

Comparison of Breeding Methods for Improved Alfalfa Yield

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Alfalfa breeders have developed cultivars with improved forage yield, but progress has been slow. Future increases in forage yield through alfalfa breeding might be accelerated by selecting parent plants based on the performance of selfed-progeny. Selfing an alfalfa plant and evaluating progenies from selfed seed in a field nursery may allow the breeder to select genetically superior plants compared to plants selected by phenotypic observations of the parent plants. The objective of this research project was to compare forage yield of cycle 0 alfalfa populations with alfalfa populations developed by one of three breeding methods: 1) mass selection, 2) progeny test of seed from parent plants that were selfed one generation (S1), and 3) progeny test of seed from parent plants that were selfed two generations (S2). Each breeding program (Cornell University, Ithaca, New York (NY), USA, D. Viands and AAFC, Ste-Foy, QC, Canada (CAN), R. Michaud) developed six alfalfa populations by completing two cycles of selection for each of the three breeding methods at the breeders' respective locations. The synthetic generation 2 seed from the six populations and the base population from each of the two breeding programs was planted in forage plot trials at seven locations in 2006 (Iowa, Minnesota (MN), and NY; and Lethbridge, Saskatoon, and SteFoy (2 trials)). Three production years of harvest data were collected at MN and NY. The other trial sites were either harvested for one or two production years or winterkilled. The results of total season yield from the two locations that completed three production years are presented. Within each trial location (NY and MN) and for each of the two breeding populations (NY and CAN), the cycle 0 populations were compared to the six breeding method populations using orthogonal contrasts.

For the MN yield trial, none of the contrast estimates were statistically significant for either breeding population. For the NY yield trial both the NY and CAN mass selection cycle 1 populations were not significantly increased in yield compared to the cycle 0 populations. The mass selection cycle 2 population, however, was significantly higher in yield than the cycle 0 population but only for the NY population (2.9 Mg ha⁻¹, $P < 0.01$). For the cycles of selfed selection in the CAN population, the breeding method populations all yielded less than the cycle 0 populations except for the S2 cycle 1 population, which was not significantly different in yield than cycle 0. Similarly, the NY S2 cycle 1 population was not significantly different in yield than cycle 0. However, the two S1 populations yielded significantly more than the cycle 0 population (S1 cycle 1 yielded 2.3 Mg ha⁻¹ more ($P < 0.01$) and S1 cycle 2 yielded 2.2 Mg ha⁻¹ more ($P < 0.05$)). The breeding method where the S2 or second generation selfed plants were used in the progeny test was quite detrimental to breeding progress since the populations developed with this method yielded significantly less than the cycle 0 population for both NY and CAN (-3.2 Mg ha⁻¹, $P < 0.01$; -1.8 Mg ha⁻¹, $P < 0.05$). Based on the NY population and NY trial results from total season yield over three production years, two cycles of mass selection and one cycle of S1 selection were the best breeding methods to use to increase forage yield. Lack of progress at the MN trial indicates that genotype x environment interaction is significant; thus selection should be done based on data from more than one location.