



**Interdepartmental Plant Physiology Major
Fall Seminar Series (P Phy 696)**

Perspectives in Plant Biology

**Wednesdays 4:10 – 5:30 pm
Fall, 2007
210 Bessey**

Date	Speaker	Topic
August 29	Andrea Scarpa (IPPM, Agron, VP) Andrew Foudree (GDCB, IPPM VP) Kan Wang (Agron, IPPM Chair)	<ul style="list-style-type: none"> • Issues regarding P Phy 696 • Fall Retreat
September 12	Rob Wallace (EEOB)	Plant Molecular Systematics and its role in understanding Angiosperm Phylogeny
September 19	Matt Liebman (Agronomy)	Growing Green: Ecological Strategies for Sustaining High-Production Agriculture in the American Midwest
October 3	Robert Thornburg (GDCB)	Development and Function of the Ornamental Tobacco Nectary
October 10	Steve Cannon (USDA)	Evolution of the Nucleotide Binding Site-Leucine Rich Repeat disease resistance gene family
October 17	Jackie Shanks (CBE)	Plant Metabolic Engineering: Lessons from Gothic Cathedrals
October 31	Lynn Clark (EEOB)	Bamboo Biology and Evolution
November 14	Bing Yang (GDCB)	Xanthomonas oryzae activates its host rice gene expression as a virulence strategy
November 28	Andrea Scarpa (IPPM, Agron, VP) Andrew Foudree (GDCB, IPPM VP) Kan Wang (Agron, IPPM Chair)	<ul style="list-style-type: none"> • Fall P Phy 696 conclusion • Arrange spring seminar series • Elect new officers for the IPPM Graduate Student Organization
December 5	Off-campus speaker	To Be Determined

Light refreshments will be available prior to seminar

Direct questions or comments to Andrea Scarpa at 4-5940/ ascarpa@iastate.edu or Andrew Foudree at 4-1767 afoudree@iastate.edu



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Invited Speaker: Dr. Robert Wallace (EEOB)

September 12, 2007

Plant Molecular Systematics and its role in understanding Angiosperm Phylogeny

Abstract

Plant systematists have historically sought evolutionary information which can provide a better understanding of the phylogenetic relationships within and among the angiosperms. The need to rigorously assess which flowering plant groups should be deemed "primitive" versus those that are derived, is especially apparent when proposing hypotheses of evolutionary diversification, and further enables the development of a more satisfying interpretation of morphological, physiological, and ecological characters found throughout the group. A review of significant impacts that the study of molecular variation of the various plant genomes has had on interpreting angiosperm phylogeny will be presented, in the context of a modern interpretation of the major lineages of angiosperms. Nucleotide sequence variation, as well as structural rearrangements within the plastid genome will be presented, with the goal of identifying phylogenetically-important molecular characters which assist in the definition of major lineages of flowering plants.

Brief Bio data of Dr. Robert Wallace:

Robert Wallace is a native of Cedar Grove, New Jersey, and received his BS in Biology from Wilkes University (Pennsylvania), M.S. and Ph.D. degrees in Botany and Plant Physiology from Rutgers University (New Jersey), and was a Postdoctoral Associate at the University of Connecticut for 2.5 years. He has been on the faculty at Iowa State University since 1990, and has focused his research on investigating phylogenetic relationships of a variety of desert plants (particularly those within Order Caryophyllales), especially the family Cactaceae (the Cactus Family), using morphological and molecular methods. He has done field research in Andean South America (Chile, Peru), South Africa, Mexico, Europe, and throughout the United States. At ISU, he teaches undergraduate courses in Evolution, Plant Systematics, Economic Botany, and a graduate course in Biogeography.

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210 Bessey Hall

Invited Speaker: Dr. Matt Liebman (Agron)

September 19, 2007

Growing Green: Ecological Strategies for Sustaining High-Production Agriculture in the American Midwest

Abstract

We conducted a 9-ha field experiment near Boone, IA, to test the hypothesis that yield, weed suppression, and profit characteristics of low-external-input (LEI) cropping systems can match or exceed those of conventional systems. Over a four-year period, we compared a conventionally managed 2-yr rotation system [corn (*Zea mays* L.)/soybean (*Glycine max* (L.) Merr.)] with two more diverse LEI systems: a 3-yr corn/soybean/small grain + red clover (*Trifolium pratense* L.) rotation, and a 4-yr corn/soybean/small grain + alfalfa (*Medicago sativa* L.) alfalfa rotation. Synthetic N fertilizer use was 59% and 74% lower in the 3-yr and 4-yr systems, respectively, than in the 2-yr system; similarly, herbicide use was reduced 76% and 82% in the 3-yr and 4-yr systems. Corn and soybean yields were as high or higher in the LEI systems as in the conventional system, and weed biomass in corn and soybean was low (≤ 4.2 g m⁻²) in all systems. Giant foxtail (*Setaria faberi* Herrm.) seed densities in the surface 20 cm of soil declined in all systems; velvetleaf (*Abutilon theophrasti* Medik.) seed densities declined in the 2-yr and 4-yr systems and remained unchanged in the 3-yr system. Without subsidy payments, net returns were highest for the 4-yr system (\$540 ha⁻¹ yr⁻¹), lowest for the 3-yr system (\$475 ha⁻¹ yr⁻¹), and intermediate for the 2-yr system (\$504 ha⁻¹ yr⁻¹). With subsidies, differences among systems in net returns were smaller, but the rank order of systems was maintained. Higher profitability of the 4-yr rotation as compared with the 2-yr rotation derived from a 28% reduction in production costs. Biological nitrogen fixation, nutrient cycling, and weed seed predation by rodents and insects were three ecological processes that promoted cost reduction and maintenance of high yields in the LEI systems. Low-external-input farming systems are likely to become increasingly important as society seeks to reduce dependence on petrochemical inputs and minimize environmental pollution by agrichemicals.

Brief Bio data of Dr. Matt Liebman:

Matt Liebman is a Professor of Agronomy and was named the Henry A. Wallace Endowed Chair for Sustainable Agriculture in July 2007. He received a B.A. in biological sciences from Harvard University in 1978 and a Ph.D. in botany from the University of California–Berkeley in 1986. Dr. Liebman held the Pioneer Agronomy Professorship during 2001-2004 and is a co-author of "Ecological Management of Agricultural Weeds," published by Cambridge University Press in 2001. His research focuses on the development of farming systems that are productive, profitable, and healthy for people and the environment.

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Invited Speaker: Dr. Robert Thornburg (GDCB)

October 3, 2007

Development and Function of the Ornamental Tobacco Nectary

Abstract

Many angiosperms have an unusual sexual habit. They utilize animals as intermediaries in the transfer of gametes between flowers. These angiosperms attract these visiting pollinators by offering a reward of metabolite-rich nectar to these visiting pollinators. Our interests lie in understanding the biochemistry, development and function of the floral organ that is the source of this metabolite-rich nectar, the nectary gland. Nectar is a rich concoction of sugars, amino acids, vitamins, metal ions and proteins. Our analysis indicates that the proteins mediate a novel biochemical pathway we call the Nectar Redox Cycle. This pathway produces extremely high levels of hydrogen peroxide to protect the gynoecium from invading microorganisms vectored to the flower by visiting pollinators. This pathway is expressed late in nectary gland development. Analysis of the Nectarin I (*nec1*) promoter has permitted the isolation of the transcription factor, *MYB305*, that binds to the *nec1* promoter. RNAi knockouts of *MYB305* demonstrate that this factor regulates *nec1* expression. We have also examined the nectary developmental processes that lead to nectar formation. We have found that the ornamental tobacco nectaries store sugar as starch during the first eight days of floral development. Then 24 hours before anthesis, the starch is broken down to produce high levels of sugar for nectar. In addition, the sugar from starch also flows into the formation of potent antioxidants (ascorbate and β -carotene). These antioxidants are thought to protect the nectary and gynoecium from the high levels of hydrogen peroxide generated by the nectar redox cycle. Analysis of the genes involved in nectary development, demonstrate that starch metabolism appears to be regulated at the gene level and we have identified a major developmental event termed the metabolic shift. The result of this shift is that the starch anabolic genes are this down-regulated and coordinately starch catabolic genes are up-regulated. The mechanism of this coordinated metabolic shift is the current focus of research in the Thornburg laboratory. Surprisingly, the *MYB305* knockout plants show that this factor also participates in the metabolic shift.

Brief Bio data of Dr. Robert Thornburg:

Robert Thornburg is a native of Tennessee. He graduated from the University of Tennessee with a BS in Chemistry. He went to graduate school at the University of South Carolina, where he received his PhD in 1981, also in Chemistry. His thesis work under the direction of John Baynes examined host-parasite interactions from the host's point of view. He did postdoctoral studies at the University of Texas-Health Science Center in San Antonio, Department of Microbiology, where he worked on host-parasite interactions from the parasite's point in the laboratory of Joel Baseman. After his first postdoctoral stint, he moved to the Institute of Biological Chemistry at Washington State University where he worked with CA Ryan. As a postdoctoral fellow, Dr. Thornburg was the first person to isolate a wound-inducible gene and characterize it in transgenic plants. In 1986, Dr. Thornburg moved to the Department of Biochemistry and Biophysics at Iowa State University. Dr. Thornburg is currently Professor of Biochemistry in the BBMB Department.

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Wednesdays 4:10 – 5:30 pm
210 Bessey Hall

Invited Speaker: Dr. Steve Cannon (USDA / Agron)

October 10, 2007

Evolution of the Nucleotide Binding Site-Leucine Rich Repeat disease resistance gene family

Abstract

Plants have evolved sophisticated mechanisms to recognize and guard against pathogens. In the past decade, disease resistance genes (R genes) have been cloned from numerous plant species, conferring resistance to a wide range of plant pathogens including bacteria, fungi, oomycetes, viruses, and nematodes. Despite the wide range of pathogen taxa involved, R genes seem to encode a limited set of proteins consisting of conserved domains. An important question, therefore, is how R genes evolve and stay ahead of pathogens. The largest class of R genes encodes proteins with a nucleotide-binding site (NBS) and a leucine-rich repeat (LRR) region. I will describe two projects that track the evolutionary dynamics of the NBS-LRR gene family in the legume plant family. The first project traces how NBS-LRRs have evolved in the model legume *Medicago truncatula* (a close relative of alfalfa, *M. sativa*). We find evidence for 400-500 NBS-LRRs in *M. truncatula*, or more than three times as many as in *Arabidopsis thaliana*. We also find that most of these genes have arisen recently in large NBS-LRR "nurseries", that the genes are relatively mobile in the genome, and that there are clusters of especially diverse NBS-LRRs. This gene family clearly has had a large impact on the structure of the genome, both through ectopic translocations (which may serve as "pioneers" for new NBS-LRR clusters), and through superclusters that dominate and change the evolutionary patterns of large parts of several chromosomes. The second project traces the evolution of NBS-LRRs in a million-basepair region in the soybean genome, and the corresponding region in a duplicated region in soybean and in six other legume genomes. In this region, we find evidence of rampant recombination between the genes.

Brief Bio data of Dr. Steven Cannon:

Steven Cannon is a Research Geneticist with the USDA Agricultural Research Service, and an adjunct Assistant Professor in Agronomy. He works on two genome sequencing projects (soybean and *Medicago truncatula*), on patterns of genome and gene family evolution, and on bioinformatic methods for aligning, comparing, and exploring genome sequences. Dr. Cannon's background includes B.S. degrees in math and biology, M.S. in urban planning, several years' work experience as a software designer in an educational software company. He received his Ph.D. in plant biology in 2003 at the University of Minnesota, and worked as a postdoctoral researcher on the *Medicago truncatula* genome sequencing project. He moved to the USDA-ARS at ISU in 2006.

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Invited Speaker: Dr. Jacqueline Shanks (CBE)

October 17, 2007

Cathedral roseus*

***and other interesting tales in Plant Metabolic Engineering**

Abstract

Plants produce a wide variety of secondary metabolites many of which are economically important in the areas of pharmaceuticals, nutrition, flavors and fragrances, fine chemicals, and cosmetics. In most cases, production of these compounds are limited to plants because synthetic routes of producing these structurally complex molecules are often more expensive than producing them natively within the plant even though the yields within the plant are small. Thus it is desirable to use the techniques of metabolic engineering to increase the yield of specific metabolites within the plant.

We have chosen to study the terpenoid indole alkaloid (TIA) pathway in *Catharanthus roseus* hairy roots as a model system because it produces two pharmaceutically important anticancer drugs vinblastine and vincristine which are used in the treatment of cancers such as lymphoma and leukemia. This talk will highlight the engineering approaches to systematically increase TIA production and in doing so, offers lessons in plant metabolic engineering. We have used the tools of precursor feeding studies, elicitor studies, flux analysis and expression profiling of target genes by Q RT PCR to better understand the bottlenecks within the indole and terpenoid pathways. Using this information, we then constructed transgenic *C. roseus* hairy root lines by using molecular biology tools to overexpress one or more strategic genes in the terpenoid and/or indole pathway under the control of an inducible promoter system. In addition, we determined the effects of these genetic manipulations on TIA production by focusing on the levels of 6 TIA compounds, where the authentic standards were available. We have begun to further characterize other unidentified metabolites from these transgenic hairy root lines using LCMS and tandem LSMS/MS data.

Brief Bio data of Dr. Jacqueline Shanks:

Jacqueline V. Shanks is a native of Granger, Iowa and received her B.S. degree in chemical engineering from Iowa State University and her Ph.D. degree in chemical engineering from the California Institute of Technology. She progressed through the academic ranks (assistant, associate, full professor) in the chemical engineering and bioengineering departments at Rice University. In Fall 1999, she joined the faculty at Iowa State University and is professor in chemical engineering at Iowa State University and an adjunct professor in bioengineering at Rice University. Dr. Shanks' research interests include plant metabolic engineering of secondary metabolites, nuclear magnetic resonance spectroscopy (NMR) techniques for metabolic flux analysis, phytoremediation of explosives and related nitroaromatics, and production of valuable products from biorenewable resources.

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Invited Speaker: Dr. Lynn G. Clark (EEOB)

October 31, 2007

Natural History of Bamboos (*Poaceae: Bambusoideae*)

Abstract

Grasses are among the most ecologically and economically important groups of plants. The cereals, sugarcane, bamboos, forage and weedy grasses are pre-eminent in human economy and civilization. Grasses occur in virtually every terrestrial habitat, covering as much as 1/5 of the Earth's land surface, and are often dominant in the vegetation cover. The economic and ecological significance of the grasses, and the use of some species as model organisms, has led to widespread interest in their evolution and classification. In recent years, the use of DNA sequence data for phylogenetic reconstruction has given us a much improved understanding of the major clades within the family and its pattern of diversification. Grasses originated in tropical forests of the southern hemisphere probably as much as 70-80 million years ago (mya) but apparently did not undergo significant radiation until about 40 mya. By 5 mya, all major clades of grasses were present, according to the fossil record. The grass family presently includes approximately 10,000 species in over 700 genera.

Bamboos are the only major clade of grasses to have diversified in forest habitats, where they often constitute a major component of the vegetation, and comprise approximately 1,400 species worldwide. Within the grass family, it is still not clear if bamboos are sister to the rices and their allies or bluegrasses and their allies. Bamboos comprise two major groups, the woody bamboos and the herbaceous bamboos, with the bulk of the species diversity (ca. 1,300) found within the woody bamboos. Woody bamboos exhibit several unusual life history features, including complex vegetative branching and gregarious, monocarpic flowering, whereas herbaceous bamboos have unisexual spikelets and some are insect-pollinated. An on-going collaborative effort to reconstruct a global phylogeny for the bamboos using plastid DNA sequence data and morphological data has produced some interesting results, including evidence of extensive reticulation, and provides a framework to explore the evolution of some of the unusual biological features of bamboos.

Brief Bio data of Dr. Lynn G. Clark:

Lynn G. Clark is a native of Alexandria, Virginia and received her B.S. degrees in botany and horticulture from Michigan State University and her Ph.D. degree in botany (plant systematics) from Iowa State University (ISU). After her major professor retired, she was hired in the Dept. of Botany at ISU and progressed through the academic ranks (assistant, associate, full professor) and then joined the Dept. of Ecology, Evolution and Organismal Biology after the re-organization of the biological sciences at ISU. Dr. Clark's research interests focus on the systematics and evolution of grasses, with a major emphasis on bamboos. Recent work includes a collaborative phylogeny of the grass family (the Grass Phylogeny Working Group); establishment of the Bamboo Phylogeny Group (currently 18 collaborators from around the world) to reconstruct a robust phylogeny for the bamboos; continued description of new species of primarily Neotropical bamboos (over 75 to date); floristic inventory and monographic work on Neotropical bamboos; and the Grasses of Iowa, a web-based resource including a database and eventually an interactive key.

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Invited Speaker: Dr. Bing Yang (EEOB)

November 14, 2007

***Xanthomonas oryzae* activates its host rice gene expression as a virulence strategy**

Abstract

The bacterial blight of rice, one of the most severe rice diseases in Asia and Africa, is caused by the bacterial pathogen *Xanthomonas oryzae* pv. *oryzae* (Xoo). The pathogen uses the type III secretion system (T3SS) to deliver and internalize a group of bacterial proteins called type III effectors into its host cells. These effectors are characteristic of eukaryotic transcription activator that contains the nuclear localization signals as well as transcription activation domain. The effectors, we refer to as transcription activator-like (TAL) effectors, serves as virulence factors for pathogen to promote bacterial multiplication, colonization and disease development. I will present the data that the TAL effectors (PthXo1, AvrXa7) specifically activate the host gene expression and such elevated changes in gene expression are associated with host disease susceptibility. Using DNA microarray analysis we found that the rice gene *Os8N3*, a member of *MtN3* gene family from plants and animals, was elevated upon infection by PXO99 and specifically depended on *pthXo1*, a major virulence gene for PXO99. Silencing of *Os8N3* by RNA interfering (RNAi) resulted in transgenic plants that lost the susceptibility to infection by PXO99, but remained susceptible to other strains of the pathogen. The effector gene *avrXa7* from strain PXO86 enabled PXO99 susceptibility on *Os8N3*-silenced plants which can be explained by our recent work that *avrXa7* targets another member of *MtN3* in rice for disease susceptibility. AvrXa7 is another member of TAL effector family. *avrXa7* is also a major virulence factor for PXO86 to cause disease on the otherwise susceptible rice. AvrXa7 up-regulates the expression of *Os11N3*, a relative of *Os8N3* and also a member of *MtN3* family. The knockdown or silencing of *Os11N3* expression by RNA interfering (RNAi) approach using a fragment of gene specific to *Os11N3* results in transgenic plants that lost the susceptibility to *avrXa7*-dependent strains. Our data suggests that Xoo strains use the TAL effectors to reprogram the host gene expression and explore the host genetic vulnerability to disease. Our data also supports a model for gene-for-gene susceptibility in bacterial blight of rice.

Brief Bio data of Dr. Bing Yang

Bing Yang joined the Department of Genetics, Development and Cell Biology as the assistant professor early this year. He got his Ph.D. in Plant Pathology at Kansas State University in 2000. At ISU, he will continue working on the bacterial blight of rice as a model pathsystem to address some fundamental biological questions, such as, how plant becomes diseased, how plant evolutionarily adapts to infection of microbial pathogen. The long term goal of Dr. Yang's research is to better understand the plant disease, to gain knowledge that will help engineer disease immune crops.

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