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ORGANIZING VARIABILITY IN RELEVANCE WITH LATE LEAF SPOT DISEASE AND YIELD ATTRIBUTES IN TMV 2 BASED SEGREGATING POPULATIONS OF GROUNDNUT (*ARACHIS HYPOGAEA* L.)

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ABSTRACT

Genetic variability for disease resistance is very important for efficient crop improvement in groundnut. An investigation was carried out to understand genetic variability in F_4 generation of crosses TMV 2 × ICGV 86699 and TMV 2 × GBFDS 272 for Late Leaf Spot (LLS) disease resistance and yield attributing traits. Analysis of results revealed moderate GCV and PCV, moderate to high heritability coupled with GAM for pod yield related traits like matured pods plant^{-1}, pod yield plant^{-1}, kernel yield plant^{-1}, shelling percentage, SMK per cent in F_3 and F_4 generation for both the crosses. High GCV, PCV with high heritability coupled with GAM was observed for per cent disease index at 60, 75, 90 and 105 DAS. Hence, selection for LLS disease resistance could be carried out in all the crosses of F_4 generation. Estimates of association analysis resulted with strong correlation among matured pods plant^{-1}, kernel yield plant^{-1}, SMK per cent, shelling per cent with pod yield plant^{-1} and showed negative correlation with LLS disease related traits. Superior performing progenies for LLS disease resistance coupled with high pod yield in all the crosses were selected and will be advanced to next generation.

Key words : Genetic variability, Heritability, Correlation, Late leaf spot, Disease resistance.

Introduction

Groundnut (*Arachis hypogaea* L.) is a widely cultivated crop in over 100 nations across the tropics and subtropics. It ranks among the world's most nutritious oilseed and legume crops. With a global cultivation area exceeding 28.5 million hectares, it yields approximately 45.95 million tons of pod yield (FAOSTAT, 2020). In India, groundnut is cultivated in an area of 5.70 million hectares with a production of 10.14 million tons and productivity of 1777 kg ha^{-1} (India stat, 2022). In Karnataka, it is grown in an area of 0.58 million hectares with a production of 0.49 million tones and productivity of 846 kg ha^{-1} (India stat, 2022).

Groundnut, often termed as the "poor man's almonds," is valued for its rich nutritional composition, where fat and protein constitute 80% of the seed content. This makes it a crucial element in combating malnutrition. Additionally, it serves as a rotational crop, enhancing soil fertility through nitrogen fixation and disrupting disease and pest cycles. Howbeit, groundnut is a crucial component of countless delectable dishes and industrial goods (Pandey and Varshney, 2018). It was created over 3,500 million years ago through the hybridization of two wild species, *A. duranensis* and *A. ipaensis* and is an allotetraploid (2n = 4x = 40) with a high genome size of 2800Mb/1C (Favero *et al.*, 2006 and Seijo *et al.*, 2018).

Low productivity in groundnut cultivation is attributed

Abbreviations: GCV- Genotypic Coefficient of Variance; PCV- Phenotypic Coefficient of Variance; GAM- Genetic Advance of Mean; SMK- Sound Mature Kernel; DAS- Days After Sowing

to various factors, including diseases, pests, unpredictable rainfall, drought, unfavorable soil conditions, market fluctuations, and the absence of locally adapted high-yielding varieties (Narh *et al.*, 2014). In most regions of the world, foliar fungal infections limit the yield of groundnuts. The most detrimental, pervasive and economically significant foliar diseases of the groundnut are late leaf spot [*Phaeoisariopsis personata* (Berk. and Curt.) Deighton] and rust [*Puccinia arachidis*], which cause major crop damage (McDonald *et al.*, 1985). They can collectively lower yield by 50-70 per cent (Subrahmanyam *et al.*, 1984) depending on the stage of plant.

Research on Late Leaf Spot (LLS) and rust resistance in groundnut suggests that resistance to these fungi is complex and polygenic, controlled by multiple recessive genes (Motagi, 2001; Dwivedi *et al.*, 2002). Chemical control measures for these diseases can raise production costs by 10%, posing a challenge for small and marginal farmers who dominate groundnut production (Coffelt and Porter, 1986).

Therefore, using genetic mechanisms like host plant resistance is an economical approach for managing these diseases in resource-limited farming systems of developing countries. LLS disease resistance is considered a quantitative trait in various studies (Khedikar *et al.*, 2010; Dwivedi *et al.*, 2002; Motagi *et al.*, 2001), implying its complex inheritance. This complexity complicates direct selection for LLS disease resistance in breeding programs.

Effective selection in plant breeding programs relies on comprehending the connection between yield and related characteristics. Prioritizing highly heritable yield characteristics is more successful than solely relying on direct yield selection (Prabhu *et al.*, 2016). Assessing the heritable and non-heritable aspects of trait variation is complex due to the influence of genetic and environmental interactions on plant characteristics. Separating these components is vital (Nath and Alam, 2002) and the study of genetic advance with heritability can identify traits that can be improved through selection (Korat *et al.,* 2009).

Correlation analysis reveals the characteristics suitable for genetic improvement in yield by exposing relationships between plant traits (Memon *et al.*, 2019). It is a top breeding goal to create high-yielding cultivars resistant to various disease, especially LLS, in order to lessen the effects of disease and boost groundnut production. It is anticipated to be possible to improve breeding for these qualities by having a better understanding of the genetic foundations of early leaf spot resistance components and agronomic traits (yield and its components).

The effectiveness of selection relies on the availability of substantial genetic variability in the breeding material for the target trait and its heritability. Additionally, the success of selection is influenced by the direction and magnitude of the association between the traits to be improved. Therefore, plant breeders must possess a solid understanding of genetic variability and trait associations for effective resistance breeding.

The current study aims to i) assess genetic variability in F_3 and F_4 populations for late leaf spot (LLS) disease resistance and yield-related traits and ii) it seeks to understand the inter-relationships through association studies between LLS disease and yield characteristics in groundnut.

Materials and Methods

The study was conducted in summer 2020 and *Kharif* 2020 at the experimental plots of K-Block, Department of Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Bangalore. The study material comprises segregating populations (F_3 and F_4) attained from the two previously made crosses *viz.*, TMV 2 × ICGV 86699 (ICGV 86699 VB- Virginia bunch [(*A. batizocoi* × *A. duranensis*) × *A. hypogaea* (*cv.* NC 2)] CS 29 (C1)) and TMV 2 × GBFDS 272 (C2) (Table 2). Table 1 provides characteristic features of the parent plants utilized for hybridization. An augmented block design was established to assess populations for the genetic variability characteristics in both the summer (F_3) and *Kharif* (F_4) seasons. Overall work flow of the study (Fig. 1).

Screening and evaluation for late leaf spot (LLS) disease

During the *kharif* season, F_4 populations from the two afore mentioned crosses were grown in separate blocks alongside control varieties and their respective parent plants. An augmented design was employed, and data was collected from each F_4 individual. TMV 2 was used as a spreader row because it is highly susceptible to Late Leaf Spot (LLS) disease, creating a natural epiphytotic condition for disease spread. The spreader row was replicated every six lines. Only yield related parameters were taken up in summer season as disease incidence is absent as the moisture levels are low.

PDI – Percent disease index (Subrahmanyam *et al.*, 1995)

$$PDI\,(\%) = \frac{\text{Sum of individual rating}}{\text{Number of observations assessed}} \times \frac{100}{\text{Maximum disease rating}}$$
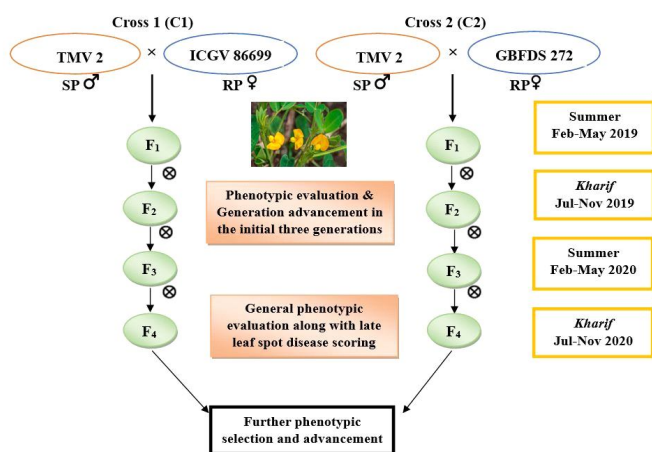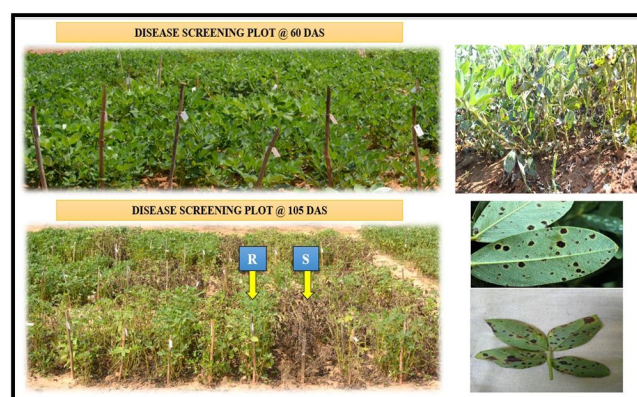
Fig. 1 : Overall work flow of the study.

Fig. 2 : Late leaf spot disease screening @60 DAS & @105 DAS under natural epiphytotic condition during *kharif*.

Table 1 : Salient features of parental lines involved in crosses of groundnut.

S. no.	Parents	Disease score	Mature Pods plant^{-1}	Pod yield plant^{-1} (g)	Reaction towards LLS disease
1.	TMV 2 (Female)	8.30	19	9.40	Susceptible
2.	GBFDS 272 (Male)	2.50	29	19.97	Resistant
3.	ICGV 86699 (Male)	2.50	30	16.57	Resistant

Table 2 : List of crosses along with number of progenies evaluated in F_3 and F_4 populations in groundnut.

Crosses	Cross abbreviation	Progenies in F_3 population	Progenies in F_4 population
TMV 2 × ICGV 86699	C1	52	48
TMV 2 × GBFDS 272	C2	52	48

Table 3 : 9-point scale disease screening (Subrahmanyam *et al.*, 1995).

Disease reaction	Score
Resistant	0 - 3.50
Moderately Resistant	3.51 - 4.5
Moderately susceptible	4.51 - 5.5
Susceptible	5.51 & above

During the *kharif* season (Fig. 2), LLS disease resistance was assessed using a visual screening method with a modified 9-point scale (Table 3) for late leaf spot severity, following Subrahmanyam *et al.* (1995). Data on the 60th, 75th, 90th and 105th days after sowing, extending to crop maturity, were collected to compute the Percent Disease Index (PDI). Additionally, observations were made on pod yield, related traits, and yield attributing traits.

Specifically, observations were recorded for traits including days to first flowering (DFF), plant height (PH), primary branches per plant (PBP), matured pods per plant (MPP), pod yield per plant (PYP) and kernel yield per plant (KYP), shelling percentage (SH) and sound mature kernel percentage (SMK) were calculated using appropriate formulas.

Results and Discussion

In a plant breeding programme, variability appears to be a useful metric for selecting superior material. The first step in accounting for variability is to measure its constituent parts *viz.*, ANOVA. Analysis of F_3 families' variance, an unbiased measure of additive genetic variance (Van Ooijen, 1989), revealed significant differences "between F_3 families" for most traits, except PBP (Table 4). Within families, negligible differences implied uniformity, making this material suitable for rewarding selection. Findings by Shivakumar *et al.* (2016) suggested the existence of significant genetic variability between families suggests potential for improvement. Additive genetic variance predominantly controls quantitative traits, offering predictability through selection.

ANOVA for F_4 progenies in crosses C1 and C2 showed significant differences in various traits, including MPP, PYP, KYP, SH, SMK and PDI at different time points. In C1, all traits exhibited significant differences except for PDI at 75 DAS and 90 DAS (Table 5). In C2, similar differences were found, except for PDI at 60 DAS and 90 DAS (Table 6). This variability is valuable for trait selection and aligns with previous research by Zongo *et al.* (2017) and Chauhan *et al.* (2022) in groundnut, supporting its use in breeding programs.

Table 4 : ANOVA in F_3 population for yield and morpho-metric traits for two crosses in groundnut.

Crosses	Sources of variation	df	DFF	PH (cm)	PBP	MPP	PYP(g)	KYP(g)	SH	SMK
TMV 2 × ICGV 86699	Between F_3 families	51	5.33**	102.54**	0.48	136.85**	113.27**	55.15**	186.74**	94.10**
	Within F_3 families	556	2.91	8.72	0.40	11.58	4.69	2.9	15.55	23.50
TMV 2 × GBFDS 272	Between F_3 families	51	4.70**	38.86**	0.28	127.27**	96.33**	41.66**	110.80**	135.84**
	Within F_3 families	571	3.78	11.55	0.24	15.11	10.60	6.23	16.37	23.8

Genetic variability parameters

Table 7 presents the study results, encompassing variability parameters. In Table 8, traits are categorized as high, medium, or low based on the observed variability. Morphological traits such as DFF, PH, and PBP exhibited low to moderate GCV and PCV in F_3 and F_4 populations of both crosses. The presence of low to moderate PCV and GCV suggests a lack of distinctiveness in trait selection. Notably, across all studied characters, PCV values were consistently higher than GCV values.

Elevated PCV values indicate environmental influence, reducing the efficiency of selection, consistent with Vasanthi *et al.* (2015) in groundnut using 29 genotypes (18 released and 11 pre-released once). These characteristics showed a significant difference between GCV and PCV, signifying strong environmental influence, making it unsuitable for selection, similar to Rao *et al.* (2014) in groundnut.

Traits like MPP, PYP, KYP, SMK, SH, PDI @ 60 DAS, PDI @ 75 DAS, PDI @ 90 DAS, PDI @ 105 DAS has showed high GCV and PCV in both the crosses of F_3 and F_4 populations except the traits MPP, SMK and SH have showed moderate GCV in both the crosses of F_3 population. High to moderate GCV and PCV suggest that the respective characters are amenable to selection, offering opportunities to explore beneficial traits.

Results from Prabhu *et al.* (2016) suggested considerable variation in MPP in F_2 and F_3 populations, making it suitable for direct selection. Specific crosses (CO 7 × GPBD 4, TMV gn 13 × GPBD 4 and TMV 2 × GPBD 4) exhibited elevated GCV and PCV for MPP, highlighting the significance of additive gene action as a major factor contributing to higher groundnut yield.

Reports of Kumari and Sasidharan (2020) in their 50

Arachis genotypes belonging to different botanical types *viz*; spanish bunch, virginia bunch, valencia, peruviana and aequatoriana noted similar observations for PYP. The small variation between PCV and GCV points to a predominately genetic regulatory mechanism with very little environmental influence. Prabhu *et al.* (2015) similarly found that phenotypic selection for KYP in backcross populations of CO 7 × GPBD 4 and CO 7 × COG 0437 with the recurrent parent CO 7 was effective.

Traits like DFF, PH, PBP, MPP, PYP, KYP, PDI @ 60 DAS, PDI @ 75 DAS, PDI @ 90 DAS, PDI @105 DAS has demonstrated strong heritability in both crosses of F_3 and F_4 populations. In both crosses, SMK and SH has showed moderate heritability except in C2 of F_4 population which showed high heritability. All traits have showed high GAM values in both the crosses of F_3 and F_4 populations except DFF which showed moderate heritability in both the crosses of F_4 and C2 of F_3 population, whereas C1 of F_3 population has exhibited low GAM.

When high heritability and significant high GAM are combined, it indicates that additive gene action is primarily responsible for the traits under investigation. This scenario implies that the observed variations are largely due to genetic factors and are less influenced by environmental factors. In practical terms, the effectiveness of selection for these traits is higher, as changes induced through breeding efforts are more likely to be passed on to the next generation.

High PCV, GCV, heritability and medium GAM values were recorded in the crosses *viz.*, TMV 2 × VRI Gn 6, TMV Gn 13 × VRI Gn 6 and VRI 2 × VRI Gn 6 for the trait SH by Divyadarshini *et al.* (2017) in groundnut. On the contrary to our results, the results obtained by

Table 5 : Mean sum of squares of F_4 progenies derived from the cross TMV 2 × ICGV 86699(C1) for pod yield and its attributing traits in groundnut.

Sources of variation	df	DFF	PH (cm)	PBP	MPP	PYP (g)	KYP (g)	SH	SMK	PDI at 60th day	PDI at 75th day	PDI at 90th day	PDI at 105th day
Blocks	3	0.10	1.39	0.29	9.35	6.76	21.30	105.45	68.29	0.06	0.40	1.23	1.75
Treatments (progenies + checks + parents)	52	3.15**	11.55**	0.46**	65.96**	42.61**	27.77**	355.65*	346.40*	1.66**	6.64**	11.09**	16.46**
Checks	4	2.45**	27.30**	1.55**	25.30*	42.66**	39.64**	615.89*	518.42*	5.10**	34.23**	42.34**	82.98**
Progenies	47	3.22**	9.85**	0.30*	32.64**	27.35**	16.36*	318.63*	320.09*	0.16*	0.22	0.15	2.95**
Checks vs Progenies	1	2.38**	28.54**	3.84**	1794.92**	759.54**	516.72**	1054.31*	894.52*	58.31**	197.87**	385.64**	400.57**
Errors	12	0.05	0.95	0.12	6.70	2.43	6.46	130.02	118.53	0.06	0.20	0.57	1.19

Table 6 : Mean sum of squares of F_4 progenies derived from the cross TMV 2 × GBFDS 272(C2) for pod yield and its attributing traits in groundnut.

Sources of variation	df	Days to first flowering	Plant height (cm)	Primary branches plant⁻¹	Pods plant⁻¹	Pod yield plant⁻¹ (g)	Kernel yield plant⁻¹ (g)	Shelling per cent	SMK per cent	PDI at 60th day	PDI at 75th day	PDI at 90th day	PDI at 105th day
Blocks	3	0.34	2.84	0.09	2.78	6.25	5.91	12.24	55.48	0.28	1.25	1.45	0.76
Treatments (progenies + checks + parents)	52	2.48**	4.54**	0.69**	78.12**	29.90**	24.49**	151.39**	287.48**	1.95**	6.90**	8.94**	13.80**
Checks	4	0.70**	23.20**	3.55**	14.00**	28.11**	33.24**	399.59**	108.79*	8.37**	41.06**	48.01**	84.84**
Progenies	47	2.24**	2.69*	0.32**	32.66**	14.53**	6.76**	61.09**	197.67*	0.35	1.20*	0.77	0.53*
Checks vs Progenies	1	20.88**	16.77**	6.34**	2470.96**	759.19**	822.56**	392.55**	263.57**	51.47**	138.39**	236.40**	353.32**
Errors	12	0.11	1.05	0.05	0.94	2.40	1.79	3.94	60.66	0.29	0.41	0.77	0.22

*Significant @ P = 0.05; **Significant @ P = 0.01

Table 7 : Genetic variability parameters for morphometric, pod yield and its component traits in F_3 and F_4 populations derived from two crosses in groundnut

Traits	Cross	GCV (%)		PCV (%)		h^2_{bs} (%)		GAM	
		F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4
DFF	C1	2.74	4.13	3.03	4.19	81.57	97.02	8.90	11.85
	C2	3.10	3.79	3.85	3.96	64.45	91.61	10.04	11.34
PH (cm)	C1	11.49	8.19	12.37	8.90	86.28	84.81	28.66	21.35
	C2	8.42	4.69	9.76	5.94	74.49	62.30	22.78	14.45
PBP	C1	8.83	8.41	9.51	11.02	86.15	58.35	36.92	34.61
	C2	11.06	11.49	15.79	12.31	49.07	87.17	42.47	43.05
MPP	C1	17.22	18.90	19.79	20.92	75.75	81.57	43.42	45.93
	C2	18.39	21.16	21.03	21.41	76.51	97.63	45.86	47.45
PYP(g)	C1	16.78	20.84	19.58	22.06	73.41	89.23	43.89	49.59
	C2	20.07	17.19	22.07	18.64	82.66	85.11	49.40	42.34
KYP(g)	C1	21.67	21.80	28.01	27.62	59.86	62.26	61.96	61.06
	C2	24.41	21.83	28.88	23.49	71.44	86.39	64.48	53.98
SMK	C1	15.35	17.98	20.92	25.68	53.88	49.01	44.02	53.73
	C2	19.26	17.20	27.69	21.31	48.37	65.15	57.79	44.96
SH	C1	15.83	16.31	22.38	23.93	50.05	46.46	46.85	50.01
	C2	11.55	12.66	20.03	12.99	32.34	94.93	42.34	28.16
PDI @ 60 DAS	C1	-	60.39	-	62.69	-	92.79	-	191.90
	C2	-	67.46	-	78.42	-	74.01	-	216.37
PDI @ 75 DAS	C1	-	60.33	-	65.71	-	84.31	-	164.54
	C2	-	57.22	-	60.70	-	88.86	-	153.26
PDI @ 90 DAS	C1	-	48.79	-	54.35	-	80.58	-	129.64
	C2	-	41.97	-	45.75	-	84.15	-	111.73
PDI @ 105 DAS	C1	-	41.71	-	42.23	-	97.55	-	101.26
	C2	-	40.41	-	41.05	-	96.91	-	99.58

Padmaja *et al.* (2013) for SMK in the four crosses studied exhibited high/medium PCV and medium/low GCV were observed. High/medium heritability and low magnitudes of GAM values indicating the limited scope of selection for SMK.

Both crosses displayed elevated GCV and PCV for PDI at 60 DAS, despite fluctuations in relative humidity (98% in the first hour and 77% in the second hour). Notably, high heritability and GAM were consistently observed in C1 cross, even under identical relative humidity conditions. The resistant parents in these crosses were ICGV 86699 and GBFDS 272. The variability in results can be attributed to genetic backgrounds and population size. High GCV and PCV were noted for PDI at 75 DAS in both crosses, maintaining similar relative

humidity conditions (94% in the first hour and 81% in the second hour). The consistency of high heritability and GAM was observed in both C1 and C2 crosses.

Elevated GCV and PCV were evident for both PDI at 90 DAS and PDI at 105 DAS across all crosses. The relative humidity (RH) varied from 87% to 59% in the first hour and 90% to 63% in the second hour. Notably, high heritability and GAM were consistently observed in both C1 and C2 crosses for both traits. The range of relative humidity was higher for PDI at 90 DAS and PDI at 105 DAS compared to PDI at 60 DAS and PDI at 75 DAS, which coincided with high heritability and GAM. Using a resistance donor as the female parent to leverage maternal effects of resistance was found to be beneficial in improving efficiency (Varshney *et al.*, 2013).

Table 8 : Genetic variability evident across various traits in Groundnut.

Variability parameters	Crosses	High		Medium		Low	
		F_3	F_4	F_3	F_4	F_3	F_4
GCV	C1	KYP	PYP, KYP, PDI @ 60, 75, 90, 105 DAS	PH, MPP, PYP, SMK, SH	MPP, SMK, SH	DFF, PBP	DFF, PH, PBP
	C2	PYP, KYP	MPP, KYP, PDI @ 60, 75, 90, 105 DAS	PBP, MPP, SMK, SH	PBP, PYP, SMK, SH	DFF, PH	DFF, PH
PCV	C1	KYP, SMK, SH	MPP, PYP, KYP, SMK, SH, PDI @ 60, 75, 90, 105 DAS	PH, MPP, PYP	PBP	DFF, PBP	DFF, PH
	C2	MPP, PYP, KYP, SMK, SH	MPP, KYP, SMK, PDI @ 60, 75, 90, 105 DAS	PBP	PBP, PYP, SH	DFF, PH	DFF, PH,
Heritability	C1	DFF, PH, PBP, MPP, PYP	DFF, PH, MPP, PYP, KYP, PDI @ 60, 75, 90, 105 DAS	KYP, SMK, SH	PBP, SMK, SH		
	C2	DFF, PH, MPP, PYP, KYP	DFF, PH, PBP, MPP, PYP, KYP, SMK, SH, PDI @ 60, 75, 90, 105 DAS	PBP, SMK, SH			
GAM	C1	PH, PBP, MPP, PYP, KYP, SMK, SH	PH, PBP, MPP, PYP, KYP, SMK, SH, PDI @ 60, 75, 90, 105 DAS		DFF	DFF	
	C2	PH, PBP, MPP, PYP, KYP, SMK, SH	PBP, MPP, PYP, KYP, SMK, SH, PDI @ 60, 75, 90, 105 DAS	DFF	DFF, PH		

Also, results revealed that the occurrence of late leaf spot disease is aided by high relative humidity and low temperatures. This variability can be utilized by selecting for LLS disease resistance genotypes (Zongo *et al.*, 2017).

Maximum infection with high PDI occurred at 20°C with at least 12 hours of high RH (90-95%) in groundnut, as noted by Shew *et al.* (1988). The duration of high relative humidity required for infection depends on the level of partial resistance in the host. The study involved two crosses with different male parents, resulting in varying resistance LLS disease. Cross C1, with the resistant parent ICGV 86699, demonstrated higher resistance compared to crosses with parent GBFDS 272 (C2).

Results for PDI at 60 DAS, 75 DAS, 90 DAS and 105 DAS indicated high heritability and significant Genetic Advance (GAM) in the F_4 population for both the crosses. Dwivedi *et al.* (2002) also emphasized the importance of a field-measured trait, the remaining green leaf area on the plants, which is a component of the disease score, as

a major selection criterion for resistance to LLS disease.

Phenotypic correlation coefficient among pod yield attributing traits in F_3 and F_4 populations and disease traits in F_4 populations in groundnut

In the present investigation association of yield with different yield components in both F_3 and F_4 populations in both the crosses were estimated and presented in Table 9. Moderately strong to very strong significant positive associations were observed between PYP and mature MPP in cross C1 in the F_3 population and in both crosses in the F_4 population. Significant positive correlations were found between KYP and MPP in both crosses in both F_3 and F_4 populations. Significant positive associations were noted for KYP with PYP in two crosses in both F_3 and F_4 populations. Significant positive associations were observed for SMK with KYP in cross C1 in the F_3 population and in both crosses of F_4 population. In cross C2 in the F_4 population, significant positive associations were found for SH.

These results highlight the significance of yield-related

Table 9 : Phenotypic correlation coefficient among growth parameters, pod yield and its attributing traits in F_3 (above diagonal) and F_4 (below diagonal) populations derived from two crosses in groundnut.

| Traits	Crosses	DFF	PH (cm)	PB	PN	PY	KY	SMK	SH
DFF	C1	-	-0.23	0.08	-0.11	-0.30*	-0.37**	-0.25	-0.20
	C2	-	0.21	0.07	-0.18	-0.09*	-0.14	0.24	-0.05
PH (cm)	C1	0.11	-	0.10	0.20	0.24	0.21	-0.03	-0.01
	C2	0.26	-	-0.01	0.03	0.07	0.04	-0.26	-0.20
PBP	C1	0.23	0.17	-	-0.03	0.03	0.05	-0.04	-0.09
	C2	0.02	0.17	-	-0.13	-0.02	-0.19	-0.06	-0.02
MPP	C1	-0.16	-0.16	0.22	-	0.71**	0.57***	0.66***	-0.09
	C2	0.31*	0.09	-0.02	-	0.713**	0.59***	-0.12	0.07
PYP	C1	-0.18	-0.09	0.12	0.88***	-	0.75***	0.09	0.07
	C2	0.24	-0.04	-0.20	0.52*	-	0.94***	0.67**	0.13
KYP	C1	-0.07	-0.06	0.26	0.77***	0.83***	-	0.69***	0.07
	C2	0.32*	-0.01	0.05	0.45**	0.47*	-	0.19	0.24
SMK	C1	0.14	0.12	-0.15	0.17	0.31*	0.31*	-	0.17
	C2	-0.08	-0.01	0.05	-0.16	-0.07	0.22*	-	0.33*
SH	C1	0.04	-0.14	-0.24	-0.21	-0.19	0.21	0.15	-
	C2	-0.06	-0.01	-0.01	0.36*	0.23	0.35*	0.33*	-
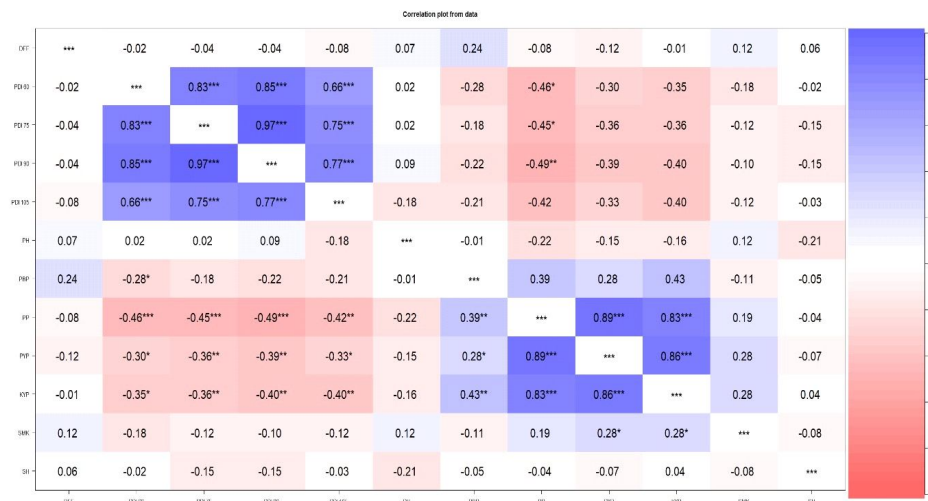
Fig. 3 : Correlation among pod yield attributing traits and disease traits in F_4 populations in the cross TMV 2 × ICGV 86699 (C1).

traits, such as PYP, MPP, SMK and SH, which demonstrated moderately strong to very strong significant positive correlations with KYP-related traits. After pod development, indirect selection can be a valuable strategy in groundnut breeding to attain high-yielding varieties.

These traits are crucial as yield attributes, and they deserve attention when breeding for high MPP and KYP in groundnut. Focusing on these characters in the selection process can contribute to improved overall yield in groundnut. The findings align with the results reported

by Ashutosh *et al.* (2017) in groundnut and with the results of Memon *et al.* (2019) in the F_2 generation, which emphasized the importance of traits like pods per plant, kernel yield per plant, shelling percentage, biological yield per plant, and harvest index as selection criteria for enhancing pod yield per plant in groundnut.

Correlation coefficient in F_4 population for PDI at 60 DAS, PDI at 75 DAS, PDI at 90 DAS and PDI at 105 DAS is presented in Table 10. As the study involves segregating generations, selection is based on percentage defoliation in the field. The disease score, mainly derived from the extent of defoliation, represents the culmination of all resistance factors and achieving their optimal combination results in a lower score.
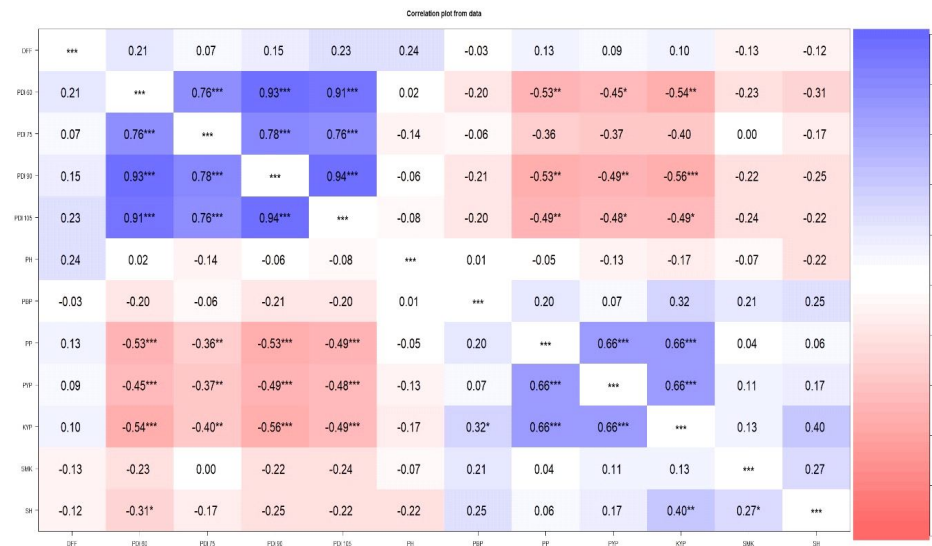
Also, the graphical representation of phenotypic correlation coefficient in F_4 population of both the crosses is depicted in the Figs. 3 and 4. The results indicated significant negative association of PDI at 60 DAS in both the crosses for MPP, PYP, KYP, SH and SMK.

Table 10 : Phenotypic correlation coefficient analysis among PDI for LLS disease resistance at different intervals with pod yield attributing traits in F_4 population in groundnut.

Traits	Crosses	MPP	PYP	KYP	SMK	SH
PDI @ 60 DAS	C1	-0.62*	-0.57**	-0.64**	-0.48*	-0.63**
	C2	-0.59*	-0.45*	-0.53*	-0.54*	-0.51*
PDI @ 75 DAS	C1	-0.60*	-0.57*	-0.71**	-0.45*	-0.71**
	C2	-0.52*	-0.41*	-0.61*	-0.53*	-0.53*
PDI @ 90 DAS	C1	-0.61**	-0.63**	-0.73**	-0.51*	-0.70*
	C2	-0.60*	-0.65**	-0.65**	-0.61*	-0.63**
PDI @ 105 DAS	C1	-0.66*	-0.67**	-0.72**	-0.50*	-0.75*
	C2	-0.41	-0.51*	-0.64**	-0.68*	-0.63*

Table 11 : LLS disease reaction of selected superior plants and Selection intensity with high pod yield from F_4 population in both the crosses of groundnut.

Cross	R	MR	Total (No. of superior selected plants)	Total No. of plants in each cross from progenies	Selection intensity (SI) *per cent*
C1	29	9	38	462	8.23
C2	32	8	40	496	8.06

Fig. 4 : Correlation among pod yield attributing traits and disease traits in F_4 populations in the cross TMV 2 × GBFDS 272 (C2).

The negative associations observed indicate that the occurrence of LLS disease from 60 DAS to 105 DAS, spanning from pod development to pod maturity stages, leads to substantial yield loss. Therefore, the selection of resistant individuals with higher pod yield can be accomplished by choosing plants with low PDI values, given the negative relationship between pod yield-related traits and PDI.

These findings align with the results reported by Zongo *et al.* (2017), who found positive correlations between resistance parameters for Early Leaf Spot (ELS) and kernel yield as well as its components in cross QH243C × NAMA. This suggests a linkage between low productivity and ELS susceptibility, emphasizing the genetic control of many traits that can be improved through classical selection.

Significant negative correlation was observed for PDI at 75 DAS with MPP, PYP, KYP, SMK, SH in both the crosses in F_4 population. In the present study correlation analysis revealed that PDI at 90 DAS was negatively associated with MPP, PYP and SMK in both the crosses. Results for the correlation coefficient for PDI at 105 DAS showed significant negative correlations in both crosses between KYP and SH. Additionally, a significant negative association of PDI at 105 DAS with MPP was observed in cross C2, while PYP and SMK displayed significant negative associations with PDI at 105 DAS in both crosses.

Identification of superior segregants in F_4 population for LLS disease resistance with high pod yield and pod characters

The breeding process success is assessed by the breeder's equation [$\Delta G = (h^2 \sigma_p I)/L$], which calculates the genetic gain rate (ΔG) using narrow sense heritability
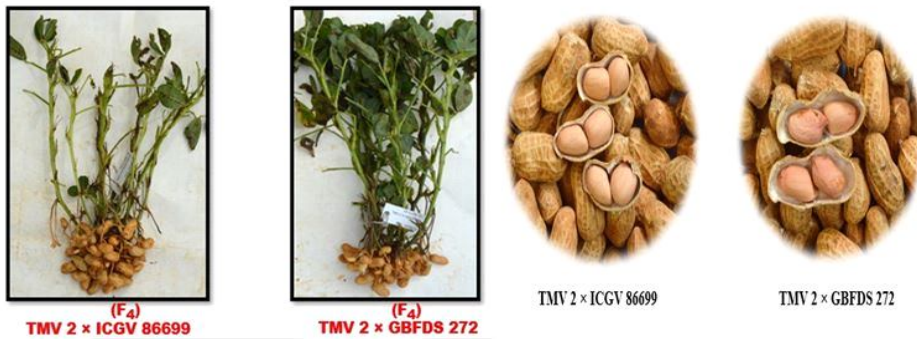
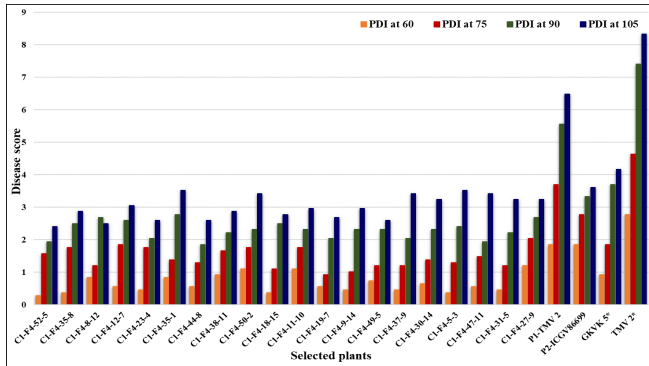**Fig. 5 :** Plant, pods and kernels of selected superior F_4 segregating population.

Fig. 6 : Disease score graph for superior selected plants of F_4 population in the cross TMV 2 × ICGV 86699 at four different intervals in groundnut.
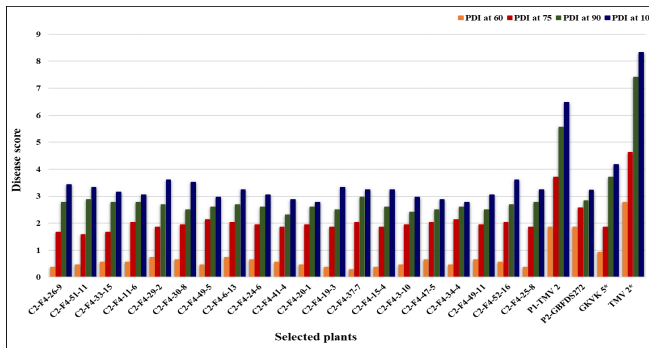

Fig. 7 : Disease score graph for superior selected plants of F_4 population in the cross TMV 2 × GBFDS 272 at four different intervals in groundnut.

(h^2), phenotypic variance (σ_p), selection intensity (I) and breeding cycle length (L), following Eberhart's (1970) recommendations.

Selection intensity, impacting the percentage advancing to the next generation, influences genetic gain. Elevated selection intensity boosts genetic gain, but excess can deplete diversity. To counter this, a larger population size is advised, generating more progeny from each breeding cross (Moose and Mumm, 2008). Superior lines with desired traits were selected from 188 F_4 progenies in Table 11. Selection criteria for specific crosses included MPP (≥30), PYP (≥20g), KYP (≥15g), SH (≥65%) and PDI score (≤4.50).

In the cross C1, 38 plants (8.23% selection intensity) were selected, with 29 resistant and nine moderately resistant. In the cross C2, 40 plants (8.06% selection intensity) were chosen, with 32 resistant and eight moderately resistant. Both C1 and C2, being TMV 2 type-based crosses, produced bold seeds with medium constriction, a slight beak, and 2-seeded pods, resembling TMV 2 seeds, which are highly preferred by consumers (Fig. 5). As previously mentioned in the paper, C1 exhibits superior disease resistance and, consequently, higher yields compared to C2. Therefore, it can be concluded that ICGV 86699 is a preferable parent for managing LLS disease, when compared to GBFDS 272.

High selection pressure can induce allelic erosion via genetic drift in large populations, necessitating a low selection intensity. However, higher selection intensity can yield a more pronounced response in desired traits, so it was applied selectively, especially in crosses with fewer progenies. Nonetheless, it's essential to exercise caution, as excessive selection pressure can perturb gene frequencies due to sampling errors in larger populations, prompting the use of a less stringent selection intensity when necessary.

In Figs. 6 and 7, a disease score graph displays PDI scores at four intervals (PDI @ 60 DAS, PDI @ 75 DAS, PDI @ 90 DAS, and PDI @ 105 DAS) on the Y-axis. On the X-axis, it shows the top superior selected plants for LLS disease resistance and pod yield attributing traits, along with their respective parents and checks of C1 and C2, respectively. The bar graphs indicate that most of the superior segregants had PDI scores lower than or equal to the resistant parent, signifying the inheritance of LLS resistance in the progenies.

Conclusion

The analysis of variance for F_3 and F_4 population progenies in both crosses showed notable differences in traits linked to pod yield and its components. This observed diversity underscores its suitability for incorporation into breeding programs. Moderate GCV and PCV, along with moderate to high heritability and GAM were noted in the populations for pod yield and its components. Notably, cross C2 exhibited the highest variability parameters, indicating its superiority over C1.

A highly significant positive correlation between pod yield (PYP) and traits like MPP and KYP suggests that

enhancing MPP in both crosses could lead to improved yield. The negative correlation between LLS disease and pod yield-related characters at various time intervals (PDI @ 60 DAS, PDI @ 75 DAS, PDI @ 90 DAS and PDI @ 105 DAS) underscores the adverse impact of LLS disease on pod yield per plant.

Based on least per cent yield reduction, per se performance and seed type 38 plants in the cross C1 and 40 plants in the cross C2 were selected as the top superior segregating plants for LLS disease resistance and high pod yield. To address these findings, selected resistant plants with minimal yield reduction, even under favourable conditions, should be advanced to the F_5 generation. F_6 families with increased pod yield and improved resistance to LLS disease can be obtained by further pedigree selection. Subsequently, uniform family selection in the F_6 generation and the pooling of seeds from these selected families are recommended.

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