

## Detection of putative QTLs for general appearance, lodging resistance and spring vigor traits in alfalfa (*Medicago sativa* L.)

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### Abstract

Alfalfa (*Medicago sativa* L.) is a very important forage crop throughout the continental U.S. Good general appearance, lodging resistance and spring vigor are important agronomic traits that are conditioned by quantitative inheritance and environmental effects. The objective of the study was to identify molecular markers associated with desirable general appearance, tolerance to lodging, and spring vigor. A backcross population (BC<sub>1</sub>) composed of 180 progeny was developed by crossing the contrasting parent DW000577 (susceptible to lodging) and NL002724 (tolerant to lodging) and back crossing the resulting F<sub>1</sub> to DW000577. A linkage map was developed based on the segregation of 336 markers among the backcross progeny. A total of 72 sequence related amplified polymorphism (SRAP) and 134 amplified fragment length polymorphism (AFLP) markers were distributed among 24 linkage groups that covered 1449.3 cM. A total of 120 markers were insignificantly linked or unlinked.

Replicated clones of both parents and all BC<sub>1</sub> progeny were evaluated for general appearance, tolerance to lodging, and spring vigor in the field in 2007 and 2008 in WA and WI. Trait analysis among the BC<sub>1</sub> progeny showed a normal distribution for tolerance to lodging and slightly skewed distributions in the direction of good general appearance and spring vigor. QTL analysis was performed using the combined data of both locations for 2007 and 2008. One unlinked AFLP marker, ACAXCTC(205), demonstrated significant associations with general appearance over both years [(2007; LOD = 3.04, explains 10.3% of trait variance) (2008; LOD = 3.01, explains 10.3% of trait variance)]. Two markers, the SRAP F7XEM2c and the AFLP ACAXCTC (251), present at 36-40cM locus in linkage group 22 showed significant associations for lodging resistance over both years [(2007; LOD = 4.32, explains 14.4% of trait variance) (2008; LOD = 4.08, explains 13.6% of trait variance)]. For spring vigor the same unlinked AFLP marker associated with general appearance, ACAXCTC(205), was significantly associated with the trait in 2007 only (LOD = 3.22, explains 11% of trait variance). The SRAP marker F7XEM2c is the most likely candidate marker for further consideration of use in marker assisted selection, as SRAP markers are considerably more reproducible and easier to generate than AFLP markers. The SRAP marker can easily be resolved on agarose gels, which will facilitate the subsequent sequencing of this marker and its conversion to a sequence characterized amplified region (SCAR). A SCAR marker could be rapidly resolved based on the presence or absence of a single amplicon, which would lend itself to the rapid examination of many plant samples. Efforts will continue to identify more SRAP markers associated with general appearance, spring vigor and lodging tolerance and to integrate these results into a consensus map of tetraploid alfalfa.