

Assessing Genetic Changes in the Alfalfa Cultivar CUF 101 Across 40 Years

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Abstract

The long-term stability of alfalfa cultivars throughout their commercial lifetime could be jeopardized when initial breeder and foundation seed lots are exhausted. Alfalfa cultivars with extended commercial lifetimes could potentially change genetically across sequential seed production cycles. High throughput DNA marker technologies like genotyping-by-sequencing (GBS) can be used to assess genetic changes within a population due to natural selection, genetic drift, inadvertent outcrossing with other populations, or seed mixtures. In this experiment, we hypothesize that the genetic constitution of the non-dormant alfalfa cultivar CUF 101, released by the University of California in 1976, could have changed over the past 40 years during which seven sequential foundation seed lots have been produced. Our objective was to test this hypothesis by analyzing these seed lots using GBS-based markers and assessing whether they show evidence of changes in their genetic structure. Recent studies in our lab have shown that GBS-based single nucleotide polymorphism (SNP) markers can readily distinguish an original population from populations derived from it by three generations of moderately strong selection on a single trait. These results suggest we could identify even slight changes in the overall genetic structure of a cultivar. GBS will be used to genotype the seven foundation seed lots that have been created for CUF 101 in its lifetime. As these lots have been developed sequentially (that is, one foundation lot serves as the source of the next lot), genetic changes are clearly possible. Based on the marker data, the relatedness of the populations and genetic shifts among them will be assessed through changes in allele frequencies. This study has implications for assessing the lifespan of a registered cultivar and also for describing the distinctiveness of new cultivars.