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Genetic Variability Heritability and Expected Genetic Advance in Peanut (Arachis hypogaea L.) Genotypes at Pawe, Northwestern Ethiopia

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ABSTRACT
Peanut (Arachis hypogaea L.) is one of the most significant oil seed crop of the world and the second most important source of vegetable oil in Ethiopia. But productivity is insufficient as compared to the world average productivity because of low genetic variability, biotic and abiotic stress, and poor seed system. This experiment was designed to evaluate genetic variability for 64 groundnut genotypes using 8x8 simple lattice design at Pawe northwestern Ethiopia, in 2021/22.The objectives of the study were to estimate the genetic variability among the genotypes. Analysis of variance revealed that, there was highly significant difference among the sixty four genotypes for all traits studied. Kernel yield showed the highest GCV and PCV values, while the lowest was seen in the shelling %.Harvest index (41.13), number of branches per plant (39.79), number of pods per plant (42.96), hundred seed weight (42.70), kernel yield (41.97), biomass yield (41.78), and pod yield (42.96) all showed moderate heritability and high genetic progress as a percentage of the mean (35.55). The results of this study showed that the genotypes had enough variation, therefore there was a good chance of identifying genotypes for future breeding programs that would be promising.

1. INTRODUCTION

Peanut (Arachis hypogaea L..) is a self-pollinated, annual, herbaceous, allotetraploid legume having genome AABB with somatic chromosome number (2n = 4x = 40), which belonging to the family Leguminoceae (Stalker and Wilson, 2015). Peanut is usually produced for food, cash earnings, and animal feed its haulms and leaves are serve as a rich source of cattle feed and its oil is the most crucial made from the crop, which is use for both domestic and commercial functions with many benefits having easily digestible proteins, high-quality oils, and important elements such as iron and zinc which are important especially in children it also increases soil fertility and productivity by fixing atmospheric nitrogen (Francisco and Resurreccion, 2008; Pasupuleti et al., 2013; Jibrin et al., 2016; Hamidou et al., 2018). The world leading producer of Peanut was china with 18,300 mt followed by Indian 7,000 mt and Nigeria 4,500 mt of the world production (FAOSTAT, 2020 and USDA, 2022). In Africa Peanut is grown with huge economic income at households and national level with average productivity of 0.96 t/ha which is poor when compared to the china (3.9 t/ha) and USA (3.5 t/ha) (FAOSTA, 2020). In Ethiopia Peanut is grown by smallholder farmers in the lowland areas and plays a significant economic role (Abady et al., 2019; Kebede et al., 2017). In 2022 cropping season the total area coverage of Peanut in Ethiopia is 113,514 ha with a total production of 2050.6 tone having productivity of 1.8 t/ha (CSA, 2021). The largest Peanut producing region in Ethiopia are found in Oromia (57,721 ha) and Benshangul-Gumuz (28,898 ha) regional states with average national productivity of 1.8 t/ha (CSA, 2021) respectively. Peanut production in the study area has been increasing but the productivity was too low due to lack of improved variety and poor seed system. Generally the average national productivity was lower than the global yield due to different production constraints those are lack of improved varieties, narrow genetic potential of released varieties, poor soil fertility, pre-harvest diseases, use of low-yielding varieties, and limited availability of improved varieties (Abady et al., 2019). On the other side, the demand for oil crop production is increasing due to expansion of agro-processing industries, and urbanization (Hagos and Bekele, 2018). Producers in the study area have high demand for varieties with desirable traits, high yield, wider adaptability, biotic and abiotic stress tolerance. This can be achieved through phenotypic and molecular characterization of plant genetic resource Govindaraj et al. (2015). So, to improve the yield of Peanut, plant breeders should have a better understanding of the genetic variability of yield and its components and

development of high yielding cultivars as breeding programs depends on the amount of variability available in the existing population (Vinithashri et al., 2019).

Objectives of the Study

❖ To estimate the magnitude of genetic diversity for yield, yield related and quality traits of Peanut genotypes

2. Material and method

2.1. Description of Experimental Sites

The experiment was conducted at Pawe Agricultural Research Center on station during the main cropping season of 2021/22. Pawe Agricultural Research Center is located at (11018`49.6``N and 036024`29.1``E) in Metekel zone. It is located 570 km away from Addis Ababa, the capital city of Ethiopia (Figure 1). The elevation of the area ranges from1150 meters above sea level (m.a.s.l).The site receives 1586mm rainfall annually. The mean annual maximum and minimum temperatures are 32.60c and 16.50c, 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 station is characterized as nitosol or loam (PARC, 2017).

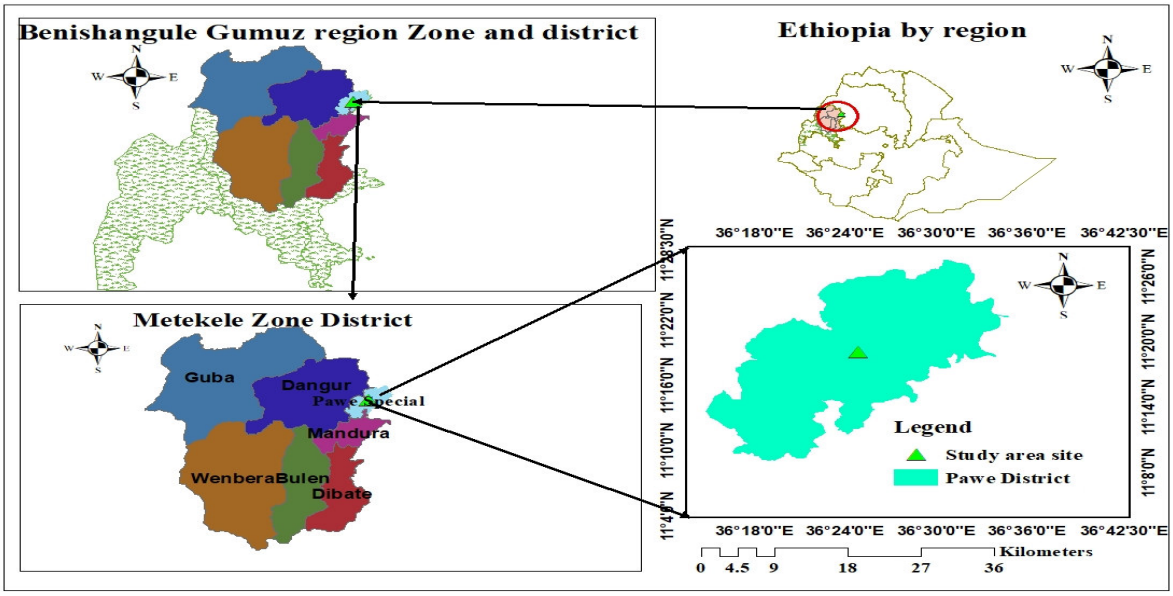

Figure 3.Map of the study area location

2.2. Experimental Materials

A total of 64 introduced groundnuts were used for the experiment. These genotypes were obtained from Pawe Agricultural Research Center.

2.3. Experimental Design, Procedure, and Trial Management

A total of 64 introduced groundnuts were used for the experiment. These genotypes were obtained from Pawe Agricultural Research Center. The experiment was laid out in 8x8 simple lattice designs with 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 applied during planting. Weeding and other agronomic management practices was done as per the recommendation for groundnut.

3. Data collected

Data was collected on a plot and plant basis. Data on days to 50% flowering, days to 95% maturity, protein content (%), oil content (%), Shelling percentage, kernel yield (kg), stand count, hundred seed weight, pod yield, harvest index, biomass and yield were recorded on plot base. Whereas plant height, number of branch per plant, number of total pod per plant, number of pod per plant, number of seed per pod was recorded on plant base. On a plant basis, five individual plants was selected randomly as sample plant from the middle two-rows leaving others rows as borders. Kernel yield per plot was measured from the middle two rows and converted to hectare bases. For the determination of the quantity of oil and protein, one hundred grams of dried seed samples from each genotype will be grinded in the laboratory room.

3.1. Data collected from phonological character.

Days to 50% emergence: was recorded as the number of days from sowing to the date when 50% of the plants in a plot will be emerged from the soil.

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.

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. The physiological maturity was determined by the hardness of the pods, the appearance of darkened veins of the inner portion of the shell, vascular stands on the shell became more distinct and pinkish full-grown kernels, gradually withered and the inside of the wall pod became shiny and dark to brown IBPGR, (1992).

3.2. Data collected from growth traits

Plant height: was recorded by measured from 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.

Number of Branch per plant: was calculated by counting the number of branches from five randomly selected plants and averaged to the number of plants considered.

3.3. Data collected from yield related traits

Biomass yield t/ha: Above ground, biomass was measured per net plot at harvest after sun drying and converted into ton per hectare.

Stand count at harvest: was recorded by counting the number of plants at harvest from the net plot.

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.

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.

Hundred seed weight (g): was recorded by counting hundred seeds randomly from a bulk of shelled seeds and weighed using a sensitive balance.

Pod yield (kg/ha): was calculated from the net plot and expressed in kilograms per hectare after sun drying for 6 days and converted in to hectare base.

Shelling percentage (%): was calculated by taking sample of 200g mature pods per plot randomly and will be calculated as:

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

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.

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.

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

3.4. Data Collected from Quality Traits

Oil

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. The ether, being very non-polar, dissolves the fat in the substance and allows it to pass through the filter and out of the sample. The amount of fat in a substance can be determined by taking the mass of the substance before and after the extraction. The extraction was done based on the following steps; seeds were cleaned and dried in an oven at 105 ºC for 48 h before the extraction procedure. Ten grams of seeds of each genotype were crushed using an electrical crusher and transferred into a thimble topped with cotton. This was followed by oil extraction using a conventional Soxhlet method with petroleum ether (40–60 °C) for 4 h using a Soxhlet apparatus. 1gm of sample for the Soxtec 2043 model was used on a fat free filter paper to an accuracy of. 28 ±1mg. The thimble was dried at 80 ºC for two hours then cooled at room temperature in desiccator. Groundnut oil extraction was double extracted (AOAC, 1990).Oil percentage of the samples was analyzed at Pawe Agricultural Research center quality laboratory. The percent of oil content of the seeds and oil yield was determined using the following formulas;

$$Oil\ in\ ground\ sample\ \% = \frac{Weight\ of\ oil(g)}{Weight\ of\ sample\ (g)} \times 100$$

Protein

Protein content was determined according 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. The digested sample was distilled in bunchi 339 distillation units to liberate ammonia using (40% NaOH). The liberated ammonia was trapped in a weak boric acid solution and titrated with a standardized 0.1N sulphuric acid. Then the amount of nitrogen and crude protein were calculated as follow.

$$\% \text{ Kjeldahl Nitrogen} = \frac{(VS - VB) \times N \times 14.01}{W \times 10}$$

Where, Vs = ml of standardized acid used to titrate a sample
Vb = ml of standardized acid used to titrate a reagent blank
N = normality of standard H2SO4, 0.1000 = normality of standard H2SO4
14.01 = atomic weight of nitrogen, W = weight, in grams, of sample or Standard
10 = factor to convert mg/gram to percent
% Crude Protein = % Kjeldahl Nitrogen x F
F = factor to convert nitrogen to protein, 5.46

3.5 Estimation of genetic parameters

Estimation of variance components

The phenotypic and genotypic variability of each trait was estimated as phenotypic and genotypic variances and coefficients of variation. The phenotypic and genotypic variances and coefficients of variation was estimated according to the method suggested by (Singh, 1985) as follows:

Environmental variance (σ 2e) = MSe

Genotypic variance (σ 2g) = $\left[\frac{MS_g - MS_e}{r}\right]$

Phenotypic variance (σ 2p) = σ 2g + σ 2e

$$Phenotypic\ Coefficient\ of\ variation\ (PCV) = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$$

$$Genotypic\ Coefficient\ of\ variation = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

Where, $\bar{x}$ = grand mean of traits.
r = number of replications,
MSg = mean square due to genotypes and
MSe = mean square of error.

According to Deshmukh et al. (1986), PCV and GCV can be categorized as low (<10%), moderate (10-20%), and high (>20%).

Heritability in broad sense

The heritability was estimate or calculated by (Robinson et al., 1949) as follows 0 - 30% = low,30 - 60% = medium and >60% = high.

Broad sense heritability (H2), as a percentage, was derived for each character using variance components as explained by (DeLacy et al., 1996)

$$h^2 = \left[\frac{\sigma^2_g}{\sigma^2_p}\right] x100$$

Estimation of Expected Genetic Advance from Selection

Genetic advance in the absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated following the methods illustrated by (Johnson et al., 1955) as:

GA = K σ ph2

Where GA=Genetic advance
K=the standardized selection differential at 5% selection intensity (K = 2.063)

σ p =Phenotypic standard deviation on mean basis
h2 =heritability in broad sense

Genetic advance as percent of mean (GAM)

Genetic advance as percent of means was calculated to compare the extent of predicted advance of different traits under selection, using the following formula

$$GAM = (GA/\bar{x}) \times 100$$

Where, GAM = Genetic advance as percent of mean

GA = Genetic advance

The GA as percent of mean was categorized as low, moderate and high as suggested by (Johnson et al., 1955) as follows.

0 - 10% = Low, 10 – 20% = Moderate, and >20% = High

4. RESULTS AND DISCUSSION

Results obtained on variability assessment, associations among yield and yield related characters and genetic divergence are presented. Implications of such studies in Peanut improvement and breeding program for higher seed yield and other quality traits of interest are also discussed.

4.1. Analysis of Variance

The analysis of variance revealed that there was a highly significant ($p < 0.01$) difference among genotypes for all the studied traits indicating the presence of sufficient variability among the genotypes for those studied traits. The mean square values of 14, traits and 64 peanut genotypes are presented in Table2 and table3. Plant height, branch per plant, biomass yield, pod yield, harvest index, hundred seed weight, shelling percentage and kernel yield showed highly significant difference at ($p<0.001$). Similar to the present finding, (Chavadhari et al., 2017) reported significant difference among peanut genotypes for the traits day to maturity, plant height, and number of branches per plant, pod yield, kernel yield, shelling percentage and harvest index. The presence of significant differences between genotypes suggests that each character is variable and gives the greatest chance for choosing genotypes with the desired character for improvement.

Table 1.Mean squares of eight traits tested in lattice design

Traits	Rep (1)	Genotype adjusted (63)	Block with in rep adjusted (14)	Inter block (49)	RE over RCBD	R square
PHT	119.4	3246.07**	23.38	9.51	116.98	0.92
NBPP	7.13	228.85**	0.55	0.41	101.81	0.94
BY	132.6	13998645.12**	24086	19905	100.78	0.94
PY	2345	18180146.08**	51507	21844	115.41	0.95
HI	0.86	7636.54**	28.75	11.79	116.66	0.94
HSW	199	6483.06**	8.79	8.11	100.14	0.95
Sh	3.47	2114.68**	9.1	8.61	100.07	0.87
KY	2184	11501481.03**	35856	15936	113.74	0.95
Oil%	8.34	2065.12**	0.2	0.14	102.1	0.99

Note: PHT = plant height, NBPP =number of branch per plant, BY = biomass yield, PY =pod yield, HI =harvest index, HSW = hundred seed weight, Sh =shelling percentage, KY = kernel yield.

Table 2.Mean squares of four traits of groundnut genotypes tested in RCBD.

Traits	Replication (1)	Genotype (63)	Error (63)	CV%	R- square
DF	0.78ns	20.30**	0.83	1.96	0.96
DM	0.38ns	79.87**	4.68	2.17	0.94
NPPP	7.13ns	16.46**	3.24	14.75	0.84
NSPP	11.40ns	49.57**	14.64	18.11	0.77
PC	0.13ns	4.20**	0.18	1.98	0.96

Note: ** = Significant at 1% probability level. Ns= non-significant, RCBD= Randomized complete block design DF= Degree of freedom. DF = Days to 50% flowering, DM = Days to maturity, NPPP = Number of pod per plant, NSPP = Number of seed per pod, Pc = Protein content.

4.1.1. Estimation of variance components

Estimate of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are provided in Table4. High GCV and PCV was recorded for number of branch per plant (23.5), (37.25), number of pod per plant (21.08), (36.39), biomass yield (22.38), (34.62), pod yield (26.34), (40.19) and kernel yield (27.37), (42.25). These higher GCV and PCV values suggested that the genotypes in this study had a diverse genetic basis and high

variability, allowing for efficient genetic improvement via selection based on phenotypic expression of these traits. Similar results have been noted by different authors such as (Mubai et al., 2019), who observed high value for number of branches per plant, number of pods per plant and kernel yield, Chavadhari et al., (2017) found high GCV and PCV values for kernel yield and pod yield. Moderate GCV and PCV were recorded by plant height (12.33), (21.01), number of seed per pod (14.34), (17.92) and oil content (8.93), (12.68). Low GCV and PCV values were obtained from days to flowering (6.7), (9.91), days to maturity (6.15), 9.22), shelling percentage (4.86), (8.93), and protein content (6.54), (9.67). similar findings were reported for days to flowering and days to maturity by (Mitra et al., 2021) for shelling percentage by (Babariya and Dobariya, 2012; Ashna, 2014). The indication for low value of GCV and PCV was that they are controlled largely by non-additive gene action and selection would be less effective, so there is opportunity to create variability through hybridization or mutation followed by selection. Generally in this study the PCV value is greater than the GCV value indicating that large influence of environment for the expression of all the studied traits as result selection based on the GCV and PCV values are not much rewarding for higher kernel yield of Peanut genotypes. Similar finding was report by (Rao, 2016).

4.1.2. Estimation of heritability and Genetic advance

The estimates of broad sense heritability and genetic advance as percentage of the mean ranged from 24.5-49.57% and 5.45-36.57%, respectively. Moderate heritability with high GAM were recorded for number of branch per plant, number of pod per plant, biomass yield, harvest index, hundred seed weight, and kernel yield. Similarly, moderate heritability with high GAM was reported for harvest index and pod yield by (Kumar et al., 2019) for hundred seed weight by (Khaliqi, 2021), for Pod yield, number of pod per plant and kernel yield by (Sardar et al., 2017). Therefore, number of branch per plant, number of pod per plant, biomass yield, harvest index, hundred seed weight, and kernel yield will be improved easily than other traits. While, the other traits showed moderate heritability and low genetic advance as percent of the mean, which makes the improvement of Peanut genotypes for higher grain yield based on those traits or characters are difficult. In the current study low heritability with low GAM were observed for shelling percentage (29.58%), (5.45). Similarly, finding was also reported for shelling percentage by (Mofokeng et al., 2021). The indication for low heritability with low GAM was that environmental influence was high and less heritable (Holland et al., 2003).

Table 3.Estimates of range, mean, genetic components of variance, heritability and genetic advance of Peanut genotypes for 14 characters at Pawe on station.

Trait	Mean	Range		σ2p	σ2g	GCV %	PCV %	H2b %	GA (k=2.06)	GAM %
		Min	Max							
DF	46.47	35	51	21.2	9.7	6.7	9.91	45.74	4.29	9.24
DM	99.73	82	108.5	84.56	37.59	6.15	9.22	44.46	8.08	8.1
PHT (cm)	37.18	23.9	47.8	61.04	21.01	12.33	21.01	34.42	5.55	14.92
NBPP	5.4	3.6	9.6	4.05	1.61	23.5	37.25	39.79	1.65	30.57
NPPP	12.2	5.8	19.7	19.7	6.61	21.08	36.39	33.55	2.84	23.27
NSPP	21.13	11.5	37.8	58.54	14.34	17.92	36.21	24.5	3.87	18.3
BY(kg/ha)	1421.196	711.1	2211.95	242106.04	101147.7	22.38	34.62	41.78	424.1	29.84
PY(kg/ha)	1386.318	594.91	2581.21	310417.75	133364.88	26.34	40.19	42.96	493.78	35.62
HI%	39.47	22.2	57.1	133.01	54.71	18.74	29.22	41.13	9.79	24.79
HSW	37.98	23.2	65.4	111.01	47.4	18.13	27.74	42.7	9.28	24.44
Sh%	72.71	54.13	80.48	42.18	12.48	4.86	8.93	29.58	3.96	5.45
OC%	45.26	35.06	53.03	32.92	16.32	8.93	12.68	49.57	4.97	10.98
PC%	21.66	18.69	24.98	4.38	2.01	6.54	9.67	45.8	1.81	8.37
KY(kg/ha)	1054.52	436.2	1994.71	198499.05	83313.67	27.37	42.25	41.97	385.76	36.58

Note: DF = days to 50% flowering, DM = days to maturity, PHT = Plant height (cm), NBPP = Number of branch per plant, NPPP = Number of pod per plant, NSPP = number of seed per pod, BY= Biomass yield (kg/ha), PY =Pod yield (kg/ha), HI% = Harvest index, HSW = Hundred seed weight, sh% = Shelling percentage, KY = Kernel yield (kg/ha), OC% = Oil content percent, PC% = Protein content. σ2g = Genotypic variances, σ2p = phenotypic variances, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, H2b = broad sense heritability, GA =expected genetic advance and GAM = genetic advance as percent of the mean

Conclusion and Recommendations

The result on the present study revealed the existence of highly significant difference (P<.001) among the tested Peanut genotypes. The study shows that there is highly significant difference for all quantitative and qualitative traits. The highest GCV and PCV was recorded by number of branch per plant, number of pod per plant, biomass yield, pod yield and kernel yield. These indicates that high GCV and PCV values suggested that the genotypes in this study had a diverse genetic basis and high variability, allowing for efficient genetic improvement via selection based on phenotypic expression of traits. Generally this study was performed on single location for only one season since phenotypic expression is affected by environmental conditions, the data generated in this study may not be similar over location. Therefore materials on this study will be checked in different environment for more season to get more promising genotypes. However, molecular genetic variability would provide more appropriate and satisfactory result therefor there is a need to perform molecular characterization on those genotypes in order to identify the genetic variability, and heritability of yield and yield related traits at molecular level.

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