

Genetic Diversity & Population Structure Analysis of the Global Germplasm Collection of *Medicago lupulina*

Oluwatosin Adebajo, University of California-Davis

Daniel Potter, University of California-Davis

Brian Irish, USDA-ARS

Charles Brummer, University of California-Davis

Medicago lupulina L. (black medic) is a self-pollinated relative of alfalfa with a global distribution and of value for use in sustainable forage systems, primarily as a component of diverse pasture mixtures. Two characteristics of the species are also of interest evolutionarily: (1) it has single seeded pods, unlike all other *Medicago* species except the rare *M. secundiflora* and (2) variation in growth form, with both perennial and annual accessions in the species. Despite its broad geographic distribution and promising characteristics, the genetic diversity and population structure of the species is uncharacterized. The objective of this study was to assess the genetic diversity of a global collection of *M. lupulina* from the USDA-ARS National Plant Germplasm System and a personal collection of Dr. Brummer, representing accessions originating from over 54 countries. Plants were grown in the greenhouse and pictures of the accessions taken as they set seed to document major phenotypic differences among them. We extracted DNA from leaf samples for genome-wide SNP genotyping using the alfalfa 3k marker panel from Diversity Array Technologies. From this marker data, we will discuss the results of population genetic analyses, including principal component analysis (PCA), the relationship between genetic and physical distance of the original collection sites of accessions, and association of markers with selected agronomic traits. Results will provide insight into the genetic diversity in *M. lupulina* providing useful information to inform selection of accessions for use in forage improvement programs or for genetic experiments.