ACCESSING THE GENETIC DIVERSITY AND DRY MATTER YIELD PERSISTENCE IN ALFALFA GERMPLASM WITHIN BRAZIL

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Introduction

Alfalfa (*Medicago sativa* L.) is considered "the queen of forages" and plays a key role in highly specialized dairy herds. Alfalfa has the potential to be grown in different edaphoclimatic regions, though its cultivation in tropical regions is still limited. Because yield persistence is one of the bottlenecks of alfalfa breeding in tropical regions, efforts should be done to overcome this problem.

Objective

This study aimed to investigate whether the alfalfa germplasm held by Embrapa Southeast Livestock has satisfactory genetic diversity regarding bromatological and agronomic traits. The investigation also looked into yield persistence, how to access it, and how to select persistent accessions based on random regression models and artificial neural networks (ANN).

Materials and methods

BLUPs of nine traits of 77 alfalfa accessions from a temperate genetic background evaluated in 8 harvests were used to estimate the phenotypic diversity. Microsatellite markers assessed the molecular diversity. Self-organizing maps clustered and organized the accessions accordingly with their scores with regards to the phenotypic and molecular diversity. Dry matter yield taken from 24 harvests was used to assess persistence. A random regression model based on Legendre polynomials with a diagonal residual variance structure was used to fit persistence curves for each accession.

The scores of the curves were clustered using the k-means method and persistence groups were established. An ANN was adjusted to classify accessions based on the persistence groups established by the k-means algorithm.

Results and discussion

Self-organizing maps revealed the presence of genetic diversity for both phenotypic and molecular data.
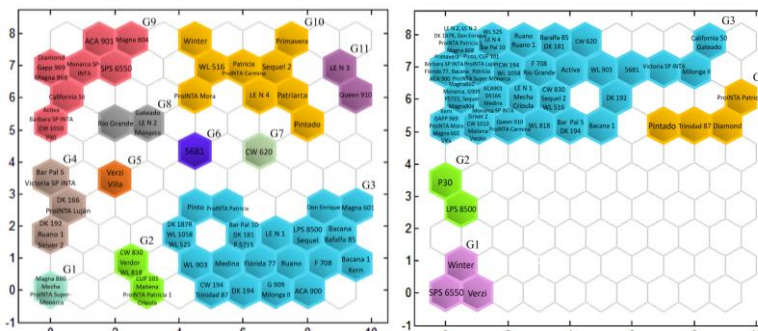

Fig 1. Self-organizing map for phenotypic (left) and molecular (right) data. Accessions belonging to the same group were identified using equal colors on the map. G1, G2, …, Gn corresponds to groups 1, 2, …, n, respectively.

The fitted curves showed amplitude regarding dry matter yield over time, which suggested a high variability regarding persistence. The three-step method for accessing persistence presented in this study has the advantage of to evaluate different alfalfa accessions using the same ANN.
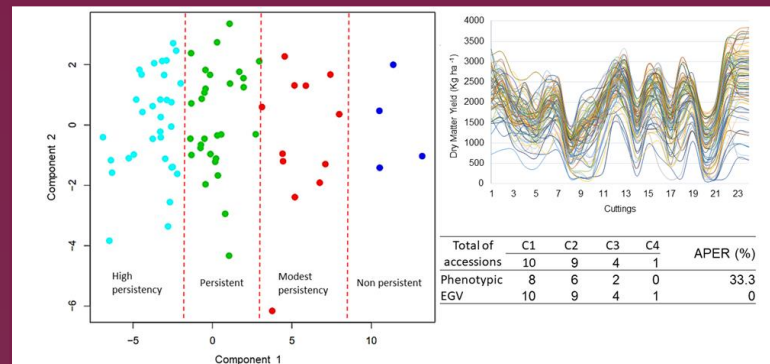

Total of accessions	C1	C2	C3	C4	APER (%)
	10	9	4	1	
Phenotypic	8	6	2	0	33.3
EGV	10	9	4	1	0

Fig 2. Clustering of alfalfa accessions based on EGV over 24 harvests (left). DMY trajectories for each accession (upper right) show cycles of high or low yield through the harvests. Apparent Error Rates (APERs) for validation of the phenotypic and EGV ANN are shown in the lower right table.

Once new accessions are evaluated, they will be classified according to their genetic value scores using the same ANN previously fitted, with no need for a new clustering step.

Conclusion

The alfalfa germplasm has the potential for developing base populations adapted to tropical conditions. The persistence method can help alfalfa breeders in the decision-making process.

Acknowledgments