

M-146

Gene expression and transposable elements as causes and effects of resistance to genome fractionation in soybean

*Brain Nadon\**, Institute of Plant Breeding, Genetics and Genomics, University of Georgia, Georgia, USA

*Chunming Xu*, Center for Applied Genetic Technologies, University of Georgia, Georgia, USA

*Scott Jackson*, Institute of Plant Breeding, Genetics and Genomics, University of Georgia, Georgia, USA

*Moaine El Baiddouri*, Institute of Plant Breeding, Genetics and Genomics,

Essentially all plants show a whole-genome duplication (WGD) or an ancient polyploidy event somewhere in their evolutionary history. While many plants remain polyploid today, many have become diploids over time. This process of diploidization is generally followed by extensive genome reorganization called fractionation, where duplicated genome segments are deleted, differentiated, and re-ordered over evolutionary time. Soybean (*Glycine max* L.) is a prime example of this process at work, with at least 3 detectable WGD events in its lineage. While many plants with a similar history of WGDs show extensive reorganization or deletion of duplicate genome segments over time, soybean shows little of this. Most soybean genes are present in duplicate, and duplicate genes from ancient WGDs in soybean are present in extensive syntenic blocks across the soybean genome. While many previous studies have noted that soybean shows little fractionation and is highly duplicated, it is still unclear how other genomic features like transposable elements, gene expression, and cytosine methylation contribute to or result from this. This study found that soybean's duplicated gene blocks are longer and cover more of the genome than in other similar legumes like common bean or *Medicago truncatula*, and contain more transposon-related sequence per base pair. Furthermore, expression levels of soybean genes are less different between paralogous copies within WGD duplicated blocks than in common bean, with genes arising from the most recent Glycine-specific duplication showing the least differentiation. Further analysis, such as investigating the relationship of TE content to expression and methylation levels, may reveal the putative cause(s) of over-retention of duplicate genome segments in soybean.