Development of genetic markers for drought tolerance in *Festuca-Lolium* complexes

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Keywords: genetic markers, drought tolerance, *Festuca-Lolium* complexes

Introduction 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 limiting, the development of drought tolerant lines becomes important. However, the progress in breeding turfgrass for drought resistance has been very slow, primarily because of the genetic complexity of drought stress responses and lack of screening procedures for rapid selection of germplasm with superior drought tolerance. Marker assisted selection (MAS) provides breeders with valuable tools to develop newer germplasm with improved drought tolerance (Quarrie *et al*., 1999). Drought tolerance involves a cascade of events and is controlled genetically by multiple genes. To clarify the genetic network involved, key agronomic traits need to be clarified into individual components to reduce complex analysis (Tollenaar and Wu, 1999). After specific components of the genes corresponding to drought tolerance are isolated and cloned, they can be converted into PCR-based markers to assist the selection and allow us to rapidly identify genetic lines that had the desired allele and discard those without.

M**aterials and methods** *Festuca mairei* (Fm) plants were selected from an Fm population collected from Morocco which was adapted to the hot and dry summers of Northwest Africa (Borrill *et al*., 1971). Two genotypes of *Lolium perenne* (Lp) were obtained from the turfgrass cultivars 'Citation II' (Lp1) and 'Calypso' (Lp2) and also 16 *Festuca-Lolium* plants were grown.

Results Plants were deprived of water until they were severely stressed. Leaf (lamina) elongation, leaf water potential, leaf water content, soil water content, osmotic potential, root length and mass, and tiller survival rate were detected or evaluated during the stress period on both control and stressed plants. The differentially expressed fragments (cDNA fragment) identified from Fm during the drought stress were re-amplified from both the drought tolerant and susceptible complexes to correlate the differential expression pattern of the re-amplified bands and the drought tolerance performance.

References

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