

MSU'S TURFGRASS BREEDING PROJECT

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Bentgrass

The main objective of the bentgrass breeding program at MSU is to develop new and improved bentgrass germplasm and cultivars for the region's golf courses and conduct research that is useful to turfgrass breeders throughout the world. The main component of our breeding program involves germplasm evaluation, breeding, selection and evaluation of advanced breeding material. Our primary focus is to improve creeping bentgrass for resistance to gray snow mold caused by *Typhula incarnata*. In 2000 and 2001 we collected over 1000 clones of creeping bentgrass from older golf courses throughout Michigan. All of the collected clones were tested artificially for reaction to an isolate of *T. incarnata* during the spring of 2001 and 2002. Over 30 clones showed significant resistance to this disease. These clones will be used in diallel crossing to choose compatible parents for our next resistant cultivar release. The artificial screening requires cold controlled temperature and incubation of the pathogen in media and corn meal for over 2 months. Another 2 months is required to identify which plants are resistant or susceptible. Selection of diverse parent plants based on both phenotype and genotype is important for developing improved bentgrass cultivars. The phenotype (expressed genes) of plants can be evaluated through conventional means. However, the conventional tools cannot determine the overall genetic profile (a measure of both expressed and non expressed genes) of plants. Selection of desirable plants based on DNA markers is termed marker-assisted selection (MAS) and is more effective. We are applying DNA markers for selection of diverse parents for mapping population and for developing improved cultivars. The incorporation of MAS with conventional breeding approaches will accelerate the development of improved bentgrass cultivars.

Genetic diversity studies using DNA markers can provide useful information regarding the overall genetic profile of a plant. Over 110 plant introductory lines (PI) represent 14 different species of bentgrass collected from all over the world. The DNA molecular marker amplified length polymorphism (AFLP) that we have optimized in our laboratory revealed seven cluster groupings that indicate the degree of relatedness or similarity between plant introductory lines. The high heterogeneity that we found exhibited implies a potential for improving bentgrass with desirable characteristics from different species within the genus. The ultimate objective of this project is to identify and evaluate markers for improved characteristics such as disease resistance and stress tolerance.

Introgression of *Lolium perenne* and *Festuca mairei*

Drought stress is one of the most complex environmental constraints on turf. It is a major factor limiting the growth of cool-season turf grasses in a wide range of climatic regions. As water conservation becomes increasingly important, the development of drought tolerant lines becomes more important. In the past 30 years, turfgrass researchers have put significant effort into developing and evaluating drought tolerance in turfgrass and studying physiological mechanisms underlying drought tolerance. However, the progress in breeding turfgrass for drought tolerance has been very slow, primarily because of: 1) the lack of screening procedures for rapid selection

of germplasm with superior drought tolerance, 2) narrow genetic diversity, 3) inconsistency in testing environment and interaction between stages of plant growth and environment, and 4) dependence on timing and severity of moisture stress.

Understanding the relative importance of major molecular markers with drought tolerance would help to identify key traits and facilitate breeding for drought tolerance turfgrass cultivars. Our main focus of this research is to identify major genes expressed for drought tolerance from *Festuca mairei* collected from Morocco, and introduce the genes into perennial ryegrass for development of cultivars adapted to stress environments in the United State.

The first objective of this research is to utilize the highly informative single sequence repeat (SSR) markers identified from ryegrass species to assess the genomic introgression of *F. mairei* into perennial ryegrass. Out of 40 SSR markers tested, 13 markers covering seven linkage groups fully discriminated the parents. Nine markers revealed that *F.mairei*'s genome was transferred in the hybrid and the back cross derivatives.

The second objective of this research is to use cDNA-AFLP (amplified fragment length polymorphism) to detect the differentially expressed fragments in *Festuca mairei* before- and after- drought stress. Also to convert them to putative cDNA-AFLP fragments into PCR-based markers for drought tolerance and confirm the genes' contribution to drought stress by testing the co segregation of the markers with drought tolerance in the BC₁F₁ progeny from the cross of *Festuca mairei* and perennial ryegrass. Genomic DNA and RNA from stressed and non-stressed *Festuca mairei* plants were extracted and the research is in progress.

Also participating in this research:

- Mr. Dean Smith, Research Assistant
- Dr. Yuexia Wang, Postdoctoral Fellow
- Mrs. Gina Vergara, Ph.D. Candidae
- Mrs. Jianping Wang, Ph.D. Candidate
- Mr. Zhao Han, Ph.D. Candidate