Genetic Relationship & Diversity of 14 Alfalfa Populations Collected From Long-Term Grazing Sites

Hu Wang, University of Saskatchewan Bill Biligetu, University of Saskatchewan Yuguang Bai, University of Saskatchewan Bruce Coulman, University of Saskatchewan Xiao Qiu, University of Saskatchewan

Information on local adaptation of alfalfa populations under long-term grazing is largely lacking. The objectives of this study were to evaluate phenotypic and genomic variations of alfalfa populations from long-term grazing sites, and to identify adaptive loci associated with environmental factors under long-term grazing across four soil zones of Saskatchewan, Canada. In this study, 14 alfalfa populations were collected from long-term grazing sites (>25 yrs) across four soil zones of Saskatchewan. Seven agro-morphological and three nutritive values traits were evaluated from 2018 to 2020. The genotyping-by-sequencing (GBS) data of the 14 alfalfa populations and 11 commercial alfalfa cultivars released between 1926-1980 were used to conduct genetic diversity and genotype-environment association (GEA) analyses. The STRUCTURE analysis showed that the 14 alfalfa populations had varying percentages of the alfalfa sub-species Medicago sativa and M. falcata. In addition, there was a genetic shift by soil zone with the populations from the Black and Brown soil zones being the most unique, inferred by discriminant analysis of principal components (DAPC). Significant differences (p < 0.05) were observed for seven agro-morphological and three nutritive value traits among alfalfa populations and soil zones. The highest yielding four populations (MacDowall, Duck Lake, Dalmeny and Arcola) was clustered closely with the *M. sativa* sub-species according to the best linear unbiased prediction (BLUP) values of 10 agro-morphological traits. The genotype-environment association (GEA) found 70 SNPs that were significantly associated with eight environmental factors of the long-term grazing sites. Candidate genes underlying these environmental factors were associated with a variety of proteins, which were involved in plant growth and development, and plant responses to abiotic stresses, i.e., high salinity, drought, and cold, and biotic stress, i.e., defense against pathogens.