

Research Article

Trait Correlations and Path Analysis for Kernel Yield Improvement in Groundnut (*Arachis hypogaea* L.) Genotypes

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Abstract

Groundnut (*Arachis hypogaea* L.), or peanut, is a self-pollinating legume valued for its oil-rich kernels and nitrogen-fixing roots. Given the limited availability of enriched germplasm in Ethiopia, indirect selection through association studies is pivotal for identifying traits linked to high kernel yield. This study evaluated fifteen groundnut genotypes using a Randomized Complete Block Design with three replications to analyze correlations and path coefficients for yield improvement. Significant differences among genotypes were observed for key traits, including days to flowering and maturity, number of mature pods per plant, 100-kernel weight, and kernel yield, indicating the presence of variability among the genotypes in terms of these traits. Correlation analysis revealed a significant negative phenotypic correlation between kernel yield and days to maturity, but positive correlations with number of mature pods per plant and number of kernels per pod. The result revealed that late maturing genotypes produce high number of pods in turn exhibit higher kernel yield than early maturing ones. Genotypic correlations reinforced these findings, highlighting number of mature pods per plant as a critical determinant of yield. Path coefficient analysis indicated that the number of mature pods per plant had the highest direct positive effect on kernel yield, suggesting that enhancing this trait could significantly boost productivity. These results underscore the importance of selecting for high number of mature pods per plant in groundnut breeding programs to enhance kernel yield.

Keywords

Genotypic Correlation, Kernel Yield, Phenotypic Correlation, Pod Per Plant, Shelling Percentage

1. Introduction

The groundnut (*Arachis hypogaea* L.), also known as the peanut, is a self-pollinating legume crop. Groundnut kernels are consumed in various ways by humans, while its branches and leaves are used as animal feed. Agronomically, groundnut roots contribute to soil fertility by fixing nitrogen. Nutritionally, groundnuts are rich in oil, containing 31.7-57% oil [1], and protein, with a content of 22.78-25.69% [2]. This crop is cul-

tivated in over 100 countries for its value as food, oil, and feed [3]. According to the Food and Agriculture Organization of the United Nations (FAO) [4], the top five groundnut-producing countries are China (18,357,437 tons), India (10,244,000 tons), Nigeria (4,607,669 tons), the United States (2,898,140 tons), and Sudan (2,355,000 tons). In 2021, Ethiopia produced 207,759 tons of groundnuts on 110,000 hectares, with an av-

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Received: 16 November 2024; Accepted: 5 December 2024; Published: 27 December 2024



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erage productivity of 1.88 tons per hectare. In the Benishangul Gumuz region, 84,372 private peasant households produced 55,405.50 tons on 28,898.73 hectares, yielding an average of 1.9 tons per hectare [5]. Notably, groundnut productivity can reach up to 5.50 tons per hectare in Israel [4].

To boost groundnut productivity in Ethiopia, the primary focus of groundnut breeding is on developing varieties with high kernel yield and disease resistance. Since groundnut is not native to Ethiopia and was introduced in 1920, its improvement relies heavily on genetic resources obtained from germplasm donor institutes, such as the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). The lack of enriched germplasm makes it challenging to obtain elite groundnut genotypes with desirable traits such as high kernel yield through direct selection. Consequently, improving groundnut kernel yield might be more effectively achieved through indirect selection and combining traits associated with kernel yield.

Association studies are particularly valuable in crop improvement, especially when germplasm availability is limited. These studies enable breeders to identify traits linked to the desired yield traits and use this information to combine multiple favorable alleles into a single genotype, by which the performance of the crop is enhanced, even with limited germplasm resources. Correlation analysis plays a crucial role in crop improvement by helping plant breeders identify relationships between different traits, such as crop yield and its related traits. Any crop improvement effort in increasing yield should consider yield related components which have direct and indirect share towards the yield [6]. On the other hand, path coefficient analysis which is a powerful multivariate statistical tool which enables to separate correlation coefficient into direct and indirect effects [6-10]. Furthermore, path coefficient analysis can aid in prioritizing traits for breeding programs by quantifying their relative importance.

Therefore, this experiment was conducted to analyze the correlation and path coefficients in groundnut genotypes.

2. Materials and Methods

2.1. Description of Experimental Field

The experiment was conducted during 2022 cropping season at Assosa Agricultural Research Center, which is situated in Benishangul Gumuz region of Northwestern Ethiopia. The experimental site is located at 1553 meters above sea level, and at latitude and longitude of 10°02'05"N and 34°34'09"E, respectively. The experimental site has a unimodal rainfall pattern, which starts at the end of April and extends to mid-November, with maximum rainfall received from June to October, with a total annual average rainfall of 1275 mm. The minimum and maximum temperatures are 16.75 and 27.92°C, respectively. The dominant soil type of Asossa area is Nitisols with the soil pH ranging from 5.0 to 6.0 [11].

2.2. Plant Materials and Design

Fifteen groundnut genotypes (Table 1), comprising thirteen advanced lines from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and two checks (Babile-4 and Sartu) were the plant materials evaluated in the experiment. The evaluation was conducted using a Randomized Complete Block Design (RCBD) with three replications. Each plot contained five rows, each 5 meters long, with 60cm between rows. The spacing within rows was set at 10cm at the time of planting. Additionally, all recommended agronomic practices were followed to ensure optimal crop growth conditions.

Table 1. Groundnut genotypes used in the experiment.

S. No	Genotype	Status
1	ICGV0266	Advanced line
2	ICGV05155	Advanced line
3	ICGV06420	Advanced line
4	ICGV07220	Advanced line
5	ICGV10315	Advanced line
6	ICGV103249	Advanced line
7	ICGV10355	Advanced line
8	ICGV10358	Advanced line
9	ICGV10365	Advanced line
10	ICGV13254	Advanced line
11	ICGV13265	Advanced line
12	ICGV13277	Advanced line
13	ICGV13278	Advanced line
14	Babile-4	Check-1
15	Sartu	Check-2

2.3. Data Collected

Days to 50% flowering (DF) and 90% maturity (DM) were recorded for each plot. To evaluate the resistance of groundnut genotypes against late leaf spot (LLS), caused by *Cercosporidium personatum*, data were collected from 10 randomly selected plants located within the middle three rows of each plot. The disease severity was assessed using the scale developed by Sarwar and Haq [12], which categorizes severity as follows: 0 = 0%, 1 = 0.1–5%, 2 = 5.1–10%, 3 = 10.1–20%, 4 = 20.1–50%, 5 = 50.1–70%, and 6 = >70%, corresponding to immune, highly resistant, resistant, moderately resistant, moderately susceptible, susceptible, and highly susceptible, respectively. The number of mature pods per plant (MPPP) was assessed on 10 randomly selected plants per plot, while

the number of seeds per pod (SPP) was determined from 10 random pods. Shelled kernel yield (ShKY) was measured from the harvest obtained from the middle three rows of each plot, and the weight of 100 kernels (HKW) was determined by weighing 100 kernels sampled from the plot harvest.

2.4. Data Analysis

A The analysis of variance (ANOVA) for the traits in this study was performed using the *doebioresearch* package [13] within the R software [14]. The ANOVA model used is defined as follows:

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

Here, y_{ij} represents the observation of the i^{th} genotype (G_i) in the j^{th} replication (R_j); μ is the overall mean; G_i denotes the effect of the i^{th} genotype; R_j signifies the effect of the j^{th} replication; and ε_{ij} is the error term. Fisher's Least Significant Difference (LSD) test was used to compare the means among genotypes, with a significance level set at 5% probability.

The *corr_plot* function within the *metan* package [15] of R software was used to estimate the phenotypic and genotypic correlations among the traits. Adjusted means of genotypes for considered traits were used to determine genotypic cor-

relation analysis. To ascertain the direct and indirect effects of traits on kernel yield, a path coefficient analysis was conducted for traits that showed significant genotypic and phenotypic correlations with kernel yield. This analysis was performed using the *path.analysis* function within the *agricolae* [16] package within R software.

3. Result and Discussion

3.1. Analysis of Variance and Mean Performance for Yield and Yield Related Traits

The analysis of variance revealed significant differences ($P < 0.05$) among groundnut genotypes for key traits including days to 50% flowering, days to 90% maturity, number of mature pods per plant, 100-kernel weight, and kernel yield. However, there were no significant differences among the tested genotypes regarding the number of kernels per pod and resistance to late leaf spot disease. Similarly, Chandran et al. [17] and Pachauri and Shikarvar [18] reported genetic variability in groundnut for the number of pods per plant, hundred kernel weight, and kernel yield.

Table 2. Analysis of variance for kernel yield and its related traits of groundnut genotypes evaluated at Assosa in 2022.

	Block	Genotype	Error
Degree of freedom	2	14	28
Days to 50% flowering	0.26	14.52**	4.64
Late leaf spot	3.24	0.68	0.74
Days to 90% maturity	9.48	38.75***	4.56
Number of mature pods per plant	9.77	118.67***	19.86
Number of kernels per pod	0.06	0.03	0.02
Hundred kernel weight (g)	23.46	95.60***	15.36
Shelled kernel yield (kg ha ⁻¹)	106475	542625***	39811

The mean performance of groundnut genotypes, as detailed in Table 3, shows that days to 50% flowering ranged from 51.00 to 60.33, and days to 90% maturity ranged from 156.00 to 169.67. The disease scores for late leaf spot (on a 1-9 scale) varied significantly, with ICGV 10365 recording the lowest score of 1.70 and ICGV 13265 the highest score of 3.67. Despite having lower 100-kernel weights (37.38 g for ICGV 05155 and 46.62 g for ICGV 06420), both genotypes pro-

duced the highest number of mature pods per plant. The highest 100-kernel weight was observed in ICGV 0266 at 60.84 g, followed by ICGV 10315 at 57.68 g and ICGV 10355 at 57.04 g. Notably, the farmers' variety, Sartu, a runner type, achieved the highest shelled kernel yield at 1913.45 kg/ha, followed by ICGV 05155 at 1425.49 kg/ha. In contrast, the standard check variety Babile-4, a Virginia type, recorded the lowest shelled kernel yield at 455.65 kg/ha.

Table 3. Mean performance of groundnut genotypes evaluated at Assosa during 2022 cropping year.

Genotype	DF	DM	LLS	MPPP	KPP	HKW	ShKY
Babile-4	51.00d	162.33efg	2.67	5.20de	1.47	47.36de	455.65fg
ICGV 0266	52.33cd	164.00def	2.80	11.47cde	1.40	60.84a	791.53de
ICGV 05155	53.67cd	156.00h	3.20	26.93a	1.80	37.38f	1425.49b
ICGV 06420	53.33cd	161.00fg	2.67	19.13b	1.67	46.62e	1082.15cd
ICGV 07220	55.00bc	164.67cde	2.40	12.40bcd	1.60	56.12abc	842.94de
ICGV 10315	55.00bc	169.33ab	2.53	4.73e	1.40	57.68ab	451.23fg
ICGV 103249	55.67bc	165.67cde	2.87	5.73de	1.47	52.03bcde	545.09efg
ICGV 10355	53.67cd	169.67a	2.10	10.27cde	1.47	57.04abc	533.99efg
ICGV 10358	53.33cd	167.00abcd	3.17	6.67de	1.60	48.75de	562.10efg
ICGV 10365	54.67bc	167.67abc	1.70	11.07cde	1.60	53.43bcd	711.13efg
ICGV 13254	54.00cd	165.00cde	2.40	7.33de	1.60	50.52cde	399.89g
ICGV 13265	60.33a	166.00bcd	3.67	10.47cde	1.60	53.69bcd	659.87efg
ICGV 13277	55.33bc	160.33g	2.30	19.33b	1.67	49.33de	1256.59bc
ICGV 13278	55.00bc	166.00bcd	2.40	8.93de	1.53	49.00de	762.68def
Sartu	57.67ab	166.00bcd	2.53	16.73bc	1.67	51.57bcde	1913.45a
Mean	54.6	164.71	2.62	11.76	1.56	51.42	826.25
CV (%)	3.94	1.29	2.89	37.89	10.61	7.62	24.14
LSD at 5% probability	3.60	3.57	ns	7.45	ns	6.55	333.71

DF=days to 50% flowering, DM=days to 90% maturity, LLS=late leaf spot, MPPP=number of mature pods per plant, KPP=number of kernels per pod, HKW=hundred kernel weight in g, ShKY=Shelled kernel yield (kg ha⁻¹), CV=coefficient of variation, and LSD=least significant difference

3.2. Phenotypic and Genotypic Correlation Coefficients

In the present study, shelled kernel yield exhibited a significant negative phenotypic correlation with days to 90% maturity ($r_p = -0.45^{**}$), indicating that as the maturity period increases, the kernel yield tends to decrease. In the previous study, days to maturity exhibited negative correlation with kernel yield [19]. However, there were significant positive phenotypic correlations between shelled kernel yield and both the number of mature pods per plant ($r_p = 0.68^{***}$) and the number of kernels per pod ($r_p = 0.44^{**}$). Additionally, days to 90% maturity had a positive phenotypic correlation with 100-kernel weight ($r_p = 0.67^{***}$), but a negative correlation with the number of mature pods per plant ($r_p = -0.55^{***}$) and the number of kernels per pod ($r_p = -0.34^*$). The number of kernels per pod showed a positive phenotypic correlation with

days to 50% flowering ($r_p = 0.30^*$) and the number of mature pods per plant ($r_p = 0.48^{***}$). Moreover, 100-kernel weight had a significant negative phenotypic correlation with the number of mature pods per plant ($r_p = -0.35^*$).

Shelled kernel yield demonstrated a significant positive genotypic correlation with both the number of mature pods per plant ($r_g = 0.82^{***}$) and the number of kernels per pod ($r_g = 0.68^{**}$). Days to 90% maturity showed a significant positive genotypic correlation with 100-kernel weight ($r_g = 0.74^{**}$), but a negative correlation with the number of mature pods per plant ($r_g = -0.75^{**}$) and the number of kernels per pod ($r_g = -0.63^*$). The number of kernels per pod exhibited a strong positive genotypic correlation with the number of mature pods per plant ($r_g = 0.80^{***}$). Additionally, 100-kernel weight had a significant negative genotypic correlation with both the number of mature pods per plant ($r_g = -0.55^*$) and the number of kernels per pod ($r_g = -0.74^{**}$).

DF	DM	LLS	MPPP	KPP	HKW	ShKY	
	0.11	0.023	-0.029	0.3 *	0.14	0.18	DF
		-0.13	-0.55 ***	-0.34 *	0.67 ***	-0.45 **	DM
			0.089	0.13	-0.14	0.11	LLS
				0.48 ***	-0.35 *	0.68 ***	MPPP
					-0.25	0.44 **	KPP
						-0.27	HKW
							ShKY

Figure 1. Phenotypic correlation among agro-morphological traits of groundnut at Assosa during 2022 cropping year. DF=days to 50% flowering, DM=days to 90% maturity, MPPP=number of mature pods per plant, KPP=number of kernels per pod, HKW=hundred kernel weight, ShKY=shelled kernel yield.

DF	DM	LLS	MPPP	KPP	HKW	ShKY	
	0.24	0.29	0.075	0.24	0.16	0.28	DF
		-0.31	-0.75 **	-0.63 *	0.74 **	-0.49	DM
			0.089	0.16	-0.29	0.037	LLS
				0.8 ***	-0.55 *	0.82 ***	MPPP
					-0.74 **	0.68 **	KPP
						-0.38	HKW
							ShKY

Figure 2. Genotypic correlation among agro-morphological traits of groundnut at Assosa during 2022 cropping year. DF=days to 50% flowering, DM=days to 90% maturity, MPPP=number of mature pods per plant, KPP=number of kernels per pod, HKW=hundred kernel weight, ShKY=shelled kernel yield.

3.3. Phenotypic and Genotypic Path Coefficients

In the current study, the phenotypic path analysis (Figure 3) revealed that the number of mature pods per plant had the most substantial direct positive effect (0.56) on kernel yield. In contrast, days to 90% maturity and the number of kernels per pod showed minor direct negative (-0.19) and positive (0.13) phenotypic effects, respectively. Although the maturity period had a minor direct effect on kernel yield, it exhibited a more significant indirect phenotypic effect (-0.30) on kernel yield through the number of mature pods per plant. Additionally, the number of kernels per pod demonstrated a larger indirect positive phenotypic effect (0.26) on kernel yield via the number of mature pods per plant.

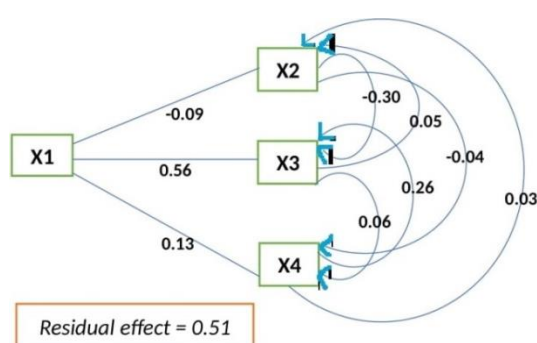


Figure 3. Phenotypic path coefficient. X1=Shelled kernel yield; X2=days to 90% maturity; X3=number of matured pods per plant; X4=number of kernels per pod. Dashes indicate direct effects, and arrowed arcs indicate indirect path coefficients.

The results indicate that increasing the number of mature pods per plant can significantly enhance kernel yield in groundnut. A notable indirect negative impact of the maturity period on kernel yield, through the number of mature pods per plant, suggests that early maturing groundnut genotypes tend to produce fewer pods, which is a critical factor for kernel yield. Additionally, the relatively higher positive indirect phenotypic effect of the number of kernels on kernel yield, via the number of mature pods, implies that groundnut genotypes with more kernels per pod can be considered high-yielding and capable of producing a greater number of pods per plant. The genotypic path coefficient analysis (Figure 4) further showed that the number of mature pods per plant had the most substantial direct positive genotypic effect (0.76) on kernel yield. Conversely, the direct genotypic effect of the number of kernels per pod on kernel yield was insignificant (0.06); however, this trait exhibited the highest indirect positive genotypic effect (0.61) on kernel yield through the number of mature pods per plant. Therefore, both phenotypic and genotypic path coefficients suggest that kernel yield in groundnuts can be effectively improved by indirectly selecting for the number of mature pods per plant. The residual effects from the phenotypic (0.51) and genotypic (0.32) path coefficients in-

dicate that the traits under examination accounted for only 49% and 68% of the variability in kernel yield, respectively. The remaining 51% (phenotypic path) and 32% (genotypic path) of the variance may be attributed to environmental factors and/or other kernel yield-related traits in groundnuts that were not included in the study.

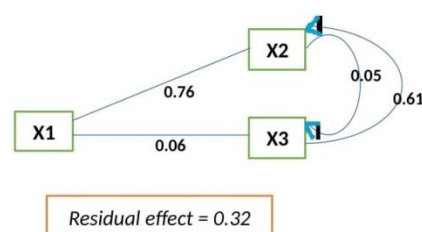


Figure 4. genotypic path coefficient. X1=Shelled kernel yield; X2=number of matured pods per plant; and X3=number of kernels per pod. Dashes indicate direct effects, and arrowed arcs indicate indirect path coefficients.

4. Conclusion

This study highlights the significant variability among groundnut genotypes in terms of flowering time, maturity, mature pods per plant, 100-kernel weight, and kernel yield, underscoring the potential for targeted breeding. Notably, no significant differences were found in kernel number per pod and resistance to late leaf spot disease. The analysis identified a strong positive correlation between kernel yield and both the number of mature pods per plant and kernels per pod, while a negative correlation with days to maturity was observed. Path coefficient analysis further emphasized the critical role of mature pods per plant in enhancing kernel yield, suggesting that indirect selection focusing on this trait could be highly effective. The study revealed that early maturing genotypes tend to produce fewer pods, negatively impacting yield. However, genotypes with more kernels per pod showed higher yields, indicating their potential as high-yielding varieties.

The study implied that late maturing genotypes produce high number of pods in turn exhibit higher kernel yield than early maturing genotypes. Furthermore, the study indicated the importance of selecting for high number of mature pods per plant in groundnut breeding programs to enhance kernel yield.

Abbreviations

DF	Days to 50% Flowering
DM	Days to 90% Maturity
LLS	Late Leaf Spot
MPPP	Number of Mature Pods Per Plant
KPP	Number of Kernels Per Pod
HKW	Hundred Kernel Weight
ShKY	Shelled Kernel Yield

Author Contributions

Sintayehu Gedifew is the sole author. The author read and approved the final manuscript.

Conflicts of Interest

The author declares no conflicts of interest.

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