**Graduate research in the School of Plant Sciences • Spring 2014**

**MS and PhD students in Plant Science and Plant Pathology**

**Kayla Arendt, Plant Pathology, MS**

Fungi are capable of producing many unique secondary metabolites used in industry and medicine. Current studies geared at mining fungal metabolites often fail to consider symbionts of fungi as important players. By encouraging and manipulating natural associations between fungi and bacterial symbionts, we may be able to alter the production of these important metabolites without genetic modification – and may influence plant-fungal interactions in ways that may prove useful for both biofuels and agriculture applications.

My work focuses on the phenotypic effects of bacteria-fungal-plant symbioses in nature and laboratory settings. I use a range of classic microbiological techniques, molecular tools, genomics in the field and lab.

**Ana Sofia Avelar, Plant Pathology, MS**

The absence of molecular tools for detecting some viruses in asymptomatic plant tissue can lead to growers and distributors falsely declaring plants ‘virus free.’ The resulting spread can cause crop losses and threaten food security.

My work focuses on viruses in sweet potato in Central America, and cotton viruses (especially from Pakistan). I am designing molecular tools to detect a variety of plant viruses based on the latest sequence data, validating the assays with controls, and screening a variety of field samples for the viruses of interest.

**Wen Chen, Plant Sciences, PhD**

Small-RNA-mediated gene silencing is critical to many cellular processes, from development to environmental responses. Previous research has focused on the molecular mechanism underlying the pathway, yet little is known about the relation between the sub-cellular localization patterns of the components involved in the pathway and their roles. I seek to identify regulatory mechanisms for sub-cellular localization and to link these with functional roles in plant systems.

My work focuses on discovering the molecular events in *Arabidopsis* that regulate the sub-cellular localization of small RNA-mediated transcriptional silencing components. I use standard molecular and genetic techniques to prepare mutants, fractionate cells, and examine organelles. I use bioinformatics tools for analysis of sequence data.

**Noma Chingandu, Plant Pathology, PhD**

Cocoa production in West Africa is threatened by several viruses. Infected trees die and plantations are abandoned as the viruses spread. Some infections can go unnoticed, further increasing chances of viral dissemination. It is important to develop methods that can detect viruses early in the infection cycle. Current methods are often ineffective due to genetic variation within viral groups. Screening plant material for genetic variation in viruses, and studying known species to understand mechanisms of infection, will enhance the viability of the cocoa industry, which is not only important for confectioneries and beverages, but also for cosmetics and medicinal purposes.

I study the genetic makeup of viruses affecting cocoa production, and seek molecular methods to enhance detection of viruses in infected trees at an early infection stage. I am using molecular biology tools to study virus-infected plant material collected different regions of West Africa.

**Timothy Dabbert, Plant Sciences, PhD**

More than half of the cotton production acres in the United States rely on rainfall and have no supplemental irrigation. A warming climate exacerbates cotton’s ability to survive in these rainfed areas. My research will help elucidate genetic components underlying heat and drought stress tolerance in cotton, with the goal of helping improve cotton production and cultivar development.

My work focuses on dissecting the genetic components of tolerance of cotton to heat and drought and applying them to improve cultivar performance in dry, arid regions of the United States. I study natural variation in cotton germplasm using advanced field selection and screening, genomics, and market analysis to improve cotton cultivar development.

**Sarah Doore, Plant Pathology, PhD**

Viruses are everywhere. Multiple virus species may even infect the same host cell at the same time. This can lead to "mixing" of genetic information, which sometimes results in the formation of new virus species. The emergence of new viruses can have dramatic effects on human health, crop production, and biogeochemical cycling. My research focuses on the barriers that prevent mixing, and which environmental factors could allow these barriers to be overcome.

I examine how viruses assemble in an infected host cell, and how this assembly process relates to the concept of viral species. I investigate virus assembly using sophisticated genetics, molecular biology, and experimental evolution.

**Evan Forsythe, Plant Sciences, PhD**

Maintaining linear chromosomes is a challenge that all Eukaryotes overcome by adorning stretches of repetitive DNA (telomeres) at chromosome ends.  Telomeres are essential for sustained cell division and are intimately involved in the process of aging as well as in many diseases, including cancer. Great strides have been made in understanding telomeres in animals, fungi, and protists by comparative studies. However, relatively little is known about plant telomeres. My research aims to fill in this gap and will likely identify novelty that will illuminate our understanding of an ancient and critical cellular function.

My research aims to discover and characterize molecular components involved in the maintenance of linear DNA molecules (chromosomes) in plants. I use a comparative approach to understand both the function and evolution of telomere components in plants, making use of cutting-edge molecular, genetic, and genomic technologies.

**Karla Garcia, Plant Sciences, PhD**

Controlled environment agriculture can help to develop new practices for sustainable food production that save water and reduce the use of chemicals such as fertilizers and pesticides. In turn, greenhouse structures allow environmental control, which permits the manipulation of multiple variables than can enhance plant development and yield, enhancing production in new ways even in off-season growth.

My work focuses on expanding the knowledge of strawberry physiology with the purpose of developing strategies for production under controlled environmental conditions. I study plant development in controlled environmental conditions using hydroponics and physiological assessments.

**Yu-Ling Huang, Plant Sciences, PhD**

Plants on the earth provide habitat and food for many organisms, and are the foundations of the biosphere. Fungi growing in trees bring benefits or damage to the trees may affect the whole ecosystem. Therefore, it is important to understand the role of fungi in the plants in order to protect our environment.

I am interested in plant-microbe interactions, with a focus on symbiotic fungi in plant leaves (fungal endophytes). I examine endophyte growth in leaves and mechanisms of their host specificity using microscopy, biostatistics and molecular biology.

**Lauren Jackson, Plant Pathology, MS**

With a population expected to exceed 9 billion people by the year 2050, it is imperative that we find new ways to safely and sustainably increase our food production.  Fungi, many of which are edible and nutritious, are the primary decomposers of the Earth and can be cultivated using a variety of waste products.  The capacity of many fungi to degrade, adsorb, or accumulate a wide array of substances make them among the most versatile options for remediation efforts.

My work involves detoxifying a carcinogenic substance using fungal enzymes, and investigating the use of organic waste products for the production of gourmet mushrooms.I study the yield and nutrition response of edible fungi cultivated on different waste products, as well as the levels of toxins present in materials before and after treatments using the most accurate detection methods available.

**Paul Kachapulula, Plant Pathology, PhD**

Feeding an ever-increasing population requires proper utilization of every single ounce of grain, fruit and tuber crop we produce. Unfortunately, some fungi such as members of the genus *Aspergillus* produce potent human carcinogens in some of these crops, endangering not only human and animal health but also food security.

My work seeks to understand the diversity of toxin producers as a way of curtailing their hazardous effects on human health and agricultural productivity. I use field studies and sampling to capture the diversity and molecular biology tools to understand it.

**Chantelle Khambholja, Plant Pathology, MS**

Fungal pathogens are increasingly recognized as important causes of novel emerging infectious diseases. *Batrachochytrium dendrobatidis* (Bd) and *B. salamandrivorans* are the only two documented vertebrate pathogens in an ancient fungal lineage called the Chytridiomycota. Bd is implicated in the extinction of amphibians worldwide and has a variety of alternate hosts. It is important to understand the origins of Bd in Arizona, its interaction with aquatic microbiomes, and the way in which a non-native crustacean, crayfish, can influence its spread and maintenance.

My work focuses on the microbial ecology of an invasive species, and how the dynamics of introduced species influence native biological communities. I use field surveys of crayfish populations throughout Arizona, and both culture-based and high-throughput sampling via next-generation molecular tools.

**Courtney Magness, Plant Sciences, MS**

Soil salinity is one of the major abiotic stresses affecting agricultural productivity, limiting the growth and yield of most crop species which are unable to tolerate even modest levels of salinity (glycophytes). Genetic variability for salt tolerance exists with some plants (halophytes) adapted to environments with high salinity. Understanding mechanisms underlying halophyte adaptation will lead to effective strategies to improve crop salt tolerance.

The goal of my research is to determine if gene duplication has contributed to the adaptation of salt tolerance in plants. I am using molecular genetic and evolutionary approaches to determine what underlies halophyte adaptation.

**Carlos Maldonado,** Plant Sciences, Ph.D.   
  
With the perspective of a growing human population, a finite amount of agricultural resources, and changing environmental conditions, plant breeding programs are looking for more efficient crops with higher yield, less input requirements, and higher nutritional value.  The wild relatives of cultivated species are an important reservoir of genetic variability and agronomically important traits that can be included in plant breeding programs to fulfill current and future requirements.

My work focuses in the analysis of genetic variability and comparative genomics of wild plants closely related to domesticated species. I study wild species using available plant collections (kept in international germplasm banks) and controlled crosses between them, and retrieving genetic information using the state of the art tools in molecular biology, genomics, transcriptomics and computational analysis.

**Jen Noble, Plant Sciences, PhD**

On a global level, the amount of arable land is not increasing as fast as the rise in the global population.  A method to increase the food supply for the growing population is to increase the amount of seed we produce.  Successful seed production is important because seeds are a major plant source that humans consume (rice, corn, wheat).

My research provides insight on how to increase seed production by understanding what initial interactions between the father and the mother are necessary for a successful seed to be produced.  I focus on understanding initial cell-cell communication in plant reproduction in order to increase seed production to meet the increasing demand of global food supply. I use a model organism and its most closely related species and tools developed for plant molecular biology, bioinformatics, and comparative genomics.

**Mana Ohkura, Plant Pathology, PhD**

*Aspergillus flavus* is a fungus that contaminates crops with its carcinogenic mycotoxin. Individual strains within *A. flavus* vary greatly in their ability to produce the toxin:  some strains produce high levels of toxin whereas other strains are non-toxigenic.  Understanding the biology of highly toxic strains can lead to better detection and awareness of environmental conditions that are conducive to contamination outbreaks.  On the other hand, because non-toxin producing strains can compete out toxic strains, studying these strains can aid in developing biological control strategies to reduce contamination.

I am comparing the genomes of *A. flavus* strains that are known to be consistently toxigenic to those that vary greatly in toxigenicity.  The aim is to identify genomic signatures that reflect the different environments to which these strains may be adapted.

**Jorge R. Paredes, Plant Sciences, PhD**

*Bemisia tabaci* is a top invasive species able to transmit plant viruses in several crops. Due to its cryptic species status and the lack of genomic information, constructing a reliable phylogeny have been a matter of study for decades. Our major goal is to construct the global invasion history of this species and in parallel, to provide more markers for facilitating its tracking worldwide.

In order to unravel the *B. tabaci* complex and track its gene flow worldwide, I am using a global whitefly collection and population genetics tools, including microsatellites and RAD sequences analysis.

**Justin Shaffer, Plant Pathology, PhD**

Tropical forests are some of the most diverse ecosystems on the planet, and provide our society with important agricultural, medicinal, and socioeconomic goods and services that are largely unique to such habitats. Crucial to the conservation and sustainable use of tropical forests is a comprehensive understanding of the forces that shape them through both space and time. Plant-associated fungi and bacteria can strongly influence plant health, but also affect certain plants in unique ways. My work aims to understand what drives this variation by carefully examining the effects on plants of a diversity of microbial communities.

I focus on discovering and understanding cryptic microbial interactions that influence forest trees. I study plant-microbe interactions using collections of microbes and plants from Central America, in a framework that combines the tools of traditional plant biology with advanced and high-throughput methods of molecular biology and genomics.

**Pummi Singh, Plant Pathology, PhD**

Aflatoxin is a highly carcinogenic secondary compound made by *Aspergillus flavus* and certain other species of *Aspergillus*. Their main hosts are crop plants such as maize, groundnuts, red chilli, pistachio. Aflatoxin contamination can cause huge economic losses and detrimental health effects: exposure to aflatoxin can cause stunted growth in children, liver damage in adults along with liver cancer, and fatality in certain situations. It is important to understand the population structure and adaptations of these fungi to control them. Fungal biocontrols (strains of *Aspergillus* that do not make toxin) have been proposed and applied in fields to reduce contamination as a successful strategy.

My research involves working with carcinogenic aflatoxin producing fungi that mainly impact crop plants. I use microbiological techniques, molecular techniques, field work based approaches and genomics.

**Brian Smith, Plant Pathology, PhD**

Horizontal gene transfer (HGT) is frequent and important in biology, especially in bacteria that influence human health and sustainability. HGT often is associated with advantageous traits in hosts (e.g., acquisition of antibiotic resistance). However, the costs of large-scale HGT are not well studied. Such costs could render pathogenic bacteria ineffective, renew antibiotic sensitivities in multi drug resistant strains, or increase susceptibility to other organisms. Understanding the genetics of these costs could translate to crop protection or medical treatments. I investigate current gaps in understanding the relationship of HGT and microbial pathogenesis.

I study horizontal gene transfer and microbial pathogenesis through various *Pseudomonas sp.* and a 1Mb megaplasmid. I use tools from microbiology, genetics, genomics, and molecular biology.

**Muhua Wang, Plant Sciences, Ph.D.**

The demand for food of Africa is estimated to increase 20% before 2020. Rice has become a major staple food in Africa in the last decade, but most rice consumed in Africa is imported from Asian countries, but exports from Asia are decreasing. African rice was originally domesticated and adapted to the environment in Africa, and it is resistant to biotic and abiotic stresses endemic to the African continent. Understanding the domestication history of African cultivated rice will provide the genetic basis for rice breeders to develop new rice varieties for Africa.

I aim to identify the center of domestication and the domestication history of African cultivated rice (*Oryza glaberrima*). I study the domestication of African cultivated rice using a group of African cultivated rice and its wild progenitors with the cutting-edge tools of molecular biology, population genetics, comparative genomics, and genetics.

**Josh Weaver, Plant Sciences, PhD**

The replacement of fossil fuels with sustainable alternatives is important for our growing global population. Identification and characterization of previously unidentified plant variants is important to understand gene function. My work focuses on enhancing the biofuel-relevant genetics of switchgrass, a bioenergy crop.

I use biotechnology techniques to propagate uniquely identified genotypes and cutting-edge tools of molecular biological and genomics for screening variant phenotypes and trait mapping.

**Michael Whalen, Plant Sciences, MS**

Greenhouse agriculture is an important and growing field of both industry and research.  Crops grown in a greenhouse produce far higher yields per area than those grown in the field, and they can be grown for a longer period of the year.  Understanding how crops behave in different greenhouse environments is key to maximizing quality and productivity to provide a sustainable source of food for the world's rapidly growing population.

I study plant morphology and productivity by conducting a wide variety of measurements, both in the lab and greenhouse, on an assortment of greenhouse crops grown under varying conditions.

**Junpeng Zhan, Plant Sciences, PhD**

The importance of cereal endosperm is two-fold: Biologically, endosperm accumulates large reserves of protein and starch to support seedling germination. For humans, a significant proportion of calories are derived from cereal endosperm, either directly or indirectly through animal feed. Furthermore, cereal endosperm is used as a raw material for numerous industrial products. Therefore, an understanding of storage function regulation in cereal endosperm will contribute to improving yield of cereal crops with beneficial effects on human nutrition and economic development.

My work focuses on identifying the gene regulatory networks that control the storage protein and carbohydrate deposition in maize endosperm. I am using systems approaches to identify genes regulated by key transcription factors in endosperm. These include genome-wide analyses using next-generation sequencing and bioinformatics tools, and techniques of biochemistry, molecular biology and genetics.