

NABC NEWS

Spring 2016 No. 51

*Providing an open forum
for exploring issues in
agricultural biotechnology*



NABC'S PRINCIPAL OBJECTIVES ARE TO:

- provide an open forum for persons with different interests and concerns to come together to speak, to listen, to learn, and to participate in meaningful dialogue and evaluation of the potential impacts of agricultural biotechnology
- define issues and public policy options related to biotechnology in the food, agricultural, biobased industrial product, and environmental areas
- promote increased understanding of the scientific, economic, legislative, and social issues associated with agricultural biotechnology by compiling and disseminating information to interested people
- facilitate active communication among researchers, administrators, policymakers, practitioners, and other concerned people to ensure that all viewpoints contribute to the safe, efficacious and equitable development of biotechnology for the benefit of society
- sponsor meetings and workshops and publish and distribute reports that provide a foundation for addressing issues.

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Letter from the Chair...

NABC: Where Does It Go from Here?

*Without popular support,
nothing is possible. With popular
support anything is possible.*
-Abraham Lincoln

In 1988 the National Agricultural Biotechnology Council was established with four founding members: Cornell University, Iowa State University, the University of California, Davis, and the Boyce-Thompson Institute. Its chair was Ralph W.F. Hardy, then the head of BTI, and its purpose was to encourage public discussion of biotechnology and the impact of rapidly evolving technologies on issues especially relevant to agriculture. A number of universities have joined this activity, including a few from Canada, which led to a name change to the North American Agricultural Biotechnology Council, but the abbreviation NABC was retained.

One of the major activities of NABC since its founding has been an annual meeting, hosted by a member institution, that focuses on some specific aspect of biotechnology, sometimes coming at the issue from the standpoint of the technology, sometimes from a market perspective, and sometimes from a policy point of view. The proceedings of these meetings have been widely distributed to member institutions and others interested in the issues. Most of these are now to view or download at http://nabc.cals.cornell.edu/Publications/Reports/pubs_reports.html. Scanning the list of titles shows that most meetings have dealt with some aspect of genetic engineering, but some meetings have dealt with water and food security, resource management, and related topics. In all cases, an effort was made to gather experts who contributed presentations that summarized the most current state of the issue.

In addition to organizing these meetings,



Michael Kahn
Washington State University
NABC Chair 2015 —2016

NABC has issued a number of white papers on various topics (see <http://nabc.cals.cornell.edu/Pubs.html>). Especially interesting in light of some current political discussions is a set of papers called “Labeling of Biotechnology Food Products” published in 1994. There has been a lot of progress since then in defining the science that might affect food labeling, but the controversy remains. This summer, a law in Vermont will require labeling of food products that contain GMO ingredients—with an interesting exception for cheeses, including Vermont cheddar, that contain bacterially produced protease.

From the perspective of the member institutions, NABC meetings have provided an open forum in which to discuss how investments in particular technologies and areas of emphasis might contribute to solving problems in North American and world agriculture. Because these meetings tend to present the science without many of the technical details, the meeting summaries provide a current and accessible overview of that year’s topic. To my knowledge, this pattern is unique. Other groups recurrently emphasize particular subject areas, often integrating overviews with more technical

NABC 28—Mark Your Calendars

A Growing Agricultural Genetic Tool Box: Applications for Plant and Animal Improvement

June 1 and 2, 2016

Pullman, WA

Michael L. Kahn

Washington State University

The College of Agricultural, Human and Natural Resource Science at Washington State University will host the 28th annual conference of the North American Agricultural Biotechnology Council (NABC) at the Washington State University campus in Pullman Washington on June 1-2, 2016. The conference—A Growing Agricultural Genetic Tool Box: Applications for Plant and Animal Improvement will focus on various technologies that are often associated with classical genetics that have, however, over the last several years become much more powerful as a result of changes in information science, DNA sequencing and improvement of tools for phenotype determination.

The meeting will consist of six sessions focusing on various ways in which activities such as recording and managing information, generating and using variants, mapping genes, determining phenotypes are contributing to improved strategies for breeding and identifying plants and animals with improved traits for agriculture.

Session 1, Wednesday AM Coping with copious information

The amount of information being generated in many parts of biology is truly amazing and, unlike data streams in many other areas of science, each bit actually may have significant meaning in determining or deciphering how things work. Communities are being organized around this data and determining efficient strategies for saving, accessing and interrogating the data is essential.

- Dorrie Main (Washington State University) *The Database Dilemma – Keeping All the Data While Strategically Working with Some*
- TBD

Session 2, Wednesday AM Generating and exploiting variation

A major part of agricultural breeding involves bringing desirable variants together in one organism. New genetic and epigenetic strategies have been developed for generating variants and assessing how genes work.

- Luca Comai (University of California, Davis) *Understanding and Designing the Genome of Crop Plants*
- Kiran Mysore (Noble Foundation) *Gene Function Analyses by Virus-induced Gene Silencing and Insertional Mutagenesis*

- Sally MacKenzie (University of Nebraska) *Modifying Epigenetic Behavior in Crop Plants as a Production-enhancing Strategy*

Session 3, Wednesday PM Connecting phenotypes to genotypes

Mapping genes that contribute to phenotype has been a major research activity for about a hundred years but the ability to take large genetic and phenotypic data sets and figure out where genes that contribute to polygenic inheritance of complex traits are located is a relatively new capability.

- Jared Decker (University of Missouri) *Livestock Genomics: New Approaches for Connecting Basic Biology to Genetic improvement*
- Carolyn Lawrence (Iowa State University) *Information Management Platform Development for the Genomes to Fields Initiative*
- Steven White (USDA-ARS, Pullman, WA) *Accelerating Genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project*

Session 4, Wednesday PM Extending the envelope

Two capabilities now within the category of “we always wanted to know how these things worked” are characterizing the identities and nature of the microorganisms that provide an important component of an organism’s environment and understanding how to deliberately manipulate useful metabolic pathways.

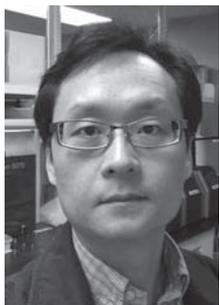
- Tim Paulitz (USDA-ARS, Pullman, WA) *Soil and Plant Microbiomes in Agriculture: Going Beyond the Descriptive to Answering Relevant Questions*
- Larry Forney (University of Idaho) *Seeing the Unseen: Approaches to Understanding the Ecology of Microorganisms*
- Mark Lange (Washington State University) *Modeling Metabolism – How to Really Integrate ‘omics’ data*

Session 5, Thursday AM Phenomics

Because it has become relatively easy to obtain genetic information and because computational methods for finding associations between genetic or phenotypic characteristics in large data sets has improved, gathering

continued on page 7

Speakers



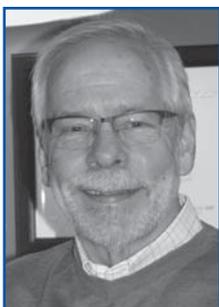
Seungho Cho is a Varietal Crop Germplasm Discovery Scientist at Monsanto. He received a Ph.D. in Genetics and Cell Biology from Washington State University in 2003 for his study on fungal disease resistance in chickpea. After postdoctoral research in the Department of Agronomy and Plant Genetics, focused on molecular genomics of cereal crops, he joined BASF Plant Science in 2006 and worked on molecular genomics platform development and HTP lab operation. In 2010, he joined Monsanto as Molecular Breeder specializing in cotton and now supporting all varietal crops in the areas of trait genetics and breeding technology discovery ■



Luca Comai is a professor of plant biology at the Genome Center of the University of California, Davis. He has a B.S.-equivalent in agricultural sciences from the Università di Bologna; an M.S. in plant pathology from Washington State University; and a Ph.D. in plant pathology from UC Davis. In his Ph.D. thesis he elucidated the genetic basis of IAA production in bacteria, later found to be homologous to that encoded by Agrobacterium T-DNA. In 1981 Dr. Comai joined the biotechnology start-up Calgene, where he worked on crop plant modification, providing the first demonstration that glyphosate resistance could be engineered through alteration of EPSP synthase. In 1990, he joined the faculty at the University of Washington, where he initiated work on the genetics and genomics of polyploidy and co-developed TILLING with colleagues. Since joining UC Davis, he continues to develop approaches to functional genomics and genome analysis with an emphasis on function and regulation of chromosomes and polyploid genomes. Dr. Comai has authored over 100 publications, has an H impact factor of 63, and is a Fellow of the American Association for the Advancement of Science. ■

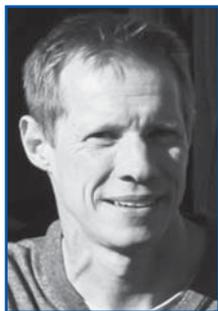


Jared Decker is an assistant professor in the University of Missouri Division of Animal Science and a beef genetics extension specialist. He is also a member of the Genetics Area Program and the University of Missouri Informatics Institute. Decker received his B.S. from New Mexico State University, with a major in animal science and a minor in biology, and received his Ph.D. at the University of Missouri in genetics, with a minor in statistics. Jared is working to help stakeholders in the beef industry better understand rapidly changing genetic technologies. His research focuses on understanding the history and selection of cattle breeds and improving the cost and accuracy of genomic prediction tests. He is active on social media and his website, A Steak in Genomics ■



Larry Forney is a University Distinguished Professor in the Department of Biological Sciences at the University of Idaho. He is currently director of an NIH-funded Center of Biomedical Research Excellence and until recently was director of the Institute for Bioinformatics and Evolutionary Studies (IBEST) at the University of Idaho. Prior to this he was professor of microbial ecology at the University of Groningen in The Netherlands, associate director of the Center for Microbial Ecology at Michigan State University, and a senior scientist at Synergen, Inc. His scientific expertise is in the evolutionary ecology of prokaryotes and microbial community ecology. He has pioneered the development of molecular microbial ecology methods to understand the extent and distribution of microbial diversity, to characterize within- species genetic diversity, and to study the evolution of novel microbial traits. His accomplishments in microbial evolution and ecology and scientific leadership have been recognized through various awards and by appointment as a Fellow of the American Academy of Microbiology ■

Go to <http://nabc.cals.cornell.edu/Pubs.html> to download NABC publications



Bernd Markus (“Mark”) Lange is currently an associate professor at the Institute of Biological Chemistry at Washington State University. He received an M.S. from the University of Bonn and a Ph.D. from the University of Munich. Following postdoctoral studies at the University of Tübingen and Washington State University, Mark spent several years as a team leader in the biotechnology industry, working for Novartis, Syngenta, and Diversa. In 2004, he joined the faculty at Washington State University and built a program focused on understanding metabolism in specialized plant cells that are responsible for the synthesis of essential oils, oleoresins, and pharmaceutically relevant natural products. Mark has directed biotechnological, and more recently, breeding efforts to develop mint cultivars with enhanced oil yield and composition. His laboratory is employing mathematical modeling to quantitatively describe oil and resin biosynthesis at various scales from individual genes or enzymes to entire plants ■



Carolyn Lawrence-Dill is an associate professor in the Department of Genetics, Development and Cell Biology at Iowa State University. She has devoted the last 15 years to developing computational systems/solutions that support the plant research community. Her work enables the use of existing and emerging knowledge to establish common standards and methods for data collection, integration, and sharing. Such efforts help to eliminate redundancy, improve the efficiency of current and future projects, and increase the availability of data and data analysis tools for plant biologists working in diverse crops across the world. Carolyn led the USDA’s maize model organism database MaizeGDB (<http://maizegdb.org/>) for a decade; currently coordinates the development of the information platform for the US maize Genomes to Fields Initiative (<http://www.genomes2fields.org/>); and is an active member of the

community working to put in place methods for phenotype data access, analyses, and re-use.

Carolyn has served in advisory roles as a member of groups including the Maize Genetics Executive Committee (2014 chair), the iPlant/CyVerse Scientific Advisory Board, the maize nomenclature committee, the Legume Information System Working Group, and the SoyBase Working Group. To learn more about her contributions to plant biology and information access, visit <https://scholar.google.com/citations?user=bHQPmtEAAA&hl=en> ■



Sally Mackenzie is the Ralph and Alice Raikes Distinguished Chair of Plant Science at the University of Nebraska-Lincoln. She began her career at Purdue University in 1989 and joined the faculty at the University of Nebraska in 1999 in the Department of Agronomy and Horticulture. Her laboratory research focuses on plant organellar properties that influence epigenetic behavior, and the exploitation of these interactions to induce changes in plant growth properties. Sally is a Quishi Chair Professor at Zhejiang University in Hangzhou, and serves as president-elect for the American Society of Plant Biologists ■



Doreen Main is a professor of bioinformatics in the Department of Horticulture at Washington State University. She received her M.S. in information management and a Ph.D. in bioscience and biotechnology from the University of Strathclyde, Glasgow. For the last 15 years her research has largely focused on the development of sequence analysis pipelines, online informatics tools, and genomic, genetic, and breeding databases to enable basic, translational, and applied crop research. Her industry- and federally supported program currently hosts databases for 25 crops, including tree fruits, berries, cool-season legumes, and cotton, using the generic, resource-efficient, open-source Tripal database platform ■



Kiran Mysore is a professor at the Plant Biology Division at the Samuel Roberts Noble Foundation. He also holds a adjunct professorship at the Department of Entomology and Plant Pathology, Oklahoma State University. He received his bachelor’s degree in agriculture at the University of Agricultural Sciences, Bangalore, master’s degree in horticulture at Clemson University, and Ph.D. in genetics at Purdue University in 1999. He did his postdoctoral training in plant genomics at the Boyce Thompson Institute for Plant Research, Cornell University. His research interests center on molecular plant-microbe interactions and plant genetic resource development. He has published over 150 papers and book chapters ■



Henry T. Nguyen is Curators' Professor of Plant Sciences and Endowed Chair in Soybean Genomics and Biotechnology at the University of Missouri and has served as Director of the National Center for Soybean Biotechnology from 2003 to 2015. Prior to this, he was the Board of Regents' Paul Whitfield Horn professor at Texas Tech University with a joint appointment with Texas A&M University. He is internationally recognized for his research in plant adaptation to stress environments. His research team conducts genetic analysis of major traits and applies molecular marker technology to soybean improvement. Dr. Nguyen has gained recognition through many awards such as the National Science Foundation's Presidential Young Investigator Award and the Young Crop Scientist Award. He was elected as Fellow of the Crop Science Society of America, Fellow of the American Society of Agronomy, and Fellow of the American Association for the Advancement of Science. He has published more than 250 refereed articles and 35 book chapters. He chairs the Abiotic Stress Workshop at the International

Plant and Animal Genome Conference and coordinates a large scale soybean genome sequencing project aimed toward the development of next generation genomics-assisted trait discovery and breeding strategies ■



Tim Paulitz earned a B.Sc. in botany with a minor in plant pathology from California State Polytechnic University in Pomona in 1979. In 1984, he received a Ph.D. in plant pathology from the University of California, Riverside. He was a visiting assistant professor at Colorado State University from 1984 to 1987 and a research associate with the USDA-ARS in Corvallis, Oregon, from 1987 to 1989. He was professor at Macdonald College of McGill University in Ste. Anne de Bellevue, Quebec, from 1989 to 2000. He is presently a research plant pathologist with the USDA-ARS Wheat Health, Genetics, and Quality Research Unit at Washington State University in Pullman. He investigates root diseases and soil-borne pathogens of wheat, barley, brassicas, and other rotation crops, with an emphasis on fungi (Rhizoctonia, Pythium, and Fusarium) and nematodes (cereal cyst and root lesion). He has focused on the ecology, epidemiology, spatial analysis, and molecular detection and quantification of soil-borne pathogens, and the development of cultural management techniques for root diseases, especially

in direct-seed systems. In the last seven years, he has studied microbial communities in disease-suppressive soils using next-generation sequencing. He is presently looking at the impacts of tillage, cultivars, glyphosate, and other herbicides on microbial communities in wheat ■



Sindhuja Sankaran joined Washington State University in 2013 as an assistant professor in the Department of Biological Systems Engineering. She received a B.S. in zoology, a dual M.S. in environmental science and environmental engineering, and a Ph.D. in agricultural and biosystems engineering (2009) from North Dakota State University. She was also postdoctoral associate at the University of Florida until 2013. Her research interests are in advanced sensing techniques for high-throughput crop phenotyping. Her work also involves development and characterization of opto-electronic and biomimetic chemical sensor technologies for noninvasive, rapid, and continuous crop monitoring applications. In 2015, she organized the conference "Advances in Field-based High-throughput Phenotyping and Data Management" in collaboration with colleagues from WSU and other US institutions ■



Rollin G. Sears retired in 2015 from Syngenta, where he was a senior science fellow and senior manager leading research and development for cereals in North America. As a wheat breeder, he focused on improved wheat production efficiency through the release of improved wheat cultivars. Dr. Sears has been able to combine high yield with improved milling and baking properties in widely adapted wheat cultivars in North America. Rollie earned his degrees at Montana State University (M.S.) and Oregon State University (Ph.D.) and joined Kansas State University as an assistant professor in 1980, rising to professor before joining Syngenta in 1999. He has received the Kansas Farm Bureau's Distinguished Service to Agriculture Award, The Kansas Association of Wheat Growers' Wheat Man of the Year Award, a Distinguished Graduate Faculty Award from Kansas State University, the American Society of Agronomy Agronomic Research Award, and the 2007 Oregon State University Distinguished Service Award. Oregon State University School of Agriculture recognized him with their Alumni Legacy Award in 2013. Dr. Sears is a Fellow of both the American Society of Agronomy and the Crop Science Society of America ■



Edgar Spalding received a B.Sc.H. degree from Acadia University in 1985 and a Ph.D. in biology from Penn State in 1990. He conducted postdoctoral research in plant membrane transport at Yale University until beginning an assistant professorship in the Department of Botany at the University of Wisconsin–Madison in 1994, where he is now a full professor. Dr. Spalding considers himself to be a plant physiologist with a penchant for getting computers to measure details of seedling growth and development, especially when the results can be used to learn about gene functions or basic physiological processes such as auxin transport and signaling. ■



Jeff White has a B.A. in biology from Harvard University and a Ph.D. in botany from the University of California, Berkeley. He is a research plant physiologist with the USDA Agricultural Research Service and is stationed at the Arid Land Agricultural Research Center near Phoenix, Arizona. Before joining USDA, Dr. White worked as a crop physiologist at the International Potato Center (CIP; Lima, Peru), the Centro Internacional de Agricultura Tropical (CIAT; Cali, Colombia), and the International Maize and Wheat Improvement Center (CIMMYT; El Batán, Mexico). Dr. White is a Fellow of the American Society of Agronomy.

Dr. White has a long interest in understanding physiological and genetic mechanisms of adaptation to temperature and water deficits. He pioneered inclusion of genetic information in ecophysiological models. Current research emphasizes development of high-throughput systems suitable for phenotyping large populations in field trials under water deficit and high-temperature stresses ■



Steven White is a Research Geneticist with the USDA-ARS Animal Disease Research Unit in Pullman, WA and is a member of the international Steering Committee for FAANG, the Functional Annotation of ANimal Genomes project. He also holds adjunct faculty appointments in the Department of Veterinary Microbiology & Pathology and the Center for Reproductive Biology at Washington State University. He earned a B.S. in Biology from Duke University, and then a Ph.D. in Genetics from Texas A&M University. His research focuses on genomics of susceptibility to infectious and inherited disease, genetics of complex traits, and development of applied genetic technologies for many ruminant livestock and other domestic animal species. Projects include scrapie resistance in domestic goats, sheep genes that restrict lentiviral replication and ovine progressive pneumonia, and a range of other topics in genetics of cattle, wild ruminants, and companion animals.

To learn more about Dr. White, please visit: <https://scholar.google.com/citations?user=3TBrXlMAAAAJ&hl=en&oi=ao> ■

continued from page 1

sessions. Universities can also be members of groups that sequentially consider topics, but the presentations do not generally become publicly available information.

The question that leads this summer letter, Where does it go from here?, has a short answer. There will be a summer meeting this year in Pullman, Washington, that is described elsewhere in this newsletter. There is a more extended answer, that a 2017 meeting will occur in Winnipeg, Manitoba. But what happens after 2017 is a deeper question that concerns the future

of the organization. Allan Eaglesham, who was involved with NABC for many years as a contributor, organizer, and editor, retired last year. Ralph Hardy has told the Executive Committee that he will not continue as president after 2017. And Susanne Lipari, who has been an essential person for many years in organizing the logistics of everything, is also planning to retire. So new people are needed.

The Executive Committee has rephrased this problem of leadership as a problem of mission and is asking members and potential members to consider two options. NABC can declare

victory and disband, leaving the meeting volumes as a record of the role that the group has played over the last ~30 years in discussing emerging science and its relationship to the changing practice of agriculture. Alternatively, members can ask what is needed to help agricultural biotechnology in the future, who needs it, and how they can contribute. If there is a need for the types of activities that NABC has carried out over the years, the structure and leadership of a new NABC will need to be discussed.

Agriculture is a central component of the *continued on page 8*

continued from page 2

large amounts of phenotype information has become a limiting factor for many projects. As a result, developing methods to measure the relevant components of the phenome has become a priority.

- Sindhuja Sankaran (Washington State University)
Advanced Sensing Tools and the Future of Phenomics
- Edgar Spalding (University of Wisconsin)
Phenotyping Maize Seed and Seedlings Using ImageProcessing and High-throughput Computing
- Jeff White (USDA-ARS, Maricopa, AZ)
Field phenotyping Basics for Adaptation to Heat and Water Deficits

Session 6, Thursday AM Breeding for agriculture

Implementing a modern breeding strategy using “classical” methods is complex but is potentially much more powerful than it was even a few years ago. DNA markers can be used to follow traits, like disease resistance or components of polygenic inheritance, which can be difficult to assay directly. High throughput phenotypic assays can be used to screen populations and eliminate individuals that are outside of the desired range of parameters. DNA sequencing can be used to verify the presence of specific alleles in selected individuals and to establish identities for IP protection.

- Seungho Cho (Monsanto)
Transformation of Plant Breeding to Deliver Increased Genetic Gain
- Rollin Sears (Kansas State University)
Wheat Improvement Towards 2035: Building on Success into the Future
- Henry Nguyen (University of Missouri)
Next Generation Genomic Tools for Soybean Improvement

Thursday PM NABC Council meeting: Where does NABC go from here?

Because the topic of this meeting concerns the future of NABC, Council members and representatives from institutions that might become NABC members are invited to attend.

About Pullman:

Pullman is in southeastern Washington state, near the Idaho state line. In early June the average temperatures are 68/44 and sunny weather. The days will be about 16 hours long. The local region, called the Palouse, was a prairie that is now a significant agricultural region and in June the rolling hills will be covered with fields of green wheat and barley, interspersed with dry peas, lentils and chickpeas. The hills are also a component of the WSU campus—land that had little value because it was too steep to plow could be made useful in this way.

Getting to Pullman:

Pullman has an airport served by Horizon Airlines (Alaska) but flights are not very frequent. Van service provided by the hotels is available as are taxis. Two other airports are most relevant, Lewiston, Idaho (LWS) and Spokane, Washington (GEG). Lewiston is about 45 minutes drive from Pullman; Spokane is about 90 minutes. Lewiston is served by Delta and Alaska, Spokane by several major airlines. A shuttle (<http://www.wheatlandexpress.com/>) connects Pullman to both airports but reservations are required in advance. The WSU French Administration Building is the stop that riders want. There is no shuttle on Memorial Day. For those interested in a longer drive it is about 5 hours to Seattle airport (SEA) but rental cars in Seattle are relatively cheap compared to the usual flight to Pullman from Seattle. The drive is not complicated once you leave the area around the airport and crosses the Cascade Mountain Range through Snoqualmie Pass.

Accommodations

A block of rooms has been reserved for NABC 28 participants at the Residence Inn Marriott (Phone: 509-332-4400; <http://www.wsuresidenceinn.com/>) at a rate of \$109/night and this includes breakfast. Please be sure to mention you are with the North American Agricultural Biotechnology Council to receive the group rate. The Residence Inn is about 0.7 miles from the Compton Union Building (CUB) conference site, an easy walk except for about two blocks of hill at the end. Three other motels are suggested. Rooms at

the Holiday Inn Express (1.3 miles; Phone: (509) 334-4437; <https://goo.gl/iSRd9z>) can currently be reserved on-line for ~\$120/night. The Hilltop Inn (1.6 miles; Phone: (509) 332 0928; www.hilltopinnpullman.com/) is available at \$106/night. The Quality Inn (1 mile; Phone: (509) 332-0500; <https://goo.gl/DAGVwr>) is available for \$90/night. All include breakfast.

Conference Website – <http://cm.wsu.edu/nabc28>

Registration

Registration may be completed online at <http://cm.wsu.edu/ehome/nabc28/364010/>. The \$300 fee (\$180 for students), payable by credit card (Master Card, Visa, Discover, or American Express) or check (payable to Washington State University), will cover refreshments at all breaks, lunches, and the evening reception and banquet.

Poster Reception

We extend the opportunity for graduate students to present posters during the reception on Wednesday, June 1 at 5 PM in the Lewis Alumni Center. Poster topics should be related to agricultural biotechnology, but do not necessarily need to address the specific foci of NABC 28. If you are bringing a poster, please let us know.

Banquet. The banquet will be held in the Lewis Alumni Center on Wednesday night.

Questions, comments and suggestions may be directed to:

Michael Kahn (kahn@wsu.edu)
Sheila Brooks (sbrooks@wsu.edu)■

continued from page 6

NABC has contributed to these objectives by summarizing trends in science on the cutting edge and by helping administrators consider how to approach this edge strategically. Unlike regional experiment station directors' meetings, which focus on how to manage states' agricultural research portfolios, the NABC meetings focus on what might be added to those portfolios and how this might be done on a national scale.

On June 2, after the end of the 28th meeting in Pullman, the membership will meet to discuss the future of NABC.

Representatives of institutions that are not currently members are welcome to attend this meeting, since their input is important to the future. However, I think we should all keep in mind something Mark Twain said: "If you want money, ask for advice. If you want advice, ask for money■"



THE STUDENT VOICE AT NABC

**TRAVEL STIPEND AND FREE REGISTRATION TO ATTEND NABC 28
FOR ONE GRADUATE STUDENT FROM EACH NABC MEMBER INSTITUTION**

<http://nabc.cals.cornell.edu/StudentVoice.html>

Media Mail

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