

Genetic variation in cold tolerance and dormancy in a bi-parental segregating population derived from a wide dormancy cross

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Alfalfa is increasingly adopted in the Southeastern USA as a companion crop in bermudagrass pastures. Based on the bermudagrass acreage in the region, there is a potential of over 20 million acres for the production of alfalfa. The high rainfall and mild winters in these environments would allow growing non-dormant alfalfa cultivars and produce forage most of the year round provided withstanding the occasional freezing temperatures. Cold tolerance is mostly present in dormant alfalfa germplasm. Transferring the trait to non-dormant alfalfa using conventional breeding is a major challenge requiring making wide crosses and several years of evaluation in multiple locations of large size populations. The objectives of this research are to characterize the genetic variation in fall dormancy and cold tolerance in a segregating population derived from a wide-dormancy cross. An F1 mapping population was developed by crossing the fall dormant, cold tolerant cultivar 3010 (FD= 2, WSI 2) with the non-dormant, cold susceptible CW1010 (FD=10). The F1 hybrids were confirmed using SSR markers. The 2 parents, standard checks, and mapping population were evaluated in Watkinsville and Blairsville, GA for fall dormancy and winter survival according to NAAIC protocols. They were also evaluated from freezing tolerance in a freezing chambers. The results showed a clear segregation of both traits in the progeny and a low correlation, suggesting that it is possible to break the association of the two trait and incorporate cold tolerance in non-dormant alfalfa germplasm. Genotyping by sequencing (GBS) will be conducted on the bi-parental population to identify QTL and markers associated with both cold tolerance and dormancy.