

RESEARCH ARTICLE



# Genetic variability and association studies in F<sub>2</sub> populations of Groundnut (*Arachis hypogaea* L.)

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# Abstract

Groundnut is an extensively self-pollinating crop with a narrow genetic base; therefore, it relies on the F<sub>2</sub> generation for optimal segregation and recombination. The genetic variability resulting from segregation and recombination is essential for effective selection in crop improvement programmes.  $F_2$  populations derived from the crosses BSR 2 × GPBD 4 and BSR 2 × TMV 2 were assessed for examining genetic variation, and correlation coefficients along path coefficients. Twenty-four yield-attributing, physiological, as well as biochemical characteristics were covered in the research, in the Kharif season of 2024. The assessment of the PCV along with GCV revealed that a majority of yield-related traits, including the number of pods, kernels, and pod yield, demonstrated high PCV along with GCV in both crosses, indicating substantial genetic variation. Regarding yield-related characteristics, high GAM along with high heritability in a broad sense were noted for both the crosses, suggesting that a breeding approach based on simple selection can be successful in increasing groundnut yield. Correlation and path coefficients indicated that the number of mature kernels and pod yield calculated for each plant possessed a high positive direct effect on kernel yield. Transgressive segregants were identified over twice the standard deviation of the better parent mean for various traits. These findings can serve as a foundation for future breeding programmes aimed at enhancing the yield and oil content.

# **Keywords**

groundnut; variability; broad sense heritability; GAM; correlation coefficient; path coefficient

# Introduction

The groundnut commonly referred to as the 'King of oilseeds' in India represents an essential legume crop cultivated extensively within the equatorial and semi-arid regions of the globe. This provides an important component of edible oil and protein as well as plays a crucial role in the agricultural economies of many developing countries like India, Nigeria, Sudan, Senegal, and Argentina (1). Groundnut kernel contains about 49% oil, 25% protein, 20% carbohydrates, and a significant amount of vitamins and minerals (2). Genetic variation remains a crucial requirement of an efficient breeding initiative because it provides necessary variation during selection. The effectiveness of selection is determined by the degree of genetic variation existing within the available breeding stock (3).

Estimates of PCV along with GCV serve as beneficial indices for assessing the genetic variation that exists within the population. Heritability in a broad sense represents a heritable component of the entire variation & Genetic Advance (GA) represents the expected genetic gain under the selection process (4). It is more useful in predicting the magnitude and direction of selection. High heritability (bs) along with high GAM for a character signifies the majority of additive gene action followed by the process involved in selection is potentially rewarding (5). Correlation analysis, on the other hand, provides insights into the interdependence of various yield and yield-contributing attributes, which is essential for designing effective selection strategies. Path coefficient analysis is a refined technique of multiple regression that partitions Pearson's correlation coefficient values into direct and indirect effects for several characteristics on the factor that is dependent and assists in identifying the most influential traits. Transgressive segregants with high yield potential can be identified from the segregating generations, which can be further exploited in breeding programmes (6). Therefore, a current investigation has been carried out to study the genetic variation, heritability in a broad sense, GAM, and association analysis for yield with associated characteristics within the F<sub>2</sub> population of groundnut.

#### **Materials and Methods**

# **Research material**

Experimental material utilized in the current investigation involves three cultivars BSR 2, TMV 2, and GPBD 4, along with two  $F_2$  populations derived from the crosses BSR 2 × GPBD 4 and BSR 2 × TMV 2. In the crossing programme, BSR 2 was used as the female parent, while TMV 2 and GPBD 4 were used as the male parents. The  $F_1$  generation was raised from the crossed seeds, and  $F_2$  seeds were subsequently obtained from the oilseeds department of the institute, Tamil Nadu Agricultural University.

# Methodology

The two F<sub>2</sub> populations derived from the cross BSR 2 × GPBD 4 and BSR 2 × TMV 2 were cultivated over the *Kharif* season of 2024 under surface irrigation conditions. The F<sub>2</sub> populations were cultivated in an unreplicated trial along with parents with 30 × 10 cm spacing in 3m rows. Standard agronomic practices and targeted pest and disease control measures were implemented throughout the growing season.

Observations were recorded on 144 plants of the cross BSR 2 × GPBD 4 and 156 plants of the cross BSR 2 × TMV 2 and 10 randomly tagged plants of parental lines at various growth stages on 24 quantitative, physiological, and biochemical characteristics *viz.*, Days to first flowering (DFF), Plant Height (PH), Number of Branches per Plant (NBP), Number of Pods per Plant (NPP), Number of Mature Pods per Plant (NMPP), Number of Immature Pods per Plant (NIPP), Number of Kernels per Plant (NKP), Number of Mature Kernels per Plant (NMK), Number of Immature Kernels per Plant (NIMK), Sound Mature Kernel Percentage (SMK), Hundred Pod Weight (HPW), Hundred Kernel Weight (HKW), Pod Yield (PY), Single Plant Yield (SPY), Shelling Percentage (SP), Number of Pegs per Plant (NPE), Peg to Pod Ratio (PPR), SPAD Chlorophyll Meter Reading (SCMR), Oil Content (OC), Linoleic Acid (LA), Oleic Acid (OA), Palmitic Acid (PA), Stearic Acid (SA), and Oleic to Linoleic Ratio (OLR). The collected data has undergone various statistical analyses, viz., analysis of variability parameters like, computation of genetic variables like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h<sup>2</sup>), and genetic advance as a percent of the mean (GAM) as per established statistical procedures proposed by (7), correlation coefficients (8), and path coefficients (9) using TNAUSTAT software (10). The significance of the mean value of parents for all the traits was determined based on the grand mean and critical difference values. Transgressive segregants with values exceeding the better parent, mean by at least twice the standard deviation of the F<sub>2</sub> population, were identified.

# **Results and Discussion**

# Mean performance of parents

The mean performance for the three groundnut cultivars BSR 2, TMV 2, and GPBD 4 used in the crosses for various traits are provided in Table 1. The analysis demonstrated that parents varied at a level of 5% significance for all examined characteristics, except linoleic and oleic acid content. This suggests the diverse genetic background of the parental lines used in the hybridization. The mean performance of the parents ranged from 27.3 (TMV 2) to 34.7 (BSR 2) for days to first flowering and from 16.6 (TMV 2) to 28.1 (GPBD4) over the number of pods in each plant. The mean performance for pod yield varied from 15.43(GPBD4) to 20.21(BSR 2), and for single plant yield, it ranged from 10.03 (GPBD 4) to 15.32 (BSR 2).

#### Analysis of variability parameters

Genetic variability parameters were computed for the  $F_2$  populations of the two crosses, alongside the outcomes given in Table 2. Variations in the average performance for various characteristics were observed. The  $F_2$  population BSR 2 × GPBD4 reported a higher mean value for the characters *viz.*, number of pods(17.73), number of mature pods (14.01), number of kernels (21.99), number of mature kernels (20.4), pod yield (11.58), and single plant yield (6.92) compared with the  $F_2$  population in the cross BSR 2 × TMV 2.

The magnitude of the PCV is substantially greater in comparison with its associated GCV over almost every characteristic, which suggests that the evident variation was not just caused by the genotype but additionally attributed to the effect of the environment. High PCV along with GCV has been observed in characteristics like the number of pods, mature & immature pods in each plant, number of kernels, mature & immature kernels in each plant, pod yield, single plant yield, and number of pogs in both F<sub>2</sub> populations, suggesting the presence of substan-

Table 1. Mean Performance of Parents used in the crosses for various	characteristics
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Traits	BSR 2	TMV 2	GPBD4	Grand mean	CD @5%	CD @ 1%
DFF	34.70**	27.30	32.60**	31.53	0.48	0.69
PH (cm)	33.15	44.50**	37.10	38.25	0.77	1.12
NBP	6.10**	4.00	5.50*	5.20	0.20	0.30
NPP	26.10**	16.60	28.10**	23.60	1.45	2.10
IMPP	20.70**	13.50**	19.80*	18.00	1.26	1.83
IIPP	5.40	3.10	10.40**	6.30	0.52	0.76
IKP	47.10**	24.70	32.40	34.73	1.66	2.40
ІМК	45.30**	22.10	29.30	32.33	1.68	2.44
ШМК	1.80	2.60	3.10**	2.50	0.22	0.32
МК	96.36**	89.62	89.98	91.98	0.83	1.20
IPW	75.11	113.33**	96.91	95.12	3.60	5.21
IKW	34.40	43.44**	45.86**	41.23	1.36	1.97
ΥY (g)	20.21**	16.34	15.43	17.33	0.82	1.19
PY (g)	15.32**	11.40	10.03	12.25	0.51	0.74
Р	65.11	68.72**	66.64	66.83	1.12	1.63
IPE	46.00**	25.20	38.20	36.47	1.81	2.63
PR	1.29**	1.51	1.34*	1.38	0.03	0.05
CMR	48.37**	41.94	49.33**	46.55	0.55	0.80
DC	43.33	47.36**	42.28	44.32	0.49	0.70
A	43.48	43.44	38.18	41.70	0.62	0.90
A	45.46	43.65	45.39	44.83	0.70	1.01
A	14.96**	13.73	14.20	14.30	0.38	0.55
A	6.78**	6.08	6.71**	6.52	0.12	0.17
DLR	1.05	1.11	1.22**	1.13	0.04	0.06

\*: Significant at 5% Probability level, \*\*: Significant at 1% Probability level, CD - Critical Difference.

Table 2. Estimates of Variability in  $F_2$  Generation of Groundnut..

Traits	Crosses	Mean	PCV %	GCV%	h²%	GAM%
	C1	35.20	10.31	9.48	84.60	17.97
DFF	C2	35.71	11.11	10.71	92.87	21.26
DLI	C1	29.91	16.20	13.54	69.86	23.31
FII	C2	43.18	20.42	12.41	36.93	15.54
NRD	C1	5.00	34.76	19.42	31.22	22.36
NDF	C2	5.26	27.58	16.12	34.18	19.42
NDD	C1	17.73	46.87	40.00	72.83	70.32
NF F	C2	13.76	62.66	50.28	64.40	83.13
NMDD	C1	14.01	49.48	42.77	74.72	76.16
NMEE	C2	10.94	64.48	51.98	64.99	86.32
NIDD	C1	3.72	73.79	34.24	21.53	32.73
INIF F	C2	2.93	89.95	43.72	23.62	43.77
NKD	C1	21.99	50.34	44.06	76.62	79.46
NKF	C2	16.83	56.42	43.93	60.63	70.47
NIMK	C1	20.40	54.05	46.78	74.91	83.41
INIMITY	C2	15.42	68.13	54.27	63.45	89.05
NIMK	C1	1.75	86.12	48.20	31.32	55.57
NIMIX	C2	1.72	88.47	39.05	19.48	35.50
SMK	C1	90.73	11.76	10.86	85.27	20.66
JMIN	C2	89.71	13.52	12.58	86.48	24.09

OLK	C2	5.90	10.56	7.28	47.44	10.32
	C1	6.00	11.77	4.59	15.18	3.68
SA	C2	6.04	15.52	8.35	28.95	9.25
54	C1	6.30	18.99	11.07	33.97	13.29
۲A	C2	14.24	13.22	7.38	31.17	8.49
DA.	C1	14.82	15.91	11.00	47.79	15.66
UA	C2	43.31	12.77	4.00	9.83	2.59
04	C1	44.69	13.93	6.23	19.98	5.73
LA	C2	41.37	10.29	5.47	28.26	5.99
	C1	41.32	12.29	6.75	30.15	7.63
	C2	43.73	11.79	9.52	65.24	15.84
06	C1	40.18	11.65	10.19	76.63	18.38
SCMIK	C2	45.81	8.57	7.64	79.52	14.03
SCMP	C1	48.13	8.26	6.58	63.59	10.82
ΓĽΚ	C2	1.20	27.38	23.16	71.54	40.36
DDD	C1	1.23	20.83	13.26	40.53	17.39
INFE	C2	16.37	60.32	50.82	70.97	88.20
NDE	C1	21.81	54.28	34.66	40.79	45.60
37	C2	61.28	13.14	11.64	78.38	21.22
SD	C1	60.23	15.46	14.21	84.41	26.89
<b>3</b> F I	C2	5.44	69.84	55.18	62.41	89.80
CDV	C1	6.92	58.21	49.27	71.66	85.93
FT	C2	9.33	62.98	50.39	64.00	83.04
PY	C1	11.58	57.81	45.83	62.85	74.86
	C2	39.40	28.54	16.21	32.25	18.96
нкм	C1	38.43	31.28	25.72	67.58	43.55
I IF VV	C2	83.66	28.40	17.17	36.56	21.39
	C1	82.73	29.24	23.00	61.88	37.27

C1 – BSR 2 × GPBD4, C2 – BSR 2 × TMV 2, PCV – Phenotypic Coefficient of Variation, GCV - Genotypic Coefficient of Variation, h<sup>2</sup> – Heritability, GAM – Genetic Advance as a Percentage of Mean.

tial genetic variation for those characteristics that might be exploited for efficient selection. These outcomes were consistent with the conclusions of Mitra (11), Kannappan (12), Shuro (13), and Shendekar (14) on the characteristics number of pods, pod yield, kernels, and mature kernels in each plant, and single plant yield. A moderate PCV & GCV has been found in the characteristics, viz., sound mature kernel percentage and shelling percentage. A low PCV and GCV have been found for SPAD chlorophyll meter readings in both crosses and for other characteristics low to moderate levels of phenotypic and genotypic coefficients of variation have been identified for both the crosses, suggesting limited potential for such characteristics to being enhanced through a selection process. A coefficient of variation merely implies the range associated with the observed variation, whereas the computations of heritability and GAM provide a more comprehensive understanding of the underlying genetic mechanisms governing the manifestation of the characteristics.

High broad sense heritability in combination with high GAM has been noted for the characteristics *viz.,* the number of pods, mature pods, kernels, and mature kernels in each plant, sound mature kernel percentage, shelling percentage, pod yield, and single plant yield for both crosses, indicating that the expression in such characteristics, was mostly regulated through additive gene action, therefore, for such characteristics the process of selection would be efficient. Vinithashri (15), Mohapatra and Khan (16) also reported similar findings for the trait's number of pods and mature pods in each plant, pod yield, and single plant yield of groundnut.

The  $F_2$  population of the cross BSR 2 × GPBD 4 reported a high heritability in combination with high genetic advance as a percentage of the mean to the traits *viz.*, plant height, hundred pod weight, and hundred kernel weight. The  $F_2$  population for the cross BSR 2 × TMV 2 recorded high broad sense heritability along with high genetic advance as a percentage of the mean to the traits, *viz.*, days to first flowering, number of pegs per plant, peg to pod ratio. A similar result was observed by Mohapatra and Khan (16), Byadagi (17) for the characteristics of plant height, number of pegs per plant, and hundred pod weight.

# Transgressive segregants analysis

Identifying superior  $F_2$  individuals exhibiting transgressive segregation would likely assist the breeder in selecting

favourable genotypes. The crosses generated a substantial number of  $F_2$  individuals exhibiting transgressive segregation for various traits in Tables 3 and 4. This is indicative of the presence of complementary gene action and epistasis, which could be further exploited in advanced generations for developing superior genotypes.

and peg to pod ratio. Similarly, the cross BSR2 × TMV 2 generated a substantial number of transgressive segregants for the traits, oleic to linoleic ratio, and the number of immature kernels per plant. The results showed that the parental genotypes involved in the study differed substantially in their genetic composition, which in turn

Table 3. Transgressive Segregants identified for various characteristics in F<sub>2</sub>generation of the cross BSR 2 × GPBD 4.

Traits	MBP	Mean Value of Transgressive Segregants													
DFF	34.70	43.00	43.00	40.00	42.00	42.00	42.00	40.00	42.00	41.00	9				
NBP	6.10	13.00	-	-	-	-	-	-	-	-	1				
NPP	28.10	45.00	47.00	-	-	-	-	-	-	-	2				
NMPP	20.70	38.00	39.00	35.00	-	-	-	-	-	-	3				
NIMK	3.10	7.00	7.00	7.00	-	-	-	-	-	-	3				
PY (g)	20.21	34.21	37.43	34.32	-	-	-	-	-	-	3				
SPY (g)	15.32	23.92	23.99	-	-	-	-	-	-	-	2				
NPE	46.00	74.00	-	-	-	-	-	-	-	-	1				
PPR	1.34	1.92	2.50	1.94	2.15	2.39	2.26	2.58	-	-	7				
OC	43.33	54.62	-	-	-	-	-	-	-	-	1				
LA	43.48	55.73	-	-	-	-	-	-	-	-	1				
OA	45.46	59.80	61.63	60.24	58.03	61.03	58.37	62.35	-	-	7				
PA	14.96	19.76	20.29	20.36	18.92	-	-	-	-	-	4				
SA	6.78	9.90	10.97	-	-	-	-	-	-	-	2				
OLR	1.22	2.00	1.95	1.99	1.76	1.92	-	-	-	-	5				

MBP – Mean of Better Parent, NTS – Number of Transgressive Segregants.

Table 4. Transgressive Segregants identified for various traits in F<sub>2</sub> Population of the cross BSR 2 × TMV 2.

Traits	МВР	Mean Value of Transgressive Segregants												
DFF	34.70	43.00	-	-	-	-	-	1						
PH	44.50	63.00	63.00	66.00	-	-	-	3						
NBP	6.10	9.00	9.00		-	-	-	2						
NPP	26.10	45.00	50.00	47.00	-	-	-	3						
NMPP	20.70	37.00	36.00		-	-	-	2						
NIPP	5.40	16.00	16.00	15.00	13.00	-	-	4						
NIMK	2.60	7.00	6.00	9.00	8.00	9.00	-	5						
HPW	113.33	178.00	-	-	-	-	-	1						
HKW	43.44	67.5	-	-	-	-	-	1						
PY	20.21	38.43	38.12	-	-	-	-	2						
SPY	15.32	23.17	23.78	-	-	-	-	2						
SP	68.72	85.58	88.95	-	-	-	-	2						
NPE	25.20	74.00	-	-	-	-	-	1						
PPR	1.51	2.80	-	-	-	-	-	1						
OC	47.36	60.14	59.94	56.41	55.70	-	-	4						
LA	43.48	53.70	54.83	52.20	-	-	-	3						
OA	45.46	62.21	56.78	-	-	-	-	2						
PA	14.96	18.91	19.13	22.12	19.32	-	-	4						
SA	6.78	9.09	8.95	-	-	-	-	2						
OLR	1.11	1.87	1.60	1.59	1.68	1.57	1.73	6						

MBP – Mean of Better Parent, NTS – Number of Transgressive Segregants.

The  $F_2$  generation from the cross between BSR 2 and GPBD 4 exhibited a greater frequency of transgressive segregants for days to first flowering, oleic acid content,

facilitated the creation of a large degree of genetic variability within the  $F_2$  progeny.

# Association analysis

Improving yield relies on enhancing the constituent traits that affect its expression, highlighting the importance of refining these component traits for better outcomes. The simple correlation coefficient for yield and associated characteristics in the  $F_2$  Population of the cross BSR 2 × GPBD 4 and BSR 2 × TMV 2 are represented in the correlogram (Fig. 1 & Fig. 2). The single plant yield showed a significant positive correlation to the traits viz., number of branches (0.51,0.46), number of pods (0.8,0.85), number of mature pods (0.86,0.91), number of immature pods (0.27,0.32), number of kernels (0.91,0.93), number of mature kernels (0.91,0.94), sound mature kernel percentage (0.42,0.36), hundred pod weight (0.72,0.56), hundred kernel weight (0.51,0.59), pod yield (0.93,0.94) and number of pegs per plant (0.59,0.71) in both crosses consequently. These outcomes were consistent with the findings of Kannappan (12), and Reddy (18).

The single plant yield from the  $F_2$  generation of the cross BSR 2 × GPBD 4 had a significant positive correlation coefficient for the characteristics *viz.*, days to first flowering (0.31), plant height (0.23), as well as oil content (0.25). These findings were following Godhani (19) for the trait days to first flowering and plant height. In the  $F_2$  population derived from the cross BSR 2 × TMV 2, the single plant yield exhibits a significant negative correlation coefficient to the trait peg-to-pod ratio. This suggests that the lower conversion rate of pegs to pods may have contributed to the reduced single-plant yield observed in this particular  $F_2$  population.

The correlation coefficients reveal both the intensity and direction of associations among the characters yet do not address their direct and indirect effects. To comprehensively evaluate these effects on single plant yield, path coefficients were computed, and the results are detailed in Table 5. Understanding the

	DFF	Hd	NBP	NPP	NMPP	NIPP	NKP	NMK	NIMK	SMK	MPW	HKW	ΡY	SP	NPE	РРВ	SCMR	8	۲	AO	PA	SA	OLR	SPΥ		
DFF	1	-007	0∕∕1	0.35	0.31	0.31	0.34	0.32	×	ø <b>≫</b> 3	0.23	×	0.31	-0×3	0.32	-0004	-0006	<b>X</b>	-005	0)36(4	<b>)</b>	<b>X</b> 3	0 <b>)\$</b> (5	0.31	「 '	1
PH	-007	1	0.27	<b>%</b>	0.24	- 🔀 3	0.25	0.25	0)\$63	0)36(1	ø <b>≫</b> 2	0)1	0.24	-0/2	0.24	0.24	0)36(4	<b>X</b> 8	-002	0.39	Х	<b>)%</b>	<b>%</b> 2	0.23		
NBP	ø <b>≫</b> 1	0.27	1	0.35	0.4	0)26(4	0.42	0.4	0)×3	0)366	0.36	0.31	0.46	<b>)%</b> 3	×	-0,05	-004	×	-0,04	0.23	-0001	<b>)%</b>	<b>%</b> 5	0.51		
NPP	0.35	<b>%</b>	0.35	1	0.96	0.64	0.92	0.91	<b>)%</b>	0.34	0.34	∞⁄1	0.92	-0.33	0.87	<b>)</b>	-007	×	0.31	-005	0.33	<b>X</b>	-0009	0.8	- 0.7	75
NMPP	0.31	0.24	0.4	0.96	1	0.4	0.95	0.94	0)36(4	0.35	0.4	<b>%</b>	0.97	-0.33	0.81	<b>)%</b>	-005	<b>)</b>	0.26	<b>)X(1</b>	0.3	) <b>%</b> 2	-005	0.86		
NIPP	0.31	-0×3	∞4	0.64	0.4	1	0.41	0.4	0)\$68	0)\$	0)462	-005	0.35	-0008	0.63	<b>%</b>	-0008	-0 <mark>.2</mark> 4	0.28	-000	0.27	<b>)%</b>	-9 7	0.27		5
NKP	0.34	0.25	0.42	0.92	0.95	0.41	1	0.99	⋈	0.36	0.49	0.25	0.94	-0/2	0.77	0)36(4	-002	×	0.24	<b>)</b> \$\$	0.26	) <b>%</b> 2	-006	0.91	- <b>.</b>	.5
NMK	0.32	0.25	0.4	0.91	0.94	0.4	0.99	1	-0×3	0.45	0.5	0.25	0.94	-0/1	0.77	<b>)</b> \$\$3	-002	×	0.25	0)\$(2	0.28	) <b>%</b> 2	-9008	0.91		
NIMK	<b>%</b>	0)*(3	<b>X</b> 3	<b>) %</b>	<b>) %</b> (4	<b>)</b> ×(8	∢	-\$\$\$	1	-0.72	-0009	-0004	<b>)</b> X(1	-0/1	<b>)</b>	<b>)</b>	) <b>%</b> (2	<b>)</b> X(1	-0008	0)\$62	×	-90(1	<b>)</b> ()	-0001		25
SMK	<b>X</b> 3	<b>)X(1</b>	<b>)%</b> (6	0.34	0.35	0∕∕5	0.36	0.45	-0.72	1	0.4	ø <b>≫</b> \$	0.38	⋈	0.28	-0/7	-000	<b>)</b> \$\$	<b>※</b>	0)462	<b>※</b>	<b>%</b> 5	-9009	0.42	0.2	20
HPW	0.23	<b>%</b> 2	0.36	0.34	0.4	0 <b>)4(</b> 2	0.49	0.5	-0009	0.4	1	0.77	0.59	0.4	0≫4	-0.36	0)\$5	0.29	<b>)</b> \$(3	0.23	<b>%</b> 5	-0009	<b>)%</b> (8	0.72		
HKW	∢	Ø <b>X</b> 1	0.31	Ì∕1	<b>※</b>	- 0 5	0.25	0.25	-0⁄24	∞\$	0.77	1	0.36	0.39	×	-0 <mark>.2</mark> 5	0.24	0.33	-007	0.37	-907	-9008	<b>X</b>	0.51		0
PY	0.31	0.24	0.46	0.92	0.97	0.35	0.94	0.94	0) <b>X</b> (1	0.38	0.59	0.36	1	-000	0.73	-0,0(3	-90(1	∞\$	0.23	<b>)</b>	0.26	-002	-\$\$\$	0.93		
SP	-0⁄43	-0/2	<b>) X</b> (3	-0.33	-0.33	-948	-) 2	- 🙀 1	-0/1	⋈	0.4	0.39	-000	1	-0.4	-0.28	<b>)%</b> (9	0.22	-04	<b>)</b>	-0 <mark>.2</mark> 5	-909	×	∞1		
NPE	0.32	0.24	⋈	0.87	0.81	0.63	0.77	0.77	<b>)</b>	0.28	∞⁄4	×	0.73	-0.4	1	0.48	-000	-003	0.37	-0/1	0.43	<b>)</b> \$(5	- 🕅 3	0.59	0	25
PPR	-9⁄4	0.24	-9⁄05	<b>)%</b> 9	<b>)%</b> (6	<b>%</b> 3	<b>%</b> (4	<b>)</b> \$(3	<b>)%</b>	-007	-0.36	-0 <mark>.2</mark> 5	-0×03	-0.28	0.48	1	-0009	-0/7	×	-005	0.25	-90(1	-0009	-0×1		
SCMR	-906	<b>) %</b> (4	-9004	-907	-9⁄05	-9008	-002	-9⁄2	0)362	-0009	∞\$	0.24	-0001	<b>)%</b>	-000	-000	1	×	<b>)</b> \$(1	0)\$62	-0×3	-0003	-90(4	<b>}</b>		
OC	<b>%</b>	<b>X</b> 8	⋈	×	<b>)%</b> 9	-0 <mark>.2</mark> 4	∢	⋈	<b>%</b> (1	) <b>X</b> 5	0.29	0.33	∞\$	0.22	-0×3	-0/7	×	1	-0.4	0.43	-0.27	-006	0.28	0.25		15
LA	-9⁄45	-002	-9004	0.31	0.26	0.28	0.24	0.25	-0008	ø <b>≫</b> ®	) <b>X</b> (3	-9007	0.23	-0/4	0.37	2	<b>)</b> X(1	-0.4	1	-0.67	0.62	<b>)</b> \$(3	-0.75	0×6		
OA	0)*(4	0.39	0.23	-•••5	<b>)</b> X(1	- 🕅 8	<b>)X</b> (3	0)4(2	0)362	0)362	0.23	0.37	0)\$6	<b>)%</b> (8	-0/1	-005	0)4(2	0.43	-0.67	1	-0.48	Ø€1	0.77	<b>%</b> 3		
PA	<b>)%</b> 9	×	-90(1	0.33	0.3	0.27	0.26	0.28	*	×	<b>)%</b> 5	-007	0.26	-0 <mark>.2</mark> 5	0.43	0.25	-0×3	-0.27	0.62	-0.48		*	-0.39	<b>%</b>	0	.75
SA	<b>%</b>	<b>)%</b> (6	<b>)%</b> (6	<b>)</b> X(3	<b>)%</b> (2	0×6	<b>)%</b> 2	0)4(2	-9×1	) <b>%</b> 5	-000	-0008	-0002	-0009	<b>)%</b> 5	-90(1	-0,03	-906	<b>)</b> \$\$	¢¥(1	<b>X</b>	1	-907	-0,04	~	
OLR	0)\$(5	<b>%</b> 2	∞5	-0009	-005	-007	-906	-908	<b>)%</b>	-000	0)36(8	<b>※</b>	-0×03	×	-0×3	-000	-9004	0.28	-0.75	0.77	-0.39	-0007	1	-0001		
SPY	0.31	0.23	0.51	0.8	0.86	0.27	0.91	0.91	-0001	0.42	0.72	0.51	0.93	∞(1	0.59	-0/1	0)\$(5	0.25	<b>%</b>	<b>X</b> 3	<b>X</b> 3	-0004	-001	1		

Fig. 1. Correlation analysis for F2 Population of the cross BSR 2 × GPBD 4.

	DFF	Н	NBP	NPP	NMPP	NIPP	NKP	NMK	NIK	SMK	MdH	HKW	ΡY	SP	NPE	РРВ	SCMR	8	ΓA	OA	PA	SA	OLR	SPΥ		
DFF	1	-0×3	-008	->>	-000	- 04	-000	-001	0)/2	-000	-0/7	-0/2	-0 <mark>.2</mark> 1	-0001	-0.26	-007	0≫4	-0,03	×	0)\$(5	0)*(1	<b>%</b> 2	-0004	-000	'	
PH	-)×(3	1	-003	-0,03	0)\$(1	×	-0001	-0,02	0)366	-0×5	-0,03	0 <b>)\$(</b> 3	×	-000	<b>)%</b> 7	0.25	<b>)%</b>	*	-0/1	-007	-0×6	<b>)X</b> (1	-003	-002		
NBP	-) 🔆 8	-0,03	1	0.47	0.48	0.22	0.42	0.44	-005	0.26	∞	0.28	0.48	-0009	0.39	-0.22	-0009	×	<b>)</b> \$(3	0)%(1	-002	-0001	-0001	0.46		
NPP	*	-0,03	0.47	1	0.96	0.67	0.91	0.9	0.26	0.23	0.28	0.33	0.88	-0.34	0.9	-0.35	-907	-0006	-006	<b>%</b> 2	-001	-0/1	<b>%</b>	0.85	- 0.75	
NMPP	-900	<b>) (</b> 1	0.48	0.96	1	0.42	0.95	0.94	0.23	0.26	0.32	0.38	0.94	-0.36	0.85	-0.38	-006	-006	-0/1	∞⁄4	-002	-0×3	∞⁄6	0.91		
NIPP	-9×4	×	0.22	0.67	0.42	1	0.42	0.4	0.21	<b>)%</b>	) <b>x</b> (5	<b>%</b> (7	0.33	-006	0.64	-0×4	-007	-0×3	<b>)%</b> 9	<b>)</b> \$\$	×	×	<b>)</b> \$\$	0.32	- 05	
NKP	-900	-90(1	0.42	0.91	0.95	0.42	1	0.99	0.3	0.22	0.35	0.36	0.9	-0 <mark>.2</mark> 3	0.81	-0.38	-002	-9×6	-0008	∞5	-002	-0×4	∞⁄2	0.93	0.0	
NMK	-921	-902	0.44	0.9	0.94	0.4	0.99	1	ø <b>≫</b> \$	0.35	0.39	0.38	0.9	-000	0.8	-0.38	-904	-0⁄43	×	<u>کر</u>	-002	-94	9≫(4	0.94		
NIK	<b>%</b> 2	<b>%</b>	-945	0.26	0.23	0.21	0.3	∞5	1	-0.72	-0×3	-90(1	ø <b>≫</b> (8	-0.28	0.23	-0008	<b>)%</b> (9	-0 <mark>.2</mark> 2	<b>%</b> 2	-906	<b>) (</b> 1	-90(4	-908	<b>%</b>	- 0.25	
SMK	-900	-005	0.26	0.23	0.26	<b>%</b>	0.22	0.35	-0.72	1	0.38	<b>※</b>	0.3	0.22	∞\$	-0 <mark>.2</mark> 3	-945	<b>※</b>	-9008	<b>%</b> 2	-002	-90(3	<b>)%</b> 9	0.36	0.20	
HPW	-0/7	-0,03	⋈	0.28	0.32	<b>%</b> 5	0.35	0.39	-0×3	0.38	1	0.73	0.55	<b>)%</b> (8	<b>※</b>	-9×(4	-9⁄05	⋈	-9008	<b>)</b> \$(5	->>	-0/1	<b>)%</b> (6	0.56		
HKW	-0/2	<b>)</b> \$(3	0.28	0.33	0.38	<b>)\$</b> (7	0.36	0.38	-0001	<b>%</b>	0.73	1	0.54	0.26	0.21	-0×5	-9⁄4	<b>)\$(</b> 7	-0/2	0)***2	->>	-005	<b>)</b> \$\$	0.59	- 0	
PY	-0.21	×	0.48	0.88	0.94	0.33	0.9	0.9	∞⁄%	0.3	0.55	0.54	1	-0.32	0.78	-0.34	-005	-0008	-0/1	∞1	-9004	-0×4	0≫5	0.94		
SP	-90(1	-948	-909	-0.34	-0.36	-006	-0 <mark>.2</mark> 3	-9019	-0.28	0.22	0)36(8	0.26	-0.32	1	-0.4	-0003	<b>X</b>	0∕∕5	<b>)\$(</b> 5	-9004	-9⁄41	-04	-\$\$\$	->>>		
NPE	-0.26	<b>%</b> (7	0.39	0.9	0.85	0.64	0.81	0.8	0.23	∞\$	×	0.21	0.78	-0.4	1	-0001	≫	-0/2	) <b>%</b> (2	<b>)%</b> (7	-9004	-0×3	∞1	0.71	0.25	
PPR	-907	0.25	-0 <mark>.2</mark> 2	-0.35	-0.38	- 04	-0.38	-0.38	-0008	-0 <mark>.2</mark> 3	-0×4	-005	-0.34	-0,003	-9⁄2(1	1	-9004	-0/7	<b>%</b>	-9×8	-9008	-90(1	-907	-0.4		
SCMR	∞4	<b>)</b>	-909	-907	-906	-907	-9⁄2	-9004	<b>)%</b>	-0005	-0,05	-904	-0⁄45	<b>%</b>	≫	-90(4	1	-000	) <b>%</b> (2	-0⁄43	<b>)%</b> 9	-90(1	0)4(3	-002		
OC	-003	×	∢	-906	-906	-\$\$\$	-906	-\$\$\$	-0.22	<b>※</b>	>	<b>)%</b> (7	-9008	0)>>5	-0/2	-0/7	-000	1	-0×5	0.33	-0/1	-0/2	<b>)%</b> (8	-\$\$\$(1	0.5	
LA	×	-0/1	<b>)X</b> (3	-906	-0/1	<b>)</b> ()	-900	×	ø <b>≫</b> 2	-0008	-0008	-0/2	-9×1	<b>)%</b> 5	0)\$42	<b>%</b>	) <b>%</b> 2	-0×5	1	-0.62	) <b>%</b> (2	¢≫(1	-0.71	-006		
OA	<b>)</b> \$(5	-907	0×(1	¢ <b>≫</b> (2	6≫(4	<b>)</b> X(3	∞5	<b>%</b> 7	-006	0)%2	0 <b>)\$(</b> 5	) <b>%</b> (2	ø <b>≫</b> i	-000(4	) <b>%</b> (7	-0008	-0003	0.33	-0.62	1	->>>	-0/2	0.33	<b>X</b> 3		
PA	<b>)X(1</b>	-006	-902	-•••	-002	×	-002	-002	0)*(1	-002	×	×	-904	-9×(1	-90(4	-0008	<b>)</b> ()	-0/1	) <b>%</b> 2	×	1	<b>%</b> 3	-9⁄0(4	-0005	0.75	
SA	<b>%</b> 2	<b>)</b> \$(1	-001	-01	- 3	×	- 04	-•••4	-0004	-0,003	-0×1	-0×5	-9×(4	-0×(4	-0×(3	-0001	-0001	-0/2	Ø∭(1	-0/2	<b>X</b> 3	1	-0001	-007		
OLR	-9004	-90(3	-•••1	0×5	<b>6</b>	<b>\$\$</b> (5	<b>%</b> 2	₫	-0008	<b>)</b>	<b>)%</b>	0)36(8	ø <b>≫</b> \$	-0,03	∞(1	-9007	0)4(3	<b>)</b> (*	-0.71	0.33	-9⁄4	-90(1	1	*		
SPY	-) (8	-002	0.46	0.85	0.91	0.32	0.93	0.94	0)×3	0.36	0.56	0.59	0.94	×	0.71	-0.4	-002	-9×(1	-006	<b>%</b> 3	-005	-0/7	<b>X</b> 7	1	- 1	

**Fig. 2.** Correlation analysis for  $F_2$  Population of the cross BSR 2 × TMV 2.

direct and indirect influences for various characteristics upon yield through path coefficients is critical for identifying the most suitable traits to employ in indirect selection approaches.

For both  $F_2$  populations, pod yield (0.81, 0.38) and number of mature kernels (0.38,0.31) showed a high positive direct effect on the dependent variable of single plant yield. The characteristics, *viz.*, a number of pods and mature pods in each plant had a high positive indirect effect on single plant yield employing the characteristics of number of mature kernels and pod yield, respectively. The trait number of kernels exhibited a high positive indirect effect on single plant yield through the trait number of mature kernels and pod yield, similar findings had been reported by Kannappan and Viswanathan (12). In the  $F_2$ population of the cross BSR 2 × GPBD 4, pod yield exhibited a high positive indirect effect on single plant yield through the characteristic number of mature kernels (0.36) and the trait number of mature pods (-0.48) exhibited a negative direct effect on single plant yield. The  $F_2$  population of the cross BSR 2 × TMV 2 exhibited a high positive direct effect on single plant yield for the trait number of kernels (0.36). The trait pod yield had a high positive indirect effect on single plant yield through the trait number of kernels per plant (0.32). Sridevi (20) also observed equivalent outcomes for the number of mature pods.

# Conclusion

By current investigations, it might be concluded that the additive gene action contributes a significant part in regulating various yield-related traits for both  $F_2$  populations. Therefore, selection might be a promising approach to

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Table 5. Path Coefficients for yield and its associated traits in Segregating Population of Groundnut for two crosses.

		DFF	РН	NBP	NPP	NMPP	NKP	NMK	SMK	HPW	нкw	PY	r
D.55	C1	0.0014	0.0023	0.0083	-0.0271	-0.1491	0.0714	0.1239	0.0005	0.0151	0.0104	0.2495	0.307**
DFF	C2	0.0283	0.0007	-0.0008	0.0211	0.0146	-0.0640	-0.0646	-0.0118	0.0029	-0.0231	-0.0814	-0.1783*
DU	C1	-0.0001	-0.0319	0.0205	-0.0124	-0.1150	0.0518	0.0943	0.0011	0.0078	0.0222	0.1959	0.233**
РН	C2	-0.0036	-0.0055	-0.0003	0.0028	-0.0004	-0.0032	-0.0059	-0.0096	0.0005	0.0057	0.0016	-0.0177ns
	C1	0.0002	-0.0085	0.0770	-0.0270	-0.1947	0.0869	0.1541	0.0002	0.0236	0.0324	0.3689	0.513**
NDP	C2	-0.0022	0.0001	0.0010	-0.0481	-0.0364	0.1497	0.1390	0.0168	-0.0034	0.0562	0.1816	0.4633**
	C1	0.0005	-0.0051	0.0270	-0.0769	-0.4629	0.1913	0.3503	0.0013	0.0220	0.0119	0.7434	0.803**
NPP	C2	-0.0058	0.0001	0.0046	-0.1031	-0.0720	0.3282	0.2845	0.0150	-0.0048	0.0664	0.3351	0.8484**
	C1	0.0004	-0.0076	0.0311	-0.0739	-0.4815	0.1971	0.3618	0.0013	0.0258	0.0197	0.7831	0.857**
NMPP	C2	-0.0055	0.0001	0.0048	-0.0985	-0.0754	0.3411	0.2977	0.0168	-0.0055	0.0760	0.3591	0.9106**
	C1	0.0005	-0.0079	0.0321	-0.0705	-0.4550	0.2085	0.3805	0.0014	0.0320	0.0261	0.7606	0.908**
ININE	C2	-0.005	0.0001	0.0041	-0.0940	-0.0714	0.3599	0.3110	0.0144	-0.0061	0.0727	0.3414	0.9271**
NIMIZ	C1	0.0005	-0.0078	0.0309	-0.0703	-0.4545	0.2070	0.3833	0.0017	0.0328	0.0267	0.7626	0.913**
NMK	C2	-0.0058	0.0001	0.0044	-0.0931	-0.0712	0.3553	0.3151	0.0229	-0.0067	0.0758	0.3432	0.9398**
SMK	C1	0.0002	-0.0003	0.0043	-0.0259	-0.1676	0.0760	0.1735	0.0038	0.0262	0.0159	0.3089	0.415**
SIMIN	C2	-0.0052	0.0008	0.0026	-0.0239	-0.0196	0.0800	0.1111	0.0648	-0.0066	0.0376	0.1135	0.3553**
עאמ	C1	0.0003	-0.0038	0.0279	-0.0261	-0.1911	0.1026	0.1934	0.0015	0.0650	0.0809	0.4740	0.725**
пги	C2	-0.0047	0.0002	0.0020	-0.0285	-0.0240	0.1275	0.1228	0.0247	-0.0172	0.1462	0.2108	0.5597**
	C1	0.0001	-0.0067	0.0237	-0.0087	-0.0905	0.0519	0.0974	0.0006	0.0501	0.1050	0.2867	0.51**
пкм	C2	-0.0033	-0.0002	0.0028	-0.0344	-0.0287	0.1313	0.1197	0.0122	-0.0126	0.1994	0.2050	0.5913**
DV	C1	0.0004	-0.0077	0.0352	-0.0708	-0.4672	0.1965	0.3622	0.0014	0.0382	0.0373	0.8071	0.933**
FI	C2	-0.006	0.0001	0.0047	-0.0907	-0.0710	0.3225	0.2837	0.0193	-0.0095	0.1072	0.3811	0.9413**

Residual effect: C1: 0.2190; C2: 0.1915, \* Significant at 5% level, \*\* Significant at 1% level, r – correlation coefficient of Single plant yield (Kernel yield), C1 – BSR 2 × GPBD 4, C2 – BSR 2 × TMV 2.

enhancing these characteristics in subsequent generations. The transgressive segregants observed can be further exploited using disruptive selection approaches to isolate genotypes exhibiting superior performance. The identification and selection of these segregants present a promising opportunity for their integration into breeding programmes aimed at improving yield and oil content in groundnut. Future research could focus on evaluating the identified segregants across different environments to ensure their stability and adaptability.

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# **Authors' contributions**

Methodology: DMH and UM; writing review and editing: DMH; Supervision: UM, RR and KR; Software and data analysis: DMH, VK, RR, and KR; All authors read and approved the final manuscript.

# **Compliance with ethical standards**

**Conflict of interest**: Authors do not have any conflict of interests to declare.

Ethical issues: None

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