Research Article

Genetic Variability, Traits Association and Path Coefficient Analysis in Advanced Lines of Groundnut (*Arachis hypogaea* L.)

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Abstract | Groundnut (*Arachis hypogaea* L.) is an important grain legume crop. However, there is still great need to develop superior varieties and lift its production. Germplasm characterization plays a vital role in improved cultivars' development. The current study was conducted to estimate genetic variability, traits association, and path coefficient analysis in eleven groundnut advanced breeding lines together with check *vis* BARD-479, using randomized complete block design with three replications at National Agricultural Research Centre, Islamabad, Pakistan. Through One-Way Analysis of variance significant discrepancies were found among the genotypes for most of the traits. In this study 100 kernels weight was found in significant positive correlation (0.821 **) with twenty pods length, while in significant negative correlation (-0.850 **) with plant width. Similarly, the trait of dry pods yield was in significant positive correlation (1.216**) with plant height, while was significant negatively correlated (-.850**) with number of branches. A strong positive direct effect was observed between twenty pods length (5.548), shelling percentage (4.630), 100-kernels weight (3.738), and leaflet length (2.950) with dry pods yield, indicating the importance of traits linkage in groundnut genotypes improvement. A weak direct effect was found among morphological traits i.e., number of branches (1.419), plant height (.311), and plant width (1.058). A strong indirect effect was witnessed by Leaflet width (-2.225) with dry pods yield. Furthermore, genotypes PG-1221, PG-1259, PG-1254, and PG-1266 were found with promising yield potential of 3637 Kg/ha, 3430 Kg/ha, 3286 Kg/ha, and 3176 Kg/ha, respectively, hence recommended for further evaluation through future breeding program.

Received | August 25, 2020; **Accepted** | November 30, 2020; **Published** | March 30, 2021
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Citation | Jahanzaib, M., Nawaz, N., Arshad, M., Khurshid, H., Hussain, M. and Khan, S.A., 2020. Genetic; variability, traits association and path coefficient analysis in advanced lines of groundnut (*Arachis hypogaea* L.). *Journal of Innovative Sciences,* 7(1): 88-97.
DOI | http://dx.doi.org/10.17582/journal.jis/2021/7.1.88.97
Keywords | Groundnut, Genetic variability, Yield, Character association, Path coefficient analysis

1. Introduction

Groundnut (*Arachis hypogaea* L.) is an allotetraploid (2n=4x=40), most probably originated in the region of eastern foothills of Andes, Southern Bolivia, and Northern Argentina (Hampannavar and Khan, 2019). It is widely grown as an oilseed and food crop in more than 144 countries worldwide, where commercial production mostly confined between 40°S and 40°N latitudes. Groundnut is presumed to be domesticated in South America about 6 thousand years ago followed by widely distribution in post-Columbian times. As a rich source of seed oil (~46–58%) and protein (~22–32%), it has great potential to cope with the problem of malnutrition and to ensure food security (Zhuang *et al*., 2019). Groundnut is also a good source of minerals and vitamins including vitamin E, niacin, phosphorus, falcin, calcium, riboflavin, magnesium, zinc, iron, thiamine, and potassium (Jibrin *et al*., 2016). Besides, the haulm is a good source of animal feed as well as industrial raw material. More importantly, groundnut contributes in soil fertility by fixation of atmospheric nitrogen (Nigam, 2014). Groundnut is widely known as poor man's almonds due to its high nutritional contents as well as fat and protein level, making up 80% of seeds contents. Furthermore, groundnut is also a vibrant ingredient in numerous delicious commercial products (Pandey *et al*., 2012; Pandey and Varshney, 2018). Besides, groundnut being a legume crop is an important candidate for crop rotation resulting soil enrichment and fertility via atmospheric nitrogen fixation and breaking pest and disease cycles (Pandey *et al*., 2020).

Growing demand for food security has spiked the need of genetic improvement of crop germplasm. Genetic variability being a best option for crop cultivar improvement has intensively used in the past (Jaganathan *et al*., 2020). Unfortunately, the process of new cultivar development in groundnut has been remained a bottleneck due to its comparatively low level of variability among the available germplasm and its complex genome size. Genetic discrepancies among the germplasm of any crop are the basic requirement for crop improvement. Worldwide groundnut germplasm collections are preserved including India with 15,445 accessions, followed by USA with 9310 accessions, and China with 7837 accessions (Pandey *et al*., 2012). The *Arachis* genera can be alienated into nine sections comprising of 81 species from two ploidy groups (diploid and tetraploid) with enormous diversity of genomes including A, B, AB, D, F, K, EX, T, PR, H, C, T, E, R1 and R2 (Stalker, 2017). Effectiveness of superior genotype selection is primarily reliant on the availability of large genetic variability in the germplasm for the trait of interest and the degree of its heritability (Hugar and Savithramma, 2015; Padmaja *et al*., 2015). The selection is further valued by the direction and extent of association between the traits of interest (Shrey *et al*., 2015). The association analysis creates statistics about the relationship among the traits of interest and thus possibility of indirect selection, when required. Similarly, path coefficient analysis provides knowledge about the direct and indirect effects of specific trait on other traits and finally on the trait of yield. In case of peanut selection for productive lines based on phenotypic traits is not so effective due to hypogeal nature of its fruit. Direct or indirect selection option for yield-related traits is highly worthwhile, most suitable in case of segregating populations. In this regards correlation analysis is useful since information about the nature and magnitude of interrelationships among various traits is not only important in defining the selection potential of an isolated trait but also identifies the effects on a particular trait based on the selection for another trait (Cruz and Regazzi, 1997). The significance of the traits correlations in genetic improvement defends on how the variation in one trait has the ability to affect others during a selection process (Santos *et al*., 2000). Though, selection strategies which are based on the correlations between traits can only encourage errors, since their association with each other might be linked to a third trait or even to a group of traits in most cases (Cruz and Regazzi, 1997). The correlation coefficient between any two traits cannot give a comprehensive picture of a complex trait like yield, which is jointly determined by several traits in the form of direct and indirect effects. Therefore, the level of applicability of correlations can more clearly be understood using the path analysis. Path analysis allows the division of correlation into direct and indirect effects resulting as a valuable tool in various breeding programs in a wide array of crops (Gomes *et al*., 2007; Gomes and de Almeida Lopes, 2005; Oliveira *et al*., 2007).

Keeping in view the importance of the above mentioned provisions in new cultivar development this study was carried out with the objectives to estimate the genetic variability, traits association, and path coefficient analysis for yield and yield-related traits in groundnut germplasm comprising eleven advanced lines. This study will help in harnessing the existing genetic variability among evaluated advanced lines and selection of superior lines in future breeding programs.

2. Materials and Methods

2.1 Study area and experimental material

The current study was conducted at the Oilseed Research Program, National Agricultural Research Centre (NARC), Islamabad, Pakistan (33.6701° N, 73.1261° E latitude with 540 meters altitude). The experimental design used was randomized complete block design (RCBD) with three replications. Groundnut germplasm evaluated in this study comprised of eleven advanced breeding lines along with check cultivar, BARD-479 (Table 1).

Table 1: Genotypes used in the study.

S. No.	Code	Identity
1	479	BARD-479
2	PG-1221	ICG-6590
3	PG-1254	BARD-479 x PG-1058
4	PG-1255	BARD-479 x PG-1058
5	PG-1256	BARD-92 x PG-1053
6	PG-1258	BARD-92 x PG-1053
7	PG-1259	BARD-92 x PG-1053
8	PG-1261	PG-1050 x PG-1074
9	PG-1262	PG-1050 x PG-1074
10	PG-1265	PG-1058 x PG-668
11	PG-1266	PG-5 x PG-1058
12	PG-1267	PG-5 x PG-1058

2.2 Crop husbandry

Recommended cultural practices were applied during the crop growing season. For seedbed preparation two ploughings were made, followed by planking. The genotypes were planted on 15th of April, 2019, on sandy loam soils in three rows of 4 meters length for each entry with a row-to-row distance of 50 cm and plant to plant 15 cm. The seed rate at sowing was kept 75 kg/ha. Nitrogen, Phosphorus, and Potassium (NPK) fertilizer was applied @ rate of 20-80-50 kg/ha and other cultural operations such as weeding, hoeing, and use of insecticides were applied.

2.3 Data recording and statistical analysis

Five plants from each advanced line as well as check cultivar were randomly selected and data were recorded. Data were recorded and analyzed on nine traits including number of branches, plant height, plant width, twenty pods length, shelling percentage, 100-kernel weight, leaflet length, leaflet width, and dry pods yield. For all the studied genotypes and characterized traits One-Way Analysis of Variance (ANOVA) was calculated using Statistix 8.1 (2003). The genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were calculated according to Burton (1952), the genotypic and phenotypic correlations were determined according to Al-Jibouri *et al.* (1958), and the path coefficient analysis was calculated according to Dewey and Lu (1959). Data were analyzed statistically by using software Statistix 8.1 (2003) and Microsoft Excel (2010).

3. Results and Discussion

ANOVA revealed significant differences among the genotypes for most of the traits (Table 2). Differences found among the genotypes for the characterized traits showing the presence of genetic variability among these genotypes for the studied traits.

Table 2: Analysis of variance for the characterized traits in the study.

S. No	Traits	Means ± SD	CV	Differences
1	Number of branches	10.250 ± 2.260	22.050	NS
2	Plant height	65.820 ± 10.470	15.910	**
3	Plant width	107.110 ± 15.170	14.160	**
4	Twenty pods length	67.920 ± 7.480	11.010	**
5	Shelling Percentage	66.280 ± 4.190	6.330	**
6	100-kernel weight	72.140 ± 13.180	18.270	**
7	Leaflet length	5.370 ± 0.880	16.310	NS
8	Leaflet width	1.980 ± 0.470	23.810	**
9	Dry pods yield	1578.280±323.340	20.490	NS

** Significant difference at the 0.01 probability level; NS, Non-Significant Difference.

3.1 Number of branches per plant

Most of the agronomic traits contribute positively towards yield in peanut. Number of branches per plant is one of these traits. In this study no significant discrepancies were observed among the genotypes for the trait of number of branches (Table 2; Figure 1), which may be the same genetic makeup of the genotypes for the said trait. Highest number of branches was found in advanced line PG-1255 (12.67), followed by PG-1267 (11.67), and check cultivar BARD-479 (11). PG-1266 was found with the lowest number of branches per plant (8). Our finding is in close agreement with that of Chavadhari *et al.* (2017), who also reported number of branches within the range of 4.07 to 10.

3.2 Plant height

Like other crops the trait of plant height is a key factor in determining peanut architecture traits and has an exceptional effect on resistance to lodging and competence to mechanized harvesting, and more importantly improved yield (Fernandez *et al.* 2009). Significant variability was observed among the genotypes for the characterized trait of plant height (Table 2; Figure 2). Tallest plants were noted in PG-1265 (82.33 cm), followed by PG-1254 (78.33 cm), and BARD-479 (73.33 cm), while the lowest plant height was found in PG-1258 (47.67 cm). The differences in plant height can be attributed to the genetic variation found among the evaluated genotypes. Our findings are supported by Raza *et al.* (2017) and Borker and Dharanguttikar (2014), they also reported significant differences for the trait of plant height. Plant height being an important trait, is extensively studied in other studies in peanut (Chavadhari *et al.*, 2017; Yol *et al.*, 2018; Lv *et al.*, 2018).

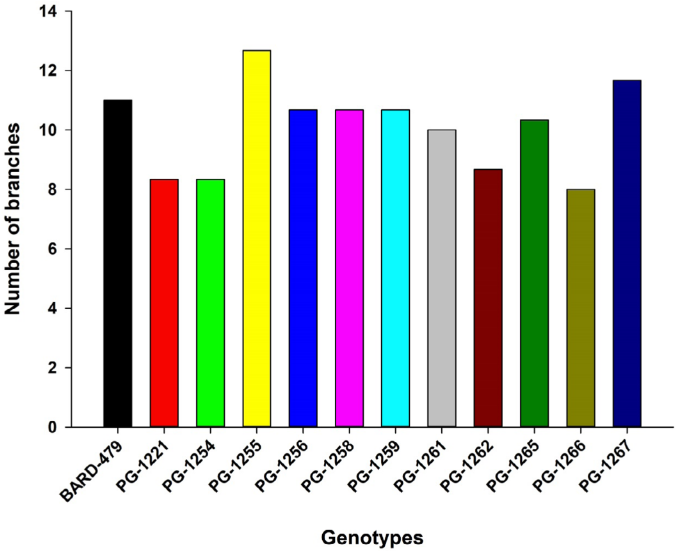

Figure 1: Discrepancies among the genotypes for the trait of number of branches.

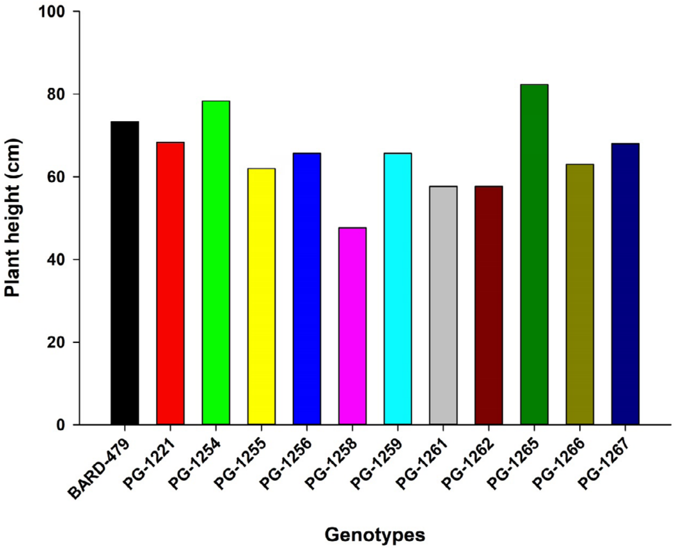

Figure 2: Discrepancies among the genotypes for the trait of plant height.

3.3 Plant width

Plant width is another important trait in crops effecting other traits as well as yield potential due to its direct link to the extent of spacing. Overcrowding of crops reduce yields as well as quality because of plants competition for light and soil nutrients. Knowing the plant width can help in maintaining proper plant to plant and row to row distance. In our findings we found significant differences in evaluated genotypes for plant width (Table 2; Figure 3). Widest plant width was noted in PG-1256 (128.67 cm), followed by check cultivar BARD-479 (121 cm) and PG-1262 (114.33 cm). The lowest plant width was found in PG-1267 (83.33 cm). Knowing the plant width, we can maintain proper spacing accordingly and can get optimum yield.

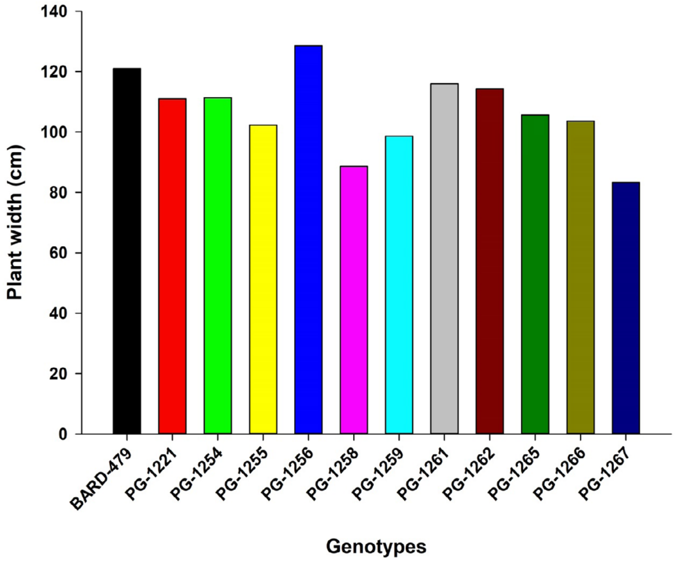

Figure 3: Discrepancies among the genotypes for the trait of plant width.

3.4 Twenty pods length

Pod and kernel size are direct contributors in peanut yield. Besides, pod and kernel size plays significant role absorbing nutrients from the soil (Singh *et al.*, 2004). Highly significant differences found among the evaluated genotypes for the trait of twenty pod length (Table 2; Figure 4). Lengthiest twenty pods length found in this study was in advanced line PG-1221 (85 cm), followed by PG-1266 (75.33 cm) and PG-1267 (74.67 cm). The shortest twenty pods length of 56.67 cm was observed in PG-1259. Since domestication of groundnut the traits of pod and kernel size have been remained under high selection pressure. Morphological as well as genetic bases have been identified for the improvement of these traits (Chu *et al.*, 2020).

3.5 Shelling percentage

Shelling percentage has been considered as an important trait in groundnut cultivar improvement (Lampang *et al.*, 1980). Significant variation found among the genotypes for the trait of shelling percentage in current study (Table 2; Figure 5). Highest shelling percentage was noted in PG-1266 (72.17%), followed by PG-1261 (71.83%), and PG-1258 (69.67%). The lowest shelling percentage of 57.83% was found in advanced groundnut line PG-126. Our findings are in close agreement with that of Raza *et al.* (2017), who also reported same trends in shelling percentage.

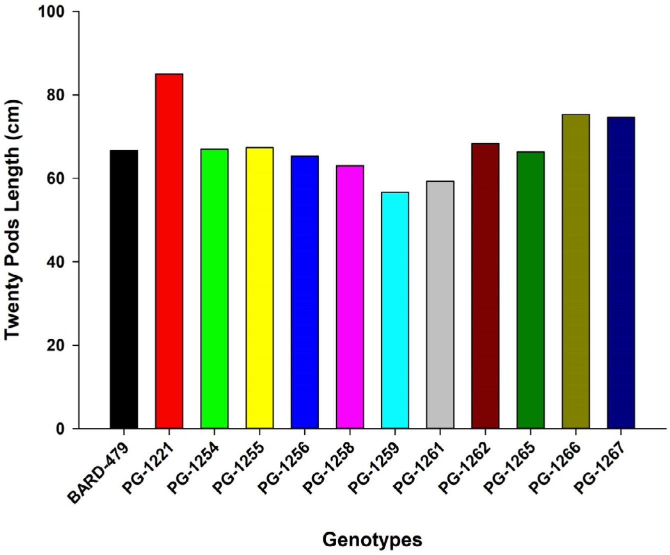

Figure 4: Discrepancies among the genotypes for the trait of twenty pods length.

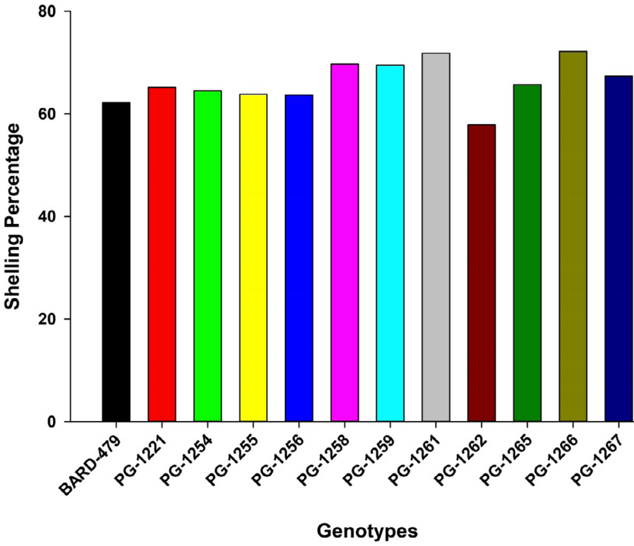

Figure 5: Discrepancies among the genotypes for the trait of shelling percentage.

3.6 100-kernels weight

Like other traits 100-kernel weight is an important yield contributing trait in groundnut (Aminifar *et al.*, 2013), affecting directly the crop yield. Significant differences were found in evaluated genotypes for the trait of 100-kernels weight (Table 2; Figure 6), showing extent of variability and the potential of high yielding cultivar development. Genotypes PG-1267 was found with highest 100-kernel weight (95.67 grams), followed by PG-1266 (94.67 grams), and PG-1221 (88.67 grams). The lowest 100-kernel weight was noted in PG-1261 (57 grams). Comparable findings for the trait of 100-kernel weight were reported by Raza *et al.* (2017) and Khan *et al.* (2009).

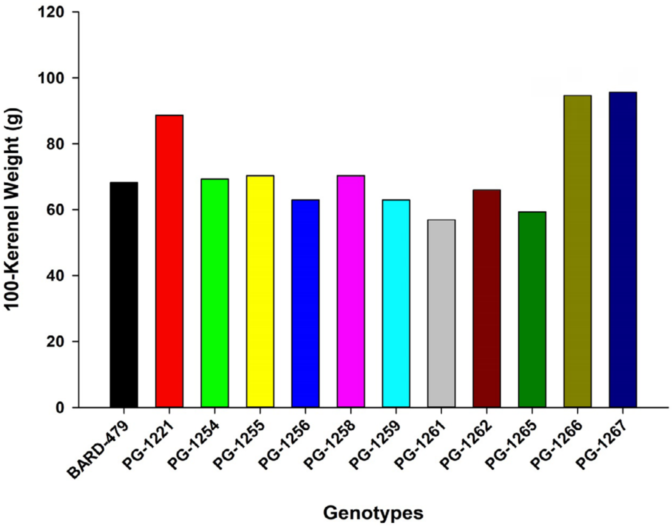

Figure 6: Discrepancies among the genotypes for the trait of 100-kernels weight.

3.7 Leaflet length

Leaflet length is among the most important traits. Leaf is the main site of photosynthesis as well as associated with various diseases in groundnut (Coffelt and Porter, 1982). Considerable differences were observed for the trait of leaflet length among the genotypes (Table 2; Figure 7). Largest leaflet length was observed in PG-1258 (6.17 cm), followed by PG-1255 (5.93 cm), and PG-1262 (5.73 cm). The shortest leaflet length was found in PG-1261 (4.33 cm).

3.8 Leaflet width

In current study significant diversity found for the trait of leaflet width among the studied genotypes (Table 2; Figure 8). Widest leaflet width was seen in advanced line PG-1221 (2.67 cm), followed by PG-1265 (2.37 cm), and PG-1267 (2.3 cm). The lowest leaflet width (1.3 cm) was noted in PG-1254.

3.9 Dry pods yield

The studied genotypes were genetically diverse for the evaluated traits (Table 2; Figure 9). Among the evaluated advanced lines highest dry pods yield was recorded in PG-1221 (1964.67 grams), followed by BARD-479 (1853.33 grams), and PG-1254 (1775 grams). The lowest (1295.33 grams) dry pods yield was noted in PG-1262.

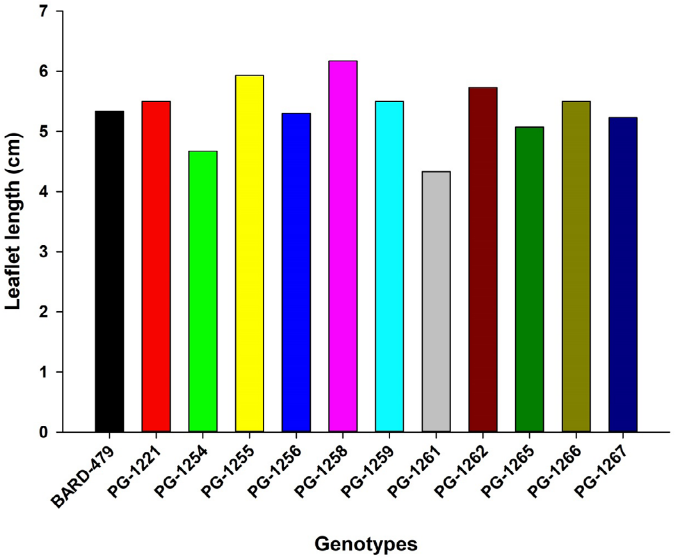

Figure 7: Discrepancies among the genotypes for the trait of leaflet length.

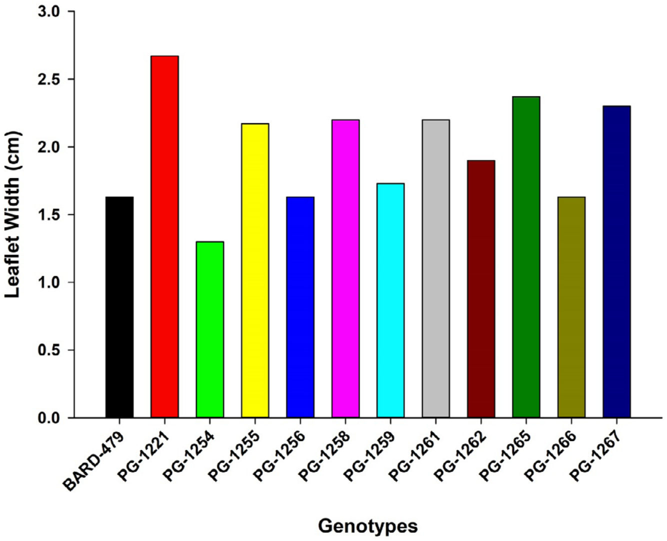

Figure 8: Discrepancies among the genotypes for the trait of leaflet width.

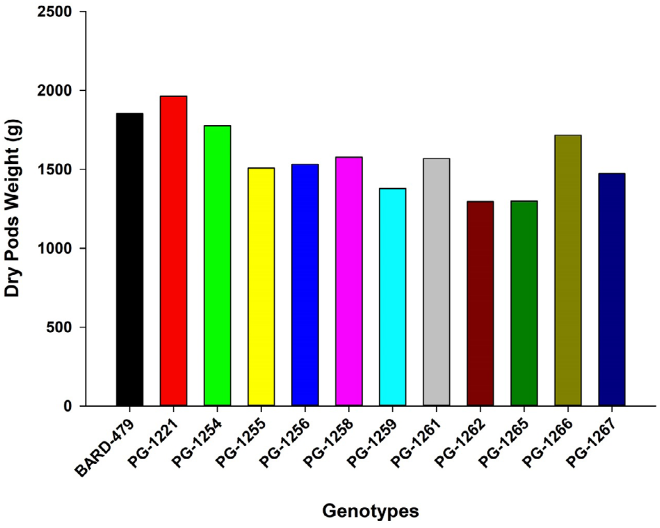

Figure 9: Discrepancies among the genotypes for the trait of dry pods yield.

3.10 Yield Kg/ha

Like most of other traits yield kg/ha was highly significant diversified in the evaluated genotypes (Table 2; Figure 10). Highest yield of 3637 Kg/ha was obtained from PG-1221, followed by PG-1259 (3430 Kg/ha), and PG-1254 (3286 Kg/ha). Advanced line PG-1261 was found with lowest yield of 1901 Kg/ha (Table 4).

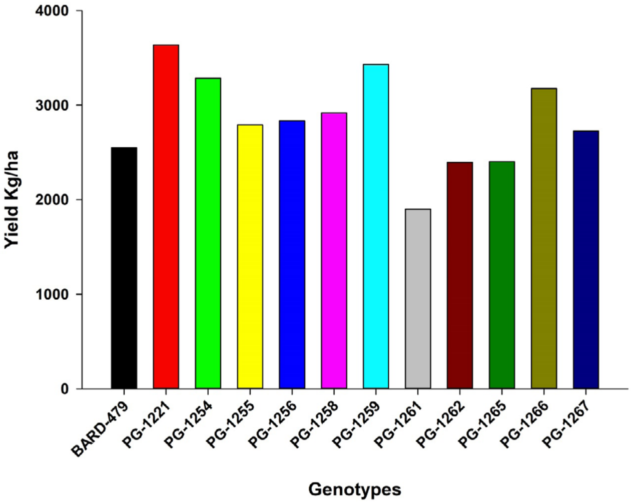

Figure 10: Discrepancies among the genotypes for the trait of dry pods yield.

In this study GCV and PCV were calculated for all pairs of characterized traits (Table 3). Out of the 36 correlation coefficients among 9 traits, 11 correlation coefficients were significant at genotypic level whereas only one correlation coefficient was found significant at phenotypic level (Table 3). Most of GCV values were higher than their corresponding PCV showing the higher level of association between two variables at genotypic level (Table 3). The phenotypic expression of the traits was reduced by environmental influence, directing towards the possibilities of effective phenotypic selection. The trait of 100-kernel weight was highly significant and positively correlated with the traits of twenty pods length (0.821 **), while highly significant negatively with plant width (-0.850 **). Dry pods yield was found in highly significant positive correlation with plant height (1.216**) and highly negative correlation with number of branches (-0.850**). A highly significant and negative correlation was observed among the traits of leaflet width and plant width (-0.984 **), shelling percentage and plant width (-0.881 **), plant height and leaflet width (-0.832**), Leaflet length and plant width (-0.795 **), and twenty pods length and number of branches (-0.785**). Similarly, the trait of twenty pods length was also found in a highly significant positive correlation (1.403**) with the trait of plant height (Table 3). In current findings, significantly high association among the traits reflects vital yield attributing traits and therefore importance should be given to these while breeding for high yield groundnut cultivar development. Significant association between pod yield plant^{-1}and PH was also recorded by Kushwah *et al.* (2016). Babariya and Dobariya (2012) also witnessed similar association of pod yield per plant with yield contributing characters.

Table 3: Genotypic and phenotypic correlation coefficient among nine studied traits.

Traits	Number of branches	Plant height	Plant width	Twenty pods length	Shelling Percentage	100-kernel weight	Leaflet length	Leaflet width	Dry pods yield
Number of branches	1	-.267	-.144	-.285	-.0129	-.187	.146	.154	-.198
Plant height	4.585	1	-.070	.141	-.084	.047	-.241	-.171	.073
Plant width	-1.082	7.846	1	-.088	-.270	-.338	-.211	-.109	.178
Twenty pods length	-.785**	1.403**	-.081	1	-.148	.790**	.137	.289	.479
Shelling Percentage	-.0746	-2.620	-.881 **	-.167	1	.198	-.185	.115	.099
100-kernel weight	-.396	-.640 *	-.850 **	.821 **	.213	1	.223	.153	.382
Leaflet length	.551	-4.680	-.795 **	.188	-.229	.268	1	.090	-.082
Leaflet width	.430	-.832**	-.984 **	.425	.125	.216	.248	1	-.134
Dry pods yield	-.850**	1.216**	.459	.546	.093	.4504	-.142	-.055	1

Significant at 5 % = * and significant at 1 %= **, Genotypic level= down ward left side of diagonal, Phenotypic level = upward ward right side of diagonal

Table 4: Direct (bold) and indirect effect among studied traits. Where dependent variable is dry pods yield and the last column shows the effects of independent variables on dry pods yield.

Traits	Number of branches	Plant height	Plant width	Twenty pods length	Shelling Percentage	100-kernel weight	Leaflet length	Leaflet width	Dry pods yield
Number of branches	(1.419)	1.427	-1.146	-4.356	-.345	1.483	1.626	-.958	-.850
Plant height	6.505	(.311)	8.303	7.787	-12.129	2.391	-13.803	1.850	1.216
Plant width	-1.536	2.442	(1.058)	-.448	-4.078	3.177	-2.346	2.188	.459
Twenty pods length	-1.114	.437	-.085	(5.548)	-.7801	-3.068	.553	-.945	.546
Shelling Percentage	-.106	-.816	-.932	-.935	(4.630)	-.795	-.676	-.278	.093
100-kernel weight	-.563	-.199	-.810	4.554	.985	(3.738)	.792	-.48	.450
Leaflet length	.782	-1.457	-.842	1.040	-1.061	-1.003	(2.950)	-.552	-.142
Leaflet width	.611	-.259	-1.041	2.356	.578	-.807	.732	(-2.225)	-.055

Table 5: Yield performance of the studies advance lines of groundnut.

S. No.	Line	Number of branches	Plant height	Plant width	Twenty pods length	Shelling Percentage	100-kernel weight	Leaflet length	Leaflet width	Dry pods yield	Yield (Kg/ha)
1	BARD-479	11	73.330	121	66.670	62.170	68.330	5.330	1.630	1853.330	2551
2	PG-1221	8.330	68.330	111	85	65.170	88.670	5.500	2.670	1964.670	3637
3	PG-1254	8.330	78.330	111.330	67	64.500	69.330	4.670	1.300	1775	3286
4	PG-1255	12.670	62	102.330	67.330	63.830	70.330	5.930	2.170	1508.330	2791
5	PG-1256	10.670	65.670	128.670	65.330	63.670	63	5.300	1.630	1531.670	2836
6	PG-1258	10.670	47.670	88.670	63	69.670	70.330	6.170	2.200	1576.670	2919
7	PG-1259	10.670	65.670	98.670	56.670	69.500	63	5.500	1.730	1378.330	3430
8	PG-1261	10	57.670	116	59.330	71.830	57	4.330	2.200	1567.330	1901
9	PG-1262	8.670	57.670	114.330	68.330	57.830	66	5.730	1.900	1295.330	2397
10	PG-1265	10.330	82.330	105.670	66.330	65.670	59.330	5.070	2.370	1299	2404
11	PG-1266	8	63	103.670	75.330	72.170	94.670	5.500	1.630	1716.330	3176
12	PG-1267	11.670	68	83.330	74.670	67.330	95.670	5.230	2.300	1473.330	2727
	LSD	3.700	10.290	17.230	2.920	4.450	4.860	1.470	0.520	505.800	353.240

To know about the direct and indirect effects of the characterized traits on dry pods yield, correlations were further divided into direct and indirect effects via path coefficient analysis (Table 4). Twenty pods length showed the highest positive direct effect (5.548) on dry pods yield, followed by S% (4.630), 100-kernel weight (3.738), and Leaflet length (2.950). Our results are supported by Kushwah *et al.* (2016), who also found positive direct effect of 100-kernel weight on pod yield plant^{-1}. A weak positive direct effect was found on dry pods yield by number of branches (1.419), plant width (1.058), and plant height (0.311). The trait of leaflet width was observed with the direct negative effect on dry pods yield (-2.225). The direct and indirect positive and negative effects of the studied traits signify the importance of these traits for groundnut yield improvement. The importance of these traits in groundnut cultivar improvement also supported by earlier studies (Kumar *et al.*, 2014; Rao *et al.*, 2014; Shoba *et al.*, 2012).

The evaluated advanced lines were further tested for yield performance. Based on the kg/ha yield performance lines PG-1221, PG-1254, PG-1259, and PG-1266 were promising with 3637 kg/ha, 3286 kg/ha, 3430 kg/ha, and 3176 kg/ha, respectively (Table 5). Further evaluation of these lines needed to develop high yielding cultivars in future breeding programs.

Conclusions and Recommendation

The highly significant association among the studied traits and direct and indirect effect of most traits on dry pods yield suggests that these traits must be considered in yield improvement of groundnut cultivar in future breeding programs. Furthermore, the current study showed that groundnut lines, PG-1221, PG-1254, PG-1259, and PG-1266 are high yielding and having great potential for high yielding cultivar development.

Acknowledgments

The authors acknowledge the contribution of the Land Resources Research Institute, NARC, Islamabad for providing technical support in terms of experimental design.

Novelty Statement

Highly significant association was found among the studied traits in this study with direct and indirect effect of most traits on dry pods yield.

Author's Contribution

NN and MA designed and supervised the experiment, MJ and MH carried out the experiment, HK performed statistical analysis, SAK wrote and revised the manuscript.

Conflict of interest

The authors have declared no conflict of interest.

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