

Phenotypic variation within local populations of meadow fescue shows significant associations with allele frequencies at AFLP loci

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Keywords: germplasm, meadow fescue, molecular diversity, AFLP, association mapping

Introduction To identify markers useful for Marker Assisted Selection (MAS), mapping families are usually constructed and used for Quantitative Trait Loci (QTL) mapping. Association mapping offers an alternative strategy for marker development using already characterized germplasm, preferably from natural populations. Simultaneous phenotypic and molecular screening of gene bank accessions can reveal associations between molecular marker alleles and phenotypic traits, and lead to a more targeted construction of mapping families for fine-mapping. In this investigation, we combine molecular (AFLP) and phenotypic data of 15 Norwegian local populations and 5 Nordic cultivars in order to identify markers associated with phenotypic traits of interest.

Materials and methods Fifteen local populations and 5 Nordic cultivars (Løken, Kalevi, Fure, Norild, and Svalöfs Sena) of meadow fescue were scored for 19 morphological and phenological traits (DUS characters), and genotyped for 74 AFLP markers (Fjellheim, 2004). Local populations covered geographic variation both for longitude, latitude, and altitude. Forty and 20 genotypes/population were scored for phenotypic characters and for AFLP markers, respectively. AFLP marker data were converted to allele frequencies (Zhivotovsky, 1999), and stepwise multiple regression analyses conducted using mean values of phenotypic traits as responses (Y) and AFLP allele frequencies from each population as predictors (X).

Results and discussion Models with the first 4 markers explained more than 90% of the variation with high associated R^2 (predicted) values (above 80) for 7 of the characters (early growth, leaf width, herbage yield 2. cut, inflorescence forming tendency, growth habit, inflorescence emergency, and width of flag leaf). Table 1 and Figure 1 present the model for leaf width.

Table 1 Stepwise multiple regression model for leaf width based on AFLP marker allele frequencies of 15 local populations (VIF=variance inflation factor)

| Marker | R^2 | R^2 (pred) | P | VIF |
|------------|-------|--------------|-------|-----|
| P77M66-62 | 73.9 | 65.0 | 0.000 | 2.8 |
| P77M72-234 | 87.7 | 79.5 | 0.003 | 2.4 |
| P77M72-139 | 94.4 | 88.2 | 0.004 | 1.3 |
| P77M66-202 | 98.1 | 91.7 | 0.001 | 2.1 |

AFLPs that map close to QTL for heading date, flag leaf length, and flag leaf width were present among markers included in the regression models for these traits, and indicate that the marker-trait associations detected are real. The results from the present analysis demonstrate that association mapping is a promising method for screening germplasm.

Reference

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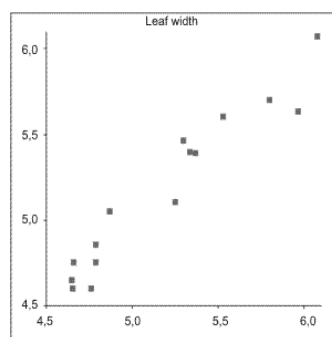


Figure 1 Predicted (Y) vs. true (X) values for the regression model of leaf width using the 4 best AFLP markers of the stepwise regression model