A fresh look at the genomic basis of autumn dormancy in cultivated alfalfa

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Selection leaves unique signatures in the allelic composition of populations, including changes in gene frequencies and/or in the amount of genetic variation, that can be used to genetically dissect traits. The trait of fall dormancy in alfalfa (Medicago sativa) is associated with growth responses in autumn, and it appears to be related to many other agronomically important traits as well, including regrowth rate, maturity, winter survival, and others. Previous inheritance studies of fall dormancy in alfalfa reported that the additive components of the genetic variance were generally greater than the non-additive components. Not surprisingly, historical recurrent selection experiments have been able to manipulate the dormancy response. We hypothesized that artificial selection for dormancy phenotypes (taller or shorter autumn growth) had shifted allele frequencies of dormancy-related genes, The objective of this experiment was to test the hypothesis by by assaying genome-wide markers in the pre- and post-selection populations from these historical selection experiments and analyzing allele frequency changes to identify dormancy-associated genomic regions. We screened bulk samples of the non-dormant cultivar CUF 101 and populations developed by three cycles of selection for taller and shorter plants in autumn with single-nucleotide (SNP) markers derived from genotyping-by-sequencing (GBS). We validated the robustness of our GBS-derived, population-specific allele frequency estimates. We demonstrated that in absence of a reference genome, window-based analyses could be successfully implemented using only those markers that map to the highly syntenic genome of Medicago truncatula. Our genomic scan for divergence found a number of genomic regions putatively associated with fall dormancy, including both those previously reported to be associated as well as new regions that had been previously undetected in other experiments. Interestingly, one of the top hits from our analysis is located within 10kb of a gene coding for a protein associated with desiccation-tolerance in a wide variety of crops. Finally, we explored the role of demography by conducting simulations of expected frequency changes under genetic drift compared with changes under selection. Our results suggest that selection mapping is a powerful means of identifying genomic regions associated with traits and that it can be exploited to provide regions on which to focus further mapping and cloning projects.