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DIFFERENTIATION OF GROUNDNUT (*ARACHIS HYPOGAEA* L.) GENOTYPES WITH DIVERSE GROWTH HABITS BY DISCRIMINANT FUNCTION ANALYSIS

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ABSTRACT

Genetic diversity of 90 groundnut genotypes belonging to different growth habits was evaluated with Discriminant Function Index. The present study indicated that genetic diversity exists among the genotypes with diverse plant type and this can be very efficiently used to exploit heterosis in groundnut.

Key words: *Arachis hypogaea* L., groundnut, growth habits, discriminant function analysis

Plant type in groundnut (*Arachis hypogaea* L.) varies from compact bunch type (Spanish bunch) with very little lateral spread to semi-spreading (Virginia bunch) and completely spreading type (Virginia runner). In order to work out the differences among the genotypes of specific growth habits, the genetic diversity was determined using paired analysis by discriminant function [1].

MATERIALS AND METHODS

Ninety genotypes of groundnut (exotic and indigenous), 30 each belonging to bunch, spreading and semispreading growth habits, were evaluated in four environments in compact family block design at the experimental area of Genetics and Plant Breeding, Punjab Agricultural University, Ludhiana. Data were recorded for pod yield, kernel yield, pod number, number of primary and secondary branches, plant height, and days to flowering. Pooled analysis of variance between groups was carried out for all the characters and discriminant function index (I) for each pair of groups was constructed as given below:

$$I = \lambda_1 X_1 + \lambda_2 X_2 + \lambda_3 X_3 + \quad \ldots\ldots + \lambda_n X_n$$

RESULTS AND DISCUSSION

Pooled analysis of variance of genotypes belonging to three growth habits over all the environments revealed significant differences among groups for all the characters under study (Table 1). This indicated that the growth habit has a distinct influence on these plant characters. The significant group x environment interactions, a function of differential response of the groups to environments gives sufficient indication of their genetic diversity. Significant differences among groups, environments, and group x environment interaction were observed for all the traits in groundnut genotypes [2].

Table 1. Pooled analysis of variance (M.S.S.) for plant traits

Source	d.f.	Pod yield	Kernel yield	Pod number	Secondary branches	Primary branches	Plant height	Days to flowering
Groups	2	1950.2^{*}	492.1^{*}	374.2^{*}	1451.5^{**}	49.3^{*}	5177.9^{**}	93.3^{**}
Environments	3	7249.2^{**}	1804.0^{**}	6281.3^{**}	123.7^{*}	50.6^{*}	516.7^{**}	26.6^{**}
Groups x envs.	6	345.2^{**}	67.2^{**}	89.8^{**}	37.8^{**}	8.3^{**}	55.1^{**}	3.4^{**}
Pooled error	12	0.2	1.2	0.5	0.4	0.1	1.4	0.1

*,**Significant at 5 and 1% levels, respectively.

The analysis of variance of discriminant function (Table 2) further confirmed significant differences in genetic architecture of the genotypes with different growth habits. The differences within groups were nonsignificant in all the cases. Discriminant function index (I) for each pair of growth habit, i.e. bunch vs. spreading, spreading vs. semispreading, and bunch vs semispreading, was constructed and tested for significance (Tables 2, 3). The differences between the groups within each pair were highly significant (Table 3), which indicated that the groups have different genetic architecture. Use of discriminant function analysis has also been found efficient in discriminating genotypes of different seed size subpopulation in pearl millet [3].

Table 2. Analysis of variance of discriminant function

Source	d.f.	Mean squares		
		bunch vs. spreading	spreading vs. semi-spreading	bunch vs. semi-spreading
Between groups	8	0.261^{**}	0.038^{**}	0.059^{**}
Within group	51	0.007	0.003	0.003

**Significant at 1% level.

The scoring of discriminant function index I for each genotype revealed the difference of mean score to be 369.5 for bunch vs. spreading group, 32.9 for spreading vs. semispreading, and 168.4 for bunch vs. semispreading groups, the contrast being maximum between bunch and spreading, followed by bunch and semispreading types. The function

Table 3. Discriminant function analysis for comparing genotypes with different growth habits

Comparison	Discriminant function	F value
Bunch vs. spreading	I = 15 1 PY + 1 KY + 30 PN – 22 SBN + 24 PBN + 147 PH + 2 DTFF	35.7**
Spreading vs. semispreading	I = 67 PY + 3 KY – 7 PN – 11 SBN – 1 PBN – 58 PH + 1 DTFF	13.6**
Bunch vs. semispreading	I = 34 PY + 4 KY + 1 PN + 1 SBN + 2 PBN + 21 PH – 4 DTFF	17.0**

**Significant at 1% level.

for various comparisons based on number of morphological characters including yield suggested that the genotypes with different growth habits have different genetic constitution.

The above findings thus clearly indicate that the genetic diversity exists among the groundnut genotypes with diverse growth habits. This genetic diversity can be very efficiently used to exploit heterosis in groundnut for different yield and quality parameters.

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