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Assessment of genetic parameters in groundnut (*Arachis hypogaea* L.) RIL population for PBND screening

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Abstract

A population consisting of 260 RILs derived from the cross JL24 × NRCGS-86 (F_{10} – F_{11} generation) was utilized for the study. The population was subjected to variability studies for pod yield, yield attributing traits and disease resistance (PBND and LLS at 60, 75, 90 and 105 days after sowing) in *Kharif* 2022. In RIL population, the analysis of variance indicated significant variation for all the yield traits and diseases, but the variation was found to be less for sound mature kernels and oil content. Moderate to high GCV and PCV with moderate to high heritability coupled with moderate to high GAM for pod yield component traits in RILs were observed but matured pods per plant and pod yield per plant showed high magnitudes of variability, indicating that selection based on these observations yields superior genotypes. Similar results were seen for PBND incidence, PDI at 60 DAS, 75 DAS, 90 DAS and 105 DAS. So, selection is rewarding for disease resistance. Moreover, these indices showcased a relatively higher level of heritability and genetic gain, thus indicating a plausible avenue for enhancing resistance.

Keywords: Groundnut, RILs, genetic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance

1. Introduction

Groundnut, scientifically known as *Arachis hypogaea* L., is a predominantly self-pollinating crop that thrives in tropical and subtropical regions. In India, it is spread over an area of 60.93 lakh hectares with a production of 102.09 lakh tonnes and 1676 kg per hectares production per unit area (Anonymous, 2021) [2]. In the country, the decline in groundnut production or productivity could be ascribed to various biotic and abiotic stress affecting growth and yield of the crop. Peanut bud necrosis disease (PBND) among many in groundnut poses a serious threat to its production in India, resulting in complete crop loss. In case of PBND, breeding for resistance to the virus or vector or both can be considered to manage viral disease to reduce economic yield losses. Evaluation of lines employed under field conditions for diseases and other traits need variability in order for the selection to be effective.

However, limited genetic diversity of groundnut necessitates the introduction of more variation in segregating materials. Genetic variability serves as the fundamental prerequisite for improving this crop, as it widens the opportunities for selection. Consequently, the effectiveness of selection depends on the type, extent and magnitude of genetic variability present in the material, as well as its heritability. Therefore, in this study, we aimed to evaluate the variability of crucial traits related to pod yield and its contributing factors. Additionally, we calculated indices of variability such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in the broad sense ($h2_{bs}$) and genetic advance as a percentage of the mean (GAM).

The knowledge of existing variability and degree of association between yield contributing characters and their relative contribution to yield is essential for developing high yielding genotypes. The observed variability is a combined measure of genetic, environmental causes and the genetic variability is heritable from generation to generation. Heritability and genetic advance are useful tools for breeders in determining the direction and magnitude of selection.

2. Materials and Methods

Two hundred sixty RILs of groundnut obtained from cross between JL24 × NRCGS-86 made during the post rainy season of 2014 at ICAR-DGR, Junagadh, Gujarat.

The JL-24 is a popular short duration Spanish bunch cultivar, which was used as female parent. It is widely grown in India, but it is susceptible to PBND. NRCGS-86 an interspecific pre-breeding line, resistant to PBND was used as donor parent.

Material was evaluated in Augmented Block Design at All India Co-ordinated Research Project on Groundnut research block, Main Agricultural Research Station (MARS), Raichur during *Kharif* 2022. Each RIL assembled at the spacing of 30 cm in between rows and 10 cm within plants and standard agronomic practices were followed as per package of practices. Findings was recorded on randomly selected five plants of each genotype and mean value was taken into consideration for statistical analysis for eleven characters namely days to 50% flowering, days to maturity, initial plant stand, final plant stand, number of mature pods per plant, pod yield per plant, hundred pod weight, shelling percentage, hundred kernel weight, sound mature kernel and oil content.

The data subjected to different statistical analysis *viz*., analysis of variance and magnitude of genetic variability were performed following the standard procedures, phenotypic and genotypic coefficient of variation as suggested by Burton (1952) [6], heritability (Broad sense) and genetic advance as followed by Allard (1960) [1].

3. Results and Discussion

3.1 Anova

For 260 RILs of groundnut, an analysis of variance was performed to assess potential differences among population means. The variance that was observed due to known and unknown sources was calculated and the findings are outlined in Table 1. The population of RILs and their parental lines exhibited moderate to high variability across majority of the traits. The ANOVA for 16 characters indicated significant differences between RILs for a number of yield-related characteristics including initial plant stand, days to 50 percent flowering, days to maturity, final plant stand, number of matured pods per plant, pod yield per plant, hundred pod weight, hundred kernel weight, and shelling percentage at both five percent and one percent levels of significance but sound mature kernels and oil content were only significant at five percent level of significance.

The variance was also analyzed for incidences of Peanut Bud Necrosis Disease (PBND) and disease indices of Late Leaf Spot (LLS) in groundnut. The results unveiled the substantial variability among RILs concerning PBND as well as the disease indices of LLS at different days after sowing (60 DAS, 75 DAS, 90 DAS and 105 DAS).

Similarly, the variance effect among checks also found significant differences for all traits examined excluding initial plant stand, final plant stand, shelling percentage and sound mature kernels. The mean sum of squares attributed to blocks (ignoring treatments) are found to be non-significant except for shelling percentage and sound mature kernels indicating the homogeneity of evaluation blocks. The effects due to interaction *i.e*., RILs *v/s* checks is also found significant indicating thereby that RILs were significantly different from checks except for hundred kernel weight and sound mature kernels.

The variance observed within the RIL population exhibited highly significant differences for most of the examined traits which indicated the existence of sufficient genetic variability between them and scope for improvement of traits through selection which justifies the use of appropriate material in the present investigation.

The obtained ANOVA results were similar to the studies by Kona *et al*., 2021 [17] and Gangadhar and Gor, 2022 [11].

3.2 Genotypic and phenotypic coefficient of variance

The outcomes of ANOVA was used for the calculation of phenotypic and genotypic coefficients of variation (GCV and PCV), heritability and to predict genetic advance as percent of mean (GAM) for traits studied. The research investigations on coefficient of variation relies on a percent mean to express variance and the results obtained on phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability and genetic advance as a percent mean are expressed trait wise in Table 2. The statistical values provide insights into the available variability, gene action and potential for improvement of these traits through selective breeding or other genetic interventions. The outcomes of PCV and GCV are depicted in fig. 1, further heritability and GAM in fig. 2.

The highest genotypic coefficient of variation (GCV) observed for final plant stand followed by matured pods per plant and pod yield per plant. The highest phenotypic coefficient of variation (PCV) observed for initial plant stand followed by final plant stand, matured pods per plant and pod yield per plant. Higher GCV and PCV were also observed for disease incidences like PBND incidence and late leaf spot index at 105 days after sowing.

These results suggest that several of the evaluated traits exhibit significant genetic variability indicating the potential for improvement through selective breeding. Traits like initial and final plant stand, number of pods, pod yield, hundred kernel weight and disease resistance traits (PBND and PDI) are particularly promising for selection efforts. Balaraju and Kenchanagoudar (2016) [4] observed high genetic variability for major yield contributing characters.

Comparable outcomes were reported by Daudi *et al.* (2021) [8] for plant stand; by Prabhu *et al.* (2016) [27] and Bhagat *et al.* (1986) [5] for matured pods per plant; by Ashutosh *et al.* (2017) [3], Omima *et al.* (2018) [22] and Wadikar *et al*. (2018) [31] for pod yield per plant; Jadhav *et al.* (2019) [15] for PBND incidences.

The difference in magnitude between PCV and GCV was minimal, suggesting that environmental effect is less or negligible and maximum reflection of genotype into phenotype of most of the traits. Therefore, selection performed based on phenotypic performance is more effective.

In the present study, moderate values of GCV were observed for initial plant stand, hundred kernel weight and late leaf spot indices at 60, 75 and 90 DAS. Also, moderate values of PCV were observed for hundred kernel weight and late leaf spot index at 90 days after sowing. Moderate values of GCV for 100-kernel weight was in accordance with the results of Patil *et al.* (2015) [25] and Ashutosh *et al.* (2017) [3].

Lower GCV and PCV were observed for days to 50% flowering, days to maturity, hundred pod weight, shelling percentage, sound mature kernels and oil content. Similar results were also reported by Vasanthi *et al.* (2015) [30] for days to 50% flowering; by Mahalakshmi *et al.* (2005) [20] and John *et al*. (2007) [16] for days to maturity; Hemanth Kumar (2004) [14] for shelling percentage; Parmeshwarappa *et al.* (2008) [24] for sound mature kernels and Hampannavar *et al.* (2018) [13] for oil content.

3.3 Heritability and genetic advance

Higher heritability were observed for initial plant stand, final plant stand, matured pods per plant, pod yield per plant, hundred pod weight, hundred kernel weight and shelling percentage. Also for disease observations like PBND incidence and late leaf spot indices at 60, 90 and 105 DAS. Results are in line with Parameshwarappa and Kallappagoudar (2005) [23] for plant stand; Devasena *et al.* (2015) [9] for pod yield per plant; Korat *et al.* (2009) [18] and Gupta *et al.* (2015) [12] for hundred pod weight; Hampannavar *et al.* (2018) [13] for hundred kernel weight; Higher broad sense heritability estimates of PBND incidence were reported by Tonsomors *et al.* (2006) [30] and of Late leaf spot reported by Dwivedi *et al.* (2002) [10] in groundnut populations.

Moderate heritability were observed for days to 50% flowering, days to maturity, sound mature kernels, oil content and late leaf spot index at 75 days after sowing. Similar findings are in line with John *et al.* (2007) [16] for days to maturity; Chavadhari *et al.* (2017) [7] for sound mature kernels.

Higher genetic advance as a percent of mean was observed for traits like initial plant stand, final plant stand, matured pods per plant, pod yield per plant, hundred kernel weight and also for disease observations like PBND incidence and late leaf spot indices at 60, 90 and 105 DAS. These findings are confirmed by Prakash *et al.* (2000) [29] for matured pods per plant; Patil *et al.* (2015) [25] for pod yield per plant; Korat *et al.* (2009) [18] and Gupta *et al.* (2015) [12] for hundred pod weight; Hampannavar *et al.* (2018) [13] for hundred kernel weight.

Moderate genetic advance as a percent of mean was observed for traits hundred pod weight, shelling percentage and late leaf spot index at 75 days after sowing.Similar results were given by Hemanth Kumar (2004) [14] and Mohan *et al.* (2012) [22] for shelling percentage.

Lower genetic advance as a percent of mean was observed for days to 50% flowering, days to maturity, sound mature kernels and oil content. Gupta *et al.* (2015) [12] reported the same for sound mature kernels.

Table 1: Analysis of variance for quantitative traits and diseases in groundnut RIL population

Sources of variation	Df	Initial plant stand	Days to fifty percent flowering	Days to maturity	Final plant stand	Matured pods per plant	Pod yield per plant (g)	Hundred pod weight (g)	Hundred kernel weight (g)
Blocks	12	4.95	0.39	0.35	7.82	1.61	1.16	7.71	24.15
Treatments (RILs + checks)	264	49.24**	4.81**	4.73**	48.09**	10.08**	8.37**	30.89**	24.26**
Checks	4	20.82	50.94**	49.36**	5.02	7.52**	5.58**	307.17**	72.59**
RILs	259	44.53**	3.90**	3.86**	43.97**	6.43**	3.92**	26.41**	23.58**
RILs *vs* Checks	1	1381.23**	56.08**	52.80**	1288.03**	966.30**	1171.33**	84.24**	8.74
Error	48	14.73	1.94	2.17	7.55	1.51	1.32	5.74	7.18

Sources of variation	DF	Shelling percentage (%)	Sound mature kernels (%)	Oil content (%)	PBND incidence (%)	LLS (PDI) at 60 DAS	LLS (PDI) at 75 DAS	LLS (PDI) at 90 DAS	LLS (PDI) at 105 DAS
Blocks	12	14.49*	16.62**	3.45	0.85	0.26	0.53	0.44	0.05
Treatments (RILs + checks)	264	36.06**	8.72*	6.93**	59.67**	0.95**	1.03**	1.20**	2.52**
Checks	4	9.89	1.56	65.98**	1794.40**	4.60**	7.42**	13.63**	37.77**
RILs	259	36.27**	8.86*	5.63*	26.00**	0.57**	0.76**	0.92**	1.66**
RILs *vs* Checks	1	85.43**	0.15	106.59**	1842.48**	84.52**	45.62**	23.06**	85.95**
Error	48	5.64	5.18	3.59	0.95	0.20	0.42	0.29	0.05

*Significant @ P = 0.05; **Significant @ P = 0.01 df = degrees of freedom, PBND = peanut bud necrosis disease, PDI = percent disease index, DAS = days after sowing, LLS = late leaf spot

Table 2: Estimates of genetic variability parameters for various traits in RIL population of groundnut

Traits	Mean	Range		GCV (%)	PCV (%)	$h^2_{(BS)}$ (%)	GAM (%)
Initial plant stand	32.20	Min.	**Max.**	16.96	20.73	66.92	28.62
Days to 50 percent flowering	33.93	19.94	50.14	4.12	5.82	50.25	6.03
Days to maturity	126.93	29.51	37.31	1.02	1.55	43.76	1.40
Final plant stand	29.36	122.74	130.34	20.56	22.59	82.83	38.59
Matured pods per plant	7.97	18.88	48.48	27.84	31.82	76.59	50.27
Pod yield per plant (g)	6.13	3.20	16.96	26.30	32.29	66.34	44.19
Hundred pod weight (g)	78.05	2.31	12.02	5.83	6.58	78.27	10.63
Hundred kernel weight (g)	30.42	64.48	101.59	13.31	15.96	69.54	22.90
Shelling percentage (%)	67.74	20.79	49.43	8.17	8.89	84.46	15.49
Sound mature kernels (%)	94.55	46.31	81.03	2.03	3.15	41.55	2.70
Oil content (%)	47.47	82.09	99.89	3.01	5.00	36.34	3.75
PBND incidence (%)	8.78	40.91	52.63	57.02	58.09	96.34	115.46
LLS (PDI) at 60 DAS	3.29	0.27	32.38	18.55	23.05	64.78	30.80
LLS (PDI) at 75 DAS	4.27	0.74	5.00	13.66	20.40	44.85	18.88
LLS (PDI) at 90 DAS	4.98	0.94	5.94	15.90	19.25	68.19	27.09
LLS (PDI) at 105 DAS	6.16	1.55	7.11	20.60	20.89	97.22	41.90
		1.94	8.42				

PBND = peanut bud necrosis disease, PDI = percent disease index, DAS = days after sowing, LLS = late leaf spot, GCV = genotypic co-efficient of variation, PCV = phenotypic co-efficient of variation, $h^2_{(BS)}$ = broad sense heritability, GA = genetic advance and GAM = genetic advance as percent of mean

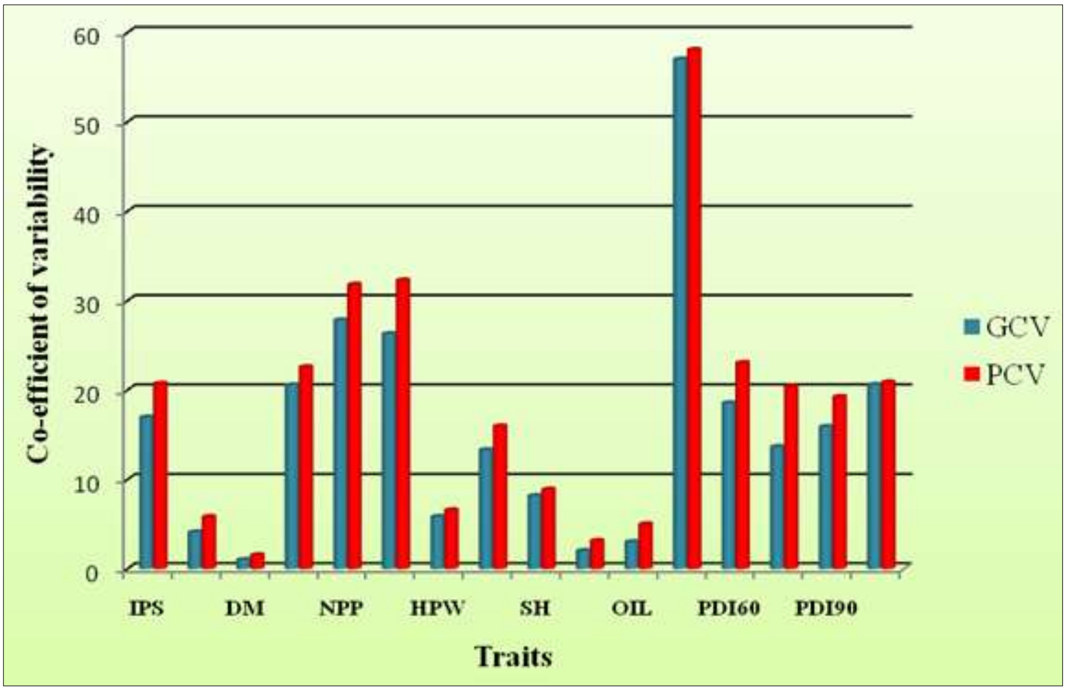

Fig 1: Genotypic and phenotypic coefficient of variation for disease resistance and productivity traits in RIL population

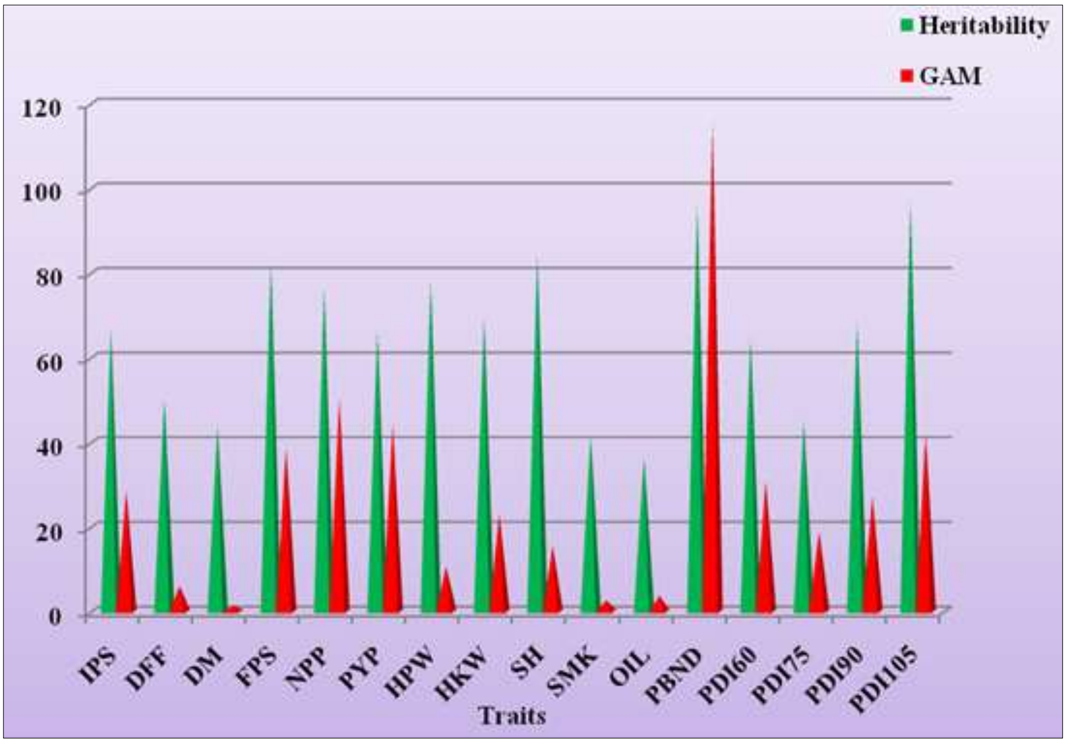

Fig 2: Heritability in broad sense and genetic advance as percent of mean for disease resistance and productivity traits in RIL population

4. Conclusion

The overall results showed the presence of adequate variability in the genotypes studied. This variation could be effectively manipulated using appropriate breeding techniques and program to develop improved varieties. High GCV and PCV were observed for most of the traits studied which indicated presence of sufficient amount of variability among the genotypes which is pre-requisite for selection. High estimate of heritability and genetic advance were observed in most of the traits, indicating the predominance of additive gene action and the possibility of direct selection through these traits for improvement of yield.

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