QUANTITATIVE GENETIC IMPROVEMENT IN AUTOGAMOUS PLANTS: APPLICATION OF RECURRENT SELECTION

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ABSTRACT

The text addresses genetic improvement in plants that reproduce by self-fertilization, focusing on characteristics such as productivity, resistance to pests and diseases, and fruit quality. Recurrent selection is highlighted as a strategy to increase genetic variability and improve the effectiveness of selection over consecutive cycles. In the study described, two soybean cultivars adapted to the target region are artificially crossed in a greenhouse, with the objective of creating a segregating population. The breeding method used is SSD (Single Seed Descent), which facilitates the obtaining of homozygous lines by reducing the time required for this and requires less space, and the populations are conducted in environments such as greenhouses.

Keywords: Genetic gain. Genetic variability. Quality of the fruit.

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INTRODUCTION

OBJECTIVES

To improve genetic gain in traits of interest, such as productivity, resistance to pests and diseases, fruit quality, among others, in plants that reproduce by self-fertilization. Recurrent selection is an efficient strategy to increase genetic variability and allow selection to be more effective over consecutive cycles.

MATERIAL AND METHODS

GENOTYPES USED AND HYBRIDIZATION

Two commercial soybean cultivars recommended for the target region of the breeding program will be used to form the segregating population. The two cultivars should show good productivity and resistance to the main diseases of the crop. The P1 and P2 parents will be artificially hybridized in a greenhouse through emasculation of the female flower and brushing of the pollen-supplying anthers on the stigma of the emasculated flower. In greenhouse conditions, where the environment is more favorable, an average of 70 to 80% of success of the crosses performed are obtained (Borém, 2001). Thus, 20 crosses will be carried out, with the expectation of obtaining approximately 15 seeds in total. These F_1 seeds will be planted in a greenhouse, to obtain seeds for the next generation.

BREEDING METHOD USED

The breeding method used will be SSD, which essentially consists of harvesting a seed from each plant of the F2 generation, using only one seed as a parent in the next population. After reaching the required level of homozygosity, each progeny is kept in mixture. In this method, the segregating population is conducted in environments that are not representative of the conditions under which they would be grown commercially (Fehr, 1987). The main characteristic of this method is the reduction of the time required to obtain homozygous lines, since the processes of evaluation and selection of genotypes only begin after obtaining the homozygous lines, and thus, several generations can be conducted in one year (Borém, 2001). One of the advantages of the method is that it requires only a restricted area for the conduction of segregating populations (Ramalho et al., 1993), such as greenhouses.

CONDUCTION OF THE SEGREGATING POPULATION

The segregating population will be conducted in a greenhouse and the seeds obtained will be sown in 3.0 L pots, where up to six plants can be grown. 5 holes will be

made in a circle and one in the center, all deep, where a seed of each plant of the segregating population will be placed per hole, originating the generation F3,0 $cm_{2:3}$. 90% germination will be considered in each generation, so 1500 F2 seeds will give rise to 1350 F2 plants. This process will be repeated until the F4:5 generation, when 1020 plants were randomly harvested individually giving rise to the F5:6 families. These will be planted in the experimental area of the Federal University of Lavras in a 32x32 lattice design with two replications, together with 4 controls. Each plot will consist of a row of two meters with spacing of , sowing 20 seeds/m. From this generation, 221 F 5:7 progenies will be selected0,5 m, which will be planted the following year in 3 locations (Lavras, Lambari and Patos de Minas), in a 15x15 lattice design with 3 replications and 4 controls. Each family will be planted in two rows of with spacing, sowing 20 seeds/m. Of these, the 20 best will be chosen based on the joint analysis of grain yield. These families will be evaluated in a randomized block design, in the same locations mentioned above, with plots of 2 rows and 3 replications, using the same controls, from where the five best will be selected to participate in the Cultivation and Use Value Trials (VCU).3 metros0,5 m4 metros

Table 1. Scheme for the management of soybean segregating populations

Generation	Year	Quantity	Local
P1 x P2	1		Greenhouse
F1	1		Greenhouse
F2	1	1500 seeds	Greenhouse
F2:3	2	1350 plants	Greenhouse
F3:4	2	1215 plants	Greenhouse
F4:5	2	1093 plants	Greenhouse
F5:6	3	1020 progenies	Field – Lavras
F5:7	4	221 progenies	Field – Lavras, Lambari, Patos
F5:8	5	20 bloodlines	Field – Lavras, Lambari, Patos
F5:9	6	5 strains	VCU

STATISTICAL ANALYSIS

Grain yield data (g/plot) will be obtained, and analysis of variance will be performed initially by location, using the following statistical model, considering all effects, except the mean, as random:

$$Yijk = m + ti + qk + bj(k) + ej(ik)$$

where :

Yijk: value observed in the plot that received treatment i, in block j, within the repetition k;

m : overall average;

Ti: Treatment effect I (i=1,2,3,...,1024)

qk : effect of the repetition k, where (k = 1,2 and 3) for $F_{5:7}$

$BJ_{(k)}$: effect of block j (j = 1.2,...,32), within the repetition k

$ej_{(ik)}$: experimental error associated with observation Y_{ijk}

For the analysis of individual variance of the evaluation data of the F5:8 progenies, the following statistical model will be used:

$$Yijk = m + t_i + r_j + e_{ij}$$

Yij: value observed in the portion that received treatment i, in repetition j;

m : overall average;

Ti: Treatment effect I (I = 1,2,3,...,24)

rj : effect of repetition j, being (j = 1,2 and 3)

eij : experimental error associated with observation Y_{ij}

Subsequently, the joint analysis of variance will be performed, with the adjusted average data of each location, using the following statistical model considering all effects, except the mean, as random:

$$Yio = m + ti + lo + (tl)_{io} + \bar{e}io$$

where :

Yio: production of treatment i, on-site o;

m : overall average;

Ti: Treatment effect I (i=1,2,3,...,1024)

lo : effect of the location o, being (o = 1,2 and 3)

$(tl)_{io}$: effect of the interaction of treatment i with site j;

ēio : medium error.

From the analysis of variance, the components of genetic variance, phenotypic variance and heritability in the broad sense will be estimated, as performed by Raposo (1999). The Realized Gain with the Selection (GRS) will also be obtained using the following expression:

$$GRS = GS_j / m_j$$

where :

GSj: is the performance in generation j of the families selected in generation i, minus the overall average of individuals in generation j;

MJ: the average of the selected families in generation J;

With the estimate of the GRS , the realized heritability will be obtained, using the expression similar to that presented by FEHR (1987), that is:

$$h2ij = [GRS] / [ds_{(\%)}]$$

where:

GRS: Realized Gain with the Selection already detailed above;

$DS_{(\%)}$: is the selection differential, that is, the average of the families selected in generation I minus the general average of the families of this generation divided by the general average of the families of generation I;

REFERENCES

1. Borém, A. (2001). *Melhoramento de plantas* (3. ed.). Viçosa: UFV.

2. Fehr, W. R. (1987). *Principles of cultivar development: Theory and technique* (Vol. 1). Ames, Iowa: Macmillan Publishing Company.

3. Ramalho, M. A. P., Santos, J. B., & Zimmermann, M. J. (1993). *Genética quantitativa em plantas autógamas: Aplicações ao melhoramento do feijoeiro*. Goiânia: UFG.

4. Raposo, F. V. (1999). *Comparação de métodos de condução de populações segregantes de feijoeiro* (Dissertação de mestrado). Lavras: UFLA.