

Mapping of Quantitative Trait Loci (QTL) for Winter Hardiness in Perennial Ryegrass

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Introduction

Perennial ryegrass (*Lolium perenne* L) is an important turf species. Perennial ryegrass has a fast establishment rate, strong seedling vigor, good tolerance to both traffic and low mowing, which makes it a good choice for use on golf course fairways and athletic fields. However, perennial ryegrass has poor ability to survive in severe winters, which limits its use in the far north of the United States including Iowa. An important breeding objective for perennial ryegrass is to improve its winter hardiness. Winter hardiness is a complex quantitative trait that is controlled by multiple genes with each having minor genetic effect. In addition, the expression of such genes is often affected by the environment, which makes it difficult to identify such genes. With the development of DNA marker techniques, it is now possible to locate these genes (quantitative trait loci, QTLs) that are associated with winter hardiness. There are abundant DNA marker variations present in natural population; some of these markers are in the same chromosome as the genes responsible for winter hardiness. These markers often transmit together with the winter hardiness genes into their progenies. The DNA markers are stable and relatively easy to identify compared to winter hardiness genes that are influenced by environment and difficult to identify with classic genetics. The long-term goal of this project is to facilitate germplasm improvement of perennial ryegrass with enhanced winter hardiness through marker-assisted selection (MAS). The specific objective of this research was to identify QTLs that are associated with winter hardiness in perennial ryegrass.

Materials and methods

A segregating population of 174 genotypes was created by crossing a perennial ryegrass cultivar 'Manhattan' which has good winter hardiness with an annual ryegrass cultivar 'Floreagon' which is very sensitive to winter killing. Four clones of each genotype were planted in the field within each replication in an α lattice design with three replications. The distance between individual clones of a genotype is 30 cm, and the distance between each genotype is 60 cm. The distance between rows is 90 cm. Fall regrowth was measured as the vertical height of regrowth in centimeters on 14 November after the last mowing. Freezing tolerance was assessed by measuring ion leakage. Winter survival was evaluated at the end of April using a scale of 1 - 5 with 1 being completely dead and 5 being no injury.

Results

Nine QTLs were identified for fall growth, freezing tolerance, and winter survival from both female and male maps. Four QTLs were identified for winter survival from both female and male maps; two QTLs were identified for fall growth measured in year 2003 and year 2004, respectively.