

DNA Marker Diversity of Big Bluestem Populations in the North Central and Northeastern USA

David Price, University of Wisconsin-Madison, Madison, WI; Paul Salon, 3266A RT 352, USDA-NRCS, Corning, NY; Michael Casler, U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI

Big bluestem (*Andropogon gerardii* Vitman) is a native grass of the North American tallgrass prairie, used as a forage crop and under development as a biofuel feedstock. It is a high quality forage species and can fill the forage availability gap between peak spring and autumn growth of cool-season grass species. Understanding the genetic diversity of big bluestem can enable better classification of accessions and increase the ability to recognize unique genetic variation for use within breeding programs. A total of 417 amplified fragment length polymorphism (AFLP) DNA markers and six chloroplast DNA (cpDNA) regions were used to measure genetic diversity both among and within three groups of big bluestem populations: natural populations collected in Wisconsin, natural populations from the northeast USA, and cultivars or accessions available through various gene bank organizations. Results indicate that the germplasm groups represent three distinct yet overlapping genetic pools. Partitioning of genetic variance for each of the three groups revealed a significant amount of variance among ecoregions and hardiness zones, and among populations within ecoregions and hardiness zones. Although significant, the percentage of explained variance was generally small. One exception was among populations for samples originating in the Northeast (20% of the variance). Additionally geographic distance and climatic variables were found to be correlated with genetic distance for samples originating in the Northeast. A total of 37 cpDNA haplotypes were identified, and confirm patterns of separate but overlapping gene pools. We conclude that unique germplasm of big bluestem is present outside of Great Plains, providing opportunities for continued improvements of big bluestem genetics and increased forage yield.