

Introgression of genome from atlas fescue to perennial ryegrass and discovery of genes for drought tolerance

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Intergeneric hybridization between *Festuca* and *Lolium* has been a long-term goal of turf and forage grass breeders to generate cultivars combining the stress tolerance of *Festuca* and the rapid establishment of *Lolium*. However, the wide distance hybridization usually results in the wild genome being eliminated from the hybrid due to incomplete chromosome pairings and crossovers. *Festuca mairei* St. Yves (Fm), commonly known as atlas fescue, is a xerophytic tetraploid ($2n=4x=28$, $M_1M_1M_2M_2$). *Lolium perenne* L.(Lp) ($2n=2x=14$, LL) has been widely used as turf with improved turfgrass quality. In this study, a serial *Festuca-Lolium* complex, generated from crosses between two Fm clones and two genotypes of Lp cultivars, were genetically analyzed with RAPD and SSR markers. All of the 16 detected complexes exhibited integration of Fm and Lp genomes by showing a wide range of ratios of Fm/Lp specific bands. The correlation of the Fm/Lp genome ratios assessed by SSR and RAPD markers was highly significant ($P = 0.0004$). Cluster analysis and principle coordinates analysis of the parents and the 16 Fm-Lp complexes based on a pairwise similarity matrix from merged SSR and RAPD data displayed four groups. Group 1 was the Fm parent group including the complexes containing more of the Fm genome. Group 2 represented the recombinants with high degree of genome blending. Group 3 was the Lp group comprising of Lp-like complexes. Group 4, composed of only one complex, was genetically differentiated from the other three groups. The results provide applicable information about the genetic composition of the *Festuca-Lolium* complexes in this study that could be utilized in breeding programs for turfgrass cultivar improvement.

Drought stress is one of the major environmental constraints on turfgrass. Turfgrass researchers have invested significant effort into developing and evaluating drought resistance in turfgrass and studying physiological mechanisms underlying drought tolerance. However, 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. Understanding the relative importance of major molecular characteristics associated with drought tolerance would help to identify key traits and facilitate breeding for drought tolerance turfgrass cultivars. The M genome in Fm is supposedly associated with a xerophytic adaptation allowing the plant to survive dry long summers. The objective of this study is to determine the whole genome expression pattern of Fm in response to drought stress and identify the genes associated with drought tolerance of Fm by using cDNA-AFLP.