

THE MSU TURFGRASS BREEDING PROGRAM

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PART I. GENETIC DIVERSITY AND DISTANCES BETWEEN BENTGRASS ACCESSIONS CHARACTERIZED BY AFLP MARKERS. G.V. VERGARA, S.S. BUGHRARA, AND M. MCGRATH.

Amplified fragment length polymorphism (AFLP) markers of *Agrostis* species on several introductory accessions was investigated. Results from 282 polymorphic bands show 20-40% variation between species. Cluster analysis revealed variation relative to chromosome number, geographic distribution, and polymorphic information content. There were three major groups at coefficient similarity index of 0.75. Group I can be divided into three subgroups: subgroup A, composed of velvet bentgrass *A. canina* and *A. vinealis*; subgroup B, with creeping bentgrass *A. palustris*, *A. stolonifera*, *A. alba*, *A. transcaspica*, and *A. scabra*; and subgroup C, of *A. lacnantha* and *A. munroana*. Group II is composed of three subgroups. Subgroup A is composed of 10 accessions of dryland bentgrass, *A. castellana* from Spain and Portugal and three accessions of colonial bentgrass *A. capillaris*, from Denmark, Italy, and the United States. These three accessions may be genetically distinct from the other four colonial bentgrass accessions which compose subgroup B. Two accessions from the United States were found to be on separate branches corresponding to the two subgroups. Subgroup C is composed of *A. trinii* (Russia) and *A. stolonifera* (Germany), the latter being phenotypically different from the other *stolonifera* species. Group III, which branched earlier in the dendrogram, is composed only of *A. mongolica* from Mongolia and *A. hygrometrica* from Uruguay. Dendrogram constructed on the basis of similarity matrices define groups consistent with the genetic origin of the species.

Part II. Using SSR Markers to Assess Introgression of Fescue into Ryegrass Genome. J. P. Wang¹, S.S. Bughrara¹, and D.A. Sleper².

The genera of *Lolium* and *Festuca* belong to the same tribe Poeae of subfamily Pooideae but offer a range of complementary characteristics of agronomic importance. Intergeneric hybridization between the two genera is expected to combine good characteristics of *Lolium* species (good turf quality and good establishment) with *Festuca* species (drought and heat tolerance and disease resistance) in turfgrass breeding.

Forty simple sequence repeat (SSR) markers were used to assess introgression of *F. mairei* (FM) genome into *L. perenne* (LP). Out of the 40 markers, 13 markers covering 7 linkage groups fully discriminated FM and LP. Nine markers revealed the introgression of FM genome into LP. Eleven of thirteen backcross derivatives showed that FM genome was introduced.

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