



GENETIC ANALYSIS OF SEED SIZE AND SEED RELATED TRAITS IN SELECTED GROUNDNUT (*Arachis hypogaea* L.) GENOTYPES

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ABSTRACT

Breeding groundnut genotypes with larger seed size enhances consumer appeal. This study investigated the genetic variability, inheritance, and relationships of seed size and yield-related traits in *Arachis hypogaea* L. using a five-parameter genetic model and correlation analysis. Two crosses, ICGV 188105 × Samnut 24 (Cross 1) and its reciprocal (Cross 2), were evaluated to F₃ generations at Institute for Agricultural Research (IAR), Samaru, during the 2021/2022 season. Significant variation was observed for seed size (SS1.506 mm), seed length (SL; 11.187 mm), seed width (SW; 7.409 mm), pod length (PL; 26.978 mm), hundred seed weight (100-SW; 42.705 g), and hundred pod weight (100-PW; 93.238 g). High broad-sense heritability ($H^2 > 70\%$) and moderate to high phenotypic (PCV: 6.33%–38.36%) and genotypic coefficients of variation (GCV: 5.89%–38.79%) suggest strong potential for genetic improvement, particularly in Cross 2. Additive, dominance, and epistatic effects were significant for seed size and related traits, indicating complex genetic control. Strong positive correlations ($p < 0.001$) were observed between SS and SL ($r = 0.87$ – 0.90), SW ($r = 0.85$ – 0.91), 100-SW ($r = 0.81$ – 0.83), and 100-PW ($r = 0.69$ – 0.93), while flowering time showed weak, non-significant associations. These findings highlight promising opportunities for selecting larger seeds and related traits while allowing independent manipulation of flowering time. We recommend implementing recurrent selection to capitalize on additive effects while maintaining heterozygosity, with Cross 2 showing superior potential for developing varieties with larger seeds and higher yield simultaneously.

Keywords: Correlation, Gene effect, Groundnut, Heritability, Seed size, Yield

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is an important legume in semi-arid and subtropical regions, valued for its high nutritional content, including oil (40–50%), protein (20–50%), and carbohydrates (10–20%) (Votapwa et al., 2024b). In 2023/2024, global groundnut production reached 51.3 million tons, with Nigeria ranking as the third-largest producer, contributing 10% of global supply and 39% of Africa's output (FAS USDA, 2024). Major groundnut-producing regions in Nigeria include the Northwest, Northeast, and Central areas (Ajeigbe et al., 2015). Groundnut plays a crucial role in food security, rural livelihoods, and soil fertility, particularly through nitrogen fixation. High-quality seeds are essential for consumer preferences, particularly in the confectionery market, and for improving yield and competitiveness (Votapwa et al., 2024a). Adoption of improved groundnut varieties (IGVs) has significantly enhanced food security, increasing household levels by 22% and generating ₦48,171.7 (\$133.1) higher gross margins per hectare for adopters (Melesse et al., 2023; Ibrahim et al., 2023). Despite these improvements, Nigeria's groundnut yields remain below their potential due to challenges such as suboptimal seed size and limited access to high-yielding cultivars (Statistical Annex, 2019). Seed size is a critical determinant of pod yield and is influenced by both genetic and environmental factors. While earlier studies suggested single-gene inheritance, recent evidence points to complex genetic interactions governing seed traits (Balaiah et

al., 1977; Guo et al., 2022; Upadhyaya et al., 1992). Advanced tools, including QTL mapping and spectroscopy, have facilitated the enhancement of seed quality and yield (Sun et al., 2022; Eevera et al., 2023; Chinnasamy et al., 2022). QTLs for seed weight and size often show environment-specific effects. For example, qSWB06.3 on chromosome B06 is a stable QTL contributing to phenotypic variance across environments (Camino & Vucinich, 2022). Epistatic QTLs, such as those involving seed maturation proteins and serine-threonine phosphatases, play a significant role in determining seed weight and quality (Joshi et al., 2024). The co-localization of QTLs for pod and kernel traits on chromosomes A05 and B06 highlights the interconnected genetic control of these traits (Fang et al., 2024; Luo et al., 2017).

Efforts to breed varieties with improved seed size—addressing traits like seed length, width, weight, and length-to-width ratio—remain critical for productivity. While research institutions like IAR Samaru have made strides in developing improved groundnut varieties, further studies on genetic variability and inheritance patterns are essential. This study aims to address these gaps, supporting the development of high-yield, large-seeded groundnut varieties to enhance Nigeria's competitiveness in the global market.

MATERIALS AND METHODS

The genetic materials used for the study comprised two groundnut genotypes—one with large seed size and the other

with small seed size—sourced from the groundnut breeding unit of the Institute for Agricultural Research (IAR), Ahmadu Bello University (ABU). The research was conducted at the IAR Research Farm, located in the Northern Guinea Savannah ecological zone of Nigeria (11°11'N, 07°38'E, and 686 m above sea level) (ABU, 2018). Crosses between the two genotypes were conducted using the hybridization procedure of Nigam et al., (1990), with modifications tailored to the IAR protocols. Emasculation of female flower buds occurred early morning before anthesis, followed by pollination with fresh male parent pollen using sterilized forceps. Successful pollinations were tagged for pod development. The resulting F1 seeds were advanced to F2 and F3 generations. Twenty seeds each from the non-segregating generations (P1, P2, and F1) and one hundred seeds each from the segregating generations (F2 and F3) were evaluated at IAR research farms during the 2021/2022 rainy and dry seasons using a randomized complete block design (RCBD) with three replications. Prior to planting, the field was cleared, harrowed, and ridged. Each plot consisted of four ridges spaced 60 cm apart, with plants spaced 10 cm apart within ridges. NPK 15:15:15 fertilizer was applied at the rate of 30 kg/ha two weeks after germination to promote healthy seedling establishment. Weed control was conducted manually, and all other agronomic practices adhered to the recommendations of IAR for optimal groundnut cultivation. At physiological maturity, the plants were harvested manually by pulling the entire plant. The harvested pods from each plot were carefully shelled by hand to obtain seeds. Dry pods and haulms were weighed separately for each plot using a weighing balance, and the weights were recorded on a per-plot basis. This standardized approach ensured consistent data collection across all generations. This process ensured genetic integrity and reliable evaluation of seed size inheritance.

Data Collection Parameters

Data were collected on individual plants based on the following parameters:

- i. Days to 50% flowering: The number of days from sowing to the point when 50% of the plants had flowered was recorded.
- ii. Number of Pods per Plant: The total number of pods per plant in each pot was counted.
- iii. Seed Length (mm): The length of seeds was measured at the longest point using a Vernier caliper.
- iv. Seed Width (mm): The width of seeds was measured at the midpoint using a Vernier caliper.
- v. Seed Size (mm): Seed size was measured using the formula;

$$SS = \frac{\text{Total weight of seeds}}{\text{Number of seeds in sample}} \quad (1)$$

- vi. Pod Width (mm): Mature pods per plant were measured at their widest point using a vernier caliper.
- vii. Pod Length (cm): The length of mature pods per plant was measured using a vernier caliper.
- viii. Hundred Seed Weight (g): The weight of 100 randomly selected, mature, and wrinkle-free seeds was recorded using a Mettler PM16-N weighing balance, model ISC07501.
- ix. Hundred Pod Weight (g): One hundred randomly selected, clean pods were weighed using the same weighing balance.
- x. Shelling Percentage (%): Shelling percentage was calculated as the ratio of seed weight to pod weight, expressed as a percentage:

$$\text{Shelling percentage (\%)} = \frac{\text{seed weight}}{\text{Pod Weight}} \times 100 \quad (2)$$

Statistical Analysis

Statistical analysis was conducted using the SAS software package (SAS, 2009). Reciprocal differences between genotypes were evaluated using a t-test. Mean and variance estimations for individual plant data were performed for each generation, and generation mean analyses were conducted following the procedure outlined by Singh and Chaudhary (1985).

The analysis of variance (ANOVA) was based on the linear model:

$$y_{ijk} = \mu + r_i + g_j + \varepsilon_{ijk} \quad (3)$$

Where: y_{ijk} is observed value for the i^{th} replication, j^{th} genotype, k^{th} block, while μ is the grand mean of the experiment, r_i is effect of the i^{th} replication, g_j is effect of the j^{th} genotype and ε_{ijk} is the residual random error.

Phenotypic (σ_p^2) and genotypic (σ_g^2) variances, as well as broad-sense heritability, were calculated using the methods described by Singh and Chaudhary (1981). Genetic advance (as a percentage of the mean) was determined following (Hill and Mackay 2004).

Phenotypic variance (σ_p^2) was estimated using:

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 \quad (4)$$

Where: σ_g^2 : Genotypic variance, and σ_e^2 : Environmental variance

Genotypic and environmental variances were derived using the "lamer" package in R software (version R-4.1.1).

The coefficients of variation were estimated using Burton Urton and Devane (1953) method:

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100 \quad (5)$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100 \quad (6)$$

Where: \bar{x} is the grand mean of the trait, PCV is the phenotypic coefficient of variation and GCV is the genotypic coefficient of variation.

Broad-sense heritability (H^2) was calculated following the method described by Allard, with heritability estimates for a single environment determined using the formula:

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100 \quad (7)$$

Where: H^2 : Broad-sense heritability (%), σ_g^2 : Genotypic variance and σ_p^2 : Phenotypic variance.

The classification of heritability values was based on Robinson et al., (1949):

Low: <30%

Medium: 30%–60%

High: >60%

Genotypic and phenotypic correlations were computed to investigate the relationships among the studied traits. Correlation coefficients were derived from components of variance and covariance, following the methodology of Shivaji and Gritton as cited in Ahamed et al., (2015). This analysis helped identify the associations among key agronomic traits, contributing to a deeper understanding of the interdependencies affecting seed size and yield characteristics.

When the additive-dominance model cannot adequately explain variation within the population, epistatic interactions are suspected. Estimation of these interactions was carried out using the five-parameter model proposed by Hayman as cited in Sheidu et al., (2020). This method allowed for the calculation of generation mean components to quantify the magnitude of suspected epistatic effects.

Scaling tests were conducted to assess the adequacy of the additive-dominance model, as described by Mather and Jinks (1971). The tests involved evaluating the *C* and *D* components, which were applied to the collected data to determine the model's suitability for explaining observed genetic variation.

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) (Table 1) revealed significant differences among generations for most of the studied traits in both crosses, indicating the presence of genetic variation and the effectiveness of our novel crossing program between ICGV188105 and Samnut 24 groundnut varieties. This unique germplasm combination, not previously documented in the literature, demonstrates considerable breeding potential. In Cross 1 (ICGV188105 x Samnut 24), highly significant ($p < 0.001$) differences were observed for NYP, 100SW, and 100PW, while significant differences ($p < 0.01$) were found for SW, PL, D50F, and SH%. Seed size (SS) and seed length (SL) also showed significant differences ($p < 0.05$). In Cross 2 (Samnut 24 x ICGV188105), highly significant ($p < 0.001$) differences were observed for SL, NYP, 100SW, and 100PW, with significant differences ($p < 0.01$) for SS, SW, PL, PW, D50F, and SH%.

These significant differences suggest that there is genetic variability among the generations for these traits, providing opportunities for selection and improvement. This result aligns with the findings of (Anwar Malik et al., 2016; Islam et al., 2015; Shamuyarira et al., 2019), who also reported high genetic variability for most of the studied traits. Our comprehensive generation analysis across P1, P2, F1, F2, and F3 generations reveals genetic inheritance patterns not captured in previous studies that typically focus only on F1 or F2 generations. The coefficient of variation (CV %) values were generally low to moderate for most traits in both crosses, indicating acceptable precision of the experiments. The mean performance of the parental lines (P1 and P2), mid-parent (MP), F1, F2, and F3 generations for each trait are presented in Table 2. Our study uniquely quantifies trait-specific heterosis for these particular crosses. Cross 1 (ICGV188105 x Samnut 24): The F1 generation showed higher mean values than the mid-parent (MP) for several traits, including SS (1.704 vs. 1.545), SL (12.57 vs. 11.11), PL (30.26 vs. 25.53), PW (13.96 vs. 11.71), and NYP (28.12 vs. 18.985), suggesting the presence of heterosis (hybrid vigor) for these traits. However, the F2 and F3 generations generally showed a decline in mean performance compared to the F1, as expected due to segregation. Comparing the parental lines, P1 generally exhibited higher mean values for seed size and seed weight related traits (SS, SL, SW, PL, PW, 100SW and 100PW) while P2 exhibited higher mean values for NYP and D50F. A distinctive contribution of our work is the analysis of

reciprocal crosses, which revealed important maternal effects. Cross 2 (Samnut 24 x ICGV188105): Similar to Cross 1, the F1 generation in Cross 2 also showed heterosis for some traits, including NYP (28.04 vs. 19.145) and 100SW (49.80 vs. 40.95). P2 generally exhibited higher mean values for size and weight related traits (SS, SL, PL, 100SW and 100PW) while P1 exhibited higher mean values for SW, PW, NYP and D50F. The F2 and F3 generations showed a decline in performance compared to the F1.

The findings demonstrated significant genetic variation among generations for most traits, as highlighted by the significant differences observed in the ANOVA and the presence of heterosis in the F1 generations. This heterosis, particularly notable in yield-related traits such as NYP and 100SW, underscores the crucial role of non-additive gene action (dominance and epistasis) in these crosses. These results align with previous findings in crops like rice and tobacco, where non-additive gene action was instrumental in hybrid vigor (Prasanna et al., 2024; Morgun et al., 2022). Our work provides specific documentation of these patterns in previously uncharacterized groundnut varieties that have regional importance. The decline in performance observed in the F2 and F3 generations can be attributed to genetic segregation, which disrupts favorable gene combinations, a phenomenon similarly noted in field bean studies (El Hosary 2020). This comprehensive tracking across multiple generations offers practical breeding implications not available from studies focused only on early generations. For breeders working with these varieties, our findings suggest that selection should focus on traits where additive gene action predominates for stable improvement, while heterosis-dependent traits may require alternative strategies such as developing synthetic varieties or maintaining hybrid seed production. This trend is consistent across multiple crops, wherein the initial heterosis in F1 hybrids is diminished in subsequent generations due to the breakdown of gene interactions (El Hosary 2020). Furthermore, the differences in mean performance between the parental lines provide a robust foundation for targeted selection and improvement of these traits. Both crosses demonstrated potential for enhancing yield and yield-related traits, making them promising candidates for further breeding efforts aimed at genetic improvement (El Hosary 2020; Prasanna et al., 2024). The regional relevance of our work with locally adapted germplasm offers direct applications to breeding programs in our specific agroecological conditions, distinguishing our contribution from studies conducted in different environments. This research advances both theoretical understanding of inheritance patterns in these specific groundnut varieties and provides practical knowledge for varietal improvement programs targeting enhanced productivity in local agricultural systems.

Table 1: The result of the analysis of variance for seed-size and seed-related traits in groundnut involving ICGV188105 X Samnut 24 cross and Samnut 24 x ICGV188105 evaluated at Samaru in 2021/2022

CROSS 1	SS	SL	SW	PL	PW	NYP	D50F	100SW	100PW	SH%
Replication	0.061	0.099	0.122	0.865	0.089	9.082	1.451	0.028	8.574	13.877
Generation	0.098*	8.984*	0.784**	16.39**	3.808**	97.43***	13.96**	162.2***	1066.8***	83.56**
Error	0.049	0.623	0.034	0.417	0.095	3.100	2.736	1.086	9.612	4.968
CV%	7.230	6.936	2.470	2.478	2.459	9.527	4.112	2.257	3.177	4.016
CROSS 2										
Replication	0.011	0.020	0.247	2.274	0.321	1.730	0.624	0.169	62.60	10.343
Generation	0.158**	13.83***	2.349**	6.187**	6.833**	105.54***	12.29**	109.07***	1112.3**	96.36**
Error	0.007	0.064	0.118	1.080	0.539	1.053	0.609	0.399	21.63	6.371
CV%	5.845	2.310	4.489	4.123	5.817	5.508	1.956	1.514	5.42	4.79

SS: seed size (mm), SL: seed length (mm), SW: seed width (mm), PL: pod length (mm), PW: pod width (mm), NYP: number of pod yield per plant, D50F: days to 50% flowering, 100KW: hundred seed weight (g), 100PW: hundred seed weight (g), SH%: shelling percentage (g)

Table 2: Mean performance of seed size and seed-related traits in ICGV188105 x Samnut 24 and its reciprocal

CROSS 1	SS	SL	SW	PL	PW	NYP	D50F	100SW	100PW	SH%
P1	1.810	13.94	7.749	28.50	13.12	23.76	36.93	48.85	137.2	81.89
P2	1.281	8.271	6.462	21.78	10.13	14.21	39.01	33.35	85.20	60.34
MP	1.545	11.11	7.105	25.53	11.71	18.985	37.98	48.975	111.25	59.12
F1	1.704	12.57	7.975	30.26	13.96	28.12	41.00	50.15	97.61	60.55
F2	1.516	11.28	7.460	27.61	12.97	14.17	44.10	41.49	87.56	57.50
F3	1.365	10.85	7.953	29.37	11.20	12.23	40.09	40.15	80.18	55.52
CROSS 2										
P1	1.413	8.102	5.785	20.33	9.420	13.39	40.09	32.90	73.32	58.77
P2	1.876	14.96	7.986	28.44	13.44	24.90	38.82	49.00	121.2	85.40
MP	1.645	11.53	6.89	25.43	11.43	19.145	39.46	40.95	97.26	57.03
F1	1.518	11.79	7.963	28.97	12.35	28.04	40.80	49.80	82.46	59.87
F2	1.254	10.02	7.984	29.39	11.58	13.23	39.44	38.00	73.15	61.69
F3	1.148	9.824	7.597	28.12	10.21	12.59	40.39	38.85	72.47	55.76

SS: seed size (mm), SL: seed length (cm), SW: seed width (mm), PL: pod length (cm), PW: pod width (mm), NYP: number of yield per plant, D50F: days to 50% flowering, 100SW: hundred seed weight (g), 100PW: hundred pod weight (g), SH%: shelling percentage (g).

Table 3 presents the partitioning of phenotypic variance (σ^2_p) into its components: environmental variance (σ^2_e) and genotypic variance (σ^2_g), along with estimates of PCV, GCV, and H^2 for each trait in both crosses. In Cross 1, high broad-sense heritability ($H^2 > 87%$) was observed for most traits, including seed length (SL; 87.01%), seed width (SW; 91.58%), pod length (PL; 95.03%), pod width (PW; 94.37%), number of pods per plant (NYP; 93.83%), 100-seed weight (100SW; 98.67%), 100-pod weight (100PW; 98.21%), and shelling percentage (SH%; 88.78%). This indicates that a large proportion of the observed phenotypic variation in these traits is due to genetic factors, suggesting that selection for these traits would be effective. Seed size (SS) also showed relatively high heritability (77.88%). Days to 50% flowering (D50F) showed comparatively lower heritability (67.22%), indicating a greater influence of environmental factors on this trait. The phenotypic coefficient of variation (PCV) ranged from 8.14% (SW) to 38.36% (NYP), while the genotypic coefficient of variation (GCV) ranged from 8.51% (SW) to 37.16% (NYP). The relatively close values of PCV and GCV for most traits suggest a limited influence of the environment on the expression of these traits. Cross 2 also exhibited high broad-sense heritability ($H^2 > 85%$) for most traits, including SL (99.07%), SW (90.40%), SS (91.40%), PW (85.37%), NYP (98.02%), 100SW (99.27%), 100PW (96.18%), and SH% (87.60%). This again indicates a strong genetic control over these traits. Similar to Cross 1, D50F showed considerably lower heritability (33.72%), confirming the greater influence of environmental factors. The PCV ranged

from 2.40% (D50F) to 39.18% (NYP), and the GCV ranged from 1.40% (D50F) to 38.79% (NYP).

High broad-sense heritability (H^2) estimates were observed in both crosses for most seed size and yield-related traits, indicating that a significant portion of the phenotypic variation is attributable to genetic factors. This suggests that direct selection for these traits could be highly effective. Notably, Cross 2 (Samnut 24 x ICGV188105) exhibited slightly higher heritability estimates compared to Cross 1 (ICGV188105 x Samnut 24), particularly for traits such as seed length (SL), seed size (SS), number of pods per plant (NYP), and 100-seed weight (100SW). These findings align with previous reports by (Sheidu et al., 2020; Sheidu et al., 2021; Sheidu et al., 2023), which also documented high heritability for these traits. The higher heritability observed in Cross 2 indicates its greater potential for genetic improvement of these traits through selective breeding (Gnanasekaran et al., 2024). In contrast, days to 50% flowering (D50F) consistently showed lower heritability in both crosses, reflecting a stronger influence of environmental factors on this trait's expression. These findings are consistent with previous studies (Gnanasekaran et al., 2024) that highlight how flowering time is significantly affected by environmental cues, such as temperature and photoperiod. Overall, the results underscore Cross 2's suitability for breeding programs targeting seed size and yield-related traits while emphasizing the need for environmental management strategies to optimize traits like flowering time.

The presence of moderate to high phenotypic (PCV) and genotypic (GCV) coefficients of variation for most traits in

both crosses indicates sufficient genetic variability within the populations to allow for effective selection (Kulus 2021; Kuru 2021). The relatively small differences between PCV and GCV values suggest a minimal influence of environmental factors on the expression of these traits (Roka et al., 2024). This implies that the observed phenotypic variation largely reflects underlying genetic differences, further supporting the potential for successful selection. These findings are

consistent with previous reports noting high heritability and genetic advance for seed yield and 100-seed weight, which emphasize the importance of additive gene action in these traits (Jou-Nteufa 2022). The combination of high heritability and substantial genetic variability provides a solid basis for developing effective selection strategies aimed at improving seed size and yield-related traits in these peanut populations (Jou-Nteufa 2022).

Table 3: Variance Component and Heritability of Seed Size and Seed Related Traits

Traits	Variance components					
	σ_e^2	σ_g^2	σ_p^2	PCV (%)	GCV (%)	H ²
Cross 1						
SL	0.62	4.18	4.80	19.25	17.96	87.01
SW	0.03	0.38	0.41	8.14	8.51	91.58
SS	0.01	0.04	0.06	15.36	13.55	77.88
PL	0.42	7.99	8.41	11.12	10.84	95.03
PW	0.95	1.61	1.70	10.36	10.06	94.37
NYP	3.10	47.17	50.27	38.36	37.16	93.83
D50F	2.74	5.61	8.35	7.18	5.89	67.22
100 SW	1.09	80.58	81.67	19.58	19.45	98.67
100 PW	9.61	528.60	538.21	23.78	23.56	98.21
SH%	4.97	39.30	44.27	11.99	11.30	88.78
CROSS 2						
SL	0.06	6.89	6.95	23.96	23.85	99.07
SW	0.12	1.12	1.23	14.49	13.78	90.40
SS	0.01	0.08	0.08	19.92	19.05	91.40
PL	1.08	2.54	3.62	6.33	7.55	70.18
PW	0.54	3.15	3.69	15.21	14.05	85.37
NYP	1.05	52.25	53.30	39.18	38.79	98.02
D50F	0.61	0.31	0.92	2.40	1.40	33.72
100 SW	0.40	54.34	54.74	17.74	17.67	99.27
100 PW	21.64	545.37	567.00	27.77	27.24	96.18
SH%	6.37	45.00	51.37	13.62	12.75	87.60

σ_e^2 = Genotypic variance, σ_g^2 = Genotype x Condition Variance, σ_p^2 = Phenotypic variance,

GCV= Genotypic Coefficient of Variation, PCV= Phenotypic Coefficient of Variation, H² = Broad-sense Heritability.

Results of the correlation analysis between seed and some agronomic traits in the two crosses (ICGV188105 × SAMNUT 24 and SAMNUT 24 × ICGV188105) are presented in figure 1 and 2. In Cross 1, strong positive inter-correlations ($p < 0.001$) were observed among the seed size and weight components. Seed size (SS) was highly correlated with seed length (SL; $r = 0.87$), seed width (SW; $r = 0.91$), 100-seed weight (100-SW; $r = 0.83$), and 100-pod weight (100-PW; $r = 0.93$), indicating that selection for larger seeds is likely to result in simultaneous increases in these related traits. The strongest association was between 100-PW and SS ($r = 0.93$, $p < 0.001$), highlighting the close relationship between overall seed size and pod weight. Pod length (PL) also exhibited strong positive correlations ($p < 0.001$) with SL ($r = 0.92$) and 100-PW ($r = 0.84$). Furthermore, number of yield per plant (NYP) was significantly positively correlated ($p < 0.001$) with several traits, including SL ($r = 0.80$), PL ($r = 0.78$), 100-PW ($r = 0.73$), and SS ($r = 0.64$), suggesting that plants with larger seeds and pods tend to produce a higher number of pods. In contrast, days to 50% flowering (D50F) showed weak and non-significant (ns) correlations with most traits; the strongest association was a negative, but non-significant, correlation with 100-PW ($r = -0.59$, ns). Shelling percentage (SH %) displayed moderate positive correlations with SS ($r = 0.74$), 100-PW ($r = 0.70$), and SL ($r = 0.65$), but only the correlation with 100-PW was statistically significant

($p < 0.05$). In Cross 2, similar strong positive inter-correlations were observed among size and weight traits. Seed length (SL) and seed width (SW) were highly correlated ($r = 0.85$, $p < 0.001$). Seed size (SS) showed a strong positive correlation with 100 seed weight (100SW) ($r = 0.81$, $p < 0.001$) and a moderate positive correlation with 100 pod weight (100PW) ($r = 0.69$, $p < 0.001$). Pod length (PL) was strongly positively correlated with both seed length (SL) ($r = 0.90$, $p < 0.001$) and pod width (PW) ($r = 0.73$, $p < 0.001$). Number of pods per plant (NYP) was also positively correlated with 100 seed weight ($r = 0.93$, $p < 0.001$) and pod length ($r = 0.76$, $p < 0.001$). Days to 50% flowering (D50F) showed weak and non-significant correlations with most other traits, with the highest negative correlation being with 100PW ($r = -0.59$, ns). Shelling percentage (SH %) exhibited moderate positive, but non-significant correlations with some size and weight traits, such as 100PW ($r = 0.67$, ns) and SL ($r = 0.64$, ns). The correlation patterns suggest a strong genetic linkage between seed size, pod size, and weight-related traits in both crosses. This implies that selection for one of these traits will likely result in correlated responses in the others. However, flowering time appears to be largely independent of these traits, suggesting that it could be manipulated relatively independently in breeding programs. These findings align with previous research on similar traits in other studies (Sheidu et al., 2023; Shamuyarira et al., 2019; Malik et al., 2011).

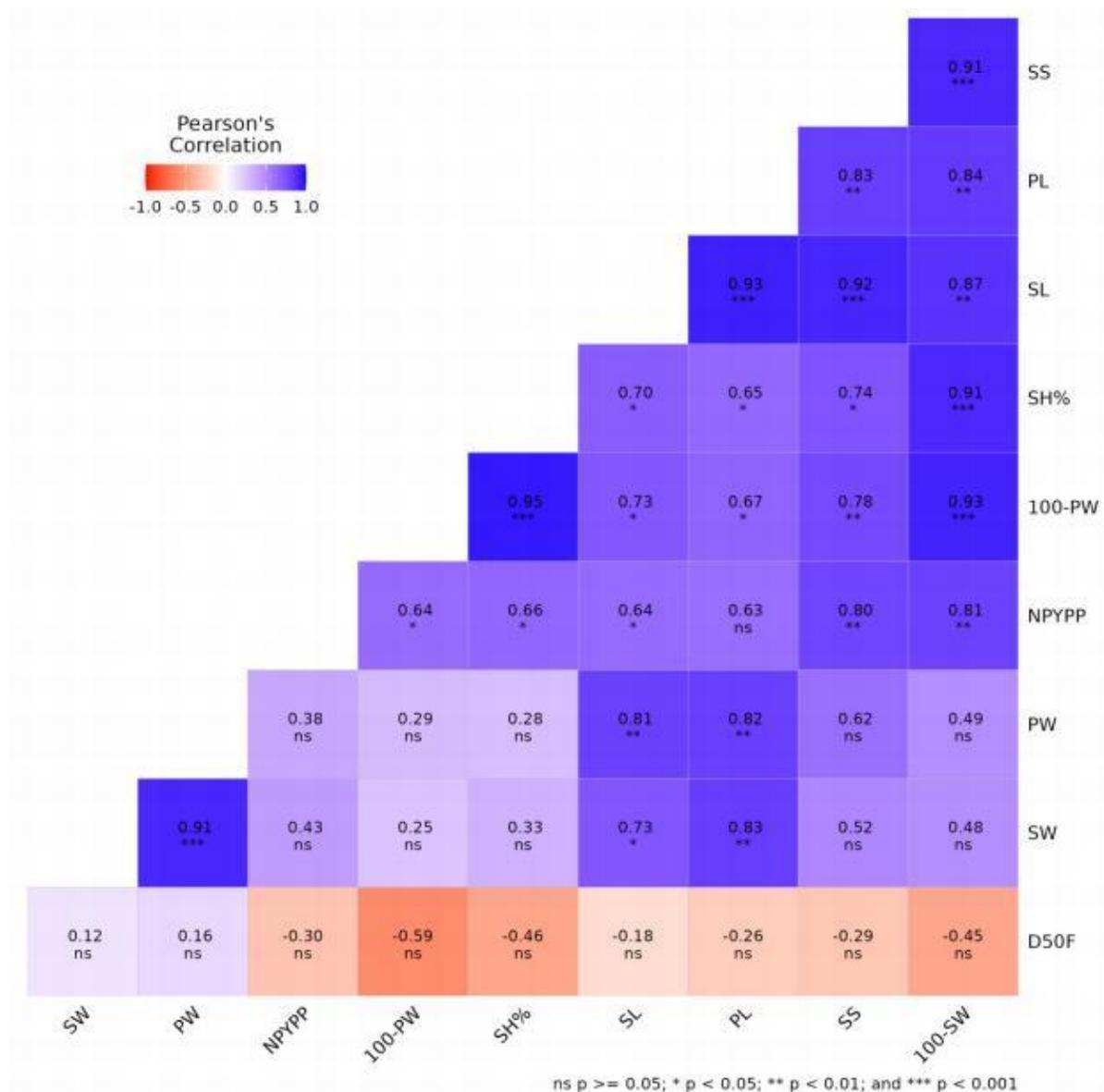


Figure 1: Associations between seed size and seed-related traits in Cross 1 (ICGV188105 x Samnut 24).
 SL: seed length, SW: seed width, SS: seed size, PL: pod length, PW: pod width, PY: pod yield, NYP: number of yield per plant, D50F: days to 50% flowering, 100SW: hundred seed weight, 100PW: hundred pod weight, SH%: shelling percentage

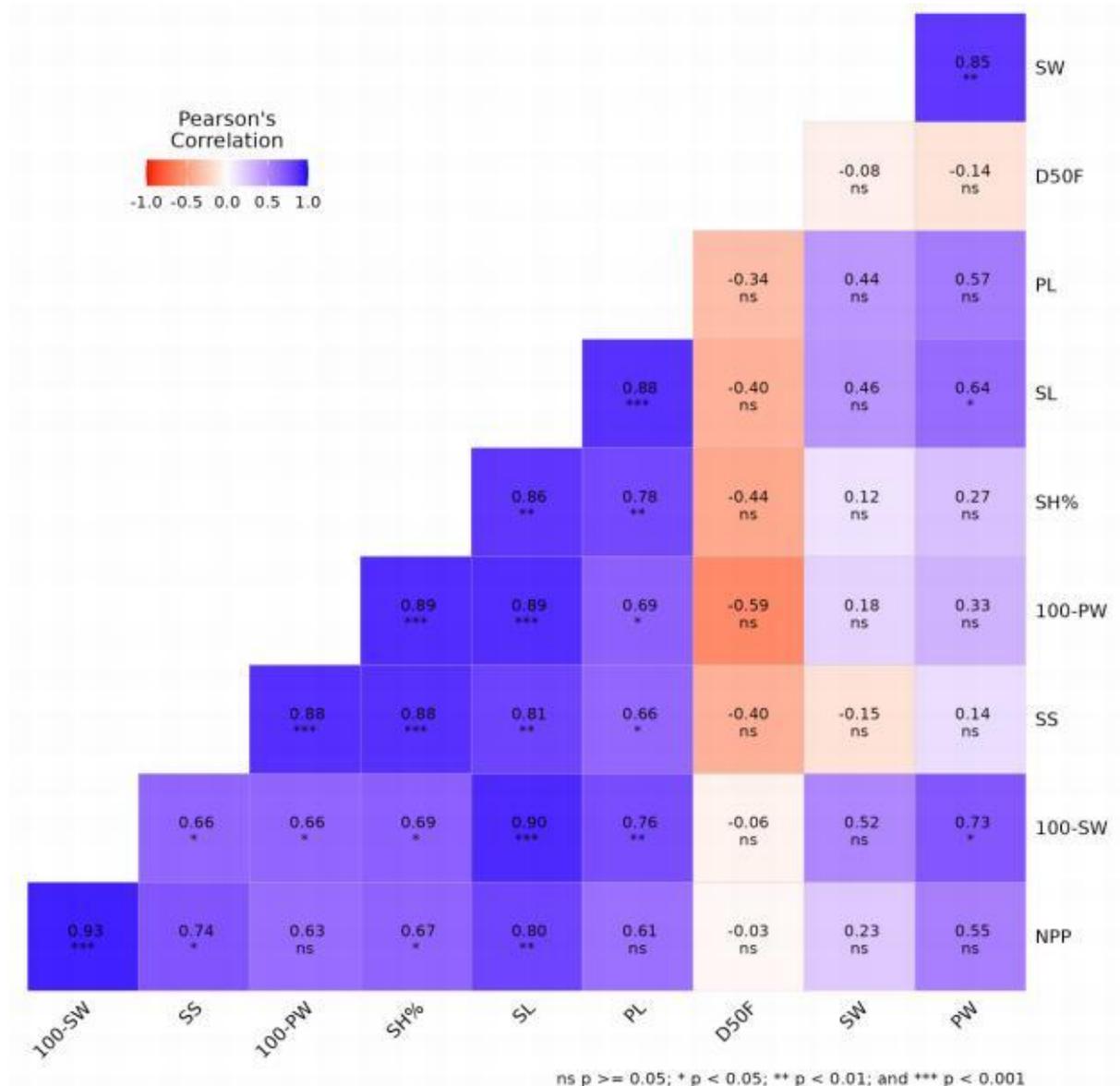


Figure 2: Associations between seed size and growth-related traits in Cross 2 (Samnut 24 x ICGV188105)
 SL: seed length, SW: seed width, SS: seed size, PL: pod length, PW: pod width, PY: pod yield, NYP: number of yield per plant, D50F: days to 50% flowering, 100SW: hundred seed weight, 100PW: hundred pod weight, SH%: shelling percentage

The scaling tests (C and D) were conducted to determine the adequacy of the additive-dominance model for explaining the genetic control of the studied traits in both reciprocal crosses (ICGV188105 x Samnut 24 and Samnut 24 x ICGV188105). The results (Table 4) revealed significant C scaling effects ($p < 0.01$) for most traits in both crosses, indicating the presence of additive x additive epistatic interactions. Specifically, the C scale values ranged from 92.22 ± 5.636 (SS in Cross 1) to 11.90 ± 3.004 (SW in Cross 2), demonstrating the varying magnitude of these epistatic effects across different traits. Significant D scaling effects ($p < 0.01$ or $p < 0.05$) were also observed for some traits, such as seed length (SL) in both crosses (60.03 ± 3.265 and 61.22 ± 6.830 , respectively) and days to 50% flowering (D50F) in Cross 2 (73.32 ± 14.98), suggesting the presence of additive x dominance epistatic interactions for these specific traits. The significance of both C and D scales indicates that non-allelic interactions play a crucial role in the inheritance of these traits and that a simple additive-dominance model is insufficient to fully explain their genetic architecture.

Estimates of genetic parameters, including mean [m], additive [d], dominance [h], additive x additive [l], and additive x dominance [i] effects, were obtained to further elucidate the genetic control of the studied traits (Table 5). Significant additive effects ($p < 0.01$) were observed for most traits in both crosses, highlighting the importance of additive gene action in determining these traits. For instance, the additive effect for seed length (SL) was 7.48 ± 0.73 in Cross 1 and 11.13 ± 0.31 in Cross 2. Significant dominance effects ($p < 0.01$ or $p < 0.05$) were also detected for several traits, such as 100 seed weight (100SW), which showed a dominance effect of 246.1 ± 118.4 in Cross 1 and pod width which showed a dominance effect of 63.7 ± 23.5 in cross 2. These significant additive and dominance effects suggest that both additive and non-additive gene action contribute to the inheritance of these traits. Furthermore, significant epistatic effects were observed for some traits, confirming the results of the scaling tests. For example, significant additive x additive [l] effects were observed for NYP in cross 1 (-74.52 ± 35.8) and significant additive x dominance [i] effects were observed for SS

(51.4±1.25), PW (78.5±26.7), 100SW (421.1±102.1) and SH% (345.8±145.5) in cross 2. The presence of significant epistatic effects further supports the complex genetic control of these traits and the need to consider non-additive genetic effects in breeding strategies. Some differences were observed in the magnitude and significance of genetic effects between the reciprocal crosses, suggesting the potential influence of maternal or cytoplasmic effects on the inheritance of these traits. For example, the dominance effect

for 100 seed weight was significant at $p < 0.01$ in cross 1 but not significant in cross 2. The results of the scaling tests and genetic parameter estimation indicate that the inheritance of seed size and growth-related traits in these peanut crosses is complex, involving significant additive, dominance, and epistatic gene effects (Venuprasad et al., 2011; Alam et al., 2013; Lal et al., 2014; Khedikar et al., 2018). These findings highlight the importance of considering non-additive genetic effects in breeding strategies aimed at improving these traits.

Table 4: C and D' scaling test and associated standard error (SE±) for seed size and seed - related traits in groundnut involving ICGV188105 X SAMNUT 24 cross and SAMNUT 24 x ICGV188105 evaluated at Samaru in 2021/2022

Parameters/Crosses	Cross 1	C _I Scale	D _I Scale
SS (mm)	Cross 1	92.22±5.636**	93.081±7.187**
	Cross 2	86.635±7.992**	15.77±10.16
SL (cm)	Cross 1	60.03±3.265**	58.49±2.967**
	Cross 2	61.22±6.830**	14.62±3.09**
SW (mm)	Cross 1	12.30±0.911**	12.76±1.142**
	Cross 2	11.90±3.004**	2.180±1.562
PL (mm)	Cross 1	209.64±8.976**	193.7±12.99**
	Cross 2	204.37±26.20**	-9.429±17.32
PW (mm)	Cross 1	99.64±4.761**	90.98±5.089**
	Cross 2	107.39±9.505**	30.54±28.02
NYP	Cross 1	184.05±16.05**	171.39±17.46**
	Cross 2	162.64±18.60**	-8.807±21.32
D50F	Cross 1	326.30±22.47**	313.4±17.01**
	Cross 2	315.97±18.56**	73.32±14.98**
100SW (g)	Cross 1	344.84±22.04**	361.54±15.58**
	Cross 2	331.54±21.09**	47.65±16.45*
100PW (g)	Cross 1	807.00±58.55**	772.8±95.23**
	Cross 2	691.01±31.79**	46.36±68.51
SH%	Cross 1	471.68±21.88**	479.5±26.37**
	Cross 2	441.68±27.52**	49.37±27.83

* and ** significantly different at 5% and 1% levels of probability.

Table 5: Estimates of five genetic parameters for seed-size and seed-related traits in groundnut involving ICGV188105 X SAMNUT 24 cross and SAMNUT 24 x ICGV188105 Evaluated at Samaru in 2021/2022

ICGV188105 X SAMNUT 24										
	SW	SL	SS	PL	PW	NYP	DFF	100 PW	100 SW	SH%
[m]	1.20±1.07	7.48±0.73**	5.95±1.04**	28.3±2.07**	13.1±1.09**	23.7±3.52**	36.91±5.30**	137.0±5.49**	49.41±5.36**	67.1±3.99**
[d]	2.91±0.37**	7.10±0.23**	6.98±0.324**	20.1±0.06**	10.7±0.48**	19.73±0.482**	33.2±1.072**	108.6±2.18**	41.3±0.726**	59.4±2.69**
[h]	30.8±33.7	54.7±658.8	40.8±30.1	134.8±170.1	71.40±3.6	121.3±191.2	221.2±119.6	507.5±549.4	246.1±118.4**	32.92±47.54
[l]	8.69±13.1	5.11±15.95	0.38 ±6.84	0.38±23.02	-9.75±10.10	-74.52±35.8**	-9.75±46.34	504.5±680.8	70.5±45.65	43.1±46.1
[i]	80.9±41.8	51.9±302.0	51.4±1.25**	203.6±184.9	93.29±310.1	196.2±154.1	298.6±514.9	706.4±218.2**	285.6±478.7	397.8±747.5
SAMNUT 24 x ICGV188105										
[m]	1.34±0.344**	7.68±0.91**	1.81±0.18**	12.01±2.64**	8.54±1.695**	15.4±4.025**	27.9±3.88**	106.9±0.716**	33.2±1.59**	50.9 ±8.65**
[d]	1.58±0.100**	11.13±0.31**	1.54±0.063**	19.7±1.181**	10.8 ±0.47**	19.78±1.024**	33.6±1.455**	416.37±209.1**	41.3±0.716**	58.2±2.91**
[h]	7.73±344.5	39.8±753.5	8.52±99.6	8.52±121.3	63.7±23.5**	110.8±232.9	210.9±581.6	165.9±119.56	213.9±344.1	285.2±175.4
[l]	-0.86±2.79	0.38±6.84	-3.636±6.01	2.82±49.15	5.034±38.34	-9.75±39.36	-2.70±29.337	99.3±151.02	27.9±34.4	27.6±52.2
[i]	10.09±5.51**	64.7±429.4	10.45±291.2	155.1±705.7	78.5±26.7**	93.8±280.2	249.4±678.3	421.1±102.1**	263.8±126.6**	345.8±145.5**

** : 1% significant level * : 5% significant level SL =Seed length, SS =Seed size, PL = Plant length, PW = Pod weight, NYP = Number of yield per plant, DFF = days to fifty flowering

CONCLUSION

This study provides valuable insights into the genetic architecture of seed size and growth-related traits in peanut. The significant genetic variation, high heritability estimates, and strong inter-correlations among key traits offer opportunities for genetic improvement through breeding. The presence of non-additive gene action and the influence of environmental factors on certain traits, such as D50F, should be considered in the development of effective breeding strategies. The identification of Cross 2 as a potentially more promising population for selection based on higher heritability estimates warrants further investigation and utilization in future breeding efforts.

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