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MULTIVARIATE SELECTION OF GROUNDNUT (*ARACHIS HYPOGAEA* L.) ADVANCE BREEDING LINES FOR IN SITU GERMINATION TOLERANCE AND SUPERIOR AGRONOMIC PERFORMANCE

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ABSTRACT
In situ germination of mature groundnut seeds at harvest is an important problem that can reduce seed quality and affect market value, particularly when rainfall occurs during harvesting. The present study was conducted to identify promising breeding lines that are tolerant to in situ germination with good yield and suitable maturity, and to examine the usefulness of different multi-trait selection approaches. Eighteen advanced breeding lines and five checks were evaluated in a randomized complete block design during *kharif* 2023–24 at Dharwad, Karnataka. Significant variation was observed among the genotypes for all traits studied. In situ germination showed high heritability (93.21%) along with high genetic advance, indicating good potential for selection. It was negatively associated with days to 50% flowering (r = −0.59) and days to maturity (r = −0.43) and was non-significantly associated with other agronomic traits. The first two principal components accounted for 58.1% of the total variation, with yield-related and phenological traits contributing substantially to genotype differentiation. Six selection indices ranked different breeding lines, however, DBG 22, DBG 20, GND 16 and R20019 × GPBD 6-1 were repeatedly selected by several indices. Overall, the identified breeding lines and multi-trait selection approaches provide useful resources for breeding groundnut cultivars with improved in situ germination tolerance while maintaining desirable yield and maturity, thereby supporting the development of cultivars better suited to harvest-period rainfall conditions.

KEYWORDS: Genetic variability; Groundnut; In situ germination; multi-trait selection; Selection indices;

INTRODUCTION
Groundnut (*Arachis hypogaea* L.), also known as Peanut, belongs to the genus *Arachis* and family *Leguminosae.* It is cultivated in over 100 countries with commercial cultivation between latitudes 40° N and 40° S. The term "*Arachis"* is derived from Greek word 'A*rachos*', meaning 'a weed' and *hypogaea*, meaning 'underground chamber', *i.e.* a weed with fruits produced below the soil surface. The domesticated groundnut originated in the region of southern Bolivia and northwestern Argentina on the eastern slopes of the Andes (1). It is a segmental allotetraploid (2n=4x=40) with A and B genome contributed by *A.duranensis* and *A.ipaensis* (2). Based on the patterns of reproductive and vegetative branching and on the pod morphology, the cultivated species is divided into two cultivated subspecies namely is *A. hypogaea* subsp. *hypogaea* and *A. hypogaea s*ubsp. *fastigata* (3). The subspecies are further divided into four botanical varieties. The subsp. *hypogaea* is divided into *hypogaea* (Virginia) and *hirsuta*, while the subsp.*fastigiata* is divided into *fastigiata* (Valencia), *vulgaris* (Spanish), *peruviana* and *aequatoriana* (4)
Groundnut is an important oilseed crop cultivated widely across tropical and subtropical regions. During 2025–26, global groundnut production is estimated at approximately 51.7 million tonnes, with China remaining the leading producer at about 19.0 million tonnes (5). India is also one of the major groundnut-producing countries, with production estimated at approximately 13.1 million tonnes during 2025–26 (6). Groundnut continues to occupy an important position in India's oilseed sector and is cultivated extensively across several states, including Gujarat, Rajasthan, Madhya Pradesh, Tamil Nadu, Andhra Pradesh and Karnataka (7).
Climate change is considered a major problem for the future. It has already reduced Groundnut productivity and quality significantly in some areas due to increased incidence of high temperature, drought stress and unpredictable rainfall at critical growth stages such as flowering and seed development (8). In situ germination is one of the major widespread constraints affecting Groundnut yield and quality due to climate change scenario (9). In situ germination of freshly matured seeds at a time of harvesting is one of such potential constraint limiting the production as well as end use quality of Groundnut kernels (10:11). Generally,Virginia genotypes are late-maturing with seeds exhibiting high tolerance, whereas the Spanish and Valencia types exhibit shorter maturity duration and less tolerance to in situ germination. In India, Groundnut is cultivated mainly in the *kharif*, *rabi* and

summer seasons. To fit Groundnut in these cropping seasons, short duration i.e early maturing cultivars are required. Presence of 2–3 weeks of fresh seed dormancy leading to tolerance for in situ germination in the early-maturing releasing groundnut cultivars is desirable in order to overcome this problem.

Although earlier studies have reported variation in in situ germination and its relationship with seed dormancy and maturity in groundnut, identifying breeding lines that combine low in situ germination with good yield and suitable maturity remains a challenge. This is particularly important for early-maturing groundnut, where shorter crop duration is desirable but may also be associated with reduced seed dormancy. In addition, most selection decisions are based on individual traits or a single selection criterion, which may not adequately capture the overall performance of a genotype for several important traits. Therefore, evaluating different multi-trait selection indices and identifying breeding lines that are consistently selected across these approaches could provide useful information for groundnut improvement.

Considering these aspects, the present study was undertaken to (i) assess the genetic variability and heritability of in situ germination and associated agronomic traits in advanced groundnut breeding lines; (ii) examine the relationships between in situ germination, phenological and yield-related traits; (iii) understand the contribution of these traits to the overall variation among the breeding lines using principal component analysis; and (iv) compare different multi-trait selection indices to identify breeding lines with a desirable combination of reduced in situ germination, good yield and suitable maturity.

Experimental material and design

Experimental area

The present investigation was carried out at the All India Coordinated Research Project on Groundnut, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad which is located at 15° 29' North latitude, 74° East longitude and an altitude of 750 m above the Mean Sea Level (MSL) and in North-Western transitional agro-climatic zone of Karnataka.

Agricultural treatments

Eighteen advanced breeding lines along with five checks (TMV-2, JL-24, Dh257, Dh86 and Dh8) were evaluated for in situ germination in a randomized complete block design (RCBD) with two replications during August 21 *Kharif* 2023–24 and harvesting was completed by third week of December. Total 99.4 mm Rainfall and temperature ranging from 18.5°C to 31.5°C has been recorded during studies. Each genotype was grown in two rows of 1 m length with a spacing of 30 (row to row) × 10 cm(plant to plant). The experimental field was prepared by thorough ploughing and leveling to obtain a fine tilth. Sowing was carried out manually, and 20 kg nitrogen, 40 kg phosphorus and 30 kg of potassium was applied. Timely intercultural operations, including hand weeding and hoeing, were undertaken to maintain a weed-free environment. Need based plant protection measures were adopted to control insect pests and diseases. The crop was raised under irrigated conditions following the recommended package of practices to ensure optimum crop growth until maturity.

Data acquisition

Observations on five randomly selected plants from each genotype in each replication were recorded for 10 characters *viz.,* Days to 50% flowering , In situ germination (%), Pod yield per plant (g/plant) , Pod yield per hectare (kg / ha) , kernel yield per plant (g / plant) , Kernel yield per hectare (kg/ha), 100 kernel weight (g), Shelling percentage (%), Sound mature kernel, Days to maturity.

Once the genotypes reached maturity, they were irrigated, and the in situ germination percentage (IGP) was recorded. In-situ germination (%) was calculated in field leaving crop upto four weeks after the physiological maturity. Due to absence of rain, manual irrigation was provided to induce in situ germination. Method and scoring scale for in situ germination (IGS) , ranging from 1 to 5, was applied based on the IGP, as outlined by Motagi et al. (2020) (12). Scale 1 represents 0–10% IGP, scale 2 corresponds to 11–20 %, scale 3 to 21–30 %, scale 4 to 31–40 %, and scale 5 indicates > 41 % IGP.

Multivariate analysis

Data obtained from the RCBD experiment were subjected to analysis of variance (ANOVA) to assess the significance of genotypic differences.The model was

$$Y_{ij} = \mu + G_i + R_j + \varepsilon_{ij}$$

where (Y_{ij}) denotes the observation of the (i^{th}) genotype in the (j^{th}) replication; (μ) denotes the overall mean; (G_i) represents the genotype effect; (R_j) represents the replication effect; and (ε_{ij}) represents the random error associated with the observation. The significance of genotype effects was tested against the experimental error mean square.

The genotypic and phenotypic variances were claculated as per the formulae given by Burton and Devane (1953) (13).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{Mean sum of squares due to treatments} - \text{Mean sum of squares due to error}}{\text{Number of replications}}$$

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

$\sigma^2 p$ = Phenotypc variance

$\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Error variance

Both phenotypic and genotypic coefficient of variability for all the characters were estimated using the formula Burton and Devane (1953) (13).
Genotypic coefficient of variability (GCV)

$$GCV\ (\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Phenotypic coefficient of variability (PCV):

$$PCV\ (\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Where,

σ_g = Genotypic variance

σ_p = Phenotypic variance

$\bar{X}$ = General mean of the characters

Heritability in broad sense will be estimated for all the characters as the ratio of genotypic variance to phenotypic variance expressed in per cent as suggested by Lush (1949) (14) and Hanson *et al*. (1956) (15)

Broad sense heritability ($h^{2)}$ = $\sigma g / \sigma_p$ x 100

σ_g = Genotypic variance

σ_p = Phenotypic variance

The extent of genetic advance that can be expected with five percent selection intensity was calculated.
Genetic advance = $i\ h^2_{bs}\ \sigma_p$
Where,
i = coefficient of selection which is 2.06 at 5% selection intensity
σp = Phenotypic standard deviation
h^2 = heritability in broad sense

Pearson's correlation coefficients among traits were computed in R, and the resulting correlation matrix was visualized using the "corrplot" package. Principal component analysis (PCA) was performed at replicated level plot values using the FactoMineR package in R (version 4.3.1). Prior to analysis, all quantitative variables were centered and standardized to unit variance (scale.unit = TRUE) to account for differences in measurement scales among traits. PCA was conducted using the correlation matrix, and the resulting principal components were visualized using the factoextra package. The first two principal components, which together explained 58.1 % of the total variation, were used for interpretation of trait associations and genotype relationships

Six multi-trait selection indices, namely Smith–Hazel, Pesek–Baker, Mulamba and Mock, Elston, Multiplicative Index, and Multi-trait Genotype–Ideotype Distance Index (MGIDI), were computed to identify superior breeding lines combining reduced in situ germination, high productivity, and early maturity. The genotypes selected across indices was summarized to assess the level of agreement among selection methods and visualized using a binary heat map. All statistical analyses were performed in R software (version 4.3.1; R Core Team, Vienna, Austria) using appropriate packages, including metan, agricolae, psych, dplyr, tidyr, ggplot2, and Complexheatmap, together with custom R scripts wherever required.

RESULTS

Genetic variability among advanced breeding lines

Analysis of variance revealed significant differences at significance level of $P < 0.05$, among the advanced breeding lines for all the traits evaluated, indicating the presence of considerable variation within the experimental material (Table 1). In situ germination exhibited the widest range, varying from complete absence of germination (0%) in DBG 21 and DBG 22 to 86.66% in GPBD 4 × ICGVO86031, with an overall mean of 35.17%. The trait also recorded high genotypic (71.03%) and phenotypic (73.58%) coefficients of variation together with high heritability (93.21%), reflecting substantial variation among the breeding lines (Table 2). Days to 50% flowering varied from 31 to 37 days, with R2001 × GPBD 5 flowering earliest, while DBG 16 and DBG 20 required the longest duration. Although heritability was high (90.87%), the low GCV, PCV and genetic advance indicated comparatively limited variation for this trait. Days to maturity ranged from 110 to 120 days and similarly exhibited high heritability (83.57%) but relatively low genetic advance. Considerable variation was also observed for the productivity traits. Pod yield per plant ranged from 10.14 to 18.80 g, whereas kernel yield per plant varied between 6.42 and 12.28 g. Pod yield per hectare ranged from 3379.99 to 6266.66 kg ha^{-1}, while kernel yield per hectare varied from 2141.09 to 4091.66 kg ha^{-1}. These traits were characterized by moderate variability associated with high heritability and genetic advance. In contrast, shelling percentage and sound mature kernel exhibited comparatively lower variability, whereas 100-kernel weight showed moderate genetic advance.

Based on the in situ germination response, R20019 × GPBD 6-1, DBG 16, and DBG 22 were classified as highly tolerant (Scale 1), while GND 7 and GND 16 exhibited a Scale 2 reaction. None of the breeding lines fell into the susceptible (Scale 4) category. Conversely, TG76 × SUNOLEIC 95 R, ICGV 07214 × ICGV 2207-2, DBG 21, GND 1, Dh 256 × G6000-2, DBG 18, GPBD 5 × GPBD 6, GPBD 5 × GPBD 4-1, ICGV2266 × Dh245-1, and

GPBD 4 × ICGVO86031 recorded comparatively higher levels of in situ germination. All the tolerant breeding lines studied were matured within 120 days.

Trait association

Pearson's correlation analysis revealed significant associations among in situ germination, phenological traits, and yield-related traits (Fig.1). The yield-related traits showed predominantly positive associations with one another. 100-kernel weight was positively correlated with KYP ($r = 0.39$), KYH ($r = 0.40$), PYP ($r = 0.35$) and PYH ($r = 0.33$). Strong positive correlations were observed among KYP, KYH, PYP, PYH with correlation coefficients ranging from 0.89 to 1.00, reflecting the close relationship among these yield components. Shelling percentage also showed positive correlations with KYP ($r = 0.30$) and KYPH ($r = 0.32$). In contrast, in situ germination showed significant negative associations with DM ($r = -0.43$) and DFF ($r = -0.59$), indicating that genotypes with higher in situ germination tended to flower and mature earlier. DFF was also negatively correlated with SMK ($r = -0.32$). Most of the remaining trait combinations showed weak and non-significant correlations. Overall, the correlation pattern indicated that higher in situ germination was associated with earlier phenological development, while the major yield related traits were positively associated with each other.

Principal component analysis

Principal component analysis (PCA) was performed to better understand the pattern of variation among the groundnut genotypes based on the traits evaluated. Eigen values and trait loadings are mentioned in Table 3 The first two principal components together explained 58.1% of the total variation, with PC1 contributing 40.3% and PC2 contributing 17.8% (Fig. 2). This indicates that a considerable proportion of the variation in the dataset could be represented by the first two components. The biplot showed a clear grouping of the yield-related traits PYP, PYH, KYP and KYH, with their vectors pointing in a similar direction. This pattern indicates that these traits were closely associated and tended to vary together among the genotypes. DFF and DM were also closely positioned, with both contributing strongly to PC2, suggesting a close relationship between these two phenological traits. In contrast, IGP was oriented in the opposite direction to DFF and DM, indicating that genotypes differing in in situ germination also tended to differ in these phenological traits. SMK showed a distinct orientation towards the positive side of both PC1 and PC2, separating it from the major group of yield-related traits. 100KW was positioned close to the centre of the biplot, indicating that it had a relatively smaller contribution to the variation represented by the first two principal components. The genotypes were distributed across different regions of the biplot, reflecting the presence of considerable phenotypic diversity in the material studied.

Selection of superior genotypes using different selection indices

To identify breeding lines combining high productivity, reduced in situ germination, and early maturity, six multi-trait selection indices were evaluated. Although all indices were applied to achieve the same breeding objective, noticeable differences were observed in genotype rankings, reflecting variation in the breeding lines prioritized by each selection method. The Smith–Hazel index ranked GPBD 5 × GPBD 4-1 as the most desirable genotype, followed by DBG 21 and GND 16. In contrast, the Pesek–Baker index identified GND 16, DBG 22, and ICGV2266 × Dh245-1 as the top-ranked breeding lines. Both the Multiplicative Index and MGIDI ranked DBG 20 first, whereas the Mulamba and Mock and Elston indices identified DBG 22 as the highest-ranking genotype. Despite the differences in individual rankings, several breeding lines were repeatedly identified across different selection methods. DBG 20, DBG 22, GND 16, GPBD 5 × GPBD 4-1, and R20019 × GPBD 6-1 appeared among the top selections of more than one index (Figure 3), whereas a number of breeding lines were unique to individual indices. This variation in genotype ranking demonstrates that the six selection methods differed in the breeding lines they prioritized, even though they were evaluated for the same set of target traits.

Various genotypes selected across different selection indices

The extent of agreement among the six selection indices was assessed based on the frequency with which breeding lines were selected among the top-ranked genotypes (Table 4). Considerable variation was observed in the frequency of selection, indicating differences in the breeding lines identified by each index. Among the evaluated breeding lines, DBG 22 showed the highest level of agreement, being selected by five of the six indices. DBG 20, JL 24, GND 16, and R20019 × GPBD 6-1 were each selected by four indices, while Dh 257, GPBD 5 × GPBD 4-1, and ICGV2266 × Dh245-1 were identified by three indices. GPBD 5 × GPBD 6, GPBD 4 × ICGVO86031, DBG 16, Dh 256 × G6000-2, and TMV 2 were selected by two indices, whereas the remaining breeding lines were identified by only a single selection method. The frequency distribution clearly distinguished breeding lines that were consistently selected across multiple indices from those identified by only one or two methods, demonstrating differences in the level of agreement among the evaluated selection procedures.

DISCUSSION

Among the traits evaluated, in situ germination exhibited high heritability together with high genetic advance, suggesting that the observed variation was largely heritable and can be effectively utilized through phenotypic selection. The narrow difference between GCV and PCV further indicates that environmental influence on this trait was comparatively low under the experimental conditions. Similar findings have been reported by Vijayabharathi & Savithramma (16) in Groundnut, where traits with high heritability and genetic advance responded effectively to selection. The relationship between high heritability and high genetic advance has long been recognized as an indicator of additive gene action and improved response to selection (17). In contrast, flowering and maturity traits exhibited high heritability but relatively low genetic advance. This combination

suggests that, although these traits were expressed consistently across the breeding lines, the expected improvement through direct selection may be comparatively limited (18). Similar trends have been reported in Groundnut, where phenological traits generally exhibit narrower variability than yield-related characters (19).Pod yield and kernel yield, however, expressed favourable levels of heritable variation, indicating that improvement in productivity can be achieved without compromising the selection for in situ germination tolerance. The high heritability and genetic advance observed for in situ germination therefore suggest that this trait can be effectively considered during selection, while yield and maturity should be evaluated alongside it to ensure that improvement in one trait does not compromise overall agronomic performance.

The correlation analysis revealed several important relationships among the studied traits. Pod yield and kernel yield traits showed strong positive associations, particularly between PYP, PYH, KYP and KYH ($r = 0.89$), indicating that improvement in one yield component could favourably influence the others (20). Hundred-kernel weight was also positively associated with the major yield traits, suggesting its contribution to productivity. In contrast, IG% showed significant negative correlations with DFF ($r = -0.59$) and DM ($r = -0.43$), indicating that higher germination was associated with shorter flowering and maturity duration. These relationships provide useful guidance for simultaneous selection of yield and germination-related traits in groundnut breeding. This relationship is important from a breeding perspective because early maturity is desirable for fitting groundnut into different cropping systems, whereas some degree of seed dormancy is desirable to prevent germination before harvest. The negative association observed in the present study suggests that selecting only for early maturity may not be sufficient when the objective is also to reduce in situ germination. However, the association was not strong enough to suggest that maturity alone could be used to predict in situ germination behaviour. Therefore, both traits need to be considered together during selection.

The PCA results highlight the presence of considerable variation among the groundnut genotypes for the traits studied. The close grouping of PYP, PYH, KYP and KYH suggests that these yield-related traits were strongly associated and may be improved together through selection. Similarly, the close association between DFF and DM indicates that flowering and maturity duration contributed considerably to the observed differences among genotypes (21). The contrasting position of IG% suggests that germination behaviour may vary independently of these phenological traits. Overall, the PCA effectively summarized the major sources of variation and identified important traits contributing to genotype differentiation, which can help in selecting diverse and promising material for groundnut improvement.The PCA therefore provided a broader view of the relationships among the traits and supported the correlation results. The separation of IG% from the major yield-related traits suggests that variation in in situ germination was not closely linked with productivity traits in the material studied. This is useful from a breeding standpoint, as it indicates that selection for reduced in situ germination may be possible without necessarily sacrificing yield performance.

The identification of breeding lines combining low in situ germination with desirable agronomic performance indicates useful variation for simultaneous improvement of these traits. Although the six selection indices were based on the same breeding objective, they differed in the lines ranked as superior because each method combines trait information differently. For instance, GPBD 5 × GPBD 4-1 ranked first under the Smith–Hazel index, reflecting its strong yield performance, whereas DBG 22 and GND 16 were favoured by other approaches that placed greater emphasis on balanced performance across traits. Such differences among selection indices are expected and have also been reported in other crop improvement programmes (22). The repeated identification of these lines is important because the breeding objective involved several traits that need to be improved together. A genotype performing well for only one trait may not necessarily be suitable for the overall breeding objective, whereas lines identified by several indices showed a more consistent combination of the target traits. Thus, the agreement among the indices provides useful support for prioritizing these lines for further evaluation.

The contrasting selection patterns can be related to the principles underlying each index. Smith–Hazel and Pesek–Baker use different approaches for defining the desired response, whereas Mulamba–Mock, Elston and the Multiplicative Index favour genotypes with relatively balanced performance across the traits considered. MGIDI differs by identifying genotypes according to their closeness to a predefined ideotype, thereby considering the overall combination of traits rather than individual characters. Despite these differences, several breeding lines were repeatedly identified. DBG 22, DBG 20, GND 16, JL 24 and R20019 × GPBD 6-1 were selected by multiple indices, indicating consistent selection across different approaches.

Agreement among selection methods provides greater confidence when identifying breeding material for complex breeding objectives. Genotypes selected by several indices are more likely to possess favourable combinations of traits rather than exceptional performance for only one character (23,24,25). In the present study, the consistently selected breeding lines combined reduced in situ germination with acceptable productivity and maturity, making them promising candidates for further multilocation and seasonal evaluation. Following validation across environments, these lines could serve as useful breeding material or potential parents for developing groundnut cultivars with improved tolerance to in situ germination while maintaining yield. It should be noted, however, that selection by several indices represents agreement among selection methods and should not be interpreted as evidence of stability across environments. Since the present study was conducted at one location and in one season, further evaluation across seasons and locations will be necessary to confirm the consistency of in situ germination tolerance, yield and maturity in these lines.

CONCLUSION

The advanced Groundnut breeding lines evaluated in this study exhibited sufficient genetic variability for in situ germination, yield and related traits, providing opportunities for simultaneous improvement of these characters. The comparison of six multi-trait selection indices showed that genotype rankings varied among methods, reflecting differences in the way each index balanced productivity, maturity and in situ germination tolerance. These findings emphasize that the choice of selection index can influence the identification of superior breeding lines when multiple traits are considered together. Despite these differences, DBG 22, DBG 20, GND 16, JL 24 and R20019 × GPBD 6-1 were consistently identified by several independent indices, indicating their stable overall performance across the target traits. The repeated selection of these breeding lines suggests that they possess a desirable balance between reduced in situ germination, competitive yield and acceptable maturity, making them valuable candidates for further evaluation. Rather than favouring a single selection method, the present results demonstrate the advantage of combining classical and modern selection indices to support breeding decisions. Using multiple indices allowed greater confidence in identifying breeding lines with consistent performance and reduced the likelihood of selecting genotypes based on the preference of a single analytical approach. Current study included only one environment and two replication since it is preliminary study for identifying tolerant lines. The consensus breeding lines identified in this study should be validated across locations and seasons before their utilization as potential cultivars or as parents in Groundnut improvement programmes aimed at enhancing in situ germination tolerance while maintaining productivity.

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Tables

Table 1 : Analysis of variance for ten quantitative characters in advanced breeding lines of Groundnut

Source of variation	df	IG%	DFF	PYP (g)	KYP (g)	SP	100KW (g)	SMK	PYH (kg/ha)	KYH (kg/ha)	DM
Replication	1	435.80	1.45	15.38	0.03	0.78	7.11	8.20	1381.94	2270.86	2.27
Treatments	22	1293.64**	4.60**	18.41**	3.89**	18.19**	22.90**	10.92**	1069126.37**	448379.36**	8.94**
Error	22	45.47	0.22	14.21	1.02	6.03	3.61	4.68	244313.90	110876.24	0.80
CV (%)		19.17	1.38	10.18	10.84	3.88	5.52	2.27	10.09	10.75	1.73

*- significance at 5% probability level ** P - significance at 1% probability level

IG % = In-situ germination percentage, **DFF** = Days to fifty percent flowering, **PYP** = Pod yield per plant, **KYP**= Kernel yield per plant,
SP = Shelling percentage, **100 KW**= 100 kernel weight, **SMK** = Sound mature kernel, **PYH** = Pod yield per hectare, **KYH** = Kernel yield per hectare, **DM** = Days to maturity

Table 2: Genetic variability parameters for in-situ germination and other productivity traits in advance breeding lines of groundnut

Character	Min	Max	Mean	σ^2g	σ^2p	GCV (%)	PCV (%)	h^2bs (%)	GA	GAM (%)
IG%	0.00	86.66	35.17	624.09	669.56	71.03	73.58	93.21	49.68	141.27
DFF	31	37	34.16	2.19	2.41	4.33	4.54	90.87	2.91	8.51
PYP (g)	10.14	18.80	14.70	2.10	16.31	9.86	27.48	12.88	1.07	7.29
KYP (g)	6.42	12.28	9.29	1.44	2.46	12.89	16.87	58.45	1.89	20.31
SP (%)	54.61	69.11	63.32	6.08	12.11	3.89	5.50	50.21	3.60	5.68
100KW (g)	27.45	47.69	34.45	9.65	13.26	9.01	10.57	72.76	5.46	15.84
SMK (%)	88.00	100.00	95.16	3.12	7.80	1.86	2.93	40.00	2.30	2.42
PYH (kg/ha)	3379.99	6266.66	4898.48	412406.24	656720.14	13.11	16.54	62.80	1048.34	21.40
KYH (kg/ha)	2141.09	4091.66	3098.65	168751.56	279627.80	13.26	17.07	60.35	657.39	21.22
DM	110	120	114.27	4.07	4.87	1.77	1.93	83.57	3.80	3.32

IG% = In-situ germination percentage, **DFF** = Days to fifty percent flowering, **PYP** = Pod yield per plant, **KYP**= Kernel yield per plant, **100KW**= 100 kernel weight, **DM** = Days to maturity, **SP** = Shelling percentage, **SMK** = Sound mature kernel, **PYH** = Pod yield per hectare, **KYH** = Kernel yield per hectare

Table 3: Eigenvectors and trait loadings of the first four principal components for in situ germination and other traits in advanced breeding lines of groundnut

Trait	PC1		PC2		PC3		PC4	
	Eigenvector	Trait Loadings	Eigenvector	Trait Loadings	Eigenvector	Trait Loadings	Eigenvector	Trait Loadings
IG	0.203	0.412	0.286	0.337	0.024	0.026	−0.493	−0.527
DFF	0.051	0.104	0.457	0.540	0.408	0.446	0.455	0.487
PYP	0.479	0.972	−0.167	−0.197	0.080	0.087	−0.031	−0.033
KYP	0.486	0.987	−0.033	−0.039	−0.045	−0.049	0.121	0.130
SP	0.087	0.176	0.432	0.509	−0.448	−0.490	0.495	0.530

Trait	PC1		PC2		PC3		PC4	
	Eigenvector	Trait Loadings	Eigenvector	Trait Loadings	Eigenvector	Trait Loadings	Eigenvector	Trait Loadings
HSW	0.012	0.024	0.218	0.257	0.744	0.813	−0.087	−0.093
SMK	−0.112	−0.228	−0.553	−0.652	0.119	0.131	0.193	0.206
PYH	0.476	0.966	−0.188	−0.222	0.084	0.092	−0.016	−0.018
KYH	0.485	0.985	−0.058	−0.068	−0.037	−0.041	0.133	0.142
DM	−0.093	−0.189	−0.320	−0.378	0.218	0.239	0.475	0.508

IG = In situ germination, DFF = Days to fifty percent flowering, PYP = Pod yield per plant, KYP = Kernel yield per plant, SP = Shelling percentage, HSW = Hundred seed weight, SMK = Sound mature kernel, PYH = Pod yield per hectare, KYH = Kernel yield per hectare, DM = Days to maturity.

Table 4 : Various advance breeding Lines selected in each selection indices

lines selected in each selection indices						
Rank	**SH**	**PB**	**MI**	**MMI**	**EI**	**MGIDI**
1	GPBD 5 × GPBD 4-1	GND 16	DBG20	DBG 22	DBG 22	DBG20
2	DBG 21	DBG 22	DBG 22	GPBD 5 X GPBD 4-1	JL 24	R20019 X GPBD -6
3	GND 16	ICGV2266 X Dh245-1	DBG 16	JL 24	DBG20	Dh 86
4	Dh 256 × G6000-2	Dh 256 X G6000-2	JL 24	ICGV 07214 X ICGV 2207-2	DBG 16	GPBD 5 X GPBD 4-1
5	ICGV2266 × Dh245-1	R20019 X GPBD -6	Dh257	ICGV2266 X Dh245-1	Dh257	GND 16
6	JL 24	DBG 18	R20019 X GPBD -6	GND1	R20019 X GPBD -6	TMV 2
7	DBG 22	GPBD 5 X GPBD6	DBG 12 mutant	DBG 21	TMV 2	GPBD 4 X ICGVO86031
8	GPBD 5 × GPBD 6	GPBD 4 X ICGVO86031	GND 16	DBG20	GND7	Dh257

SH - Smith and Hazel, PB- Pesek and Beker, MI - Subandi et al. Multiplicative Index, MMI, Mulamba and Mock Index, EI - Elston Index, MGIDI - Genotype– Ideotype distance Index

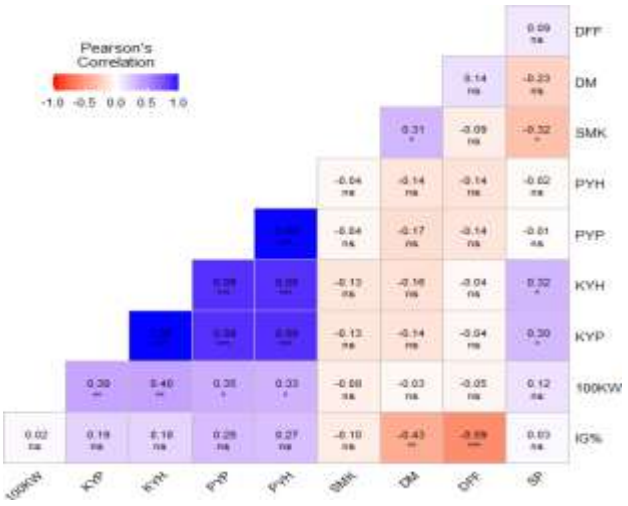

Fig 1. Correlation plot for various characters in advance breeding lines of groundnut

*- significance at 5% probability level ** P - significance at 1% probability level
(IGP = In-situ germination, DFF = Days to fifty percent flowering, PYP = Pod yield per plant, KYP= Kernel yield per plant, 100 KW= Test weight, DM = Days to maturity, SP = Shelling percentage, SMK = Sound mature kernel, PYH = Pod yield per hectare, KYH = Kernel yield per hectare)

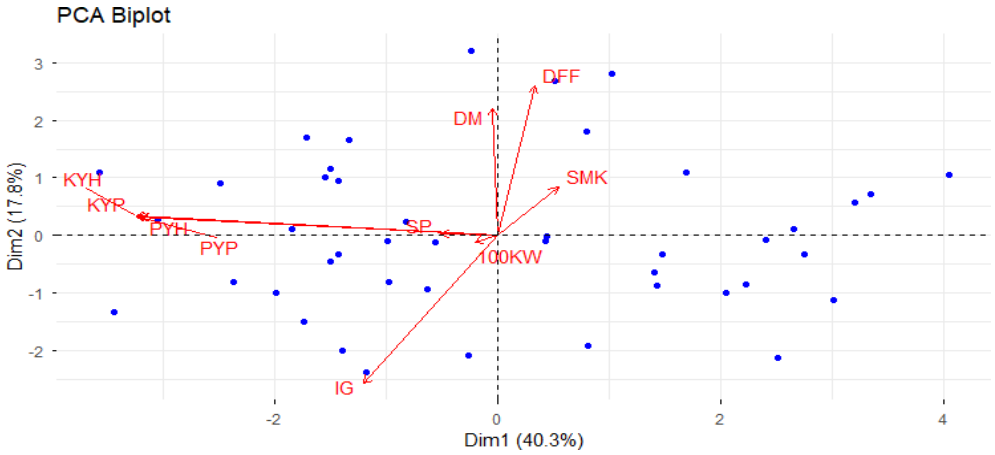

Fig. 2 Principal component analysis (PCA) of agronomic traits associated with in situ germination in Groundnut which depicts the contribution and relationships among the measured traits.

IGP = In-situ germination, DFF = Days to fifty percent flowering, PYP = Pod yield per plant, KYP= Kernel yield per plant, 100 KW= Test weight, DM = Days to maturity, SP = Shelling percentage, SMK = Sound mature kernel, PYH = Pod yield per hectare, KYH = Kernel yield per hectare

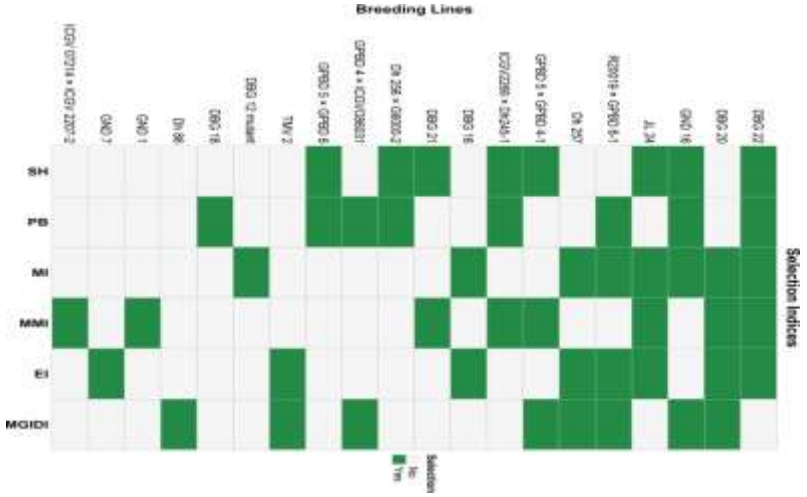

Figure 3. Binary heatmap showing the selection pattern of advanced Groundnut breeding lines across six multi-trait selection indices.
SH - Smith and Hazel, PB- Pesek and Beker, MI - Subandi et al. Multiplicative Index, MMI, Mulamba and Mock Index, EI - Elston Index, MGIDI - Genotype– Ideotype distance Index. Green cells indicate that a breeding line was selected among the top eight by the corresponding selection index, whereas grey cells indicate that it was not selected. Breeding lines are arranged according to their frequency of selection across indices, highlighting consensus and index-specific selections.