SRAP polymorphisms associated with Phytophthora Root Rot (PRR) tolerance in alfalfa

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Phytophthora root rot (PRR) caused by *Phytophthora medicaginis* is a major cause of decline of established stands of alfalfa in North America. Marker-assisted selection could help accelerate the introgression of resistance genes in germplasm of high agronomic value. In this study, populations resistant to PRR were generated by recurrent selection within two genetic backgrounds that had been previously obtained after three cycles of recurrent selection for superior tolerance to freezing (TF populations): Apica TF3 and Caribou TF3. In each background, 1500 seedlings were challenged with a blend of four isolates of *P. medicaginis* and one hundred (100) genotypes with the highest level of tolerance to PRR were selected and intercrossed to generate three cycles of PRR-resistant populations (PRR-R1, R2 and R3). DNA samples were collected from 50 genotypes of the two initial backgrounds and the six recurrently-selected populations. DNA polymorphisms associated with PRR resistance were subsequently uncovered with sequence related amplified polymorphism (SRAP) amplification of bulked DNA within each population.

Amplification profiles generated with 280 SRAP primer pairs identified several fragments differentially amplified among populations recurrently-selected for PRR within the Apica-TF3 background. The presence of these polymorphic fragments was subsequently assessed in the Caribou-TF3 background using bulked DNA from PRR-R3. Four primer pairs yielded DNA polymorphic fragments of the same size in both genetic backgrounds. Among these, an amplicon obtained with the F11-R9 primer pair present in only 16% of the genotypes in the initial Apica-TF3 background was detected in 54% of the genotypes after three cycles of selection. A similar increment ratio was observed within the Caribou-TF3 background populations. We are currently investigating the presence of these polymorphic fragments in PRR-tolerant genotypes from other alfalfa cultivars. These results show that SRAP analysis of bulk DNA from recurrently-selected populations is an effective approach to identify potential markers for disease resistance in alfalfa.