

# Genomic Selection for Alfalfa

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Esteban Rios is an Assistant Professor in Forage Breeding and Genetics in the Agronomy Department at University of Florida. He holds MSc and PhD degrees in forage breeding from the University of Florida, and a BSc degree in Agronomy Engineering from the National University of the Northeast in Corrientes, Argentina. His research program focuses on genetic improvement of warm- and cool-season grasses and legumes, and he uses traditional and modern methods to improve crops for biomass yield, nutritive value, and tolerance to biotic and abiotic stresses. He breeds numerous warm and cool season crops because they provide unique ecosystem services for a diverse livestock clientele in subtropical and tropical agroecosystems. He has experience in collecting, evaluating, and selecting germplasm for diverse breeding objectives, and he has released numerous cultivars with documented improved traits for grasses and legumes. He works closely with extension faculty and agents to disseminate the use of improved forage cultivars locally, regionally, and internationally. He investigates, develops, and applies breeding, quantitative genetics, statistical and technological innovations to make plant breeding more efficient. Focus areas in his lab: i) quantitative genetics and experimental designs, ii) high-throughput phenotyping (HTP) to accelerate data collection in field trials, and iii) utilize multi-omics approaches to link genotypes to phenotypes and implement genomic prediction in forage species. His teaching program is fulfilled by actively participating in undergraduate and graduate education through instruction, student recruitment, chairing and serving on graduate committees, supervising undergraduate research, and mentoring student clubs. He teaches four graduate-level courses: Field Plot Techniques, Advanced Plant Breeding, Survey of Breeding Tools and Methods, and Plant Chromosomes and Genomes.

Alfalfa is the most important perennial forage legume in the world because of its relatively high yield and nutritional value. Nondormant alfalfa cultivars grow in regions with little frost, such as the southern US and the Central Valley of California, where plants grow year-round and can be harvested up to 10 times per year (Bouton, 2012). In Florida, nondormant cultivars were developed for improved adaptation and yield ['Florida 66' (Horner, 1970), 'Florida 77' (Horner and Ruelke, 1981), and 'Florida 99']. These cultivars and germplasm introduced from other subtropical regions in the world were used to develop breeding populations (Acharya et al., 2020), which were subjected to various studies involving genomics (Andrade et al., 2022; Sipowicz et al., 2022), phenomics (Biswas et al., 2021), and enviromics (Fernandes Filho et al., 2022) to increase genetic gain for yield, nutritive value, and persistence. High-throughput phenotyping demonstrated to be a reliable method to aid alfalfa phenotyping for yield (Biswas et al., 2021), and bivariate models combining drone and partial ground-based measurements for yield provided higher genetic gains than univariate models. Genomic prediction showed variable predictive ability (PA) across harvests, and the inclusion of multi-harvest data in training set increased PA for yield (Andrade et al., 2022). In another study, PA for yield was compared for two genotyping platforms, namely sequence capture and a fixed array developed by Breeding Insight. A subset of markers (5000 SNPs for sequence capture and 1000 SNPs for breeding insight) outperformed the full set of markers. When using the full set of markers, breeding insight markers yielded higher PA using GBLUP models within each harvest (Sipowicz et al., 2022). Envirotyping-based data (integrating environmental information in genomic studies) aims to increase PA under multi-environmental trials by including the interaction between genomic features and environmental factors under different cross validation schemes. Models accounting for enviromics data led to higher PA for various traits in a reduced number of harvests under CV0 and CV2 scenarios (Fernandes Filho, et al., 2022). The next steps in our alfalfa breeding project are focused on combining multi-omics data with crop growth models to improve PA for complex traits and accelerate genetic gain in alfalfa.

## References

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