

DEVELOPMENT OF GENOMIC-BASED STRATEGIES FOR SCREENING AND SELECTION OF ACCESSIONS FROM A CARROT (*DAUCUS CAROTA*) GERMPLASM COLLECTION

Keo Corak

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Germplasm collections are rich sources of both genetic and phenotypic diversity but are difficult to comprehensively screen for desired traits and/or alleles. To efficiently utilize the diversity present in large germplasm collections, plant breeders often attempt to identify a subset of accessions that represents the larger collection. Methods for creating these “core collections” rely on partitioning collections into sub-clusters based on geographic, morphologic or neutral genetic similarity. These methods do not consistently capture functional diversity and may be inappropriate for highly admixed species. We are using a collection of domesticated carrot (*Daucus carota*) accessions to test genomic-based strategies that will allow breeders to create custom subsets of germplasm collections that maximize trait values of interest while maintaining adequate genetic variability. Our preliminary work has established carrot as an appropriate species in which to study these strategies. We used a large dataset of genotyped cultivars and wild accessions to study the genetic structure of carrot germplasm resources available to breeders. Within Western cultivars, genetic diversity is present but there has been continuous gene flow and admixture. Principal component analysis and hierarchical clustering of Western domesticated carrot accessions based on the genetic differences between them support the conclusion that they form one large breeding pool. While partitioning the accessions according to either geographic, morphologic or genetic similarity resulted in core sets that adequately represented the whole, these cores did not differ significantly from a random sample. We plan to develop two genomic-based selection schemes that a) balance genetic and phenotypic diversity and b) incorporate genomic prediction models to identify interesting accessions. We also plan to test the efficiency of genomic predictions compared to phenotypic selection of parental accession to incorporate quantitative traits from genetic resources into elite breeding populations. While these strategies will likely not identify subsets that maximize the diversity of the subset and are a departure from the traditional core collection concept, we expect that they will help us identify accessions and develop breeding populations that are more relevant for specific breeding goals.