

UNIVERSITY OF SASKATCHEWAN



Genetic Relationship & Diversity of 14 Alfalfa Populations Collected from Long-Term Grazing Sites Hu Wang¹, Yuguang Bai¹, Bruce Coulman¹, Xiao Qiu² and Bill Biligetu¹

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Introduction

- Alfalfa is an important cash crop to Canadian economy with certified alfalfa seed export valued at \$61.2 million and alfalfa meal and pellet export at \$37.1 million in 2020 (Tridge, 2021).
- However, alfalfa stand is frequently affected by grazing (Smith et al., 1989), and extreme environmental conditions (Bélanger et al., 2006).
- Development of new alfalfa cultivars with high regional adaptation and persistence is an important research topic for alfalfa production enhancing and increasing profitability of the beef and dairy sectors in Canada.

Objectives

- To identify the genetic relationship of the 14 alfalfa populations from long-term grazing sites and the 11 commercial alfalfa cultivars released from 1926 to 1980.
- evaluate genetic and phenotypic • To variations of alfalfa populations from long-term grazing sites.

Materials and methods

- Fourteen alfalfa-grass mixed stands with a minimum 25 years of grazing history were selected across Brown, Dark Brown, Black and Grey Wooded soil zones of Saskatchewan (SK), Canada (Fig 1).
- A nested randomized complete block design (RCBD) with two replications was established in June 2017, Saskatoon, Saskatchewan, Canada (Fig 2).
- Genotyping-by-sequencing (GBS) was applied in the genetic relationship and diversity analysis of the 14 alfalfa populations from long-term grazing sites and the 11 commercial alfalfa cultivars released from 1926 to 1980, and genotype-environment association (GEA) analysis of alfalfa populations from longterm grazing sites.





of eight environmental factors with alfalfa populations from long-term grazing sites. The colored points represent individual genotype. Blue vectors represent eight environmental factors.

Table 1. Candidate genes associated with seven environmental factors for alfalfa populations from long-term (> 25yrs) grazing sites.

Environ

Soil pH

- Ν Ρ
- n
- Summe
- tempera
- Growing precipi



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nmental factor	Number of candidate gene	Putative function
	4	Plant adaptation to environmenta salinity, cold and nutrient deprivat
	2	Pathogens resistance and drough
	14	P stress and abiotic stresses
	7	No direct association with K stres
	2	Pathogens resistance and drough
er extreme ature	14	Heat stress
ig season tation	10	Drought stress

I stresses such as drought, tion ht tolerance

ss in plants ht tolerance

Conclusions

- The UPGMA (Fig 4) and STRUCTURE (Fig 5) analyses showed that the 14 alfalfa percentages of the alfalfa sub-species Medicago sativa and M. falcata. Most importantly, the four highest forage dry matter yielding populations (MacDowall, Duck Lake, Dalmeny, and Arcola) belonging to the *M. sativa* sub-species were clustered closely according to the best linear unbiased prediction (BLUP) values of ten agronomic I traits (Fig 3).
- The GEA analysis (Fig 6) found that 70 SNPs were significantly associated with seven environmental factors of the longterm grazing sites. The 53 candidate genes (Table 1) underlying these environmental factors were associated with a variety of proteins, which were involved in plant development, and plant responses to abiotic stresses, i.e., high salinity, drought, and cold, and biotic stress, i.e., defense against pathogens.

References

- Tridge 2021. Lucerne (alfalfa) meal, pellets and seeds used for sowing. [Online resource: <u>www.tridge.com/</u>].
- Smith et al. 1989. Alfalfa persistence and regrowth potential under continuous grazing. Agronomy Journal. 81: 960-965.
- Bélanger et al. 2006. Winter damage to forage crops perennial Canada: causes, prediction. Canadian Journal of Plant Science. 86: 33-47.

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