Presentation Abstract and Biography of Speakers

Introductory Speech: Plant Breeding Education and Training: An Industry Perspective
Dr. Geoff Graham, Pioneer Hi-Bred International, Inc.

Abstract:

The industry demand for Ph.D. trained plant breeders will continue to increase over the next 10 years through increased global demand for food, feed, fuel, and fiber. In addition to being educated in traditional plant breeding methods, new breeders will be continue to be challenged to apply emerging technologies to the field. To meet the this growing demand, we recommend that industry work in collaboration with the public sector to (1) identify the most effective means of recruiting high school graduates and university undergraduates into the plant breeding field, and (2) generate a larger pool of new plant breeders by aggressively funding more graduate student training and research programs. This can be accomplished through informational programs, recruitment of students in complementary majors earlier in their careers, the broad offering of internships within industry, and the funding of graduate student fellowships.

Biography:

Geoff Graham, Research Director, North America Corn Breeding

Geoff has been working to apply new and conventional technologies to improve plant breeding systems for the past 10 years. In 2000, he joined Pioneer Hi-Bred International as a research scientist and was promoted to senior research scientist in 2004. Geoff accepted a position as director of Molecular Breeding in 2006. In January 2008, he was named director of North America Corn Breeding. In his current role, Geoff has responsibility for maize research and development in North America, including inbred and hybrid creation and evaluation; hybrid characterization and advancement; and breeding technologies. Prior to joining Pioneer, Geoff was a research scientist with Monsanto/Asgrow Seed Company for three years. He received his bachelor's degree in agronomy and master's degree in genetics and plant breeding from the University of Minnesota. He went on to receive his doctorate in genetics and plant breeding from North Carolina State University.

Keynote Address: Imagining the Future of Applied Plant Genetics
Dr. Ron Phillips, University of Minnesota

Abstract:

The recently announced 1000 Genomes Project where researches plan in three years to capture human diversity in 1000 genomes once again allows the applied plant geneticist to imagine the future with a high degree of predictability. The National Academies Report "Rising Above the Gathering Storm" recommends that we need to "sustain and strengthen the nation's traditional commitment to long-term basic research that has the potential to be transformational to maintain the flow of new ideas that fuel the economy, provide security, and enhance the quality of life." The students of today will be the ones to be "transformational" utilizing the ever-changing genetic technologies in the context of traditional plant breeding, requiring the careful selection of parents based on traits of interest, hybridization, recombination, and evaluation. The plant breeder of the future will know the complete genetic code of his/her organism, the genomic relationship of the DNA sequence to traits of interest, which genes are expressed in different genetic backgrounds and environments, and how these genes interact in networks. This approach requires the coupling of lab and field. Advances in genotyping are of little use to the applied geneticist without efficient and accurate phenotyping.

Research has shown that about half of the increases in crop productivity are due to genetic changes, and the other half is due to fertilizers, pesticides, water use, and other aspects of crop management. Since plant breeding can be considered as applied plant genetics, one has to assume that the unimaginable forward steps in genetic knowledge and technologies will enhance plant breeding efficacies, even to the point where food, fiber, feed, and fuel production will meet the needs of the additional billion people on the planet every 14 years. Our current food system is excellent but not perfect; plant breeding will address issues in the future that have received little attention in the past. Breeding will find ways to address the severe pesticide poisoning that affects more than 25 million people

in developing countries. And breeding will finds ways of reducing agriculture's use of 70% of all fresh water.

Breeding of the future will have the means to control homologous and homoeologous recombination, tools to measure genetic diversity and identify bottlenecks and new alleles, means to mutagenize and knock-out or knock-down specific genes, identify new sources of flood and drought tolerance, create more nutritious crops that have specific health effects, and crops that make our food safer and our environment healthier.

Einstein believed in using imagination. He said "I am enough of an artist to draw freely upon my imagination. Imagination is more important than knowledge. Knowledge is limited. Imagination encircles the world."

Biography:

Dr. Phillips is Regents Professor and McKnight Presidential Chair in Genomics, University of Minnesota. He earned B.S. and M.S. degrees from Purdue University and a Ph.D. from the University of Minnesota; postdoctoral training was at Cornell University. Dr. Phillips has advised over 60 graduate theses and taught a course in cytogenetics as a faculty member in the Department of Agronomy and Plant Genetics for over 40 years. Dr. Phillips received the prestigious Wolf Prize in Agriculture in Israel in 2007 for "ground breaking research in service of mankind". In 1991, he was elected a member of the National Academy of Sciences. Currently, he serves on the Board of Trustees of the premier International Rice Research Institute in the Philippines and on the Scientific Advisory Board of the Donald Danforth Plant Science Center. Other awards include an honorary doctorate from Purdue University, Fellow of AAAS (American Association for the Advancement of Science), ASA (American Society of Agronomy), and CSSA (Crop Science Society of America), the Purdue University Agriculture Distinguished Alumni Award, the Dekalb Genetics Crop Science Distinguished Career Award, and the Crop Science Society of America Research Award. Dr. Phillips served as Chief Scientist of the USDA (1996-1998) in charge of the National Research Initiative Competitive Grants Program and chaired the Interagency Working Group that wrote the plan for the NSF Plant Genome Research Initiative. He served as President of the Crop Science Society of America in 2000 and Chair of the Council of Scientific Society Presidents in 2006.

Throughout his career, Dr. Phillips has coupled the techniques of plant genetics and molecular biology to enhance our understanding of basic biology of cereal crops and to improve these species by innovative methods. His research program at the University of Minnesota was one of the early programs in modern plant biotechnology related to agriculture. He is a founding member and former Director of both the Plant Molecular Genetics Institute of the University of Minnesota and the Microbial and Plant Genomics Institute. He has served on numerous editorial boards, edited six books, and published over 140 refereed journal articles, 70 chapters, and 340 abstracts. Dr. Phillips has been invited to teach, present the results of his research, or serve in an advisory capacity at numerous university, governmental, and industrial institutions in the U.S. and abroad.

Dr. Phillips conducts research and teaching in plant genetics applied to plant improvement with an attempt to bridge basic and applied aspects. The research objectives have been to develop and apply molecular genetic information to the improvement of important traits, to evaluate somatic cell genetic systems for manipulating crop species, to develop and use genetic and molecular biological selection procedures, and to develop high-throughput genomic mapping procedures. As Regents Professor and member of the National Academy of Sciences, he participates in addressing University-wide, national, and international issues.

The Genetics of Domestication: The Evidence from Maize and Other Crops

Dr. John Doebley, University of Wisconsin-Madison

Abstract:

Ten thousand years ago human societies around the globe began to transition from hunting and gathering to agriculture. By 4,000 years ago, ancient peoples had completed the domestication of all major crop species upon which human survival is dependent including rice, wheat and maize. Recent research has begun to reveal the genes responsible for the agricultural revolution. The list of genes to date tentatively suggests that diverse developmental pathways were the targets of Neolithic genetic tinkering, and we are now beginning to understand how plant development was redirected to meet the needs of a hungry world. The lecture will focus on the genetic steps involved in the domestication of maize but draw on evidence from other crops, especially the cereals.

Biography:

Dr. John Doebley is a Professor of Genetics and a member of the Plant Breeding Faculty at the University of Wisconsin-Madison. Dr. Doebley holds a B.A. in Anthropology from West Chester State College (1974) and a Ph.D. in Botany from the University of Wisconsin-Madison (1980). He is a member of the National Academy of Sciences USA (2002), a Fellow in the AAAS (1991), and a member of Phi Kappa Phi (1975) and Sigma Xi (1980). He has received the Gamma Sigma Delta's Award of Merit for Outstanding Service to Agriculture (1992) and the Kellet Mid-Career Award at the University of Wisconsin-Madison (2000). In 2005, he served as President of the American Genetic Association. He has served a member of several editorial boards, advisor boards and panels. Doebley is a geneticist who studies how genes drive plant development and evolution with a focus on the domestication of maize. He resolved the long-standing question of the nature of the genetic differences between maize and its ancestor, teosinte, and he has cloned and characterized two of the major genes that cause the visible differences between these two very different plants. His work has advanced our understanding of how genes cause structural change in evolution and how complex traits are inherited.

Where Are We Growing? Making Sense of Plant Breeding Data Across Environments

Dr. José Crossa, CIMMYT (International Maize and Wheat Improvement Center)

Abstract:

In agricultural and plant breeding research, multi-environment evaluation trials are used to develop recommendations concerning cultivars for adoption by farmers. Linear-bilinear (multiplicative) statistical models are useful for studying genotype × environment interaction (GE) and estimating realized genotypic responses in specific sites. These models can be used within the fixed effects or mixed effects framework. In this presentation I will (1) describe the theory of the multiplicative fixed effects models and summarize results on shrinkage estimates of multiplicative models for better estimation of phenotypic performance across environments, (2) show how to use mixed linear models with coefficient of parentage (COP) for better prediction of breeding values using multi environment data, and (3) explain results of statistical models for marker-trait association by means of incorporating the COP for modeling GE . Often shrinkage estimation of linear-bilinear models produce better estimates than BLUPs of the cell means and appear to always yield better estimates than do truncated multiplicative linear-bilinear models fitted by least squares. In plant breeding, multi-environment trials may include sets of related genetic strains. In self-pollinated species the covariance matrix of the breeding values of these genetic strains is equal to the additive genetic covariance among them. This can be expressed as an additive relationship matrix **A** multiplied by the additive genetic variance. Using mixed model methodology, the genetic covariance matrix can be estimated and BLUPs of breeding values obtained. The effectiveness of exploiting relationships among strains tested in multi environments trials and the usefulness of the BLUPs of breeding values for simultaneously modeling the main effects of genotypes and genotype × environment interaction (GE) have been studied using a Kronecker (direct) product of a sites factor analytic covariance matrix and a matrix (**A)** of genetic relationships between. Results comparing this approach with traditional fixed effects and random effects models for studying GE ignoring genetic relationships showed that factor analytic structures with inclusion of matrix **A** efficiently model the main effects of genotypes and GE. Modeling GE using the relationship matrix **A** was proved to be effective for studying trait-marker association in historical wheat trials and detecting molecular markers associate to leaf rust, yellow rust, stem rusts, and grain yield.

Biography:

Dr. José Crossa has been a principal scientist at the International Maize and Wheat Improvement Center (CIMMYT) located in Mexico, D.F., Mexico, working in the Crop Research Informatics Lab as part of the Biometrics and Statistics Unit since 1998 having begun his career at CIMMYT as a post-doctoral fellow in 1984. Dr. Crossa holds a B.S. in Agriculture from Universidad de la República Oriental del Uruguay, Facultad de Agronomía (1974) and a Ph.D. from the University of Nebraska-Lincoln (1984). He is a member of the Mexican Academy of Science and a fellow of the Agronomy Society of America and the Crop Science Society of America. He has received several awards (1997, 1999, 2002, 2004, 2005, and 2006) by the Genetic Resource Conservation Division of the Crop Science Society of America for one of the three best research articles published in Crop Science. Dr. Crossa has also been an Associate Editor for a number of scientific journals, including: Crop Science (1996-200), Euphytica (1994-present), Agrociencia (2001-present), Revista Mexicana de Fitopatologia (2002-present), and has served on the editorial board of the Open Horticultural Journal. Dr. Crossa's research focuses on developing statistical models and methods to aid plant breeders. Such methods have included means for analyzing genotype X environment interactions, the design and analysis of field experiments, and developing statistical methodologies for the maintenance and characterization of genetic resources (i.e.- germplasm collections).

Big Science and Plant Breeding: Usefulness of Genomics Data

Dr. William D. Beavis, Iowa State University

Abstract:

Plant genome initiatives have promised future crop improvement based on fundamental research information. While developmental and evolutionary biologists have taken advantage of 'omics' data to generate testable hypotheses about fundamental molecular mechanisms, the same information is not being used by public sector translational researchers and applied plant breeders. This is due, in part, to the enormous gap between assigning function to a gene and developing an improved crop variety. Our premise is that reengineering genetic networks that have emerged from thousands of years of selection is, at best, a very long term goal. We believe that the ancient tool of selection will be the most effective means to translate 'omics' information into crop improvement. This translational research challenge consists of three overlapping activities: 1. Identify functional allelic variants 2. Assign breeding value to the allelic variants. 3. Determine the optimal selection strategies to bring desirable allelic variants into the crop. We'll discuss the tools and resources, with emphasis on decision support systems, that will be needed to translate omic information into applied breeding.

Biography:

Ph.D., 1986, Plant Breeding Major, Statistics Minor, Iowa State University, Ames, IA
M.S., 1981, Interdisciplinary Biology-Statistics, New Mexico State University, Las Cruces, NM
B.S., 1978, Range Management, Humboldt State University, Arcata, CA.

Most often cited for his discovery of bias in estimates of genetic effects in statistical analyses of populations with poor power (the "Beavis Effect"), Bill gained extensive experience in the application of statistical genetic methods during his twelve years at Pioneer Hi-Bred. As Chief Science Officer and Chief Operating officer at the National Center for Genome Resources in Santa Fe, New Mexico, Bill provided leadership in establishing a sustainable non-profit research institute in a predominantly Hispanic and poor region of the United States. In late 2007, Dr. Beavis joined the faculty at Iowa State University as the G.F. Sprague Chair of Crop Genomics and Sustainable Agriculture. His academic appointment is 75% research and 25% teaching.

Bill's research interests have been focused on finding the genotypic basis of complex traits for purposes of developing high throughput diagnostic tests. Towards this goal he has focused on development and application of statistical genetics, (statistical modeling and analysis of complex and quantitative traits) and bioinformatics (data modeling and integration of large biological information resources). His long term goal at ISU is to predict the breeding value of genes for traits such as biomass production and disseminate such information through an electronic decision support system. Bill's teaching interests are in assuring that the next generation of Biologists will be prepared to address complex problems with mathematical and statistical skills. In particular, he is teaching statistics and quantitative genetics to graduate students through distance and on-campus venues.

Tree Breeding: Conquering High Heterozygosity and Long Generation Times

Dr. David Neale, University of California-Davis

Abstract:

Genomic discovery in forest trees follows paradigms from both agricultural crop and livestock improvement and human medicine. Forest trees in a domesticated state can be improved using genomic-based breeding technologies whereas the health of trees in a natural and undomesticated state might be managed using those same technologies. These applications begin by first dissecting complex traits in trees to their individual gene components and for that the association genetics approach is quite powerful in trees. This is true for several reasons including large, random mating and unstructured populations and the rapid decay of linkage disequilibrium in many tree species. Once marker by trait associations are discovered they can be used in genomic-based breeding and forest health diagnostics. High-throughput DNA sequencing and genotyping technologies have enabled a new generation of research in forest genetics where combined quantitative and population genetic approaches can be used to better understand the relationship between naturally occurring genotypic and phenotypic diversity.

Biography:

Dr. David Neale has been a professor in the Department of Plant Sciences at the University of California- Davis since 2005 and has served as chair of the Genetics Graduate Group since 2006. Dr. Neale received his B.S. in Forest Science in 1976 and his M.S. in Forest Genetics in 1978, both from the University of New Hampshire, before moving to Oregon State University where he obtained his Ph.D. in Forest Genetics in 1984. Upon receiving his Ph.D., he moved to UC Davis as a postdoctoral fellow and promptly joined the USDA Forest Service, where he held several positions until 2001. In 1994 he became an Adjunct Professor in the Department of Environmental Horticulture and held that position until becoming full professor. Dr. Neale is also currently the Co-chair of the Bioenergy Research Group at UC Davis, as well as the Editor-in-Chief of the journal, Tree Genetics and Genomes. Additionally, Dr. Neale is co-author of a recently published book on forest genetics, which is likely to become the standard text on the topic for years to come.

Dr. Neale's primary research interest is in the discovery and understanding of the function of genes in forest trees, especially those controlling complex traits, through genetic mapping and genomic science technologies. His objective is to use cloned genes from pine species as tools for functional analysis. This will, in turn, lead to an understanding of complex patterns of coordinated gene expression leading to phenotypic traits, with initial emphasis being placed on traits of practical value (wood quality, growth, and disease resistance), and expanding upon those traits to include the identification of genes determining patterns of adaptation and response to environmental stresses.