SRAP polymorphisms associated with Phytophthora Root Rot (PRR) resistance within two alfalfa genetic backgrounds

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Two important traits for alfalfa productivity under cold climate conditions are tolerance to freezing and to low-temperature diseases. Castonguay's group has recently improved several alfalfa backgrounds for their tolerance to freezing (TF populations) using numerous cycles of recurrent selections under controlled conditions. Using Apica and Caribou TF3-derived populations (three cycles of selection for freezing tolerance), we carried on a first cycle of selection for resistance to Phytophthora root rot (PRR). PRR, caused by *Phytophthora medicaginis* is a major cause of decline of established alfalfa in North America.

We screened 1500 genotypes for each of these two PRR-sensitive backgrounds using a blend of three different PRR isolates. PRR-resistant Amerigraze seedlings were used as control. Less than 10% of the TF3-derived populations showed PRR resistance under our testing conditions. One hundred (100) genotypes of each background were selected and intercrossed to generate a first cycle of selection for resistance to PRR (ATF3-PRR+ and CTF3-PRR+). Bulk and individual DNA samples were collected from two groups of 50 genotypes for each background. Using a bulk segregant analysis (BSA) approach in combination with the sequence related amplified polymorphism (SRAP) technique, we uncovered several positive and negative DNA polymorphisms associated with variation to PRR resistance within our two TF3-derived populations.