

M-129

Genome-wide characterization of allopolyploid members of genus *Glycine*
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Allopolyploid is a common feature in many angiosperm genera. *Glycine max* has a duplicated genome, the result of two identifiable whole genome duplication events. Soybean is one of as many as 30 species in the genus *Glycine*. The perennial wild relatives include at least nine recently formed (within the last million years) polyploid taxa. This study examined three allopolyploid and four diploid progenitor taxa using genome wide single nucleotide polymorphisms (SNPs) and network analysis. Genotyping by sequencing (GBS) was used to generate SNPs and results were compared with previous analyses from transcriptome data. SNP genotypes for 70 accessions resulted an alignment of 22,806 bases across eight taxa with no missing data. The extended sampling made possible by GBS identified accessions that were misclassified in the GRIN/CSIRO germplasm systems or the result of mixed seed stocks. The most intriguing results are the discovery of previously unrecognized substructure within diploid taxa, and the likelihood that allopolyploids were derived from particular diploid subgroups. Separation of allopolyploid SNPs into SNPs derived from homologous progenitor species indicate that allopolyploids no longer share genotypes with their diploid progenitors but have evolved separately long enough for signals from direct progenitor genotypes to be obscured.