Buffalograss Breeding and Genetics

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Objectives:

1. *Breed, select, and evaluate seeded and vegetative genotypes with improved turfgrass quality, pest resistance, and stress tolerance.*
2. *Improve our basic knowledge of the genetics of buffalograss through modern molecular marker technologies.*
3. *Expand understanding and use of efficient management practices for best genotypic performance.*
4. *Develop protocols for best turfgrass establishment.*

Buffalograss is naturally adapted to hot and dry environments. The growing conditions over the past few seasons have been challenging with respect to heat and drought, and buffalograss is a good low maintenance alternative that survives in these conditions. While buffalograss is a great choice in many turf applications, there are still challenges that the breeding program at the University of Nebraska–Lincoln is addressing to further improve buffalograss performance. To improve overall adoption of buffalograss, we are seeking to maximize efficiency in seed production and handling, and create improved strategies for seeding to reduce cost and difficulty in establishment.

Seed dormancy issues complicate buffalograss seed production. A recurrent selection breeding strategy is underway to reduce seed dormancy. Burs from nine individual seed lots were sown to flats in the greenhouse in the absence of a seed priming treatment; a KNO_3 seed priming treatment is typically required to obtain an acceptable germination percentage. Seedlings germinating within 21 days were transplanted and maintained. Early germinating types were intermated, seed harvested, and the cycle repeated. One of the nine seed lots (NE–BFG–07–01) expressed a sufficient number of staminate and pistillate inflorescence in the greenhouse and that line was advanced. All nine lines were also established in isolated blocks in the field to induce flowering and advance the populations. After a single generation, there was a 21.3% germination increase in NE–BFG–07–01.

Establishment of a strip–plot field experiment used to identify host resistance to false smut disease.

Germination percent remains low (36.7%), but if significant gains continue with each generation and if the germination improvement is sustainable, the seed priming treatment might be alleviated, saving buffalograss producers labor, time and money.

False smut disease, caused by *Cercospora seminalis*, prevents normal caryopsis development reducing seed quality. By comparing sequencing of nuclear DNA regions to previously published *Cercospora* sequences, it is clear that *C. seminalis* is mis–identified and is not a true *Cercospora*. Additionally, molecular marker analysis revealed a high level of genetic diversity among 86 *C. seminalis* distinct isolates, suggesting the fungus reproduces sexually. These findings are significant since no prior research has been done on this important disease. With a better understanding of the pathogen, improved management practices to control false smut can be developed. Preliminary research

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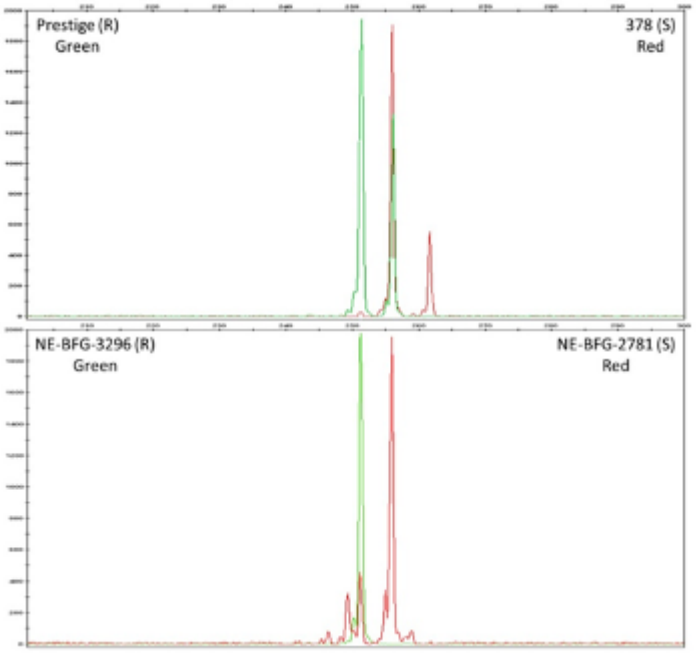
An example of a cDNA–SSR that uniquely identifies 378, Prestige, NE–BFG–2781, and NE–BFG–3296 and may be associated with chinch bug susceptibility (S) and/or resistance (R).



evaluating timing of fungicide applications suggests that fungicides applied at late flowering or at the early signs of disease is more effective at controlling false smut than fungicides applied at pre– or early flowering. A split–plot field experiment with four replications was established during the summer of 2012 consisting of 18 advanced experimental lines along with the false smut susceptible 95–55 line. These plots will be inoculated with false smut and incidence of disease evaluated to identify sources of host resistance.

Genetic markers are a useful tool for more efficiently advancing breeding efforts. A subset of 96 cDNA–SSR markers were tested on the buffalograss varieties 378, Prestige, the parents of a diploid mapping population (NE–BFG–2781 and NE–BFG–3296), and four additional experimental lines. More than 92% of the markers amplified and 50% were polymorphic in the plants tested. Of particular interest, SSRs were identified that discriminate 378 from Prestige and NE–BFG–2781 from NE–BFG–3296. Prestige and NE–BFG–3296 are resistant to chinch bug infestation, while 378 and NE–BFG–2781 are susceptible suggesting these SSR markers may be associated with chinch bug resistance. These markers will be mapped in the diploid mapping population and could be used as a screening tool to identify other sources of chinch bug resistance. Research is also underway to identify new germplasm sources with good turfgrass performance, characterize the mechanisms of gender determination, and improve the production value of buffalograss. The resources developed from this research will accelerate our ability to develop new buffalograss cultivars with desirable characteristics.

Summary Points

- Reducing seed dormancy through traditional breeding.
- Improved characterization of false smut causing pathogen *Cercospora seminalis*.
- Initiated field trials to identify sources of host resistance to *C. seminalis*.
- SSR markers identified that may be associated with chinch bug resistance and will facilitate the development of improved cultivars.

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