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Genotypic, phenotypic, and heritability studies in groundnut (*Arachis hypogaea*)

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ABSTRACT

A total of 36 different genotypes maintained under Goldking Research Centre were evaluated in Kharif, 2019 for some variability parameters like GCV, PCV, Heritability and Genetic advance as percent of mean. The statistical analysis shows that the estimates of GCV and PCV along with heritability and genetic advance were found to be high for pod yield per plant, plant height number of aerial pegs per plant, biological yield per plant 100 pod weight and harvest index which indicate that these quantitative characters are preponderantly govern by additive genes so there is a good scope of selection for further improvement in these traits and ultimately pod yield.

Keywords: Groundnut, GCV, PCV, Heritability, genetic advance

1. INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is one of the important edible oilseed crop apart from cotton, sesame, mustard, sunflower. It is a highly self-pollinated crop so there is less scope of genetic diversity. Genetic variability is the necessity for crop improvement because it provides good scope of selection. Pod yield is quantitative character govern by several quantitative traits and selection in these traits ultimately leads to increase in pod yield which is highly influence by the environmental factors. Improvement in any crop depends upon the magnitude and available genetic variability in the traits. Hence an effort was made by present investigation to assess the variability in important quantitative traits with the help of indices of genetic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability in broad sense and genetic advance as a percent of mean (GA%). This attempt will be helpful to understand the variability available in the genotypes and how to be utilised in the future selection programme.

2. MATERIAL AND METHODS

A total of 36 germplasm entries were utilized for the present investigation. The whole material was sown utilizing Randomized Block Design (R.B.D.) having three replications. The trial was sown in Kharif, 2019 at Goldking Research Centre, Goldking Biogene Pvt., Ltd., located at Village Sherpur, Ta. Idar-383 430, Di. Sabarkantha, Gujarat, INDIA. Each genotype was sown having 3.0 m length and with row:row & plant: plant spacing of 60 x 15 cm. The fertilizer was applied with 12.50: 25.00: 00 Kg ha⁻¹ (N:P:K). Other recommended cultural practices were also followed to raise a good crop. The necessary observations were recorded on five randomly selected plants in each genotype for three replications for days to 50% flowering, days to maturity, pod yield per plant (g) plant height (cm), No. of primary branches per plant, No. of mature pods per plant, No. of aerial pegs per plant, No. of underground pegs per plant, biological yield per plant (g), Mature kernels (%), 100 kernel weight (g) and harvest index (%) and the average (mean) values were utilized for statistical analysis. The mean data were utilized to different statistical analysis viz., magnitude of genetic variability were performed following the standard procedures, PCV and GCV coefficients of variation were estimated as per the procedure suggested by Burton (1952) and heritability (broad sense) and genetic advance were estimated as followed by Allard (1960).

3. RESULTS AND DISCUSSION

The statistical analysis on the value of different characters and analysis of variance showed presence of sufficient variability in the genotypes. Very wide range of phenotypic coefficient of variation was observed for Pod yield per plant, plant height, biological yield, 100 kernel weight and harvest index (Table-1). Similar observations were also found by John et al. (2005). High PCV and GCV estimates were recorded for pod yield per plant, plant height, No. of primary branches per plant, no. of mature pods, no. of aerial pegs per plant, 100 kernel weight and harvest index. These results are in accordance with Mothilal et. Al. (2004). Moderate to low GCV and PCV were observed for Days to 50% flowering, days to maturity and mature kernels. Similar results were also observed by Yogendra Prasad et al. (2002). Some characters like days to 50% flowering, days to maturity, mature kernels (%), biological yield per plant showed narrow difference between genetic and phenotypic variability estimates which means that these characters are less influenced by the interaction of genotype and environment. (Choudhary *et al.*, 2013). The presence of high magnitude of estimates of genetic variability in harvest index, 100 kernel weight, No. Of underground pegs, no. Of aerial pegs, no of mature pods indicates greater extent of genetic variability in these traits and thus provide a good scope of selection to improve the population and thereby creates a good gene pool for future breeding programme. Low values of genetic variability show the need for hybridization programme by selection of parents having maximum extent of genetic diversity with respect to trait and which may also leads to trait specific or yield oriented breeding programme. The similar observations were made by Rao (2016)

High heritability values does not indicate that there will be better progress in selection of very good genotypes. High heritability coupled with high genetic advance provide more chances of effective selection of good genotypes Johnson et al., (1955). High heritability estimates along with high genetic advance as a percent of mean were expressed by pod yield per plant, plant height, no. Of mature pods per plant, no of aerial and underground pegs per plant, biological yield, 100 kernel weight and harvest index which may be due to profound additive gene action controlling these traits, which in turn provide ample scope for selection and it also does mean that these characters are less influenced by environment. Similar results were obtained by Venkatesh et.al. (2019), Mukhesh *et al.*, (2014).The similar observations were obtained by Choudhary et al., (2013). Low magnitude of genetic advance in days to maturity, mature kernels (%) and days to 50 flowering indicates that these traits are governed by mostly non additive gene action and hence there will be very less response to selection due to higher environmental influence on the expression of these traits.

Table 2: Mean, Range and Coefficient of Variations (GCV, PCV), Heritability in broad sense, Genetic advance as percent of Mean (GA%) for different characters in Groundnut.

Characters	Mean	Range	Coefficient of variation		Heritability (%)	Genetic advance as % of mean
			Genotypic	Phenotypic		
Days to 50% flowering	45.55	43.00-53.00	6.33	7.55	64.70	8.90
Days to maturity	114.33	112.33-125.67	2.15	2.88	60.40	3.16
Pod yield per plant (g)	11.52	9.77-18.33	14.33	18.77	63.80	26.77
Plant height (cm)	20.41	11.93-30.33	19.08	33.34	65.87	29.20
No. of primary branches/plant	4.89	3.77-8.17	13.93	17.33	61.33	19.99
No. of mature pods per plant	12.52	10.33-16.53	10.77	16.88	32.50	13.66
100 pod weight (g)	95.77	63.55-150.33	17.35	18.74	95.55	37.67
Number of aerial pegs per plant	5.90	3.77-15.77	51.31	54.33	82.80	85.84
Number of underground pegs per plant	28.67	21.37-48.33	19.23	21.31	82.40	35.89
Biological yield per plant (g)	30.66	19.82-39.77	14.77	17.21	67.40	27.97
Mature kernels (%)	91.15	71.33-98.95	6.11	6.97	76.60	13.13
100-kernel weight (g)	38.45	25.33-60.67	15.93	17.66	81.50	34.09
Harvest index (%)	35.92	31.13-49.50	15.71	19.66	60.33	19.27

4. SUMMARY AND CONCLUSION

In the present investigation it was observed that sufficient genetic variability was present for many quantitative traits like pod yield per plant, plant height, no of aerial pegs, mature kernels (%), 100 kernel weight and harvest index. This shows the proper selection of the genotypes. Some characters like pod yield per plant, plant height, no. Of mature pods per plant, no of aerial pegs, 100 kernel weight and harvest index indicated high heritability along with high genetic advance (GA%) which means that these traits are govern by mostly additive gene action and these are less influenced by environmental thus it provides a very good scope of rigorous selection. Some characters show very low magnitude of genetic advance which may be due to environmental effect on the phenotypic expression of genotypes.

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