Turfgrass Breeding and Genetics

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The long-term goal of our turf grass breeding program at MSU is to develop turfgrass germplasms that are stress tolerant (biotic and abiotic) and require less pesticide application, fertilization and irrigation. Four major strategies will be used for germplasm enhancement:

1) Conventional breeding methods including ecotype selection and hybridization.

2) DNA molecular markers for assisting in selection.

3) Understanding the genetic mechanisms controlling important agronomic traits such as drought and cold tolerance.

4) Using intra and interspecific hybridization and confirm it with DNA markers such as SSR, AFLP, and RPAD.

Bentgrass Project

The main objective of the bentgrass breeding program is to develop breeding methodologies to improve creeping bentgrass for 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. Over 400 clones were tested artificially for reaction to an isolate of *T. incarnata* during the spring of 2001. Over 30 clones showed significant resistance to this disease. Those 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. Anther 2 months is required to identify which plants are resistant or susceptible. Development of quick, inexpensive and reliable screening methods are needed for this disease.

We have performed initial studies on the genetic diversity and distances of 110 plant introductory lines (PI) representing 14 species of bentgrass collected from all over the world. The DNA molecular marke5r amplified length polymorphism (AFLP) revealed three cluster groupings which 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 *Festucamairei Project*

The prime objective of this research is to utilize the highly informative single sequence repeats (SSR) markers identified from *L. perenne* to assess the genomic introgression of *F. mairei* into *L.*

perenne. 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 backcross derivatives.

Reaction to gray leaf spot disease was highly repeatable among replicates and resulted in biologically and statistically significant ($P<0.001$) differences among the backcross derivative hybrids. We intend to identify the major gene resistance in the backcross derivative hybrid to gray leaf spot disease. The genomic DNA and RNA from those backcross derived hybrids were extracted and primers from R genes cloned in rice were designed. Polymerase chain reactions (PCR) and reverse transcriptions (RT-PCR) to amplify the specific DNA fragments from grass were conducted. Those backcross derivative hybrids will be planted for further testing for release as new turfgrass cultivars.