**Postdoctoral Scholars Association (PSA) Travel Grants**

**Simon Renny-Byfield**

**Submitted Abstract**

Analysis of resequencing data has provided an in-depth look at species-wide variability in maize and teosinte, but we still have little understanding of how evolutionary processes shape diversity within individual populations.  In particular, previous efforts have shown that the vast majority of the maize genome is affected by presence-absence or copy number variation, but we do not yet understand how this genomic flux impacts diversity.  Here, we investigate within-population processes and the role of presence-absence variation by resequencing the genomes of 20 teosinte from a single natural population near Palmar Chico, Mexico.  We scan the genome for evidence of recent positive selection, and identify thousands of presence-absence variants across euchromatic portions of the genome.  We show that patterns of diversity in these regions deviate meaningfully from standard population genetic expectations, and argue that population genetic analysis in complex plant genomes must take into account the effect of such polymorphisms on genome-wide patterns of diversity.

**Statement**

I am a new post-doc in the lab of Dr Jeffrey Ross-Ibarra in the Department of Plant Science here at UC Davis. I gained my PhD from the University of London in 2012, for which I was awarded three year scholarship. I was subsequently awarded the *Irene Manton Prize* by the *Linnean Society of London*, for best thesis in botany. I then went on to a two-year post-doc in the lab of Jonathan F. Wendel at Iowa State University. During the course of my early career I have authored 14 publications in peer-reviewed journals, eight of these as first author, or joint first author.

My current research focuses on important questions regarding interspecific variation in copy-number variants in natural plant populations (in they case will maize). Investigation of domestication and natural selection in maize, and indeed many other taxa, typically do not account for such variation when examining genome-wide variability, potentially impacting inference of population level demographics and natural selection. Presenting at the maize conference will allow this crucial consideration to disseminated to current researchers engaged in such work, including those directly working in maize genetics. This will serve to increase awareness of our current research project, leading to greater impact in the future.

Furthermore, my early career focused on work in tobacco and cotton before I recently switched focus to work on maize. As such I am relatively unknown within the maize research community. Presenting my work at the Maize Conference 2015, is an ideal opportunity to integrate myself into this community. My presence at the conference will allow me to introduce myself, networking with fellow researches, promotion of work ongoing here at UC Davis, and allow for more well-rounded and productive research in the future.