

PAUL GALEWSKI¹ and MITCH McGRATH², (¹ Michigan State University and ²USDA-ARS, 1066 Bogue Street, 494 PSSB, Michigan State University, East Lansing, MI 48824). **Phenotypes, genome wide markers, and structured genetic populations: A means to understand economically important traits in *Beta vulgaris* and to inform the process of germplasm enhancement.**

Populations are the operational unit of beet improvement and thus characterizing populations is critical for gene discovery and deployment of traits to growers. Several -omics technologies are being deployed to: 1) Catalog and compare the molecular variation found within *Beta vulgaris* crop types, 2) Generate genome wide markers from 22 varieties/ germplasm representing beet crop type diversity and important phenotypic characters, and 3) Partition the phenotypic variation resulting from divergent crosses between sugar beet and crop type against the respective genome sequence. To date, 982,190 high-information-content SNPs have been identified that discriminate within and among crop types. Characterization of private variation (SNP/INDELS) found only within one population or crop type is producing evidence of global and local genome differentiation resulting from selection for end use and genetic drift within the breeding program. Global pairwise F_{st} for inter-crop type populations C896 and W357B was 0.29 versus and an F_{st} of 0.12 for populations of the same crop type C869 and L19. The MSR is an F7 inbred population derived from sugar crossed with table beet (C869 X W357B) and represents a large degree of phenotypic variability for economically important characters (i.e. percent sucrose, percent water, biomass accumulation). Locating these traits to genomic regions using genotype/phenotype associations and leveraging additional data regarding local genome differentiation and gene expression to gain better resolution of the genetic architecture of these traits is providing a useful tool to identify genes for any phenotype of interest.