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Correlation and Path Analysis among Agro-morphological Traits in Groundnut (*Arachis hypogaea* L.)

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Abstract: Twenty-six genotypes of groundnut were evaluated for estimation of genetic parameters and character inter-relationship among the yield contributing characters. These genotypes showed noticeable differences in days to maturity, test weight, sound mature kernels, harvest index, protein content, and pod yield per plant. Test weight reported the highest value for the phenotypic coefficient of variations (PCV), genotypic coefficient of variations (GCV), genetic advance (GA), and percentage genetic advance while protein content testified as the best heritable trait. During correlation analysis, days to maturity, test weight, harvest index, and protein content indicated positive relation with pod yield for genotypic (r_g) and phenotypic (r_p) correlation coefficient. Harvest index, days to 50% flowering, protein content and test weight showed direct positive effect on pod yield per plant.

Key words: *Arachis hypogaea*, agro-morphological, genetic advance, heritability.

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Groundnut (*Arachis hypogaea* L.), a self-pollinated legume is an important crop cultivated in 24 Mha the world over for extraction of edible oil and food purpose. There are about 70 species of groundnut that are grown in more than 100 different countries globally. In the last decade (2000-2010), global groundnut production increased marginally. The global annual increase in production was 0.4% which was due to both, an annual increase in yield by 0.1% and in area by 0.3% (Janila *et al*., 2013). Over 60% of global groundnut production is crushed for extraction of oil for edible and industrial uses, while 40% is consumed as food and others (Birthal *et al*., 2010). In Europe and North and South America about 75% of the production is used as food, while only 35% is used for the same purpose in Asia (Birthal *et al*., 2010). Peanut butter is the most popular groundnut product in the USA, Canada, and Australia. Groundnut seed can be consumed raw (non-heated), boiled, or as roasted, and also used to make confections and flour to make baked products. Groundnut shells are used for making particle boards or used as fuel or filler in the fertilizer and feed industry. Groundnut haulms constitute nutritious fodder for livestock. They contain protein (8-5%), lipids (1-3%), minerals (9-17%), and carbohydrates (38-45%) at levels higher than cereal fodder.

The economic importance and narrow genetic base of groundnut has motivated scientists to characterize available germplasm against current abiotic and biotic stresses based on its morphological characteristics. The study of correlation and causation of path concept reveals different ways in which component attributes influence the complex traits and this gives a clear picture of the contribution of each morphological character. Knowledge of the direction and magnitude of association between various traits is essential for achieving the goal of increased production through increasing the yield potential of the crop. Correlation is a biometrical approach that brings out the intensity of the association between two pairs of characters and provides information on those components that could serve as criteria for the selection of candidates in a breeding program. Traits that are positively correlated with yield are considered effective because selection for such traits would result in the simultaneous improvement in yield (Mahalakshmi *et al*., 2005). The correlation coefficient may be confounded with indirect effect due to the common association inherent in trait interrelationships. Path coefficient analysis measures the direct influence of one variable upon another and facilitates the separation of correlation coefficients into components of direct and indirect effects (Dewey and Lu, 1959). Therefore, information derived from the correlation coefficients can be augmented by partitioning correlations into direct and indirect effects by path coefficient analysis. In the era of climate change, screening and studying the variability of different characters in groundnut genotypes for tolerance against salinity (Singh *et al*., 2007) and drought is essential (Nautiyal *et al*., 2011). Even for using the advanced technology of genome editing in groundnut (Rajyaguru and Tomar, 2020) the presence of variability and the correlation of the trait to be edited with other traits is essential. Genetic variability and correlation have been studied in groundnut (John *et al*., 2009; Korat *et al*., 2009; Kumar *et al*., 2009; Vekariyaet *et al*., 2011) and most of the crops (Tomar *et al*., 2008) and even molecular marker have been used to study the variability at DNA level (Reddy *et al*., 2022).

The main purpose of the present study is to evaluate available groundnut germplasm through agro-morphological characteristics for determining their genetic diversity which can be helpful for the future planning of groundnut breeding programs, according to its behavior in local environmental conditions.

Materials and Methods

Twenty-six groundnut genotypes originating from different sources were collected from Main Oilseed Research Station, Junagadh Agricultural University, Junagadh. The details of the genotypes with the parentage and major characteristics have been depicted in Table 1.

Experiment design for agro-morphological characterization

All twenty-six genotypes were sown in randomized block design (RBD) at Main Oilseed Research Station, Junagadh Agricultural University, Junagadh during kharif with 45 cm x 10 cm spacing and other recommended agronomical practices were followed. Four replications were maintained and the data was statistically analysed.

Agro-morphological observations

Observations on days to 50% flowering, days to maturity, test weight(g), sound mature kernels (%), shelling percentage, harvest index, oil content (%), protein content (%) and pod yield per/plant (g) for each genotype were recorded from five randomly selected plants per replication.

Data analysis

Analysis of variance (ANOVA) (Panse and Sukhatme, 1985), GCV and PCV (Burton and Devane, 1953), heritability (h^2) and genetic advance (GA) (Johnson et al. 2008) were also estimated for field observed agro-morphological trait data.

Results and Discussion

Analysis of variance for agro-morphological characters showed a significant difference in genotypes for all traits (Table 2). Days to 50% flowering, shelling percentage, and oil content indicated highly significant results as their range of variation was 26.25-29.50, 51.89-73.19 and 43.06-50.47, respectively. Days to maturity, test weight, sound mature kernels, harvest index, protein content, and pod yield per plant showed noticeable differences in ANOVA.

Table 1. List of groundnut genotypes under study

S.No	Genotype	Origin	Pedigree	Characters
1	ICGV-91114	ICRISAT, Hyderabad	ICGV 86055 x ICGV 86533	Drought tolerant
2	R-2001-2	UAS, Raichur	ICGS 11 x ICG-4728	Resistant to PBND (Peanut Bud Necrosis Disease)
3	R-2001-3	UAS, Raichur	ICGS 11 x ICG-4728	Resistant to PBND
4	JL-24	ICRISAT, Hyderabad	selection from EC 94943	Drought tolerant
5	Pratap Mungphali-1 (PM-1)	MPAU & T, Udaipur	ICGV 86031 x ICG 2241	Moderately resistant to ELS (Early Leaf Spot), LLS (Late Leaf Spot), PBND, *Spodoptera litura* and leaf miner
6	Pratap Mungphali-2 (PM-2)	MPAU & T, Udaipur	ICGV 86055 x ICG (FDRS) 10	Moderately resistant to ELS, LLS, PBND, *Spodoptera litura*, leaf miner and thrips
7	VG-5	TNAU, Coimbatore	CG 26 x ICGS 44	More Secondary branches, high shelling and red testa
8	AK-159	PKV, Akola	JL-24 x CGC 4018	High oil content
9	TMV-13	TNAU, Coimbatore	Selection from Pollachi red	Moderately resistant to LLS, rust and bud necrosis; Tolerant of early and mid-season moisture stress
10	TPG-41	BARC, Mumbai	TG 28A x TG 22	O/L
11	TG-37A	BARC, Mumbai	TG 25 x TG 26	Moderately tolerant of Collar rot, rust and LLS
12	GPBD-4	UAS, Dharwad	KRG 1 x ICGV86855	Resistant to LLS and rust
13	GPBD-5	UAS, Dharwad	TG 49 x GPBD 4	Resistant to LLS and rust
14	Dh-101	UAS, Dharwad	R9241 x dh 51-2	Tolerant to stem rot, PBND, thrips and *Spodoptera litura*
15	GG-3	JAU, Junagadh	GAUG 1 x JL 24	Early maturity and high yielding
16	GG-5	JAU, Junagadh	27-5-1 x JL 24	Drought tolerant, leaflets stay green at maturity
17	GG-7	JAU, Junagadh	S 206 x FESR-8	Early maturity
18	GG-8	JAU, Junagadh	27-5-1 x JL 24 30-3-2-B-B	High yielding
19	GJG-9	JAU, Junagadh	GG-5 x ICGV 90116	High yielding, bold seed size and tolerant to stem rot
20	Kadiri-4	ANGRAU, Kadari	Dh 3-30 x NCAc 2230	
21	Kadiri-6	ANGRAU, Kadari	JL 24 x Ah 316/S	Tolerant of LLS
22	Kadiri-9	ANGRAU, Kadari	Kadiri 4 x Vemana	Tolerant of thrips, jassids, mite, nematodes, LLS, rust, dry root rot and collar rot
23	Kadiri Harithandhra	ANGRAU, Kadari	91/57-2 x PI476177	Resistant to multiple disease and insect pest
24	Narayani	ANGRAU, Tirupati	JL24 x Ah316/s	Tolerant to mid-season moisture stress
25	Greesma	ANGRAU, Tirupati	TIR-46 x JUG-37	Tolerant to LLS, drought, high temperature and aflatoxin
26	Abhaya	ANGRAU, Tirupati	K 134 x TAG 24	Tolerant of LLS, jassids, thrips, *Spodoptera litura*; tolerant early and mid-season moisture stress

Phenotypic and genotypic coefficient of variations values depicted test weight with highest estimates of 21.411 and 19.122, respectively followed by pod yield per plant and harvest index (Table 3). Protein content showed highest value (94.36) for heritability followed by oil content (91.28) while days to 50% flowering indicated lowest 20.29. Genetic

Table 2. Analysis of variance (ANOVA) for nine characters in twenty-six genotypes

Source	df	Days to 50% flowering	Days to maturity	Test weight	Sound mature kernels	Shelling percentage	Harvest index	Oil content	Protein content	Pod yield plant^{-1}
		1	2	3	4	5	6	7	8	9
Replication	3	4.471	2.292	4.237	0.909	91.955*	2.830	1.327*	0.451	1.867
Genotypes	25	2.740**	17.580*	186.827*	87.611*	128.089**	97.831*	15.340**	9.785*	18.678*
Error	75	1.358	4.165	11.145	7.286	47.762	12.244	0.358	0.144	1.551

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

Table 3. Phenotypic coefficients of variations, genotypic coefficient of variations, heritability, genetic advance and genetic advance value expressed as a percentage of means for various characters in groundnut

Characters	Range of variation	Mean	Phenotypic coefficient of variations (%) (PCV)	Genotypic coefficient of variations (%) (GCV)	Heritability (h2)	Genetic advance (GA)	Genetic advance value % means
Days to 50% flowering	26.25-29.50	27.548	4.738	2.134	20.29	0.54	1.98
Days to maturity	111.25-120.25	115.048	2.383	1.592	44.60	2.52	2.19
Test weight (g)	23.67-50.28	34.658	21.411	19.122	79.76	12.19	35.18
Sound mature kernels (%)	79.00-97.66	91.899	5.693	4.876	73.37	7.90	8.60
Shelling percentage	51.89-73.19	64.026	12.865	6.999	29.6	5.02	7.84
Harvest index	23.75-41.62	33.248	17.445	13.913	63.60	7.59	22.85
Oil Content (%)	43.06-50.47	47.360	4.277	4.086	91.28	3.80	8.04
Protein Content (%)	25.55-31.16	28.184	5.671	5.508	94.36	3.10	11.02
Pod yield plant^{-1} (g)	9.823-18.16	13.426	17.989	15.412	73.40	3.65	27.20

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

Table 4. Genotypic (rg) and phenotypic (rp) correlation coefficients among 9 characters in groundnut

Characters		Days to 50% flowering	Days to maturity	Test weight	Sound mature kernels	Shelling percentage	Harvest index	Oil content	Protein content
Pod yield plant^{-1}	rg	0.337**	0.384**	0.229*	-0.010	0.222*	0.482**	0.050	0.274**
	rp	0.061	0.196*	0.211*	-0.001	0.124	0.566**	0.051	0.239*
Days to 50% flowering	rg		0.264**	-0.065	0.205*	-0.017	0.185	0.083	-0.390**
	rp		0.115	-0.047	0.182	-0.012	0.131	0.064	-0.329**
Days to maturity	rg			0.284**	0.310**	-0.321**	0.419**	-0.192	0.013
	rp			0.095	0.190	-0.272**	0.338**	0.008	0.004
Test weight	rg				-0.039	0.406**	-0.025	0.139	0.672**
	rp				-0.149	0.204*	0.006	0.133	0.282**
Sound mature kernels	rg					0.162	-0.004	0.162	-0.063
	rp					-0.075	-0.036	0.059	-0.111
Shelling percentage	rg						0.191	0.012	-0.488**
	rp						0.052	0.021	-0.324**
Harvest index	rg							-0.033	0.134
	rp							0.011	0.087
Oil content	rg								-0.270*
	rp								0.031

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

advance and percentage genetic advance were also found maximum for test weight. Suneeta *et al*. (2004), Wani *et al*. (2004) and Mahalakshmi *et al*. (2005) reported that 50% flowering, days to maturity, shelling percentage and harvest index could be considered as good traits for yield improvement through agro-morphological diversity study.

Pod yield per plant depicted noticeable relation with days to maturity, test weight, harvest index and protein content during genotypic (r_g) and phenotypic (r_p) correlation coefficient estimation (Table 4). Genetic correlation was found not-significant between days to 50% flowering and shelling percentage with pod yield. Oil content did not reported significant relation with any trait under study while protein content had positive significant relation with pod yield and test weight as well as noteworthy negative relationship with days to 50% flowering and shelling percentage at both genotypic (r_g) and phenotypic (r_p) level. Oil content had negative association with protein content. Suneetha *et al*. (2004), Mahalakshmi *et al*. (2005) and John *et al*. (2009) showed relation between days to 50% flowering with pod per plant while John *et al*. (2008) reported association between shelling out turn with pod yield. Wani *et al*. (2004) indicated bond between days to maturity and harvest index with pod yield. Mahalashmi *et al*. (2005) confirmed oil content association with pod yield.

The path coefficient analysis reported with positively high direct effect of harvest index (0.9515), days to 50% flowering, protein content (0.4693) and test weight (0.2042) on pod yield per plant (Fig. 1). Bera and Das (2000), Suneetha *et al*. (2005); Korat *et al*. (2009), Vekariya *et al*. (2011), Babariya and Dobariya (2012) supported results for harvest index. Khanpara *et al*. (2010) also reported positive direct effect for days to 50% flowering while Zaman *et al*. (2011) testified for days to 50% flowering as well as test weight. Low positive direct effect for oil content is also confirmed by Korat *et al*. (2009). Babariya and Dobariya (2012) found moderately positive relation, contrary to our result for days to maturity.

Dendrogram analysis based upon agro-morphological data showed similarity range of 0.09 to 0.56 (Fig. 2). JL-24 and Kadari-6 showed highest similarity of 56.00% which indicated that genotypes under study still have diverse traits which can be useful for future.

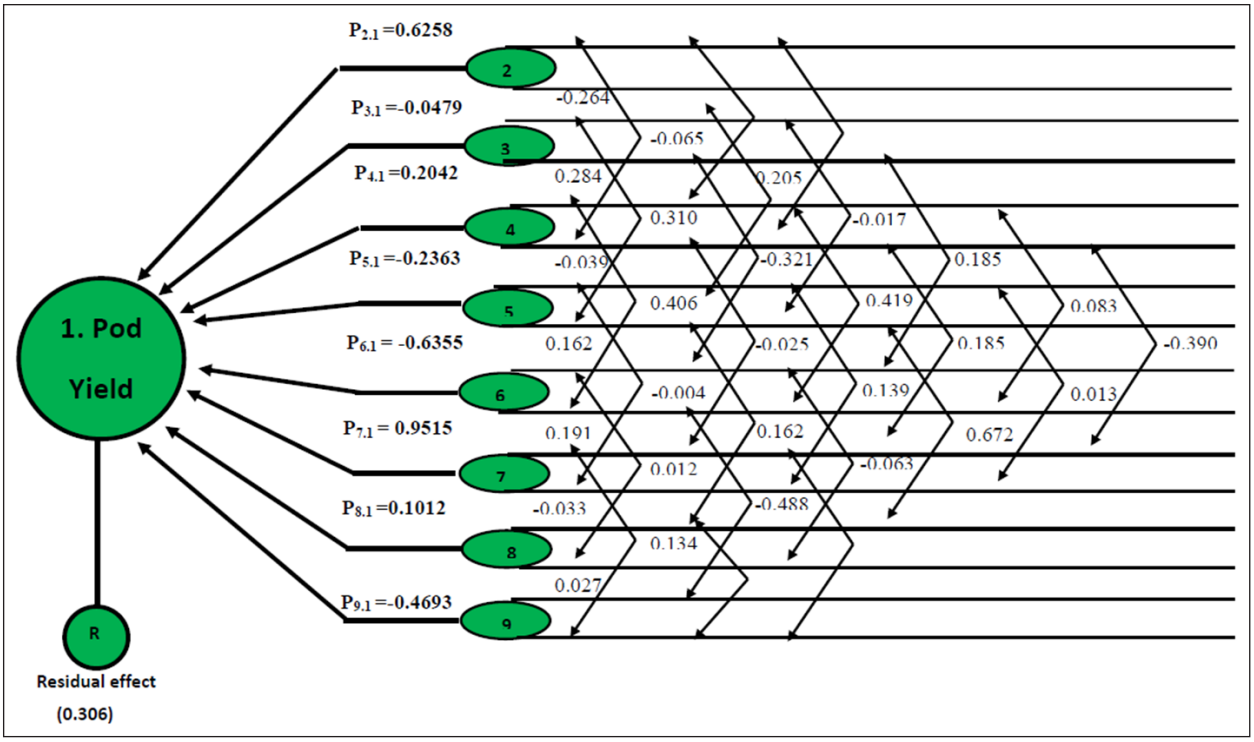

Fig. 1. Diagrammatic representation of genotypic path analysis in groundnut (2. Days to 50% flowering, 3. Days to maturity, 4. Test weight, 5. – Sound mature kernels, 6. Shelling percentage, 7. Harvest index, 8. Oil content and 9. Protein content).

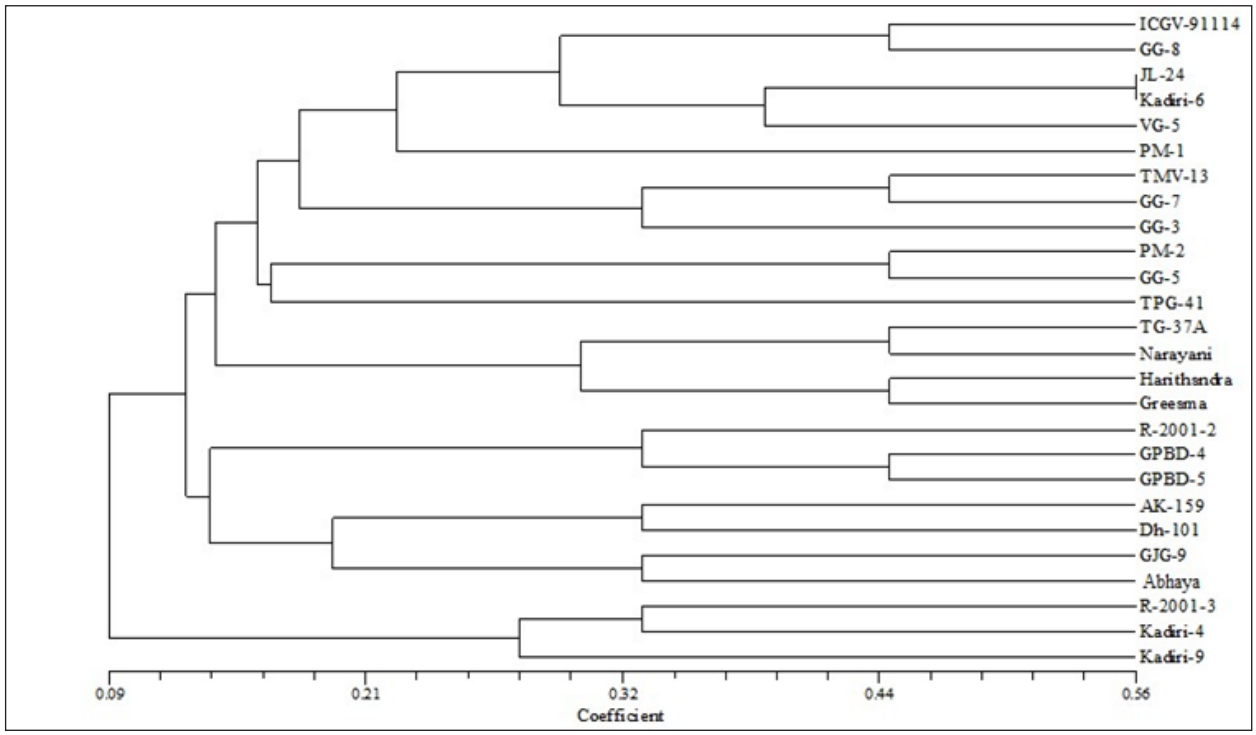

Fig. 2. Dendrogram depicting the genetic relationship among 26 groundnut genotypes based on the quantitative data.

Groundnut is highly self-pollinated crop due to cleistogamous flower which is main reason behind generating narrow genetic base. Many researchers studied agro-morphological traits of groundnut which has variation in seed related characters but these characters are ultimately governed by genetic makeup as well as its performance depend on Genomic x Environmental interaction. Groundnut genotypes having environmentally stable morphological traits with wide variation can be utilized for germplasm improvement that's why these agro-morphological traits of Spanish bunch types were evaluated for variation in this study to finally improve the productivity of groundnut.

During a diversity study based on the agro-morphological trait, all twenty-six genotypes were grouped into two main clusters. Kadiri-4 and Kadiri-9 fall into the same group as Kadari-9 was developed from Kadiri-4. AK-159, Narayani, GG-3, 5, 8 and Kadiri-6 showed similarity with its parent JL-24 as they were part of same group, among which Narayani and GG-3, 5, 8 showed relation at sub-group level while Kadiri-6 indicated highest resemblance. Though genotypes have similarity they also showed behavior difference at the plant-to-plant level depending upon the small genetic variation within it. Mungala *et al*. (2008) reported survival differences between AK-159, GG-3, 5 and JL-24 while Kadiri-6 was found in the same group of JL-24.

Narayani and Kadiri-6 indicated likenesses with each other as both have same pedigree and are cultivated in South Indian climatic conditions. Similarly, GG-3, 5, 7, 8 and GJG-9 were in the same group as they have a common pedigree and are well adopted for cultivation in Saurastra region of Gujarat.

TPG-41 and TG-37A fall in the same group, as both were developed from the parents which were developed through mutation but both had less than 20% agro-morphological similarity showing good variation at performance level. R-2001-2 and R-2001-3 also represented similar patterns as both have the same pedigree and were developed at Raichur but were found in different clusters. Swamya *et al*. (2003) conducted study on subsp. *fastigiata* and *hypogaea* during different seasons and location in India concluded that genotype performance depends upon interaction of trait with seasons and location as well as closely related genotypes performance also variety according to genotype x location interaction.

ICGV-91114 and JL-24 have drought-tolerant capacity and were developed at ICRISAT, Hyderabad but didnot show any genetic similarity but were grouped into same sub-cluster during quantitative data analysis. Pratap Mungphali-1 and 2 showed relatedness of less than 20% by grouping at agro-morphological diversity analysis. Both these genotypes have almost similar traits for qualitative and quantitative traits. Suneetha *et al*. (2015) also reported that Narayani and Tirupati 4 have similar parents JL-24 x Ah316/S but didn't show good genetic similarity. These could occur due to contribution of different genetic material as well as recombination differences in parents during the breeding program. Selection pressure also act as one key factor during variety development.

TMV-13 and VG-5 both are cultivated in the Coimbatore region of Tamil Nadu having red testa reported with good variation at both agro-morphological traits and molecular analysis. GPBD-5 has one of its parents as GPBD-4 which was found in the same cluster as per quantitative data analysis. Dh-101 also developed from Dharwad showed high genetic diversity from GPBD-4 and 5.

Assessment of agro-morphological traits and genetic diversity together provide better insight for the selection of parents with different genetic backgrounds or for creating a larger genetic base for a breeding program of groundnut improvement else gene additive effect will only be observed with the involvement of closely related genotypes (Isleib and Wynne, 1983; Upadhyaya, 2005). Genetically and agro-morphologically diverse parents improve the dominancy of the desired trait which can be increased and improved further by repeatedly being involved in the breeding program. It is also observed that 0.2 to 6.6% cross-pollination happening within the population also offers an opportunity for selecting a natural recombinant genotype for the desired trait (Idi *et al*., 2015).

Conclusions

Despite being from the same region and having common parents in its pedigree, the groundnut germplasm under study had good agro-morphological variation. Additionally, the availability of genetic variability up to 60% is good enough to be used in upcoming breeding programs. The findings also imply that early study of groundnut germplasm aids in understanding how genotype behavior changes in response to location interaction, individual diversity, and spontaneous evolution, all of which are crucial for maintaining the gene pool.

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