

Association of Traits in Peanut (*Arachis hypogaea* L.) Genotypes at Pawa Northwestern Ethiopia

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Abstract: The study was conducted to estimate correlation coefficients and direct and indirect effects by path analysis for pod yield per plant and its components by using 64 Peanut genotypes. In the current study, peanut genotypes were assessed for quantitative and qualitative traits during the main cropping season of 2021/22 in the North, Western Ethiopia Metekel zone at Pawa Agricultural Research Centre. The experiment was carried out to assess 64 Peanut genotypes in an 8x8 simple lattice design to generate information on the association of yield and yield-related traits and to ascertain the direct and indirect effects of yield-related traits on kernel yield. Data were recorded for 14 traits and subjected to analysis of variance ANOVA using SAS software version 9.4. Correlation analysis revealed a highly significant ($P < 0.001$) positive correlation between kernel yield per hectare and harvest index, number of pods per plant, number of seeds per pod, hundred seed weight, and shelling percentage at the phenotypic and genotypic levels, respectively which revealed the true relationship between the traits. Path analysis was divided into direct and indirect effects for various characters for the kernel yield per hectare. At the phenotypic level, days to maturity, oil content, and shelling percentage had the largest positive direct effects on kernel yield, whereas pod yield and shelling percentage had the highest positive direct effects at the genotypic level. The result indicated that there is a good opportunity to improve kernel yield using the tested genotypes in Peanut breeding programs. Therefore, emphasis should be given to pod yield followed by days to maturity, and shelling percentage to increase kernel yield production.

Keywords: Correlation, Path, kernel, Variety, Peanut.

INTRODUCTION

Peanut (*Arachis hypogaea* L.) is a self-pollinated, annual, herbaceous, allotetraploid legume having genome AABB and somatic chromosome number ($2n = 4x = 40$), which belongs to the family Leguminosae and sub-family Papilionaceae (Stalker and Wilson, 2015). Peanut is one of the major legumes that is grown around the world with huge economic income at households and national level in Africa with average productivity of 0.96 t/ha (Arya *et al.*, 2016). In Ethiopia, Peanut is solely grown by smallholder farmers under dryland conditions in the lowland and drought-prone areas of the country and plays a significant role in the Ethiopian economy (Kebede *et al.*, 2017; Abady *et al.*, 2019). The estimated annual groundnut production in Ethiopia was about 2050.6 tons from 113,514 ha hectares of production area. The average national yield was 1.8 tons per hectare (CSA, 2021). The crop was mainly

produced by smallholder farmers in the lowland area of Ethiopia. Currently, production is constrained by a lack of improved varieties, the narrow genetic potential of released varieties, poor soil fertility, pre-harvest diseases, the use of low-yielding varieties, and the limited availability of improved varieties (Abady *et al.*, 2019). In Benshangul Gumuz Region, Peanut is cultivated in various districts of the region under rain-fed conditions. It covers about 28,898 ha of land with a productivity of 1.7 tone/ha and the annual production of Peanut in Metekel zones was 47648.26 kg and Metekel zone takes the lion-share 24,355 ha with a productivity of 1.9 t/ha in the 2021 cropping season (CSA, 2021). The low productivity of the crop was due to the narrow genetic potential of improved varieties released in the region. Plant Breeders are attracted to the relationship that exists between or among traits and Information on the extent and nature of interrelationships among traits that help them to formulate efficient mechanisms of multiple trait

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selection. Correlation studies provide information to study the magnitude and direction of correlation of yield with its components and also among various components. The correlation of traits determined by analysis may not provide an exact picture of the relative importance of the direct and indirect influence of each of the yield components on kernel yield. The path coefficient analysis is one of the effective techniques to know the direct and indirect effects on yield through correlation values and to achieve the aim of developing a high-yielding variety in ground Peanut breeding programs, a breeder must exploit variability of quantitative characters existing within a collection of genotypes. Therefore, in Peanut breeding programs, information on relationship between various characters and their contribution to yield is important to increase Peanut production in the region as well as in a country.

Objectives

- ✓ To Assess the extent of correlation among yield, yield components, and oil content in Peanut genotypes and,

- ✓ To estimate the direct and indirect effect of yield-related traits and oil content on the grain yield of Peanut genotypes

MATERIALS AND METHODS

Description of the Experimental Sites

The experiment was conducted at Pawe Agricultural Research Center (PARC) on station during the main cropping season of 2021. PARC is geographically located between 11° 15' North latitude and 36°30' East longitudes with an altitude of 1150 m.a.s.l in Benshangul-Gumuz Regional state, Metekel Zone, Ethiopia. It is located 570 km away from Addis Ababa, the capital city of Ethiopia (Figure 1). The site receives 1586 mm of rainfall annually. The mean annual maximum and minimum temperatures are 32.6°C and 16.5°C, respectively. The soils type of Pawe district are characterized as dark 60%, red 31%, and blended 9% (Tizazu, 2019). Whereas the soil type of Pawe Agricultural Research Center (PARC) is characterized as nitosol or loam soil (PARC, 2017).

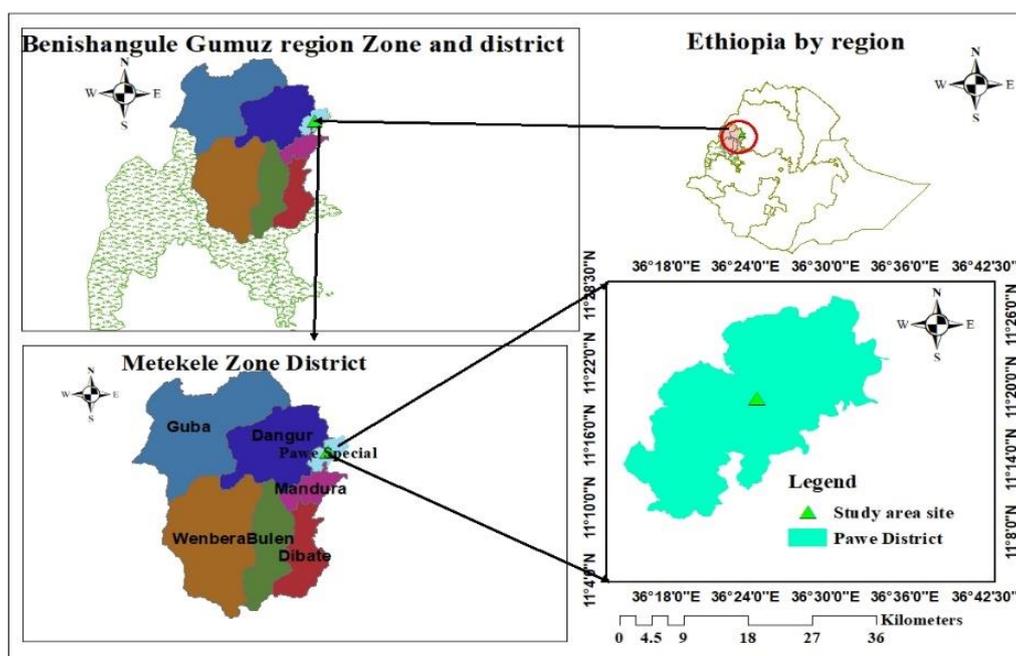


Figure 1: Map of the study area

Experimental Design, Procedure, and Trial Management

The experimental materials consisted of 64 advanced groundnut genotypes with three released Peanut varieties, namely Maniputer, babile-3, and babile-4. These genotypes were obtained from Pawe Agricultural Research Center. The experiment was laid out in 8x8 simple lattice designs with a plot size of (2.4m*3m) =7.2 m². Each plot consisted of four rows

with inter-row and intra-row spacing was 60 cm and 10 cm, respectively. The spacing between plots, blocks, and replications was 1m, 1m, and 1.5m, respectively. Two seed per hill seed rate was used with 100kg NPS fertilizer per hectare which is 72gm per plot was used and all were applied during planting. Weeding and other agronomic management practices were done as per the recommendation for Peanut.

Table 1: Description of Peanut Genotypes used in the Experiment

No	Genotype designation	Source	No	Genotype designation	Source
1	ICGV-13850	ICRISAT	33	RDRGVT ICGV SM 05723	Malawi
2	ICGV-91317	ICRISAT	34	RDRGVT ICGV SM 06519	Malawi
3	ICGV-96826	ICRISAT	35	RDRGVT ICGV SM 8528	Malawi
4	ICGV-97188	ICRISAT	36	RDRGVT ICGV SM 8533	Malawi
5	ICGV-91278	ICRISAT	37	RDRGVT ICGV SM 8538	Malawi
6	ICGV-55437	ICRISAT	38	RDRGVT ICGV 8540	Malawi
7	ICGV-91284	ICRISAT	39	RDRGVT ICGV SM 8547	Malawi
8	ICGV-03196	ICRISAT	40	RDRGVT ICGV SM 8556	Malawi
9	ICGV-03181	ICRISAT	41	ICGV 06420	ICRISAT
10	ICGV-08056	ICRISAT	42	ICGV 05155	ICRISAT
11	cn-34c noss ittga	ICRISAT	43	ICGV 07220	ICRISAT
12	ICGV-89104	ICRISAT	44	ICGV 0266	ICRISAT
13	ICGV-97094	ICRISAT	45	ICGV 10315	ICRISAT
14	ICGV-96909	ICRISAT	46	ICGV 10355	ICRISAT
15	ICGV-86024	ICRISAT	47	ICGV 10358	ICRISAT
16	ICGV-14840	ICRISAT	48	ICGV 10365	ICRISAT
17	ICGV-94434	ICRISAT	49	ICGV 103249	ICRISAT
18	ICGV-91279	ICRISAT	50	ICGV 13254	ICRISAT
19	ICGV-91315	ICRISAT	51	ICGV 13265	ICRISAT
20	ICGV-93305	ICRISAT	52	ICGV 13277	ICRISAT
21	ICGV-00350	ICRISAT	53	ICGV 13278	ICRISAT
22	ICGV-03179	ICRISAT	54	ICGV -95469	ICRISAT
23	ICGV-14858	ICRISAT	55	Manipeter	Local
24	SARTU	ICRISAT	56	Big seed	ICRISAT
25	ICGV 95469	ICRISAT	57	ICGV 89328	ICRISAT
26	RDRGVT(BAKA)	Malawi	58	ICGV 95463	ICRISAT
27	RDRGVT ICGV 14788	Malawi	59	ICGV-87108	ICRISAT
28	RDRGVT ICGV 00331	Malawi	60	ICGV-86928	ICRISAT
29	RDRGVT ICGV SM 01514	Malawi	61	ICGV-86644	ICRISAT
30	RDRGVT ICGV SM 03519	Malawi	62	ICGV -98	ICRISAT
31	RDRGVT ICGV SM 3520	Malawi	63	ICGV-98404	ICRISAT
32	RDRGVT ICGV SM 3530	Malawi	64	ICGV-94100	ICRISAT

Source: - PARC (Pawe Agricultural Research Center)

Data Collection

Data were collected on a plot basis and plant basis from the middle two rows for all parameters. For data recorded on a plant basis, five plants were randomly taken and tagged from the net harvestable plots and the mean value of these five plants was calculated using Micro soft Excel. The yield and yield component data that were collected on a plant basis and plot basis were described as follows.

Data Collected on Plant Basis

Plant height: was recorded by measuring five randomly selected plants from the harvestable rows using measuring tape from the ground surface to the top of the plant at maturity and the average will be calculated.

1. Number of Branches per plant: was calculated by counting the number of branches from five randomly selected plants and averaging the number of plants considered.
2. Number of pods per plant: was recorded as the number of pods per plant from five randomly selected plants from the net plot area and averaged.

3. Number of seeds per pod: This was determined from the pods harvested from five randomly selected plants and then counted seeds divided by total pods.

On Plot Basis

1. **Days to 50% flowering:** was recorded as the number of days from the date of 50% emergence to the date when 50% of the plants in a plot produced at least one flower.
2. **Days to 95% maturity:** was recorded as the number of days from the date of 50% emergence to the date when 90% of the plants in a plot are matured
3. **Biomass yield t/ha:** Above ground, biomass was measured per net plot at harvest after sun drying and converted into ton per hectare.
4. **Hundred seed weight (g):** was recorded by counting hundred seeds randomly from a bulk of shelled seeds and weighing using a sensitive balance.
5. **Pod yield (kg/ha):** was calculated from the net plot and expressed in kilograms per hectare after sun drying for 6 days and converted into a hectare base.
6. **Shelling percentage (%):** was calculated by taking

a sample of 200g mature pods per plot randomly and will be calculated as:

$$\text{Shelling percentage} = \frac{\text{Grain yield (g)}}{\text{Total pod yield (g)}} \times 100$$

7. Kernel yield adjusted at 8% moisture (kg/ha):

Was calculated as shelling percentage multiplied by pod yield and adjusted to standard storage 8% moisture level.

8. Harvest index (%): Is the ratio of economic yield (pod yield) to biological yield (Total dry matter with pods) and is expressed in percentage. It was calculated as the dry pod yield divided by above-ground dried biomass per plot plus dry pod yield per plot and multiplied by 100.

$$\text{HI} = \frac{\text{dry pod yield}}{\text{dry pod yield} + \text{biomass yield}} \times 100$$

9. Oil content: - Seeds from each replication were bulked by each genotype and 64 bulk samples were taken for oil content analysis. Oil content for each genotype was determined by extracting the groundnut seed in a Soxhlet apparatus with petroleum ether, which functions by dripping pure ether through a fat-containing substance.

10. Protein content: - Was determined according to Kjeldahl digestion method by digesting the sample in concentrated sulphuric acid (Thiex *et al.*, 2002). 0.5g of sample were weighted in the digestion tube containing concentrated sulphuric acid and copper tablet catalyst and digested in a block digester at 375oc for 3hr.

Analysis of variance (ANOVA)

All measured parameters were subjected to analysis of variance (ANOVA) using PROC GLM of SAS software version 9.4 (SAS, 2013) to assess the difference among the tested varieties. The difference between treatment means will be compared using DMRT at 5% probability levels.

Estimation of correlation coefficients

The phenotypic and genotypic correlation coefficient was estimated using the standard procedure suggested by (Miller *et al.*, 1958) from the corresponding variance and covariance components as:

Phenotypic correlation coefficient ($r_{p_{xy}}$) =

$$\frac{\sigma_{p_{xy}}}{\left(\sqrt{\sigma^2 p_x * \sigma^2 p_y}\right)}$$

Where, $r_{p_{xy}}$ = phenotypic correlation coefficient between character x and y

Genotypic correlation coefficient ($r_{g_{xy}}$) =

$$\frac{\sigma_{g_{xy}}}{\left(\sqrt{\sigma^2 g_x * \sigma^2 g_y}\right)}$$

$r_{g_{xy}}$ = genotypic correlation coefficients between characters x and y

The phenotypic correlation coefficient was tested for its significance using the formula suggested by (Sharma, 1998).

$$t = \frac{r}{\sqrt{\frac{1 - r^2}{n - 2}}}$$

The genotypic correlation coefficient was tested with the following formula suggested by (Robertson, 1959).

$$t = \frac{r_{g_{xy}}}{SEr_{g_{xy}}} \quad \text{where, } SEr_{g_{xy}} = \sqrt{\frac{1 - r_{g_{xy}}^2}{2h_x^2 * h_y^2}}$$

$SEr_{g_{xy}}$ = Standard error of genotypic correlation coefficient between characters X and Y

h_x^2 = heritability for character X

h_y^2 = heritability for character y

The calculated absolute t-value was tested against the tabulated t- value at a g-2 degree of freedom for both phenotypic and genotypic correlations. Environmental correlation coefficients were tested at $(r - 1) - 1$ degree of freedom. Where g is the number of genotypes and r is number of replication.

Path coefficient analysis

Path coefficient analysis will be performed using the phenotypic and genotypic correlation coefficients to know the direct and indirect effect of yield components on kernel yield using the general formula of (Dewey and Lu, 1959) by considering kernel yield per hectare as a dependent variable. The path coefficients was obtained by solving the following simultaneous equations, which express the basic relationship between correlation and path coefficient.

$$R_{ij} = P_{ij} + \sum r_{ik} P_{kj}$$

Where,

R_{ij} = Mutual association between the independent character (i) and dependent character, grain yield (j) as measured by the correlation coefficients.

P_{ij} = Components of direct effects of the independent character (i) as measured by the path coefficients and $\sum r_{ik} P_{kj}$ = summation of components of indirect of a given independent character

(i) On a given dependent character (j) via all other independent characters (k).

The contribution of the remaining unknown factor was measured as the residual factor (P_R), which is calculated

as: $P_R = \sqrt{1 - \sum r_{ij} p_{ij}}$ the magnitude of P_R indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary, 1979). That is, if P_R value is small (for instance, nearly zero) the dependent character considered (kernel yield) is fully explained by the variability in the independent characters, whereas higher P_R value indicates that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent character (seed yield).

RESULTS AND DISCUSSION

Phenotypic correlation coefficients of kernel yield with other traits

Complex traits like yield are measures of several correlated traits which directly or indirectly influence the expression of the trait. It indicates whether two variables are independent or vary together. Correlation analysis measures the relation between variables and can be positive or negative, significant or non-significant (Pavlov *et al.*, 2015). The phenotypic correlation coefficients of traits are given in Table.1 kernel yield has showed highly ($P < 0.001$) significant positive phenotypic correlation with pod yield ($r_{hp}=0.98^{**}$), harvest index ($r_{ph}=0.68^{**}$), number of Seed per pod ($r_{ph}=0.61^{**}$), number of pod per plant ($r_{ph}=0.60^{**}$), hundred seed weight, ($r_{ph}=0.45^{**}$) and shelling percentage ($r_{ph}=0.41^{**}$). The result was in agreement with the finding of (Mubai *et al.*, 2020) who reported highly significant differences among Peanut genotypes for number of pods per plant, hundred seed weight, and shelling percentage. Therefore selection based on highly positively correlated traits could maximize yield and suggests that a better exploration of these traits for the development of desirable genotypes (Myint *et al.*, 2021). Whereas, plant height ($r_{ph}=-0.25^{**}$) and oil content (-0.19^*) has a significant negative correlation with kernel yield at the phenotypic level similar finding were reported by (Venkataravana *et al.*, 2020).

Phenotypic correlation coefficients among other traits

In the present study days to flowering had shown a positive highly significant phenotypic correlation with days to maturity ($r_{ph}=0.34^{**}$) and number of branches per plant ($r_{ph}=0.31^{**}$). Similarly, positive significant phenotypic association with days to maturity in Peanut has been reported by (Kolo, 2021; Mubai *et al.*, 2020). Days to maturity has a significant

positive phenotypic correlation with number of branches per plant (0.41^{**}) and hundred seed weight ($r_{ph}=0.33^{**}$) this finding was in line with (Aliyi *et al.*, 2018) who reported positive significant correlation for number of branches per plant and hundred seed weight were plant height had negative significant phenotypic correlation coefficient with number of branch per plant ($r_{ph} = -0.56^{**}$), hundred seed weight ($r_{ph}=-0.32^{**}$), pod yield (-0.28^{**}) and hundred seed weight (-0.32^{**}). This finding was in line with the finding of (Venkataravana *et al.*, 2020) who reported that negative highly significant correlation between plant height with pod yield. Number of branches per plant has ($P < 0.001$) a positive highly significant to significant correlation with hundred seed weight ($r_{ph}=0.32^{**}$), pod yield ($r_{ph}=0.23^*$), and number of pods per plant ($r_{ph}=0.22^*$). Number of pods per plant has a positive highly significant correlation with number of seed per pod (0.91^{**}), pod yield (0.60^{**}), harvest index (0.4^{**}), shelling percentage (0.23^{**}) while oil content (-0.27^{**}) has negative significant correlation.

Number of pods per plant has a positive significant correlation with number of seed per pod ($r_{ph}=0.91^{**}$), pod yield ($r_{ph} =0.60^{**}$), harvest index ($r_{ph}=0.44^{**}$), kernel yield ($=0.60^{**}$), shelling percentage (0.23^{**}) while oil content (-0.27^{**}) has negative significant correlation. similar finding was reported for harvest index and kernel yield by (HajHussein *et al.*, 2018). Biomass yield has significant negative correlation with harvest index ($r_{ph} = -0.58^{**}$) and the rest traits has positive non-significant correlation. Pod yield had positive highly significant correlation with kernel yield ($r_{ph}=0.98^{**}$), harvest index ($r_{ph}=0.69^{**}$), hundred seed weight ($r_{ph}=0.49^{**}$), shelling percentage ($r_{ph}=0.23^*$). The finding was in agreement with (Shinde *et al.*, 2019) who reported that positive highly significant correlation for shelling percentage and hundred seed weight were as (Reddy *et al.*, 2017) for number of pod per plant, harvest index and hundred seed weight. (Jain *et al.*, 2016) also reported that, kernel yield and number of pod per plant had positive significant correlation with pod yield. Harvest index had positive significant correlation with kernel yield ($r_{ph}=0.68^{**}$), hundred seed weight ($r_{ph}=0.32^{**}$), Similar finding was reported for hundred seed weight by (Pachauri and Sikarwar, 2022). Whereas, positive significant correlation with shelling percentage ($r_{ph}=-0.18^*$). Shelling percentage has positive highly significant correlation with protein content ($r_{ph}=0.32^{**}$) and negative highly significant correlation with oil content ($r_{ph} = -0.29^{**}$). Oil content has negative significant correlation with protein content ($r_{ph}=0.20^*$).

Table 2: Phenotypic correlation coefficients (rp) of yield and yield related traits of Peanut genotypes

Traits	DF	DM	PHT	NBPP	NPP	NSPP	BMY	PY	HI	HSW	Sh%	Kernel Y	Oil%	PC%
DF		0.34**	-0.17ns	0.31**	0.16ns	0.14ns	0.03ns	0.14ns	0.10ns	0.12ns	-0.15ns	0.10ns	-0.09ns	-0.04ns
DM			-0.19*	0.41**	-0.13ns	-0.08ns	0.04ns	0.09ns	0.02ns	0.33**	-0.25*	0.04ns	0.18*	-0.17ns
PHT				-0.56**	-0.09ns	-0.09ns	-0.21*	-0.28**	-0.05ns	-0.32**	0.09ns	-0.25**	-0.04ns	-0.02ns
NBPP					0.22*	0.21*	0.03ns	0.23*	0.11ns	0.32**	-0.20*	0.17ns	0.11ns	-0.04ns
NPP						0.91**	0.07ns	0.60**	0.44**	0.04ns	0.23**	0.60**	0.27**	0.21ns
NSPP							0.03ns	0.61**	0.47**	0.02ns	0.20*	0.61**	-0.20*	0.21ns
BMY								0.16ns	-0.58**	0.09ns	0.07ns	0.16ns	0.01ns	0.06ns
PY									0.69**	0.49**	0.23*	0.98**	-0.12ns	0.20ns
HI										0.32**	0.18*	0.68**	-0.11ns	0.16ns
HSW											-0.07ns	0.45**	0.12ns	0.002ns
Sh%												0.41**	0.29**	0.32**
Kernel Y													-0.19*	0.26**
Oil%														-0.20*
PC%														

*, ** = significant at 1 % and 5% levels, respectively. DF=days to 50% flowering, DM = days to 95% maturity, PHT=Plant height, NBPP= number of branches per plant, NPP = number of pods per plant, NSPP = number of seeds per pod, BMY = Biomass yield, PY= Pod yield, HI = harvest index, HSW =hundred seed weight, SP= shelling percentage, KY= kernel yield, pc=protein content%, oil content %

Genotypic correlation coefficients of kernel yield with other traits

The genotypic correlation coefficients of traits are given in Tables. 6 kernel yield had significant positive genotypic correlation with pod yield ($rg=0.98^{**}$), harvest index ($rg=0.68^{**}$), number of pod per plant ($rg=0.64^{**}$), number of seed per pod ($rg=0.64^{**}$), hundred seed weight ($rg=0.48^{**}$), shelling percentage ($rg=0.40^{**}$), and significant correlation with protein content ($rg=0.28^{*}$) while plant height (-0.34^{**}) and oil content ($rg= -0.19^{*}$). Similar findings were reported for pod yield and harvest index by (Godhani *et al.*, 2020). while plant height has negative highly significant correlation with kernel yield ($rg=-0.34^{**}$) this finding was in line with (Venkataravana *et al.*, 2020) who reported negative highly significant correlation with kernel yield. The positive correlation of these traits with grain yield shows the presence of pleiotropic genes that control these traits in the same direction (Kearsey *et al.*, 1996). The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except few traits, which indicate the presence of inherent or genetic association among various characters.

Genotypic correlations among other traits

Days to flowering has ($P < 0.001$) positive significant correlation with days to maturity ($rg=0.36^{*}$), number of branch per plant ($rg=0.31^{**}$) similar finding was reported for days to maturity by (Kolo, 2021) were days to maturity had ($P < 0.001$) positive significant correlation with hundred seed weight ($rg=0.36^{**}$), number of branch per plant ($rg=0.34^{**}$). While shelling percentage has negative significant correlation ($rg=-31^{*}$). Plant height had ($P < 0.001$) negative highly significant genotypic correlation with number of branch per plant ($rg= -0.64^{**}$), pod yield ($rg=-0.36^{**}$), hundred seed weight ($rg= -0.38^{*}$). Number of branch per plant had positive ($P < 0.001$) highly significant correlation with hundred seed weight ($rg=0.37^{**}$) and pod yield ($rg=0.25^{*}$) this finding was in line with the (Yadlapalli, 2014; KOLO, 2021). Number of pod per plant had ($P < 0.001$) positive significant correlation with number of seed per pod ($rg=0.94^{**}$), pod yield ($rg=0.64^{**}$), harvest index

(0.47^{**}) and kernel yield (0.64^{**}). Similarly (Patil *et al.*, 2006) reported significant positive correlation for pod yield, for kernel yield by (Babariya and Dobariya, 2012). Number of seed per pod has positive significant genotypic correlation with pod yield ($rg=0.64^{**}$) and harvest index ($rg=0.49^{**}$) the rest traits has showed positive non-significant genotypic correlation coefficient. Biomass yield had ($P < 0.001$) negative highly significant association with harvest index ($rg= -0.57^{**}$) it has positive non-significant association with the rest characters.

Pod yield has positive significant genotypic correlation with harvest index ($rg=0.69^{**}$), number of pod per plant ($rg=0.64^{**}$), and hundred seed weight ($rg=0.53^{**}$) Similar finding was reported by (KUMAR *et al.*, 2019) for hundred seed weight (Ashna, 2014) for harvest index. Harvest index has positive significant genotypic correlation with pod yield ($rg=0.69^{**}$), kernel yield ($rg=0.68$) whereas, negative highly significant correlation were observed for biomass yield ($rg= -0.57^{**}$) and the rest characters had positive non-significant correlation. Hundred seed weight had positive significant genotypic correlation with days to maturity ($rg=0.36^{**}$), number of branch per plant ($rg=0.37^{**}$), pod yield ($rg=0.53^{**}$), harvest index ($rg=0.34^{**}$) and kernel yield ($rg=0.48^{**}$) whereas, negative significant correlation were observed for plant height ($rg= -0.38^{**}$) similar finding were reported for days to maturity and number of branch per plant by (Mubai, 2019) while the rest characters has positive non-significant correlation except shelling percentage. Shelling percentage has ($P < 0.001$) positive highly significant genotypic correlation with kernel yield ($rg=0.40^{**}$) the study was in line with the finding of (Ashna, 2014) for kernel yield. Were as negative significant correlation were observed for number of branch per plant ($rg= -0.29^{*}$), oil content ($rg= -0.32^{*}$). Oil content has negative significant correlation with number of pod per plant ($rg=-0.30^{*}$), while shelling percentage ($rg=-0.32^{*}$), and number of pod per plant ($rg=-0.30^{*}$), has showed negative significant correlation with oil content similar finding was reported for number of pod per plant by (Bhargavi *et al.*, 2015).

Table 3: Genotypic correlation coefficients (rg) of yield and yield related traits for Peanut genotypes.

Traits	DF	DM	PHT	NBPP	NPP	NSPP	BMY	PY	HI	HSW	Sh%	Kernel Y	Oil%	PC%
DF														
DM	0.34**													
PHT	-0.19ns	-0.21ns												

Traits	DF	DM	PHT	NBPP	NPP	NSPP	BMY	PY	HI	HSW	Sh%	Kernel Y	Oil%	PC%
NBPP	0.34**	0.44**	-0.64**											
NPP	0.18ns	-0.16ns	-0.15ns	0.23ns										
NSPP	0.16ns	-0.10ns	-0.16ns	0.23ns	0.94**									
BMY	0.027ns	0.04ns	-0.25ns	0.01ns	0.07ns	0.04ns								
PY	0.13ns	0.08ns	-0.36**	0.25*	0.64**	0.64**	0.17ns							
HI	0.08ns	0.00	-0.09ns	0.13ns	0.47**	0.49**	-0.57**	0.69**						
HSW	0.11ns	0.36**	-0.38**	0.37**	0.034ns	0.01ns	0.10ns	0.53**	0.34**					
Sh%	-0.16ns	-0.31*	0.07ns	-0.29*	0.24ns	0.19ns	0.08ns	0.23ns	0.18ns	-0.09ns				
Kernel Y	0.089ns	0.01ns	-0.34**	0.18ns	0.64**	0.64**	0.17ns	0.98**	0.68**	0.48**	0.40**			
Oil%	-0.09ns	0.18ns	-0.03ns	0.11ns	-0.30*	-0.24ns	0.01ns	-0.13ns	-0.11ns	0.13ns	-0.32*	-0.19*		
PC%	-0.04ns	-0.17ns	-0.04ns	-0.03ns	0.25ns	0.26ns	0.06ns	0.21ns	0.17ns	0.00ns	0.37ns	0.28*	-0.21ns	

*, ** = significant at 1 % and 5% levels, respectively. DF=days to 50% flowering, DM = days to 95% maturity, PHT=plant height, NBPP= number of branches per plant, NPP = number of pods per plant, NSPP = number of seeds per pod, BMY = Biomass yield, PY= Pod yield, HI = harvest index, HSW =hundred seed weight, SP= shelling percentage, KY= kernel yield, pc=protein content%, oil content %.

Path Coefficient Analysis

Path coefficient analysis, was method which partitions correlation coefficients into direct and indirect effects, allowing the estimates of contribution of each trait to seed yield (Wright, 1921). It is an effective way to find out the direct and indirect sources of correlation. The results of phenotypic and genotypic path coefficients were presented in Table 3 and 4 respectively.

Phenotypic direct and indirect effect of characters on kernel yield

High and positive phenotypic direct effects on kernel yield were exerted by pod yield (0.939), shelling percentage (0.189), and number of seed per pod (0.026), protein content (0.008), and hundred seed weight (0.006) similar, results were reported by (Reddy *et al.*, 2017; Pachauri and Sikarwar, 2022) this traits are effective for

selection of genotype with high kernel yield. The highest positive indirect effects on kernel yield were exerted by number of pod per plant (0.561), number of seed per pod (0.57), harvest index (0.65), hundred seed weight (0.46), shelling percentage (0.22) and protein content (0.19) via pod yield respectively. Oil content (-0.12) and plant height (-0.26) has showed negative high direct effect on kernel yield similarly (Bhargavi *et al.*, 2017; Venkataravana *et al.*, 2020) reported negative high direct effect. In this experiment the indication for negative direct effect of plant height on kernel yield indicating that kernel yield was increased in groundnut by selecting the plant with maximum number of pods. while small

negative indirect effect were exerted by number of seed per pod (-0.032), pod yield (-0.021), harvest index (-0.015), via number of pod per plant and hundred seed weight (-0.014) and oil content has showed negative indirect effect via shelling percentage on kernel yield similar result were reported for oil content by (Ram *et al.*, 2017) for plant height by (Zaman *et al.*, 2011). The residual effect (0.07) indicated that most of the variability in kernel yield for the genotypes under the present study has explained around 93% by the independent variables included in the analysis which implies that most of the variability are considered since, the variability explained are high.

Table 4: Direct (bold diagonal) and indirect effects (off diagonal) at phenotypic level of traits on kernel yield of Peanut genotypes tested at Pawe Agricultural Research center 2021

Trait	PHT	NPP	NSPP	PY	HI	HSW	SP%	Oil	Protein	rph
PHT	-0.005	0.003	-0.002	-0.262	0.000	-0.002	0.016	0.001	0.000	-0.25
NPP	0.000	-0.034	0.024	0.561	-0.004	0.000	0.044	0.005	0.002	0.60
NSPP	0.000	-0.032	0.026	0.571	-0.004	0.000	0.038	0.004	0.002	0.61
PY	0.001	-0.021	0.016	0.939	-0.006	0.003	0.044	0.002	0.002	0.98
HI	0.000	-0.015	0.012	0.649	-0.009	0.002	0.034	0.002	0.001	0.68
HSW	0.002	-0.001	0.000	0.462	-0.003	0.006	-0.014	-0.002	0.000	0.45
SP%	0.000	-0.008	0.005	0.216	-0.002	0.000	0.189	0.005	0.003	0.41
Oil	0.000	0.009	-0.005	-0.117	0.001	0.001	-0.055	-0.018	-0.002	-0.19
Protein	0.000	-0.007	0.006	0.186	-0.001	0.000	0.060	0.004	0.008	0.26

Residual 0.07; PHT=plant height, NPP = number of pods per plant, NSPP = number of seeds per pod, PY= Pod yield, HI = harvest index, HSW =hundred seed weight, SP= shelling percentage, protein content%, oil content %

Genotypic direct and indirect effect of various characters on kernel yield

High and positive genotypic direct effects on kernel yield were exhibited by pod yield (0.935), and shelling percentage (0.183) the result was in agreement with the results obtained by (Kumar *et al.*, 2014; Rao, 2016; Ramakrishnan *et al.*, 2017). Therefore, selection based on these traits would result in genetic improvement in groundnut. Whereas number of pod per plant (0.030), hundred seed weight (0.005) and protein content (0.011) has showed relatively small direct positive effect on kernel yield. Whereas harvest index (-0.004), plant height (-0.010) and number of pod per plant (-0.031) has negative direct effect on kernel yield similar, finding were reported by (Mitra *et al.*, 2021). Number of pod per plant (0.596), number of seed per pod (0.601), harvest

index (0.643), hundred seed weight (0.491), shelling percentage (0.218), and protein content (0.200) has exerted highest positive indirect effect on kernel yield via pod yield at genotypic level similarly, finding were reported by (Aliyi *et al.*, 2018). while negative highest indirect effect were exerted by plant height (-0.337) via pod yield this finding is in line with (Venkataravana *et al.*, 2020) who reported negative highly significant indirect effect for plant height. Were number of seed per pod (-0.029), pod yield (-0.02 harvest index (-0.015), protein content (-0.008) and shelling percentage (-0.007) has small negative indirect effect on kernel yield via number of pod per plant at genotypic level this result indicated that the true relationship between the traits which helps for improvement through selection.

Table 5: Direct (bold diagonal) and indirect effects (off diagonal) at genotypic level of traits on kernel yield of Peanut genotypes tested at Pawe Agricultural Research center 2021

Trait	PHT	NPP	NSPP	PY	HI	HSW	SP	Protein	rg
PHT	-0.010	0.005	-0.005	-0.337	0.000	-0.002	0.013	0.000	-0.336
NPP	0.001	-0.031	0.028	0.596	-0.002	0.000	0.044	0.003	0.639
NSPP	0.002	-0.029	0.030	0.601	-0.002	0.000	0.036	0.003	0.640
PY	0.004	-0.020	0.019	0.935	-0.003	0.003	0.043	0.002	0.982
HI	0.001	-0.015	0.015	0.643	-0.004	0.002	0.033	0.002	0.676
HSW	0.004	-0.001	0.000	0.491	-0.002	0.005	-0.016	0.000	0.481
SP	-0.001	-0.007	0.006	0.218	-0.001	0.000	0.183	0.004	0.402
Protein	0.000	-0.008	0.008	0.200	-0.001	0.000	0.069	0.011	0.279

Residual =0.06; PHT=plant height, NPP = number of pods per plant, NSPP = number of seeds per pod, PY= Pod yield, HI = harvest index, HSW =hundred seed weight, SP= shelling percentage, protein content %.

Phenotypic path analysis of oil content with other traits

The phenotypic direct and indirect effect of different characters on oil content is presented in Table 5. Number of seed per pod (0.26), days to maturity (0.07) followed by kernel yield (0.03) had exerted positive direct effect on oil content at phenotypic level. However, number of pod per plant (-0.45) shelling percentage (-0.20) and protein content (-0.09) had negative direct

effect on oil content. Number of seed per pod, days to maturity, and kernel yield ultimately affects oil content were the components that exerted a substantial direct effect on oil content. The residual effect determines unaccounted variability of the dependent factor (oil content). Its magnitude 0.08 indicated that the characters included in the path analysis explained 92% of the variation in oil content.

Table 6: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level for different characters on oil content in Peanut genotypes

Trait	DM	NPP	NSPP	SP	KY	PC	rp
DM	0.07	0.06	-0.02	0.05	0.00	0.02	0.18
NPP	-0.01	-0.45	0.23	-0.05	0.02	-0.02	-0.27
NSPP	-0.01	-0.41	0.26	-0.04	0.02	-0.02	-0.20
SP	-0.02	-0.10	0.05	-0.20	0.01	-0.03	-0.29
KY	0.00	-0.27	0.16	-0.08	0.03	-0.02	-0.19
PC	-0.01	-0.10	0.05	-0.06	0.01	-0.09	-0.20

Residual = 0.08; DM= days to maturity, NPP =number of pod per plant, NSPP =number of seed per pod, SP = shelling percentage, KY =kernel yield, PC = protein content, rp = phenotypic correlation with kernel yield.

Genotypic path analysis of oil content with other characters

The Genotypic direct and indirect effect of different characters on oil content is presented in Table.6 number of pod per plant (-0.24) and shelling percentage (-0.27) had showed negative direct effect on oil content. The residual (0.08) indicated that characters which are included in the genotypic path analysis explained 92% of the total variation in oil content. Path analysis indicated that number of pod per plant and shelling percentage could be used as indirect selection criteria for better oil content.

Table 6: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level for different characters on oil content in Peanut genotypes.

Trait	NPP	Sh%	rg
NPP	-0.24	-0.06	-0.27
Sh%	-0.06	-0.27	-0.29

Residual = 0.08; NPP= number of pod per plant, Sh= shelling percentage, rg= genotypic correlation with kernel yield.

CONCLUSION

Scientific information about genetic variability is very important for developing successful breeding strategies. So, genetic variability present in a population and interrelationships among Characters is also essential to design breeding strategies in crop improvement. To generate such information 64 Peanut genotypes including three released varieties (Maniputer, babile-3, and babile-4) were tested in 8x8 simple lattice designs under rain fed conditions at Pawe Agricultural Research Center in Benshangul-Gumuz regional state, Western Ethiopia. Data were collected for 14 traits on plot base as well as plant bases and subjected to analysis of variance

using SAS software proc lattice and GLM procedure. The correlation and path coefficient analysis indicated that, Kernel yield showed highly significant positive genotypic and phenotypic correlation with pod yield. Positive and high direct effect of path analysis both at genotypic and phenotypic level was observed by pod yield and shelling percentage respectively. The correlation and path coefficient analysis indicated that, Kernel yield showed a positive and strong correlation with pod yield and exerted positive highest phenotypic and genotypic direct effect both at genotypic and phenotypic levels. This trait will be useful for direct selection to increase grain yield. Therefore, the current study indicates the existence of considerable variability for most traits studied and differences in the performance of the genotypes as there were statistically significant differences among genotypes. These conditions indicated that there is a good opportunity to improve these traits using the tested genotypes in Peanut breeding programs.

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