

Germplasm Development and Management of Buffalograss Varieties

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Objectives:

1. Identify and evaluate seeded and vegetative buffalograss biotypes with improved resistance to biotic and abiotic stresses.
2. Develop protocols for establishing vegetative and seeded biotypes of buffalograss cultivars.
3. Develop improved disease and pest resistance, and stress tolerant germplasm using plant breeding methods, molecular techniques, and statistical approaches.

Start Date: 2006

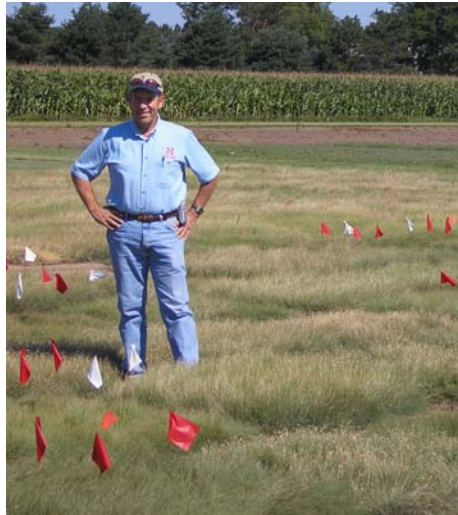
Project Duration: three years

Total Funding: \$90,000

In 2006, advanced germplasm were evaluated for turfgrass winter survival, spring green-up, color, and quality. This germplasm represented material that had been extensively evaluated for its tolerance to low mowing heights, and reduced irrigation and nutrient inputs. Genotypes with outstanding turfgrass color and quality, and superior spring green-up and winter survival were identified and placed into new management evaluations that included mowing height and nitrogen nutrition variables. Four superior genotypes (i.e. two tetraploids and two hexaploids) were identified as potential vegetative entries for the next National Turfgrass Evaluation Program (NTEP) Trial. Three genotypes (hexaploids) were identified as having superior chinch bug (*Blissus occiduus*) resistance during advanced line screening.

Seed increase was initiated on eight lines. These increases were initiated in Nebraska and Arizona. These are polycross lines comprised of genotypes that were identified for their superior bur yield potential. Bur yields from these lines were as much as two-fold those of 'Texoka' under small-plot research trial conditions. The genotypes used in these crosses had been extensively evaluated for turfgrass quality and performance prior to establishing their bur yield potential. Five of the eight lines are hexaploids and three are tetraploid. The tetraploid genotypes used were identified as having early spring green-up and excellent winter hardiness. Seed from these increases will be used for turfgrass evaluations.

In 2004, a study was initiated to determine nitrogen and phosphorus effects on 'Bowie' buffalograss bur yields, and was repeated in 2005. Three rates of each nutrient were investigated in all combinations and were compared to an untreated



The buffalograss breeding and genetics program has many advanced lines with improved turfgrass color, quality, and seed production characteristics.

control. Significant differences were observed for bur yield, pistillate flower height, stand density, and plant quality. These differences were primarily due to increased nitrogen nutrition levels. The highest yields were obtained from the highest nitrogen and phosphorus treatment combination.

Plant peroxidases are a family of related proteins possessing highly conserved domains. Degenerate oligonucleotide primers based on these conserved domains can be used to amplify DNA sequences coding for peroxidases from plants with unsequenced genomes. Polymorphisms in peroxidase genes among buffalograss [*Buchloe dactyloides* (Nutt.) Engelm.] genotypes and eight other grasses were evaluated, and potential evolutionary relationships were determined using this approach. Fourteen peroxidase specific primers with alternative forward and reverse primers using 34 rice peroxidase cDNAs were designed based on conserved motifs of this gene family.

Targeted-PCR amplification of genomic DNA from 28 buffalograss, four C₄ and four C₃ grass genotypes yielded polymorphisms, differentiating diploids

from polyploids within buffalograss and C₃ and C₄ grass species from each other. A total of 11 peroxidase gene fragments, seven belonging to buffalograss and four to the other grass species were sequenced. Five of these sequences were clustered with rice ascorbate peroxidase known to have chloroplast origin. These results demonstrate that primers targeting the peroxidase gene family can be used to study genotypic diversity and evolutionary relationships on an intraspecific and interspecific basis.

Germplasm evaluations have provided many useful sources for the appropriate parental selection in the development of crossing schemes, sampling strategies, and managing our germplasm. A diploid population has been developed. The parents and population have been evaluated for chinch bug resistance, turfgrass quality, and bur yield characteristics. It is our intention to use this diploid population to initiate developing a buffalograss genetic linkage map to test utility and distribution of available markers and identify genetic markers associated with chinch bug resistance, turfgrass quality, bur yield, and other agronomically important traits.

Summary Points

- Progress has been made in identifying genotypes with superior winter survival, spring green-up, and turfgrass quality.
- Seed increase of superior lines was initiated in 2006. Seed from these increases will be used for turfgrass evaluation and potential cultivar release.
- Targeted-PCR amplification of genomic DNA from 28 buffalograss, four C₄ and four C₃ grass genotypes yielded polymorphisms, differentiating diploids from polyploids within buffalograss and C₃ and C₄ grass species from each other.
- A diploid population has been established and evaluated and will be used to develop a genetic linkage map for buffalograss.