

A comparison of alfalfa selection schemes

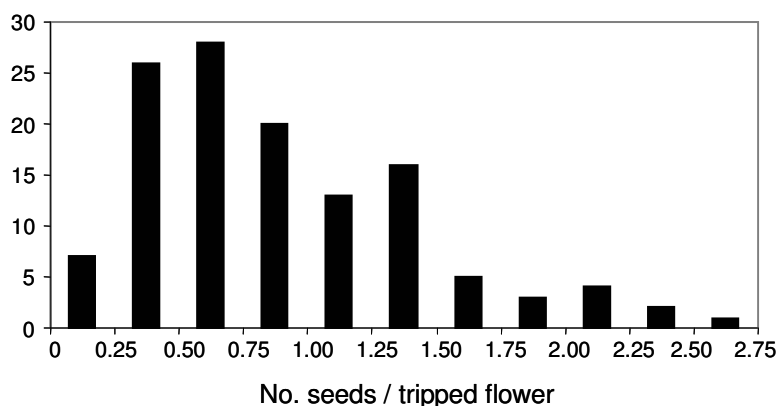
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Phenotypic selection from a large germplasm pool followed by half-sib family selection probably is the commonest breeding scheme for alfalfa. Clonal selection, S_1 family selection, and combined selection between and within S_1 or half-sib families, are major alternatives to half-sib family selection. Selecting S_2 material has been proposed to reduce the genetic load and increase the selection efficiency. Empirical comparisons of selection schemes have been fairly rare, limited to a few schemes, and sometimes relative to selection environments that differ for each scheme (Rumbaugh et al., 1988).

Some 125 genotypes chosen by stratified phenotypic selection from 4500 genotypes formed the genetic base for comparing: i) clonal selection; ii) half-sib family selection; iii) combined selection between and within half-sib families; iv) S_1 family selection; v) combined selection between and within S_1 families; vi) S_2 family selection of S_0 parents; vii) combined selection between S_0 and within S_2 families; viii) S_2 family selection of S_1 parents obtained from best S_0 genotypes; ix) S_2 family selection of S_1 parents obtained from any S_0 genotype. These schemes, and a few others that also maximize the genetic diversity among elite S_0 parents (as estimated by SSR markers), will be compared for rate of forage yield gain per year. All selections will include 12 parents selected from responses of clones, half-sibs, S_1 or S_2 genotypes grown in density in the same environment. The ability of genotypes to be cloned or selfed influences the applicability of some schemes. Results are reported on the variation among 125 S_0 genotypes for these characteristics. The percent of cloning success was assessed across 3 seasons using RCB experiments with 2 replications and 14 clones per replication. Clones were treated with 0.5% NAA and rooted in a mixture of 60% peat and 40% perlite under electronic control of air humidity and soil temperature. The number of seeds per tripped flower was assessed across two contiguous selfing cycles, tripping 15 inflorescences and 10 flowers per inflorescence for each genotype and cycle. The entry variation for average cloning success ranged from 36 % to 89% and, expressed in terms of variance component, was smaller than the genotype \times season interaction variance component. The variation in number of seeds per tripped flower was wide (see Figure 1), ranging from 0.16 to 2.53, and displayed a high broad-sense heritability ($h^2 = 0.81$). No genotype was completely self-sterile. The loss of S_0 genotypes due to insufficient ability to be cloned or selfed was very limited.

Figure 1. Distribution of frequency classes for number of seeds per tripped flower of 125 genotypes



Reference

Rumbaugh, MD, Caddel, JL, Rowe, DE 1988. Breeding and quantitative genetics. In: Hanson, AA, Barnes, DK, Hill, RR (eds), Alfalfa and alfalfa improvement. ASA, CSSA, SSSA, Madison, pp. 777-808.