**Evaluating Wild Grapevine Germplasm with Genotyping-By-Sequencing Methods for Conservation, Preservation, Genetics and Breeding**

The USDA-ARS cold hardy grapevine germplasm represents one of the best collections of publically available grapevine material for grape breeding and improvement.  The repository holds in excess of 1300 different grapevine genotypes, with roughly a quarter made up of wild grapevine species.  Efforts to increase the germplasm holdings have traditionally relied on donations from grapevine breeding programs, with minimal recent wild collections.  However, contemporary collections of wild North American species would offer the opportunity to include diverse germplasm for future breeding efforts.  As a perennial, clonal crop, grapevine germplasm preservation is costly and requires a careful examination of plant material in order to save unique material, without retaining redundant genotypes.  To evaluate wild germplasm, we used the genotyping-by-sequencing method to sequence a reduced representation genomic library of 1308 unique germplasm and wild collected grapevine samples, producing over 8 million sequenced tags.   Alignment of wild tags to the 12x grapevine reference genome resulted in unique mapping of ~2.9 million tags, or 33.3%.  Use of wild grapevine reference transcriptomes allowed mapping of 6.6-7.8% of tags, depending on species. Unfiltered data produced an initial ~1.8 million SNPs but filtering processes reduced this dataset to ~72,000 high quality SNPs. Here we present the SNP discovery method and an analysis of the genetic diversity present within the cold hardy wild grapevine collection.  In addition, we examine recent collections of wild material in order to identify new candidate accessions for phenotypic screening and preservation.