Rate of Forage Yield Breeding Gains in a Red Clover Breeding Program

Heathcliffe Riday, U.S. Dairy Forage Research Center (USDA-ARS)
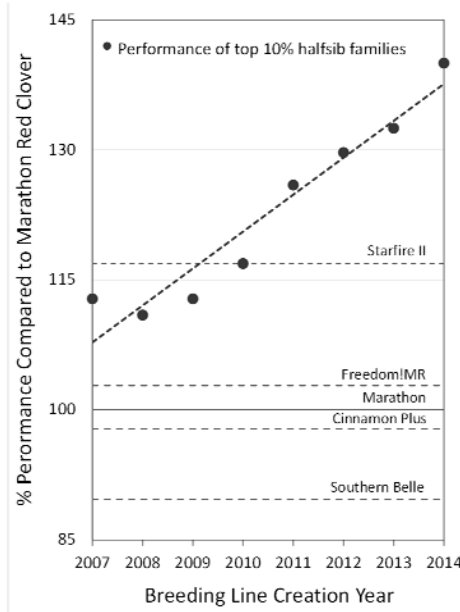
Fig. 1 Performance gain of top 10% of halfsib families derived from 2007-2014 polycrosses (4% gain yr^{-1}, $r^2 = 0.93$, $P <$

Red clover (*Trifolium pratense* L.) is a major forage legume grown on an estimated 4.5 million U.S. acres that contributes an estimated $5 billion USD in value added products to the economy per year. The U.S. Dairy Forage Research Center, USDA-ARS (USDFRC) red clover breeding program is a major red clover breeding program globally and has existed since the 1950s. Major breeding targets in red clover remain improved plant persistence and increasing biomass yield. Starting in 2006 the USDFRC initiated an intensive multi-location space-plant based red clover breeding program. From 2006 through 2015, across 61 space-plant evaluation nurseries, 694,134 repeated individual plant vigor score ratings were taken on 66,649 unique plants from 1,824 entries (e.g., halfsib families, experimental populations, or varieties), derived out of a subset of entries derived from 104 polycrosses. DNA marker paternity testing was conducted on 9,065 of the 66,649 red clover plants. Based on plant average vigor score ratings two selection strategies were practiced. 1) Phenotypic selection – digging the top 5%-8% of superior surviving nursery plants in the fall of the 4th growing season. Selected plants were intermated using bumble bees the next growing season in numerous polycrosses. From these polycrosses new halfsib family entries were derived for further selection. 2) Genotypic selection – intermating progeny from remnant halfsib seed from the 8 to 16 genotypes with the best breeding values among all genotypes ever tested in the program to generate new halfsib family entries for further selection. In this study we determined the program wide germplasm improvement rate by determining the average performance of the top 10% of entries derived each year from 2007-2014 polycrosses (Fig. 1). Assuming a linear trend we observed a 4% gain year^{-1} in average plant vigor score. The correlation between average plant vigor score and sward yield was $r^2 = 0.25$; $P < 0.05$. Based on this correlation the gain year^{-1} for sward forage yield was 1%. Finally we wanted to determine if phenotypic or genotypic selection was generating more of the superior breeding material for the program. Sufficient data was available for halfsib families derived from 2011- 2014 polycrosses. Using a χ^2-test for each year the frequency of phenotypic and genotypic derived halfsib families among all entries were compared to the frequencies of phenotypic and genotypic derived halfsib families among the top 10% performing entries (Fig. 2). In three out of four years we found significant evidence that genotypic selection was generating more than the expected number of halfsib families among the top 10% performing entries. Based on these results in future years more genotypic selection derived halfsib families will be evaluated compared to phenotypic selection derived halfsib families in hopes of accelerating the rate of genetic gain in the program.

Fig. 2 Frequency comparison of phenotypic and genotypic selection derived halfsib families from 2011-2014 polycrosses.