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1) Selecting homozygous male fertile lines from an intermating soybean population.

The synthesis of random-mating soybean populations and their use in recurrent selection programs was enhanced by the discovery of the male sterile genotype,  $\underline{ms}_1 \underline{ms}_1$  (Brim and Young, 1971; Brim and Stuber, 1973). At some point in such a recurrent selection program, a plant breeder usually wishes to select lines for testing from one or more of the improved populations. There is a difficulty in this, however, because the progeny of every fertile plant selected from a random mating population will segregate for male sterility. This is because every fertile plant is an  $F_1$  from a cross between a male sterile and a fertile plant and is therefore heterozygous at the  $\underline{ms}_1$  locus. The following describes a simple technique for deriving homozygous fertile lines from a random mating population using single-seed descent.

Begin by selecting  $\underline{x}$   $F_1$  fertile plants from the random mating population. Grow the progeny of each plant in a row. This results in  $\underline{x}$  rows, each of which represents a different  $F_2$  family. A set of lines are derived from the  $F_2$  families by sampling a single seed from  $\underline{y}$  plants in each row. This results in a total of  $\underline{x} \cdot \underline{y}$  lines which can be inbred by single-seed descent. In each generation of inbreeding, sample only the fertile plants for the next generation of inbreeding. At some generation,  $F_n$ , the fertile plants are harvested and each increased in plant rows (the  $F_{n+1}$  generation). In the  $F_{n+1}$  generation, only the fertile lines which do not segregate for sterility are saved. The result will be a group of  $F_n$ -derived lines which are homozygous for the dominant  $\underline{Ms}_1$  allele.

Table 1 shows the proportion of fertile plants which can be expected with each generation of selfing, assuming the steriles are discarded each time. It also shows the number of  $F_n$ -derived  $\underline{Ms}_1 \underline{Ms}_1$  lines which one can expect at the  $n^{\text{th}}$  generation. The number of  $F_n$ -derived lines depends upon  $\underline{x} \cdot \underline{y}$ , the original number of plants sampled. It should be noted that the proportion of  $F_n$ -derived lines increases by one-half of the proportional increase in the  $F_{n-1}$  generation.

Table 1

Proportions of homozygous male fertile lines which can be expected with each generation of inbreeding by single seed descent.  
Lines selected from a random mating soybean population

Generation	Proportion of $F_n$ fertile plants	Expected number of $F_n$ derived $\underline{Ms}_1\underline{Ms}_1$ lines	Proportional increase in expected $\underline{Ms}_1\underline{Ms}_1$ lines
$F_2$	3/4	$.500 \times x \cdot y^\dagger$	
$F_3$	5/6	$.583 \times x \cdot y$	.083
$F_4$	9/10	$.625 \times x \cdot y$	.042
$F_5$	17/18	$.646 \times x \cdot y$	.021
$F_6$	33/34	$.656 \times x \cdot y$	.010
$F_7$	65/66	$.661 \times x \cdot y$	.005
$\vdots$	$\vdots$	$\vdots$	
$F_\infty$	1	$.666 \times x \cdot y$	

<sup>†</sup>x and y represent the number of  $F_2$ -plant rows and the number of plants sampled within each row, respectively.

The table can be used to decide how many  $F_2$  plants should be sampled in order to have a specified number of  $F_n$ -derived lines for testing. For example, if 500  $F_4$ -derived lines were needed, it would be necessary to begin with a population of  $\underline{x} \cdot \underline{y} = 800$ , since  $.625 \times 800 = 500$ . The relative sizes of  $\underline{x}$  and  $\underline{y}$  would be an individual judgment based on the size of the base random mating population and the number of generations it has intermated. The results in Table 1 can also be generalized to any recessive simply-inherited trait that can be easily identified and selected out of a population with each generation of selfing.

#### References

- Brim, C. A. and M. F. Young. 1971. Inheritance of a male-sterile character in soybeans. *Crop Sci.* 11: 564-567.
- Brim, C. A. and C. W. Stuber. 1973. Application of genetic male sterility to recurrent selection schemes in soybeans. *Crop Sci.* 13: 528-530.

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