GENETIC ANALYSIS ON AGRONOMIC TRAITS IN SNAP BEAN

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Introduction

In snap bean, studies about inheritance of important agronomic traits for plant breeders are scarce. Besides, there are many controversial results considering the same characteristics (Leal et al. 1979; Rodrigues et al. 1998; Carvalho et al. 1999).

Nevertheless, planning and executing a breeding program require correct information on the genetic systems controlling interest traits, expecting gains can be maximized with use of the selection process (Vencovsky and Barriga 1992; Barelli et al. 1999).

In this case, diallel analysis is an adequate strategy, considering it offers large amount of genetic information. Among methodologies of diallel analysis, Hayman´s procedure (1954), has greatly contributed to breeding because it provides an efficient study of the genetic action involved in the control of traits and identifies the presence of epistatic interactions. It also estimates the genetic component of genotype determination and the limit of selection which may be obtained from assessed parents (Cruz and Regazzi 1995; Barelli et al. 1999; Bonett el al. 2001).

The present study was carried out using a diallel cross system based on Hayman´s methodology (1954) among five divergent snap bean accessions to obtain genetic information for agronomic traits to start a breeding program.

Materials and Methods

The snap bean accessions UENF 1429, UENF 1432, UENF 1442, UENF 1445 and UENF 1448, from vegetables germplasm bank at UENF (Darcy Ribeiro North Fluminense State University), Rio de Janeiro, Brazil, were chosen because of their divergent morphological and agronomic traits identified by Abreu (2001) and used as parents in a complete diallel without reciprocals. The hybrids were confirmed by flower color and RAPD markers. The populations consisting of 15 treatments were assessed in the greenhouse at the UENF, in a randomized complete block with fifteen replications. The Hayman`s diallel analysis (1954) was carried out based on Cruz and Regazzi (2001), considering that homozygous parents were different in only one locus (T/t), and presented desirable alleles in an u_1 ratio and undesirable alleles in a v_1 ratio. The GENES program (CRUZ, 2001) was used for this analysis.

Results and Discussion

Additive genetic effects were predominant for pod weight per plant, number of seeds per pod, height of the insertion of the first pod and number of days to flowering while non-additive effects were more important for number of pods per plant. Using the accessions 'per se' in breeding programs would be possible to obtaining genetic gain for the first four traits, while breeding system with crossing are desirable for improve other traits.

The analysis also revealed that dominant alleles increased the number of pods per plant, pod weight per plant and number of seeds per pod. Moreover, although the recessive alleles were responsible for increase in the height of the insertion of the first pod and number of days to flowering, considering practical aspects from farmers point of view, major interesting is to reduce of these traits. Achieving this objective, dominant alleles are desirable to obtain pure lines with lower insertion of first pod and plants with short yield season.

Allelic interaction was overdominance to the number of pods per plant, while the partial dominance worked on the expression of other traits. Excepting number of pods per plant, there were high coefficients of genetic determination for the other traits, indicating that superior lines may be obtained using simple selection methods.

Conclusions

1. Genes with additive action were responsible for the expression of the major traits evaluated.
2. There is great chance of developing superior genotypes in breeding programs.

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