | USA

Aging and Diseases of Aging (S2)
Organizers: Takashi Kadowaki, Leonard P. Guarente, Judith Campisi and Sean M. Oldham
Oct 22–27 | Sheraton Miyako Hotel Tokyo | Tokyo, | Japan

Immunological Mechanisms of Vaccination (S3)
Organizers: Adrian V.S. Hill, Dan H. Barouch, John T. Harty and Tania H. Watts
Dec 13–18 | Fairmont Château Laurier | Ottawa, Ontario | Canada

Type 2 Immunity: Initiation, Maintenance, Homeostasis and Pathology (J1)
Organizers: Richard M. Locksley and Judith E. Allen
Jan 10–15 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

Pathogenic Processes in Asthma and COPD (J2)
Organizers: Marsha Wills-Karp, Jay K. Kolls and Sebastian L. Johnston
Jan 10–15 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

Multiple Sclerosis (A1)
Organizers: Trevor J. Kilpatrick, Brenda Banwell and Hartmut Wekerle
Jan 11–16 | Big Sky Resort | Big Sky, Montana | USA

New Frontiers in Cardiovascular Genetics Beyond GWAS (A2)
Organizers: Jennifer L. Hall and Stephen S. Rich
Jan 13–18 | Granlibakken Resort | Tahoe City, California | USA

Frontiers of NMR in Biology (A3)
Organizers: Gerhard Wagner, Angela M. Gronenborn and Marc Baldus
Jan 13–18 | Snowbird Resort | Snowbird, Utah | USA

Hematopoiesis (A4)
Organizers: Leonard I. Zon, Stuart H. Orkin and Nancy A. Speck
Jan 14–19 | Sheraton Steamboat Resort | Steamboat Springs, Colorado | USA

Emerging Topics in Immune System Plasticity (A5)
Organizers: Steven L. Reiner, Erika L. Pearce and Yasmine Belkaid
Jan 15–20 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

Plant Abiotic Stress and Sustainable Agriculture: Translating Basic Understanding to Food Production (A6)
Organizers: Julia Bailey-Serres and Mike Hasegawa
Jan 17–22 | Sagebrush Inn and Conference Center | Taos, New Mexico | USA

Noncoding RNAs in Development and Cancer (A7)
Organizers: Joshua T. Mendell, Phillip A. Sharp, Judy Lieberman and Howard Y. Chang
Jan 20–25 | Fairmont Hotel Vancouver | Vancouver, British Columbia | Canada

Malaria (A8)
Organizers: Fidel P. Zavala, Andrew P. Waters, Kevin Marsh and Carolina V. Barillas-Mury
Jan 20–25 | JW Marriott New Orleans | New Orleans, Louisiana | USA

Metabolic Control of Inflammation and Immunity (A9)
Organizers: Vishva M. Dixit, Douglas R. Green and Maya Saleh
Jan 21–26 | Beaver Run Resort | Breckenridge, Colorado | USA

Antibodies as Drugs (J3)
Organizers: Paul Carter and Andreas G. Plückthun
Jan 27–Feb 1 | Fairmont Hotel Vancouver | Vancouver, British Columbia | Canada

Cancer Immunology and Immunotherapy (J4)
Organizers: Glenn Dranoff, Carl H. June and Suzanne L. Topalian
Jan 27–Feb 1 | Fairmont Hotel Vancouver | Vancouver, British Columbia | Canada

Adipose Tissue Biology (J5)
Organizers: Susan K. Fried and Anthony W. Ferrante
Jan 27–Feb 1 | Keystone Resort | Keystone, Colorado | USA

Diabetes – New Insights into Mechanism of Disease and its Treatment (J6)
Organizers: C. Ronald Kahn, Jens C. Brüning and Gerald I. Shulman
Jan 27–Feb 1 | Keystone Resort | Keystone, Colorado | USA

Mitochondria, Metabolism and Myocardial Function – Basic Advances to Translational Studies (B1)
Organizers: Michael N. Sack and Roberta Gottlieb
Feb 3–8 | Keystone Resort | Keystone, Colorado | USA

Neurogenesis (J7)
Organizers: Hongjun Song, Yukiko Gotoh, Yi Eve Sun and Gerd Kempermann
Feb 3–8 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

New Frontiers in Neurodegenerative Disease Research (J8)
Organizers: Li-Huei Tsai, Steven M. Paul and Michael Hutton
Feb 3–8 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

Lung Development, Cancer and Disease (B2)
Organizers: Brigid L.M. Hogan, Jeffrey A. Whitsett and Christine Kim Garcia
Feb 5–10 | Sagebrush Inn and Conference Center | Taos, New Mexico | USA

The Gut Microbiome: The Effector/Regulatory Immune Network (B3)
Organizers: Lloyd H. Kasper, Javier Ochoa-Repáraz and Sarkis K. Mazmanian
Feb 10–15 | Sagebrush Inn and Conference Center | Taos, New Mexico | USA

B Cell Development and Function (X1)
Organizers: Max D. Cooper, Andrea Cerutti and Carola G. Vinuesa
Feb 10–15 | Keystone Resort | Keystone, Colorado | USA

HIV Vaccines (X2)
Organizers: Georgia D. Tomaras, Quentin J. Sattentau and Barbara L. Shacklett
Feb 10–15 | Keystone Resort | Keystone, Colorado | USA

Autophagy, Inflammation and Immunity (B4)
Organizers: Herbert (Skip) W. Virgin IV, Beth Levine and Gökhan S. Hotamisligil
Feb 17–22 | Fairmont The Queen Elizabeth | Montreal, QC | Canada

Nutrition, Epigenetics and Human Disease (B5)
Organizers: Robert A. Waterland, David S. Rosenblatt and Patrick J. Stover
Feb 19–24 | Hilton Santa Fe Historic Plaza Hotel | Santa Fe, New Mexico | USA

Myeloid Cells: Regulation and Inflammation (B6)
Organizers: Vincenzo Cerundolo, Gwendalyn J. Randolph and David M. Mosser
Feb 19–24 | Keystone Resort | Keystone, Colorado | USA

Stem Cell Regulation in Homeostasis and Disease (B7)
Organizers: Sean J. Morrison, Iannis Aifantis and Yukiko M. Yamashita
Feb 24–Mar 1 | Fairmont Banff Springs | Banff, Alberta | Canada

PI 3-Kinase and Interplay with Other Signaling Pathways (X3)
Organizers: Christian Rommel, Kevan M. Shokat and Jose Baselga
Feb 24–Mar 1 | Keystone Resort | Keystone, Colorado | USA

2012–2013 Keystone Symposia Meeting Series

Tumor Metabolism (X4)
Organizers: Matthew G. Vander Heiden and Karen H. Vousden
Feb 24–Mar 1 | Keystone Resort | Keystone, Colorado | USA

Structural Analysis of Supramolecular Assemblies by Hybrid Methods (C1)
Organizers: Andrej Sali, Brian T. Chait and David Baker
Mar 3–7 | Granlibakken Resort | Tahoe City, California | USA

Understanding Dendritic Cell Biology to Advance Disease Therapies (C2)
Organizers: Miriam Merad and Bart N. Lambrecht
Mar 3–8 | Keystone Resort | Keystone, Colorado | USA

DNA Replication and Recombination (X5)
Organizers: James M. Berger, Wolf-Dietrich Heyer and Julia Promisel Cooper
Mar 3–8 | Fairmont Banff Springs | Banff, Alberta | Canada

Genomic Instability and DNA Repair (X6)
Organizers: Stephen P. Jackson, Alan D. D'Andrea and Susan M. Gasser
Mar 3–8 | Fairmont Banff Springs | Banff, Alberta | Canada

Growing to Extremes: Cell Biology and Pathology of Axons (C4)
Organizers: Valeria Cavalli, Michael Fainzilber and Jeffery L. Twiss
Mar 10–15 | Granlibakken Resort | Tahoe City, California | USA

Host Response in Tuberculosis (X7)
Organizers: Andrea M. Cooper and Robert J. Wilkinson
Mar 13–18 | Whistler Conference Centre | Whistler, British Columbia | Canada

Tuberculosis: Understanding the Enemy (X8)
Organizers: Eric J. Rubin, Sebastien Gagneux and Heran Darwin
Mar 13–18 | Whistler Conference Centre | Whistler, British Columbia | Canada

Precision Genome Engineering and Synthetic Biology: Designing Genomes and Pathways (C5)
Organizers: Dana Carroll and Jef D. Boeke
Mar 17–22 | Beaver Run Resort | Breckenridge, Colorado | USA

Neuronal Control of Appetite, Metabolism and Weight (C6)
Organizers: Tony K.T. Lam and Matthias H. Tschöp
Mar 17–22 | Fairmont Banff Springs | Banff, Alberta | Canada

RNA Silencing (C7)
Organizers: David C. Baulcombe and Irene Bozzoni
Mar 19–24 | Whistler Conference Centre | Whistler, British Columbia | Canada

Epigenetic Marks and Cancer Drugs (C8)
Organizer: Ali Shilatifard
Mar 20–25 | Eldorado Hotel & Spa | Santa Fe, New Mexico | USA

Molecular Clockworks and the Regulation of Cardio-Metabolic Function (C9)
Organizers: Garret A. FitzGerald and Joseph S. Takahashi
Apr 3–7 | Snowbird Resort | Snowbird, Utah | USA

Immune Activation in HIV Infection: Basic Mechanisms and Clinical Implications (D2)
Organizers: Irini Sereti, Michaela Müller-Trutwin, Damian F.J. Purcell and Mauro Schechter
Apr 3–8 | Beaver Run Resort | Breckenridge, Colorado | USA

Nuclear Receptors and Friends: Roles in Energy Homeostasis and Metabolic Dysfunction (D3)
Organizers: Antonio J. Vidal-Puig, Antonio Moschetta and Anastasia Kralli
Apr 3–8 | Alpbach Congress Centrum | Alpbach, Austria | Austria

Immunopathology of Type 1 Diabetes (Z1)
Organizers: Kevan C. Herold, Dario A.A. Vignali, Jeffrey A. Bluestone and Anne Cooke
Apr 4–9 | Fairmont Chateau Whistler | Whistler, British Columbia | Canada

Advances in the Knowledge and Treatment of Autoimmunity (Z2)
Organizers: Juan Rivera, Virginia Pascual and David M. Lee
Apr 4–9 | Fairmont Chateau Whistler | Whistler, British Columbia | Canada

Cardiac Remodeling, Signaling, Matrix and Heart Function (D4)
Organizers: Anthony J. Muslin, Jil C. Tardiff and Steven R. Houser
Apr 7–12 | Snowbird Resort | Snowbird, Utah | USA

Plant Immunity: Pathways and Translation (D5)
Organizers: Sophien Kamoun and Ken Shirasu
Apr 7–12 | Big Sky Resort | Big Sky, Montana | USA

Positive Strand RNA Viruses (D7)
Organizers: Eric J. Snijder and Ralf Bartenschlager
Apr 28–May 3 | Boston Park Plaza & Towers | Boston, Massachusetts | USA

The Innate Immune Response in the Pathogenesis of Infectious Disease (E1)
Organizers: Ricardo T. Gazzineli, Gustavo P. Amarante-Mendes, Anne O'Garra and Alan Sher
May 10–15 | Universidade Federal de Ouro Preto (UFOP) | Ouro Preto, Minas Gerais | Brazil

The Hippo Tumor Suppressor Network: From Organ Size Control to Stem Cells and Cancer (E2)
Organizers: Marius Sudol, Helen McNeill, Georg A. Halder and Giovanni Blandino
May 19–23 | Hyatt Regency Monterey | Monterey, California | USA

Human Genomics and Personalized Medicine (E3)
Organizers: Kelly A. Frazer and Geoffrey S. Ginsburg
Jun 17–21 | Clarion Hotel Sign | Stockholm, Sweden | Sweden

2013–2014 Keystone Symposia Meeting Series

The following meetings are in development as part of Keystone Symposia's 2013–2014 meeting series. Details are subject to change. Visit us online at ***keystonesymposia.org*** *or join our various mailing lists and online networks for updates as we finalize details, including dates and locations, over the next few months.*

Advancing Vaccines in the Genomics Era (T1)
Organizers: Bali Pulendran, Chris Wilson and Rino Rappuoli
Dates and venue to be determined | Brazil

Sensing and Signaling of Hypoxia: Interfaces with Biology and Medicine (A1)
Organizers: Peter J. Ratcliffe, L. Eric Huang, Michael Ohh and Cynthia M. Beall
Jan 7–12 | Beaver Run Resort | Breckenridge, Colorado | USA

The Ubiquitin System: From Basic Science to Drug Discovery (A2)
Organizers: Ingrid E. Wertz and David Komander
Jan 7–12 | Big Sky Resort | Big Sky, Montana | USA

Nuclear Receptors: Biological Networks, Genome Dynamics and Disease (A3)
Organizers: Kevin P. White, Donald P. McDonnell and Gordon L. Hager
Jan 10–15 | Sagebrush Inn and Conference Center | Taos, New Mexico | USA

Tissue-Resident Memory T Cells (A4)
Organizers: Cornelia L. Trimble, Rachael A. Clark and Leo Lefrançois
Jan 12–16 | Snowbird Resort | Snowbird, Utah | USA

Aging – Pushing the Limits of Cellular Quality Control (A5)
Organizers: Andrew G. Dillin, Daniel E. Gottschling and Thomas Nyström
Jan 12–17 | Sheraton Steamboat Resort | Steamboat Springs, Colorado | USA

Challenges and Opportunities in Diabetes Research and Treatment (J1)
Organizers: Domenico Accili, Masato Kasuga and Morris F. White
Jan 12–17 | Fairmont Hotel Vancouver | Vancouver, British Columbia | Canada

Obesity: A Multisystems Perspective (J2)
Organizers: Roger D. Cone, Barbara Cannon and Lee M. Kaplan
Jan 12–17 | Fairmont Hotel Vancouver | Vancouver, British Columbia | Canada

Emerging Cytokine Networks (J3)
Organizers: Daniel J. Cua, Hergen Spits and Federica Sallusto
Jan 17–22 | Fairmont Hotel Vancouver | Vancouver, British Columbia | Canada

Inflammatory Diseases: Recent Advances in Basic and Translational Research and Therapeutic Treatments (J4)
Organizers: Chen Dong, Jingwu Zhang Zang, Tadamitsu Kishimoto and Richard A. Flavell
Jan 17–22 | Fairmont Hotel Vancouver | Vancouver, British Columbia | Canada

Pathogenesis of Respiratory Viruses (J5)
Organizers: Adolfo García-Sastre and Peter J.M. Openshaw
Jan 19–24 | Keystone Resort | Keystone, Colorado | USA

Innate Immunity to Viral Infections (J6)
Organizers: Caetano Reis e Sousa, Kate A. Fitzgerald and Charles M. Rice
Jan 19–24 | Keystone Resort | Keystone, Colorado | USA

New Frontiers in the Discovery and Treatment of Thrombosis (A6)
Organizers: Jane E. Freedman, Bruce Furie and Dietmar Seiffert
Jan 26–30 | Keystone Resort | Keystone, Colorado | USA

Mechanisms and Consequences of Invertebrate-Microbe Interactions (A7)
Organizers: Bruno Lemaitre, Nicole M. Gerardo and Jason Rasgon
Jan 26–30 | Granlibakken Resort | Tahoe City, California | USA

Growth and Wasting in Heart and Skeletal Muscle (A8)
Organizers: Elizabeth M. McNally, Nadia A. Rosenthal and Leslie A. Leinwand
Jan 26–31 | Eldorado Hotel & Spa | Santa Fe, New Mexico | USA

RNA Silencing (A9)
Organizers: V. Narry Kim, David P. Bartel and Julius Brennecke
Jan 31–Feb 5 | Sheraton Seattle Hotel | Seattle, Washington | USA

Developmental Pathways and Cancer: Wnt, Notch and Hedgehog (J7)
Organizers: Frederic J. de Sauvage, Mariann Bienz and Jon C. Aster
Feb 2–7 | Fairmont Banff Springs | Banff, Alberta | Canada

Stem Cells and Cancer (J8)
Organizers: Tannishtha Reya, Craig T. Jordan and Philip A. Beachy
Feb 2–7 | Fairmont Banff Springs | Banff, Alberta | Canada

Cancer Epigenetics (Q1)
Organizers: Sharon Y.R. Dent, Jean-Pierre Issa and Peter A. Jones
Feb 4–9 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

Transcriptional Regulation (Q2)
Organizers: Richard A. Young, Robert G. Roeder and Joanna Wysocka
Feb 4–9 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

Plant Signaling: Dynamic Properties (B1)
Organizers: Ottoline Leyser, Junko Kyozuka and Pamela C. Ronald
Feb 5–10 | Beaver Run Resort | Breckenridge, Colorado | USA

Molecular Cell Biology of Macrophages in Human Diseases (B2)
Organizers: Frederic Geissmann, Judith E. Allen and Christopher K. Glass
Feb 9–14 | Hilton Santa Fe Historic Plaza Hotel | Santa Fe, New Mexico | USA

Prophylactic and Therapeutic Antibodies (Q3)
Organizers: Margaret Karow and Neil Stahl
Feb 9–14 | Keystone Resort | Keystone, Colorado | USA

Biology of B Cell Responses (Q4)
Organizers: Hedda Wardemann, Michael G. McHeyzer-Williams and Michel C. Nussenzweig
Feb 9–14 | Keystone Resort | Keystone, Colorado | USA

Omics Meets Cell Biology: Applications to Human Health and Disease (B3)
Organizers: Anne-Claude Gingras, Igor Stagljar and A.J. Marian Walhout
Feb 18–23 | Sagebrush Inn and Conference Center | Taos, New Mexico | USA

Mitochondrial Dynamics and Physiology (Q5)
Organizers: Rodrigue Rossignol and Heidi M. McBride
Feb 18–23 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

The Chemistry and Biology of Cell Death (Q6)
Organizers: Guy S. Salvesen, Matthew S. Bogyo and Jennie R. Lill
Feb 18–23 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

The NF-κB System in Health and Disease (B4)
Organizers: Alexander Hoffmann and Louis M. Staudt
Feb 23–28 | Keystone Resort | Keystone, Colorado | USA

2013–2014 Keystone Symposia Meeting Series

The following meetings are in development as part of Keystone Symposia's 2013–2014 meeting series. Titles are subject to change. Visit us online at ***keystonesymposia.org*** *or join our various mailing lists and online networks for updates as we finalize details, including dates and locations, over the next few months.*

Long Noncoding RNAs: Marching toward Mechanism (B5)
Organizers: Thomas Cech, Edith Heard and Ronald R. Breaker
Feb 27–Mar 4 | Eldorado Hotel & Spa | Santa Fe, New Mexico | USA

Cilia, Development and Human Disease (C1)
Organizers: Elizabeth Petri Henske, Jeremy F. Reiter and Joel Rosenbaum
Mar 2–7 | Granlibakken Resort | Tahoe City, California | USA

Parkinson's Disease: Genetics, Mechanisms and Therapeutics (Q7)
Organizers: Patrick A. Lewis, Thomas Gasser and Marcel P. van der Brug
Mar 2–7 | Keystone Resort | Keystone, Colorado | USA

Alzheimer's Disease – From Fundamental Insights to Light at the End of the Translational Tunnel (Q8)
Organizers: John Q. Trojanowski, Charles F. Albright and Hui Zheng
Mar 2–7 | Keystone Resort | Keystone, Colorado | USA

Mobile Genetic Elements and Genome Evolution (C2)
Organizers: Nancy L. Craig, Henry L. Levin and Cedric Feschotte
Mar 9–14 | Hilton Santa Fe Historic Plaza Hotel | Santa Fe, New Mexico | USA

Inflammation, Infection and Cancer (X1)
Organizers: Johanna A. Joyce, Timothy C. Wang and Frances R. Balkwill
Mar 9–14 | Fairmont Chateau Whistler | Whistler, British Columbia | Canada

Immune Evolution in Cancer (X2)
Organizers: Suzanne Ostrand-Rosenberg, Olivera J. Finn and Lisa M. Coussens
Mar 9–14 | Fairmont Chateau Whistler | Whistler, British Columbia | Canada

HIV Vaccines: Adaptive Immunity and Beyond (X3)
Organizers: Nicole Frahm, Susan W. Barnett and Galit Alter
Mar 9–14 | Fairmont Banff Springs | Banff, Alberta | Canada

HIV Pathogenesis–Virus vs. Host (X4)
Organizers: J. Victor Garcia-Martinez, Daria J. Hazuda and Dan R. Littman
Mar 9–14 | Fairmont Banff Springs | Banff, Alberta | Canada

Metabolism and Angiogenesis (X5)
Organizers: Peter F. Carmeliet and Michael Simons
Mar 16–21 | Fairmont Chateau Whistler | Whistler, British Columbia | Canada

Tumor Metabolism (X6)
Organizers: William G. Kaelin, Jr., Benjamin F. Cravatt III and Peter K. Jackson
Mar 16–21 | Fairmont Chateau Whistler | Whistler, British Columbia | Canada

Lipid Pathways in Biology and Disease (C3)
Organizers: Michael P. Czech, Tobias C. Walther and Morris J. Birnbaum
Mar 19–24 | Royal Dublin Society | Dublin, Ireland | Ireland

Fibrosis: From Bench to Bedside (C4)
Organizers: Jeremy S. Duffield, Steven R. Ledbetter and John P. Iredale
Mar 23–28 | Keystone Resort | Keystone, Colorado | USA

Chromatin Mechanisms and Cell Physiology (C5)
Organizers: Thomas Jenuwein and Shelley L. Berger
Mar 23–28 | Oberstdorf Haus | Oberstdorf | Germany

Complications of Diabetes (X7)
Organizers: Michael A. Brownlee, Matthew D. Breyer and Susan Quaggin
Mar 23–28 | Whistler Conference Centre | Whistler, British Columbia | Canada

Innate Immunity, Metabolism and Vascular Injury (X8)
Organizers: Ajay Chawla, Peter Tontonoz and Gwendalyn J. Randolph
Mar 23–28 | Whistler Conference Centre | Whistler, British Columbia | Canada

The Ins and Outs of Viral Infection: Entry, Assembly, Exit and Spread (C6)
Organizers: Karla Kirkegaard, Mavis Agbandje-McKenna and Eric O. Freed
Mar 30–Apr 4 | Beaver Run Resort | Breckenridge, Colorado | USA

Novel Therapeutic Approaches to Tuberculosis (C7)
Organizers: Christopher M. Sassetti and Thomas G. Evans
Mar 30–Apr 4 | Keystone Resort | Keystone, Colorado | USA

G Protein-Coupled Receptors: Structural Dynamics and Functional Implications (Z1)
Organizers: Christopher G. Tate and Fiona H. Marshall
Mar 30–Apr 4 | Snowbird Resort | Snowbird, Utah | USA

Frontiers of Structural Biology (Z2)
Organizers: Andrew Ward and Wayne A. Hendrickson
Mar 30–Apr 4 | Snowbird Resort | Snowbird, Utah | USA

Exploiting and Understanding Chemical Biotransformations in the Human Microbiome (D1)
Organizers: Peter J. Turnbaugh, Curtis Huttenhower and Michael A. Fischbach
Apr 1–6 | Big Sky Resort | Big Sky, Montana | USA

Epigenetic Programming and Inheritance (D2)
Organizers: Joseph H. Nadeau, Marisa S. Bartolomei, Peter Gluckman and Wolf Reik
Apr 6–10 | Joseph B. Martin Conference Center | Boston, MA | USA

Emerging Concepts and Targets in Islet Biology (D3)
Organizers: Rohit N. Kulkarni, Raghavendra G. Mirmira and Eckhard Lammert
Apr 6–11 | Keystone Resort | Keystone, Colorado | USA

Engineering Cell Fate and Function (Z3)
Organizers: Darrell J. Irvine and Sangeeta N. Bhatia
Apr 6–11 | Resort at Squaw Creek | Olympic Valley, CA | USA

Stem Cells and Reprogramming (Z4)
Organizers: Deepak Srivastava and Shinya Yamanaka
Apr 6–11 | Resort at Squaw Creek | Olympic Valley, CA | USA

Adult Neurogenesis (E1)
Organizers: Jonas Frisén and Fred H. Gage
May 12–17 | Clarion Hotel Sign | Stockholm, Sweden | Sweden

Autophagy: Fundamentals to Disease (E2)
Organizers: Christina H. Eng, Daniel J. Klionsky, Guido Kroemer and Li Yu
May 23–28 | Hyatt Regency Austin | Austin, TX | USA

The Brain: Adaptation and Maladaptation in Migraine and Chronic Pain (E3)
Organizers: Frank Porreca, David Borsook and David W. Dodick
Jun 15–20 | Keystone Resort | Keystone, Colorado | USA

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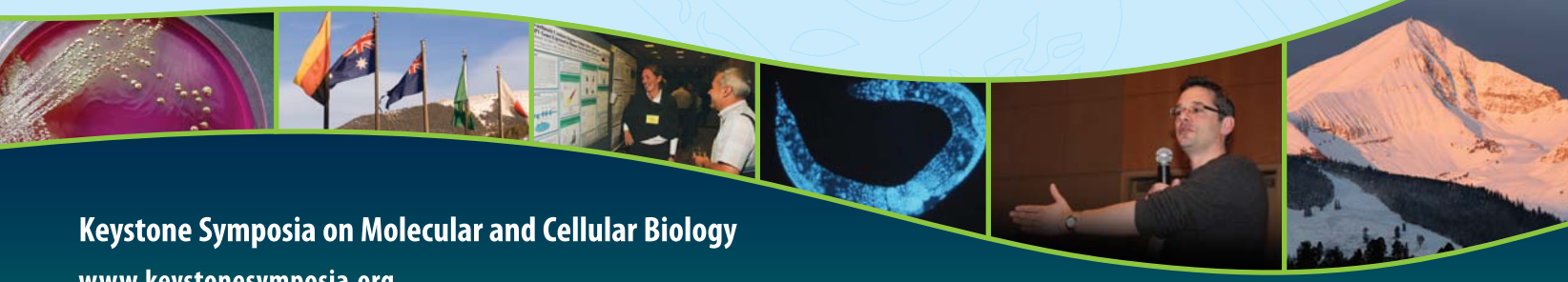

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