

Thursday, September 25, 1:30-2:00 p.m.

Douglas Cook, Ph.D.

University of California, Davis drcook@ucdavis.edu

“Taking a walk on the wild side: Combining ecology and genomics to deduce the function of legume-microbe interactions in natural and agricultural systems”

R. Varma Penmetsa¹, Alex Greenspan¹, Peter Chang^{1,2}, Noelia Carrasquilla¹, Bullo Mamo¹, Lisa Vance¹, Reyaz Mir¹, Susan Moenga¹, Eleanor A. Siler³, Janna L. Rose⁴, Asnake Fikre⁵, Bunyamin Tar’an⁶, Maren Friesen³, Sergey Nuzhdin², Bekir Bukun⁷, Abdulkadir Aydogan⁸, Jens D. Berger⁹, Abdullah Kahraman¹⁰, Eric von Wettberg⁴ and Douglas R. Cook^{*1},

¹University of California, Davis, CA, ²University of Southern California, Los Angeles, CA, ³Michigan State University, East Lansing, MI, ⁴Florida International University, Miami, FL, ⁵Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia, ⁶University of Saskatchewan, Saskatoon, Canada, ⁷Dicle University, Diyarbakir, Turkey, ⁸Central Institute for Field Crops Research, Ankara, Turkey, ⁹Plant Industry, CSIRO, Floreat, WA, Australia, ¹⁰Harran University, Sanliurfa, Turkey. drcook@ucdavis.edu.

Crops are impacted in unintended, often negative ways during their domestication and breeding. Loss of adaptive alleles, fixation of deleterious alleles, and low genetic diversity in cultivated species constrains our ability to expand their cultivation into more extreme climates, marginal soils, or to situations with reduced agricultural inputs. We are addressing this need in chickpea, the world’s second most important pulse legume, by harnessing the capacity of wild relatives to survive in harsh environments. Effective use of wild germplasm in chickpea improvement requires new and systematic surveys of genotypes from natural environments, identification of adaptive alleles to environmental extremes, and incorporation of the diversity of wild alleles into purpose driven populations for trait analysis and breeding. We focus on climate resilience, nitrogen fixation and seed nutrient density, with the goal of more sustainable and stable production systems. We combine upstream ecology and genomics to assemble and characterize wild germplasm; population development to remove barriers to use of wild alleles for trait assessment and breeding; and phenotyping and modeling of trait-gene associations to enhance the precision and rate with which wild alleles are applied to crop improvement. To date we have completed ecological characterization and genetic resource collection for ~1,200 novel accessions, used genotyping by sequencing and bioinformatics to deduce population genetic parameters, initiated whole genome re-sequencing, collected co-occurring bacterial symbionts, surveyed seed and flowering phenotypes, and initiated development of nested association mapping panels. In parallel to the analysis of plant populations we have initiated genomics and community ecology of legume-associate microbes from both wild species at their center of origin and their domesticated counterparts globally. Sequencing the genome of ~400 *Mesorhizobium* genomes reveals a history of horizontal gene transfer of symbiotic genes from the natural symbiont of *Cicer* spp to atypical genomic backgrounds, presumably to balance the need for edaphic adaptation to agricultural situations with the requirement for symbiotic competency. We have also initiated culture-independent metagenomic studies of rhizosphere and phyllosphere microbial communities throughout the plant species’ center of origin, to investigate the biogeography of plant-associate microbes. We are testing the hypothesis of plant-microbiome coevolution in a range-wide study system, as well as characterizing the population genetics of key crop pathogens in wild systems. Results from these ongoing studies will be presented.