Interdepartmental Plant Physiology Major
Spring Seminar Series (P Phy 696)

Student Seminar Presentation

Wednesdays 4:10 – 5:30 pm
1420 Molecular Biology Building

Date	Speaker (Major Professor)	Topic
January 23	**Jen Gray** (VP) **Stephanie Moon** (VP) **Kan Wang** (DOGE)	• Issues regarding P Phy 696 • Student issues • Opening
January 30	**Andrew Foudree** (GDCB, Rodermel Lab)	Immutans Chloroplast Biogenesis
February 6	**Michael V. Kolomiets (Assistant Prof., Texas AM University) (Invited speaker)**	**Functional genomics analysis of maize lipoxygenases: role in cross-kingdom signal communication with pathogens**
February 13	**Jen Gray** (BBMB, Nikolau Lab)	Molecular and biochemical characterization of a fusion protein that catalyzes two sequential reactions in the biotin biosynthetic pathway
February 20	**Alex (Lixun) Su** (GDCB, Becraft Lab)	Effect of anaerobiosis and transcription factor expression on maize embryo germination
March 5	**Qiang Wang** (BBMB, Peters Lab)	Rice gibberellic acid metabolism
March 12	**Xing Xu** (Agron, Wang Lab)	Increase expression of a recombinant pharmaceutical protein in transgenic maize: Collagen
March 19	**Spring Break**	No Class!!!
March 26	**Loomis Lecture Week**	No Class!!!
April 2	**1) Dan Hand** (Rotation)	TBA
	2) Stephanie Moon (BBMB, Nikolau Lab)	TBA
April 9	**1) Shan Li** (Agron, Bhattacharyya Lab)	TBA
	2) Gibum Yi (Rotation)	TBA
April 16	**James Register (Research Director, Pioneer Hi-Bred International) (Invited Speaker)**	**Research Life in AgBiotech Industry: how can you get prepared**
April 23	**Nicholas Boersma** (Hort, Christians Lab)	**Exit seminar:** TBA
	Kan Wang (DOGE)	Wrap up

Light refreshments will be available prior to seminar
Direct questions or comments to Kan Wang (kanwang@iastate.edu, 4-4429)

Direct questions or comments to Jen Gray at 4-0347/ jengray@iastate.edu or Stephanie Moon at 4-0347 /moonsm03@iastate.edu

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Andrew Foudree (GDCB)

January 30, 2008

Immutans Chloroplast Biogenesis: Characterization of Early Development

Abstract

A mutation in the *immutans* gene in Arabidopsis impedes the proper formation of chloroplasts during development. These mutant plants form white and green sectors that have clearly defined borders. *Immutans* is considered a photosensitive mutant and its variegation is dependent on light intensity. By map based methods, this mutation has been mapped to a nuclear gene known as plastid terminal oxidase or PTOX. To investigate the mechanism of this variegation we have chosen to look at how the chloroplasts in this mutant develop during early leaf formation.

It is thought that the immutans variegation phenotype forms early on and does not affect already differentiated plastids. Therefore, we think that the role played by *immutans* is somehow involved in the differentiation process of chloroplasts from the proplastid stage. Through molecular genetics and microscopy, we have chosen to look at the effects *immutans* has on early chloroplast formation in Arabidopsis.

Brief Bio of Andrew Foudree:

Andrew Foudree received his B.S. from the University of Minnesota in Microbiology. After graduation, he worked in industry doing forensic drug testing and analysis for three years. Andrew was admitted to the IPPM program in fall of 2005 and is currently working under Dr. Steve Rodermel.

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Jennifer Gray (BBMB)

February 13, 2008

A Novel Bifunctional Protein (BIO3/BIO1) Is Capable of Catalyzing Two Sequential Reactions In the Biotin Biosynthetic Pathway in *Arabidopsis*

Abstract

Biotin, also known as vitamin B7, is vital for all organismal survival. The water soluble vitamin facilitates carboxyl transfer by acting as a cofactor to enzymes that catalyze carboxylation, decarboxlation, and transcarboxylation reactions. These biotin-binding enzymes are found in such pathways as lipid metabolism and gluconeogenesis. Plants, bacteria, and some fungi can synthesize biotin, but humans and animals cannot. Therefore, humans must acquire biotin through their diet. The genes that encode the enzymes in the biotin biosynthetic pathway in *Escherichia coli* are well characterized, but the structural and catalytic properties of the homologous plant proteins are not yet known.

This project first set out to characterize the BIO1 gene, which encodes DAPA aminotransferase in *Arabidopsis thaliana*. Genetic studies then lead to the discovery that the BIO3 gene is located immediately upstream of the BIO1 gene in the *A. thaliana* genome. Further experiments uncovered two differentially-spliced transcripts produced from this locus. These transcripts differ in size by ten nucleotides. One transcript is denoted as BIO3/BIO1 (+10), which includes ten more nucleotides than the other transcript, and thus encodes a premature stop codon. It is capable of producing a 44.5 kD protein with catalytic property of BIO3, or dethiobiotin synthetase. Alternatively, a chimeric transcript denoted as BIO3/BIO (-10), lacks the ten nucleotides and the corresponding translation stop site. This transcript is unique in that it encodes a bifunctional 91.9 kD protein that has both BIO3 and BIO1 catalytic activity.

Further studies, such as bioinformatics prediction of this bifunctional protein structure, and also biochemical kinetic analyses will be undertaken in an effort to better understand the characteristics of this novel protein.

Brief Bio of Jennifer Gray:

Jennifer received her B.S. in Plant Biology from Michigan State University in Spring of 2006. She then joined Iowa State University's IPPM in Fall of 2006; her major professor is Dr. Basil Nikolau in the BBMB Department. Jennifer likes to spend time outdoors, and she enjoys plants for both their physiological properties and also their aesthetic value.

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Lixun (Alex) Su (GDCB)

February 20, 2008

Effect of Anaerobiosis and Transcription Factor Expression on Maize Embryo Germination

Abstract

Abscisic Acid (ABA) regulates many aspects of plant growth and development, including embryo maturation, seed dormancy, abiotic stress responses, leaf senescence, and stomatal aperture. During the maturation phase of seed development, ABA can induce the expression of many transcription factors, which can form a complex ABA responsive pathway. VIVIPAROUS1 (VP1) is a B3 domain-containing transcription factor that is central to the regulation of seed maturation in maize and is a key regulator in plant's response pathway to ABA. Oxygen concentration can affect the physiological properties of many plants. We found that a total hypoxia environment can completely inhibit maize embryo germination. Like ABA, Anaerobiosis-inhibited germination cessation also has a close relationship with the endogenous VP1 level. We are trying to find the relationship between anaerobiosis-induced and ABA-induced germination inhibition and the role of VP1 in these processes.

Brief Bio of Lixun Su:

Lixun was born and spent the first 18 years of his life in Fuzhou, China. He received his B.S. in Biological Science from Xiamen University in 2006. He was admitted to the Interdepartmental Plant Physiology Major of Iowa State University in fall of 2006. After rotation, he joined Dr. Becraft's lab in the GDCB Department.

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Qiang Wang (BBMB, Peters Lab)

March 5, 2008

Clarifying gibberellic acid metabolism

Abstract

Gibberellins (GAs) are a group of diterpenoid compounds, some of which act as growth-promoting hormones controlling such diverse processes as stem elongation, leaf expansion, seed germination, and flowering. GAs are biosynthesized from geranylgeranyl diphosphate (GGPP), a common C20 precursor for diterpenoids. Conversions of GGPP into bioactive GAs and their deactivation involve three classes of enzymes: plastid-localized terpene cyclases (copalyl diphosphate synthase, CPS; and kaurene synthase, KS), membrane-bound cytochrome P450 monooxygenases (kaurene oxidase, KO; and kaurenoic acid oxidase, KAO), and soluble 2-oxoglutarate-dependent dioxygenases (GA 20-oxidase, GA 3-oxidase, GA 2-oxidase).

Recently one novel class of GA 2-oxidase has been identified which catalyzes hydroxylation at the C2 position of 20 carbons GAs (e.g. GA_{12}). Although GA 2-oxidases have been previously identified, these are specific for 19 carbon nor-diterpenoid GAs, and the two types of GA 2-oxidases clearly fall into separate enzymatic families that share limited homology (<40% aa identity). The only characterized examples of these novel 20 carbon GA 2-oxidases are from the dicots *Arabidopsis thaliana* and spinach, although homologs can be found in the rice genome (Schomburg et al., 2003; Lee and Zeevaart, 2005). Thus, the aim of my first project is biochemical characterization of the rice 20 carbon GA 2-oxidase homologs.

AtCPS and AtKS catalyze the first two steps in GA biosynthesis. Overexpression of AtCPS and AtCPS/AtKS results in accumulation of 1000 times more *ent*-kaurene and *ent*-kaurenoic acid than wild type, but only approximately 10 times more GA_{12} than wild type, no GA overdose morphology was observed and these overexpression lines have wild-type levels of bioactive GAs. Based on these differences between early and later GA intermediates, it appears that KAO limits the production of later GA intermediates. No transcriptional regulation of AtKAO has been reported. Thus, KAO may be under biochemical regulation. My second project focuses on clarifying the role of KAO in GA metabolism regulation by biochemical and genetic approaches.

Brief Bio of Qiang Wang:

Qiang Wang obtained his BS in Biology in 2000 and MS in Botany in 2003, at Sichuan University. He enrolled in IPPM of Iowa State University in Fall 2006 and is working in Dr. Peters lab for his PhD degree.

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Xing Xu (Agronomy, Wang Lab)

March 12, 2008

Expression of Recombinant Collagen and Gelatin in Transgenic Maize

Abstract

Collagen is the most abundant protein of mammals. Collagen and its denature form gelatin have been used widely in food, pharmaceutical, cosmetic, and photography industries. More than 98% of the current collagen and gelatin sources are animal tissue-derived, which have potential risk to human health due to possible pathogen contamination in the tissues. A potential safe and low cost way to produce collagen and gelatin is to use the plant production system.

Maize is chosen for producing recombinant collagen due to its scalability, high yield and the biofuel potential. The collagen will be specifically expressed in maize seed to facilitate extraction and avoid collagen degradation. Seed specific expression can also reduce any detrimental effect of foreign protein on plant growth. While such seed can be used for collagen production, the remaining parts of transgenic maize (such as stover) can be used for ethanol production to increase the economy value of maize as a crop.

To achieve high expression of recombinant collagen in maize, we propose to use a number of signal peptides fused to the collagen gene for targeting different organelles. We will evaluate the effects of these signal peptides in the levels of collagen production. We will also attempt reducing the maize zein protein contents, a major seed storage protein in seeds, using the RNAi (RNA interference) technology. Our hypothesis is that by reducing endogenous storage protein contents we may be able to allow more collagen protein accumulation in seed. Our long term objectives are to understand the mechanisms of exogenous protein expression, trafficking and localization in transgenic plants. It is hoped that such basic study can lead to the production of high yield recombinant collagen in maize.

Brief Bio of Xing Xu:

Xing Xu obtained his BS in Biological Science at Zhejiang University, Hangzhou, China in 2006. He enrolled in IPPM program at Iowa State University in the fall of 2006 and has his home department in Agronomy.

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IPPM
INTERDEPARTMENTAL PLANT PHYSIOLOGY MAJOR

Dan Hand (IPPM Entry Seminar)

April 2, 2008

Analysis of a reduced fertility mutation in *Arabidopsis thaliana* in plant lines that display defective pollen development.

Abstract

My research focused on using *Arabidopsis thaliana* to study plant developmental biology with particular attention to anther pollen development. I studied several lines of *Arabidopsis* with previously induced mutations that were the result of a T-DNA insertional mutagenesis in which *Arabidopsis* seed was germinated on media containing the plant-transforming bacteria *Agrobacterium tumefaciens*. Successfully transformed plants should contain a segment of T-DNA containing an introduced selectable marker, the antibiotic kanamycin resistance gene, from the bacterium. The plant lines used in this study were among the more than 8000 transformants that resulted from the initial mutagenesis experiment and the lines of interest display a defect in the male reproductive structures of the flower. Through genetic and DNA analysis, it is now believed that other undesirable mutation events may have occurred, some introducing segments of *Agrobacterium tumefaciens* Ti plasmid into the plant genome while others resulted in defects within the male reproductive organs, though no DNA of bacterial origin was identifiable. This study contains two primary components; a genetic analysis of two plant lineages in an effort to isolate true-breeding lines of *Arabidopsis thaliana* displaying a reduced-fertility phenotype that segregates according to prescribed segregation ratios and the second is a phenotypic characterization of the plant lines at several stages during the course of microsporogenesis and microgametogenesis.

Brief Bio of Dan Hand:

Dan Hand is originally from Oak Creek, Wisconsin—a suburb of Milwaukee. He obtained his MS in biology in the summer of 2007 from the University of Wisconsin-Milwaukee, where he also earned his BS. He enrolled in IPPM program at Iowa State University in the fall of 2007.

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Stephanie Moon (Dr. Basil Nikolau)

April 2, 2008

Metabolomics based annotation of novel genes in *Arabidopsis thaliana*

Abstract

This project is establishing metabolomics as a functional genomics platform for Arabidopsis gene function discovery. Identifying the function of genes of unknown function (GUFs) is one of the major challenges that genome projects have presented to the biological community; for all genomes that have been sequenced approximately 30% of the annotated genes are identified as GUFs. Basic data needed to define the function of GUFs include biochemical function of the protein encoded by the gene, spatial and temporal resolution of the gene product expression and the biochemical, physical and regulatory network in which the gene product functions. In response to this need, the pilot project involving 10 US-based laboratories developed a high-throughput collaborative platform for assessing the global patterns of metabolite abundance changes in Arabidopsis.

Metabolomics is a method that identifies and measures the metabolome (global pool of small molecules of molecular weight <1,000) of a biological sample. Comparing the metabolome of a wild-type sample to that of a sample altered by a mutation at a target gene will provide clues as to the function of that gene, and thus help define the basis for a biological trait or a biochemical phenotype associated with the gene allele. The consortium of metabolomics labs generates parallel streams of metabolite data from identical biological materials. The data is then evaluated through a combination of different statistical techniques to reveal metabolites that are either hyper- or hypo-accumulating in the mutant lines, which can then be mapped on metabolic maps. The information generated using the combination of statistical analysis on the metabolite data makes it possible to construct hypotheses concerning the functionality of the GUFs.

Brief Bio of Stephanie Moon:
Stephanie is originally from Des Moines, Iowa and received her B.S. from Iowa State University in Biochemistry. She started working in the Nikolau lab as an undergraduate just over 4 years ago and decided to continue her education as a graduate student working under Dr. Nikolau.

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Shan Li (Madan K. Bhattacharyya)

April 9, 2008

Investigation of soybean – *Phytophthora sojae* interaction

Abstract

Oomycete pathogen, *Phytophthora sojae*, causes devastating root and stem rot disease in soybean. In the United States, this disease has been the second most destructive soybean disease after soybean *cyst nematodes*, and annual crop losses were valued to be about $273 million. The key to develop stable and broad-spectrum resistance soybean plants is to understand molecular mechanisms of soybean defenses against pathogen.

Constantly being attacked by various pathogens, plants have evolved a well-performed and inducible mechanism to combat against pathogen invasion. It is often demonstrated by rapid, programmed cell death known as hypersensitive response (HR). Following pathogen invasion, proteins encoded by host resistance(*R*) genes recognize pathogen proteins encoded by corresponding avirulence(*Avr*) genes and active defense responses are induced. In soybean, expression of *Rps* (resistance to *P.sojae*) genes has been providing significant protection against *Phytophthora sojae* races. Among 15 *Rps* genes, *Rps1*-k confers resistance against a large number of the *P. sojae* races and has been widely used in soybean cultivars.

Dr. Bhattacharyya's lab has cloned disease resistance gene *Rps1*-k-2 which was shown to encode a CC-NBS-LRR type protein. They also identified a type II metacaspase *GmMcII* required for expression of *Rps1*-k-mediated *Phytophthora* resistance. We plan to manipulate their expression levels through RNA interference (RNAi) approach to further understand their functions and signaling requirements for disease resistance.

Brief Bio of Shan Li:

Shan Li obtained her B.S. in Biological Sciences at China Agricultural University, Beijing, China in 2007. She enrolled in IPPM program at Iowa State University in the fall of 2007 and joined Dr. Bhattacharyya's lab in the Agronomy Department.

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Gibum Yi (Philip W. Becraft)

April 9, 2008

Exploitation of *Capsicum* EST–SSRs and an SSR-based linkage map

Abstract

Simple sequence repeat is one of the most useful markers because they detect high levels of allelic diversity, and are easily assayed by the polymerase chain reaction. The study of simple sequence repeats (SSRs) in plant genome is increasing as public sequence databases are expanding. Through analyzing 10,232 EST parent sequences 133 SSR markers were developed. These *Capsicum* ESTs were generated by Korea Research Institute of Bioscience and Biotechnology (KRIBB). Total 1196 SSRs were found in this EST database. There was one SSR in every 3.8 kb in the ESTs. Registration of these SSRs is undertaken on the *Capsicum* genetic linkage map using the F_2 population of *Capsicum annuum* cv. TF68 x *C. chinense* cv. Habanero. Some of these makers were used for comparing varieties of *Capsicum*.

Brief Bio of Gibum Yi:

Gibum Yi is from Republic of Korea (South Korea) and received his B.S. and M.S from Seoul National University in Plant Science and in Horticultural Science. He worked as a research associate for 4 years in the Kumho Life Science Laboratory, Gwangju and the Plant Molecular Genetics and Breeding Center, Seoul National University. He joined IPPM, ISU at fall, 2007.

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Nic Boersma (Nick Christians)

April 23, 2008

Fruit extracts of *Rhamnus cathartica* inhibit growth of perennial ryegrass and seed germination of six weed species

Abstract

Natural weed controls are growing in popularity in response to increased awareness of the potential hazards of many synthetic pesticides. Many studies have been conducted to test the potential of allelopathic plant residues for their inhibitory characteristics. Common buckthorn (*Rhamnus cathartica* L.) is an invasive shrub implicated as allelopathic in part due to its capability of creating monocultures in wooded areas that were previously populated by native plants. Since its introduction in North America, it has spread considerably after escaping cultivation. A study was conducted to determine the potential of common buckthorn aqueous tissue extracts for target plant inhibition. Aqueous extracts were prepared using powdered or undamaged common buckthorn fruit or leaf tissues. Extracts were tested on perennial ryegrass (*Lolium perenne* L.) to determine ideal extract preparation method and concentration for inhibition. The powdered fruit extract at 100 $g \cdot L^{-1}$ was the most effective and was subsequently tested for its inhibition potential of common clover (*Trifolium repens* L.*)*, red clover *(Trifolium pretense* L.*)*, lambsquarters (*Chenopodium album* L.), purselane (*Portulaca oleracea* L.), annual bluegrass (*Poa annua* L.), and barnyardgrass (*Echinochloa crusgalli* (L.) Beauv.), all of which were inhibited by the extract.

Brief Bio of Nic Boersma:

Nic Boersma is originally of Hospers, IA. He grew up on the farm and has been interested in plants and the outdoors since an early age. He obtained a BA in Biology: Ecological Science from Northwestern College in Orange City, IA in 2006 where he also earned a minor in Chemistry. He was accepted into IPPM as a direct admit to the lab of Dr. Nick Christians where he began working in the summer of 2006.

Direct questions or comments to Jen Grey jengray@iastate.edu or Stephanie Moon at moonsm03@iastate.edu