

Genetic Parameters for Agronomic and Morphological Traits in Annual Ryegrass (*Lolium multiflorum* Lamarck)

Esteban Rios, Agronomy Department, University of Florida

Kevin Kenworthy, Agronomy Department, University of Florida

Salvador Gezan, SFRC, University of Florida

Patricio Munoz, Horticultural Science, University of Florida

In order to develop, maintain, and use germplasm collections more efficiently, it is important to characterize their phenotypic diversity. Variance component estimates are used to calculate population genetic parameters that are crucial to make strategic decisions for more efficient management of germplasm collections. This information does not exist for annual ryegrass plant introductions (PI's) from the USDA-National Plant Germplasm System (USDA-NPGS). In this study, we estimated variance components, broad-sense heritability, genotypic values, genotype x year correlations and genetic correlations for eighteen traits in a population composed of 167 annual ryegrass lines, including USDA-NPGS germplasm. Broad-sense heritability (H^2) ranged from 0.11 to 0.93 for single year analyses, and from 0.03 to 0.86 for traits evaluated during two growing seasons, evidencing the presence of genetic variability. Genotype x year correlation ranged from 0.17 up to 0.99, indicating low and high consistency in performance of annual ryegrass lines across years. Genotypic values revealed extensive genetic variability for economically important traits in the USDA-NPGS germplasm collection. Combining multiple traits in one cultivar is a challenge for breeders, especially for traits showing negative correlations. Establishment, plant vigor, leaf width and length, and chlorophyll content were positively correlated among them, and were negatively associated with disease traits. Large variability was found for heading date, which was positively correlated with number of tillers, crown perimeter and biomass production. High positive correlations were also found between biomass and plant height, crown perimeter, number of tillers, tiller size and leaf to stem ratio. A subset of 35 diploid lines was selected based on genotypic values for forage production traits. All results presented in this study will be submitted to the USDA-NPGS for incorporation into their annual ryegrass database collection.