Mapping QTL for traits related to summer dormancy in tall fescue

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Materials and Methods
A pseudo F1 bi-parental population consisting of 200 progenies was developed by crossing a Mediterranean parent, 103-2, and a Continental parent, R43-64. Plants were phenotyped under a long day of 16-hour-light condition accompanied by 34 degrees Celsius/24 degrees Celsius (day/night) temperature for summer dormancy and 10 hours light condition accompanied with 21 degrees Celsius/16 degrees Celsius (day/night) temperature for optimum growth. Data were taken on tiller number (TN), new leaf (NL), plant height (PHT) fresh weight (FW), dry weight (DW), average tiller weight (ATW) and moisture content (MST) during three different stages, i.e., before cut back, after cut back and return to normal growth (Fig 1). Data analysis was done using PROC UNIVARIATE procedure and PROC GLM procedure of SAS 9.3. Total of 1,968 molecular markers (SSR and DAR markers) were used for linkage mapping. Linkage maps were conducted by JOINMAP 4.0. QTL analysis was conducted using the Windows version of QTL Cartographer V2.5. The difference of the mean data between two conditions was used for QTL mapping. Epistasis analysis was done using QTL IciMapping V4.0.

Results
All the traits showed normal distribution and transgressive segregation except AATW (Fig 2 and Fig 3) and were significantly correlated (Table 1).

The linkage maps pertinent to the Continental parent (R43-64) comprised 817 markers. Twenty-two chromosomal groups have been identified covering a total and average size of 1956.30 and 88.92 cM respectively. Average marker interval of the linkage maps was conducted using QTL Cartographer V2.5. A total of 17 traits were used for QTL mapping in 22 and 23 linkage groups of R43-64 and 103-2 parent respectively. Chromosome 1, 2, 3, 4, 5, 6, 7, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22 and 23 in 103-2 parent were detected with major QTL for plant height, tiller number, new leaf, fresh biomass weight and dry biomass weight. The variability explained by the number of QTL ranged from 9.91 to 22.32. Markers in the flanking region of the identified QTL will be applied for marker-assisted breeding in tall fescue for integration of summer dormancy in Continental morphotypes.

Introduction
Summer dormancy is a phenomenon found in Mediterranean tall fescue (Festuca arundinacea (Schreb.) S.J. Darbysh), which is endogenously controlled and coupled with a series of processes including growth reduction, cessation and/or senescence under nonlimiting moisture conditions during summer (Norton et al., 2006). It is an important drought adaptation trait of cool-season perennial grasses in the Mediterranean climates to survive under harsh summer conditions (Vegis, 1964). In the Southern Great Plains, the persistence and productivity of cool-season perennial grasses is significantly affected by hot and dry summers (Malinowski et al., 2005). Thus understanding and using summer dormancy mechanism in tall fescue would help in developing adaptive cultivars for the region. Marker-assisted selection (MAS) is an appealing method for selecting complex traits like summer dormancy, identifying and using markers flanked to quantitative trait loci (QTL) associated with summer-dormancy-related traits will pose a significant advantage over phenotypic selection to the breeders. The aim of the project is to identify markers and QTL regions associated with summer-dormancy-related traits for potential use in marker-assisted breeding programs.

Conclusion
QTL on chromosome 6 in male parental map and chromosome 14c in female parental map have high potential and should be targeted for marker-assisted breeding for screening summer dormancy in the hybrid population.

References


Fig 1. Schematic presentation of phenotyping procedure.

Fig 2. Phenotypic distribution of various traits under optimum growing condition.

Fig 3. Phenotypic distribution of various traits under summer-dormancy growing condition.

Fig 4. Epistatic interaction of various traits among the chromosomes of female parental maps.

Fig 5. Epistatic interaction of various traits among the chromosomes of female parental maps.

Table 1. Significant QTL involving marker intervals, LOD value and explained phenotypic variation of various traits (Fig 1) and (2) linkage groups.

Table 2. Significant QTL involving marker intervals, LOD value and explained phenotypic variation of various traits (Fig 1) and (2) linkage groups.

Table 3. Significant QTL involving marker intervals, LOD value and explained phenotypic variation of various traits (Fig 1) and (2) linkage groups.

Significant epistatic QTL were found for APHT, RNL, RPHT and BDW in the male (R43-64) parental maps (Fig 4) and for AFW, ADW, AMST, AATW and RTN in the female parental maps (Fig 5).