Open PhD work/study opportunity with Department of Entomology and Plant Pathology
University of Tennessee Institute of Agriculture

Genomics and Plant-microbe interactions PhD Work/Study employment opportunity
Email: Bode Olukolu at bolukolu@utk.edu for inquiries, apply at https://gradschool.utk.edu/admissions/applying-to-graduate-school/

Anticipated start date: March 1, 2018

Description
Funding for PhD degree in Entomology, Plant Pathology, Nematology (4 years, with full staff benefits) with concentrations in Bioinformatics, Genomics and Molecular Interactions. The Olukolu lab’s research interests encompass genomics, quantitative genetics, bioinformatics, complex disease resistance and the impact of the microbiome on plant-pathogen interactions. Several ongoing projects are described below:

1) The microbiome is increasingly being recognized as an important factor for host defense response against pathogens and pests. Beyond cataloguing taxa within microbial communities, the molecular processes underlying these interactions are not well understood. What are host-specific or broad-spectrum beneficial microbes that enhance resistance? What are host genetic factors associated with recruitment of beneficial microbes? How does the microbiome mediate enhanced resistance? Can inclusion of quantitative microbiome profiles in models increase heritability, especially for traits with low heritability? Are there practical applications in plant breeding programs and agrosystems?

2) Dosage-dependent SNP calling in a sweetpotato germplasm using an optimized genotyping-by-sequencing protocol and bioinformatic pipeline. The study will lead to a better understanding of the global population structure, further insight its evolutionary origins and the genetic architecture underlying key traits based on genome-wide association studies (GWAS). The SNP data will be used to design oligos for an inexpensive targeted-GBS array with low ascertainment bias. This resource will be scalable for low, medium and high density SNP arrays.

3) Developing a novel inexpensive strategy for whole genome sequencing and high-quality assembly of highly heterozygous and polyploid genomes, with hexaploid sweetpotato as a case study.

4) Understanding mechanisms that drive rapid crop adaptation. The Methylome profile of genetically diverse sweetpotato genotypes and various adaptation-related traits will be evaluated. Are genes responsive to selection during adaptation enriched with DNA methylation patterns?