

GENETIC VARIABILITY PARAMETERS AND CHARACTER ASSOCIATIONS AMONG YIELD ATTRIBUTING TRAITS IN ADVANCED BACKCROSS LINES OF GROUNDNUT

ABSTRACT

Groundnut is currently a major industrial oilseed crop with good commercial significance. It is highly variable in phenotypic characters and thus it is important to investigate the variations and associations of these morphological features. 20 advanced Groundnut lines were planted in Randomized Complete Block Design along with parental lines and two checks and they were evaluated for 13 traits. Significant variations were revealed in analysis of variance. High GCV (20.21) coupled with high heritability (91.2) and GAM (39.77) were observed in plant height suggested that environment had lesser influence on the expression of this trait, as this character is governed by an additive gene action, making them effective for selection. High heritability combined with low GCV and GAM were recorded in oil content, days to 50 percent flowering, shelling outturn and number of secondary branches per plant revealed that non-additive genetic variation played a significant role in the expression of this trait thus, selection for this character would be inefficient. Pod yield per plant showed a positive and significant association with seed yield per plant, plant height, number of secondary branches per plant, pod length, pod width and number of pods per plant. Path coefficient analysis have

revealed that positive direct effects towards pod yield per plant were reported for seed yield per plant, plant height, number of secondary branches per plant, pod length, pod width, and number of pods per plant. Thus the characters seed yield per plant, number of pods per plant, pod length and number of secondary branches per plant which are the most essential characters contributed significantly towards higher pod yield per plant.

Keywords-Genetic Variability, Character association, Heritability, Groundnut, Backcross, Yield traits.

INTRODUCTION

Groundnut (*Arachis hypogea* L.) ($2n=4x=40$) is one of the important oilseed crops of India and World. It is a herbaceous legume that is native to South America (Brazil) and belongs to the Fabaceae family. The crop consists edible oil (40–56%), protein (20–30%), carbohydrate (10–20%) and various nutritious components such as vitamin E, niacin, calcium, magnesium, phosphorus, zinc, iron, riboflavin, thiamine and potassium in its seeds. Groundnut fat consists of monounsaturated fatty acid, oleic acid (36-81.3%) polyunsaturated fatty acid, linoleic acid (3.9-40.2%) (Janila *et al.*, 2016).

In semi-arid regions of the world including India, the productivity and quality are likely to be impaired in coming years owing to fluctuating climatic conditions. The incidence of fungal disease like late leaf spot have increased in the recent years due to continuous cultivation of K6 and TAG24 varieties. The occurrence of late leaf spot is common in rainfed ecologies world over and studies showed that in India they cause 50 per cent reduction in pod yield (Pande *et al.*, 2003 and Singh *et al.*, 2011). The fungal pathogen (*Phaeoisariopsis personata*) causes late leaf spot disease in groundnut.

In cultivated groundnuts, sources of LLS resistance have been identified in several genotypes. Recent advancements in crop genomics have made it easier to identify molecular markers linked to specific traits that can be used to choose a superior line in a breeding programme, a process known as genomics-assisted breeding (Varshney *et al.*, 2005). The present investigation is aimed to evaluate the groundnut introgressed 20 backcross derived lines through marker assisted selection.

MATERIALS AND METHODS

The experiment was carried out at the AICRP on Groundnut Supporting Centre, Regional Agricultural Research Station, Palem, Nagarkurnool, Telangana state during the *rabi* season 2021-22. The experimentation site has a semi-arid climate and is located at 16°35'1" latitude, 78°11' longitude, and 642 m above mean sea level in the Southern Telangana Zone. Twenty advanced backcross progenies (10 BC1F₆ and 10 BC2F₅) were raised in a randomised block design with two replications with spacing of 30 cm between rows and 10 cm between the plants, together with parental lines and checks (K6, ICGV 13193, ICGV 15033, GPBD 4 and TMV 2).

The observations of Days to 50 per cent flowering, Plant height (cm), Number of primary branches per plant, number of secondary branches per plant, number of pods per plant, seed yield per plant (gm), pod yield per plant (gm), shelling outturn, pod length (mm), pod width (mm), 100 seed weight, pod constriction, pod beak, pod ridge, pod reticulation, oil content (%), protein content (%) were recorded in five plants of each backcross line and the mean values were considered for analysis.

Analysis of variance for Randomized Complete Block Design was done initially to find out the genotypic differences between the lines based on the method given by Panse and Sukhatme (1964). The calculation of genotypic (σ^2_g) and phenotypic (σ^2_p) variances was carried out based on the formula given by Burton (1952). Following this the range of variation was categorized according to Subramanian and Menon's (1973) recommendations. The formula presented by Hanson *et al.* (1956) was followed to calculate broad sense heritability [h^2 (b)]. Heritability estimations were classified as indicated by Johnson *et al.* (1955). The projected genetic gain in the next generation is given by genetic advance which was calculated by the formula of Johnson *et al.* (1955). The variance and covariance components for each pair of characteristics were calculated by the methods described by Falconer *et al.* (1964) from which the phenotypic and genotypic correlation coefficients were calculated. The estimated values of correlation coefficients were compared with table values of correlation coefficients (Fisher and Yates, 1963) at 5% and 1% levels of significance in order to test their significance. The correlation coefficients are further divided into direct and indirect effects of independent factors on the dependent variable in path coefficient analysis proposed by Wright (1921) and elaborated by Dewey and Lu (1959). All the mentioned analyses were performed using the INDOSTAT software.

RESULTS AND DISCUSSION

Genetic variability parameters

According to analysis of variance among the genotypes studied there were significant variations observed for all the characters under study among the genotypes studied. The values of Phenotypic and genotypic coefficients of variation are given in Table 1. The GCV values ranged from 1.5 for 100 seed weight to 20.2 for plant height. High GCV (>20%) was observed in plant height (21.3) indicating the presence of wide range of variation for this character, which can be improved further by individual selection. The low GCV values (<10%) were recorded for protein content (6.7), pod width (5.9), number of primary branches per plant (6.7), pod length (5.7), number of secondary branches per plant (4.0), number of pods per plant (5.1), seed yield per plant (8.9), shelling outturn (3.1), 100 seed weight (1.5), days to 50% flowering (4.6) and oil content (4.6) and which indicates that environment had a major influence on the expression of these characters. The values of

PCV were between 4.0 and 21.1. High estimates of PCV (>20%) were recorded for plant height (21.1). Seed yield per plant (10.7), 100 seed weight(10.7), pod yield per plant (11.1) were observed with moderate estimates of PCV (10-20%). Low estimates of PCV (<10%) were observed in days to flowering (5.2), number of primary branches per plant (9.2), number of secondary branches per plant (4.9), number of pods per plant (6.6), shelling outturn (4.0), pod length (6.6), pod width (7.2), oil content (4.8), protein content (7.1). PCV values are greater than GCV values across all traits, showing that variation was induced not only by genotypes but also by environmental influences. Similar results were found in studies of Kumari and Sasidharan, (2020), Aruna *et al.* (2019), Shinde *et al.*, (2019) and Mandal *et al.* (2017).

High heritability was exhibited by all the characters under study and the values are shown in table 1 also diagrammatically represented in Fig 1. High heritability (broad sense) (>60%) was recorded for plant height (91.2), oil content (91.2), protein content (89), pod yield per plant (84.8), days to flowering (78.5), pod length (76.1), seed yield per plant (68.3), number of secondary branches per plant (68.2), pod width (67.1), number of pods per plant (61.1) and shelling outturn (60.9). The high heritability indicated that the environment had little influence on the inheritance of these traits. Moderate estimates of heritability (30-60%) were observed in number of primary branches per plant (52.6). The higher estimates of genetic advance as percent of mean (>20%) were observed plant height (39.7). Pod yield (19.3), seed yield (15.1), pod width (10.0), protein content (13.0), pod length (10.3) and number of primary branches per plant (10.0) were recorded moderate values of GAM (10-20%). Low estimates of genetic advance as percent of mean (<10%) were observed in oil content (9.15) and days to 50% flowering (8.4), number of number of pods (8.3), secondary branches per plant (6.9), shelling outturn (5.0), 100 seed weight (0.4). In present study high GCV (20.2) coupled with high heritability (91.2) and GAM (39.7) were observed in plant height suggested that environment had lesser influence on the expression of this trait, as this character is governed by an additive gene action, making them effective for selection. High heritability (68.2) combined with low GCV (4.0) and GAM (6.9) were recorded in number of secondary branches per plant revealed that non-additive genetic variation played a significant role in the expression of this trait thus, selection for this character would be inefficient. These findings are in conformity with reports of Kumari and Sasidharan (2020), Aruna *et al.* (2019) and Mandal *et al.* (2017).

Character associations

The character associations of certain morphological characters to the pod yield were studied through correlation analysis and path coefficient analysis. Correlation values of all the characters depicted in table 2. In the present study, pod yield per plant showed a positive and significant association with plant height($r_g=0.7013^{**}$, $r_p=0.6691^{**}$), number of primary branches per plant ($r_g=0.3960^*$, $r_p=0.3975^*$), number of secondary branches per plant ($r_g=0.6560^{**}$, $r_p=0.6380^{**}$), number of pods per plant ($r_g=0.5208^{**}$, $r_p=0.5038^{**}$), seed yield per plant ($r_g=0.8571^{**}$, $r_p=0.8578^{**}$), shelling outturn ($r_g=0.3773^*$, $r_p=0.4175^*$), pod length ($r_g=0.5552^{**}$, $r_p=0.5284^{**}$) and pod width ($r_g=0.5316^{**}$, $r_p=0.4157^*$) and oil content ($r_g=0.3786^*$, $r_p=0.3471^*$) hence, these traits should be given more importance in the selection process. These results emphasized the effectiveness of these characters in terms of their contribution towards pod yield per plant. Pod yield per plant exhibited a significant negative association with days to 50 per cent flowering ($r_g=-0.5724^{**}$, $r_p=-0.4796^{**}$) and 100 seed weight ($r_p=0.4641^*$ at genotypic level) and protein content ($r_g=0.0740$, $r_p=0.03639$) showed positive non-significant association. Such a positive interdependence between pod yield per plant and among these traits would aid in increasing the pod yield levels and therefore more emphasis should be given to these characters. Similarly, significant positive association was reported by Kumari and Sasidharan (2020), Shinde *et al.* (2019) and Tulsi *et al.* (2017).

Path coefficient analysis have revealed that positive direct effects towards pod yield per plant were reported for seed yield per plant ($G=-0.2548$, $P=0.8793$), number of secondary branches per plant ($G=-2.3293$, $P=0.0846$), number of pods per plant ($G=2.1934$, $P=0.0116$), pod length ($G=-3.5840$, $P=0.0011$), pod width ($G=-0.7681$, $P=0.0916$), and plant height ($G=-3.5840$, $P=0.0011$) depicted in table 3. Among them, seed yield per plant had a high and positive direct effect on pod yield per plant and thus, it should be considered as an essential component for pod yield. As a result, it is advised that these traits can be considered as most important yield contributing characters for selection. Days to 50% flowering ($G=-0.5423$, $P=-0.1627$), number of primary branches per plant ($G=-0.8033$, $P=-0.0552$), 100 seed weight ($G=-0.0087$, $P=-0.0338$), shelling outturn ($G=2.0839$, $P=-0.1751$) and oil content ($G=2.4330$, $P=-0.0622$) have shown negative direct effect on plot yield. The direct and indirect effects of all the characters on pod yield are portrayed in figure 1 and table 3. These results were in accordance to the findings of Patel *et al.* (2021) , Mandal *et al.* (2017) and Mohapatra and Khan (2020).

CONCLUSION

Based on the study of GCV, PCV, heritability, genetic advance per cent of mean, correlation and path coefficient analysis among 20 advanced ground lines and parents we conclude that seed yield per plant, number of pods per plant, pod length and number of secondary branches per plant which are the most essential characters contributed significantly towards higher pod yield per plant. Such a positive interdependence between pod yield per plant and among these traits would aid in increasing the pod yield levels and therefore, while selecting groundnuts, more emphasis should be given to these characters.

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Table 1 Estimation of genetic parameters for 13 quantitative traits in 20 backcross lines and parents

S. No.	Trait	Mean	Range		GCV (%)	PCV (%)	h ² (bs) (%)	GAM (%)
			Minimum	Maximum				
1	DFF	35.2	33.0	40.0	4.6	5.2	78.5	8.4
2	PH	17.4	11.3	22.9	20.2	21.1	91.2	39.7
3	NPB/P	7.3	6.2	8.5	6.7	9.2	52.6	10.0
4	NSB/P	40.4	37.0	44.4	4.0	4.9	68.2	6.9
5	NPP	14.7	13.1	16.2	5.1	6.6	61.1	8.3
6	PY/P	12.5	10.2	14.8	10.2	11.1	84.8	19.3
7	SY/P	8.5	7.1	10.6	8.9	10.7	68.3	15.1
8	SH(%)	70.6	65.3	74.8	3.1	4.0	60.9	5.0
9	PL	26.4	23.7	30.0	5.7	6.6	76.1	10.3
10	PW	12.2	10.5	13.7	5.9	7.2	67.1	10.0
11	100 SW	41.1	28.3	44.7	1.5	10.7	20.0	0.4
12	OC(%)	55.0	49.5	60.7	4.6	4.8	91.2	9.1
13	PC(%)	24.2	21.8	28.0	6.7	7.1	89.0	13.0

DFF: Days to 50% Flowering, PH: Plant Height (cm), NPB/P: Number of Primary Branches per Plant, NSB/P: Number of Secondary Branches per Plant, NPP: Number of Pods per Plant, PY/P: Pod Yield per Plant (g), SY/P: Seed Yield per Plant (g), SH (%): Shelling outturn (%), PL: Pod Length (mm), PW: Pod Width (mm), 100 SW :100 seed weight (g), OC (%): OIL Content and PC(%): Protein Content.

Table 2 . Genotypic (G) and Phenotypic (P) correlation coefficients of yield contributing and quality traits.

Character		DFF	PH (cm)	NPB/P	NSB/P	NPP	SY/P (g)	SH%	PL (mm)	PW (mm)	100 SW	Oil content	Protein Content	Pod yield per plant (g)
DFF	r _g	1.0000	-0.5995**	0.1863	-0.3637*	-0.1012	-0.4755**	-0.1497	-0.4542*	-0.2911	0.0956	-0.2199	-0.2165	-0.5724**
	r _p	1.000	-0.5278**	0.1970	-0.2085	-0.0617	-0.3430*	-0.0866	-0.3685 *	-0.2423	0.1243	-0.2383	-0.1926	-0.4796 **
PH	r _g		1.0000	0.2587	0.5068*	0.4222*	0.7013**	0.3234*	0.6980**	0.5997**	0.4645*	0.2651	0.1637	0.7013**
	r _p		1.000	0.2553	0.4524*	0.3684*	0.6328**	0.3617*	0.6161**	0.4888 *	0.1120	0.2300	0.1118	0.6691**
NPB/P	r _g			1.0000	0.5571**	0.6966**	0.6229**	0.5090**	0.3093*	0.4105*	0.2286	0.1610	0.1460	0.3960*
	r _p			1.000	0.5565**	0.6559**	0.5774**	0.4601*	0.2885	0.2347	0.3012*	0.1122	0.0771	0.3975*
NSB/P	r _g				1.0000	0.7438**	0.7782**	0.6429**	0.5394**	0.5060**	1.3833**	0.3950*	0.2336	0.6569**
	r _p				1.000	0.7318**	0.7281**	0.5522**	0.5266**	0.4371*	0.1813	0.3039*	0.1871	0.6380**
NPP	r _g					1.0000	0.6795**	0.6249**	0.5034**	0.3145*	0.3769*	0.0668	0.1575	0.5208**
	r _p					1.000	0.6082**	0.5018**	0.4752**	0.3397*	0.1134	0.0626	0.1661	0.5038**
SY/P	r _g						1.0000	0.6835**	0.6699*	0.5405**	1.7075**	0.3178*	0.3353*	0.8571**
	r _p						1.000	0.6591**	0.5894**	0.3919*	0.2153	0.2617	0.2181	0.8578**
SH%	r _g							1.0000	0.7873**	0.4889*	3.5673**	0.1955	0.3620*	0.3773*
	r _p							1.000	0.6155**	0.2886	0.5174**	0.1643	0.2260	0.4175*
PL	r _g								1.0000	0.6808**	2.5070**	0.4413*	0.1416	0.5552**
	r _p								1.000	0.6051**	0.2269	0.3396*	0.1849	0.5284**
PW	r _g									1.0000	1.5336**	0.3444*	0.1952	0.5316**
	r _p									1.000	0.0303	0.2663	0.2269	0.4157*
100 SW	r _g										1.0000	0.3336	2.0417**	0.4614*
	r _p										1.000	0.0477	0.1225	0.0565
Oil content	r _g											1.0000	-0.5915**	0.3786*
	r _p											1.000	-0.5202**	0.3471*
Protein content	r _g												1.0000	0.0740
	r _p												1.000	0.0369

* Significance at 5 per cent level; ** Significance at 1 per cent level

DFF: Days to 50% Flowering, PH: Plant Height (cm), NPB/P: Number of Primary Branches per Plant, NSB/P: Number of Secondary Branches per Plant, NPP: Number of Pods per Plant, PY/P: Pod Yield per Plant (g), SY/P: Seed Yield per Plant (g), SH (%): Shelling outturn (%), PL: Pod Length (mm); PW: Pod Width (mm)

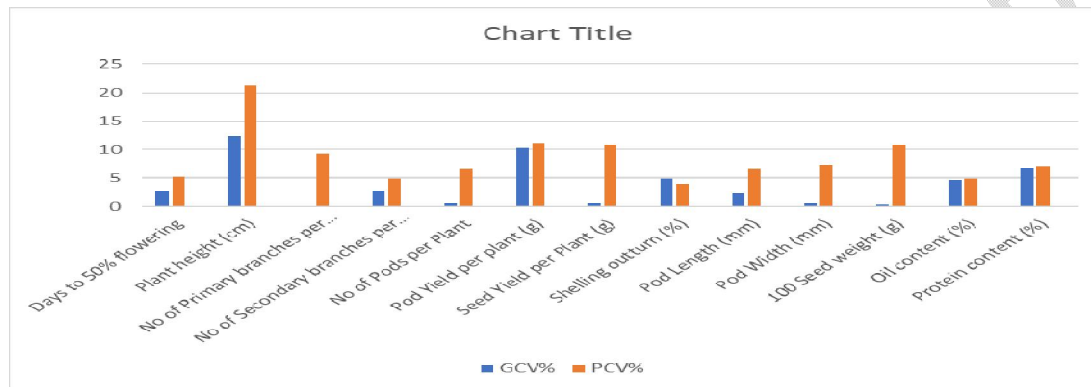
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Table 3. Genotypic (G) and Phenotypic (P) path coefficients of yield contributing and quality traits.

Character		DFF	PH (cm)	NPB/P	NSB/P	NPP	SY/P (g)	SH%	PL (mm)	PW (mm)	100 SW	Oil content	Protein Content	Correlation with pod yield / plant (g)
DFF	G	-0.5423	-0.9310	-0.1496	0.8471	-0.2220	0.1212	-0.3120	1.6279	-0.2236	-0.0008	-0.5351	-0.2520	-0.5724**
	P	-0.1627	-0.0309	-0.0109	-0.0176	-0.0007	-0.3016	0.0152	-0.0004	-0.0222	-0.0042	0.0148	0.0416	-0.4796**
PH	G	0.3251	1.5531	-0.2078	-1.1806	0.9261	-0.1787	0.6740	-2.5018	0.4606	-0.0040	0.6449	0.1905	0.7013**
	P	0.0859	0.0585	-0.0141	0.0383	0.0043	0.5564	-0.0633	0.0006	0.0448	-0.0038	-0.0143	-0.0241	0.6691**
NPB/P	G	-0.1010	-0.4019	-0.8033	-1.2977	1.5279	-0.1587	1.0607	-1.1086	0.3153	-0.0020	0.3917	0.1699	0.3960*
	P	-0.0320	0.0149	-0.0552	0.0471	0.0076	0.0577	-0.0805	0.0003	0.0215	-0.0102	-0.0070	-0.0166	0.3975*
NSB/P	G	0.1972	0.7872	-0.4475	-2.3293	1.6315	-0.1983	1.3397	-1.9332	0.3887	-0.0120	0.9611	0.2720	0.6569**
	P	0.0339	0.0265	-0.0307	0.0846	0.0085	0.6367	-0.0967	0.0006	0.0400	-0.0061	-0.0189	-0.0404	0.6380**
NPP	G	0.0549	0.6557	-0.5595	-1.7325	2.1934	-0.1732	1.3022	-1.8041	0.2416	-0.0033	0.1624	0.1833	0.5208**
	P	0.0100	0.0216	-0.0362	0.0619	0.0116	0.5348	-0.0879	0.0005	0.0311	-0.0038	-0.0039	-0.0359	0.5038**
SY/P	G	0.2579	1.0892	-0.5003	-1.8126	1.4903	-0.2548	1.4243	-2.4008	0.4152	-0.0149	0.7734	0.3903	0.8571**
	P	0.0558	0.0370	-0.0319	0.0613	0.0070	0.8793	-0.1154	0.0006	0.0359	-0.0085	-0.0163	-0.0471	0.8578**
SH%	G	0.0812	0.5023	-0.4089	-1.4974	1.3706	-0.1742	2.0839	-2.8216	0.3755	-0.0311	0.4757	0.4214	0.3773*
	P	0.0141	0.0212	-0.0254	0.0467	0.0058	0.5796	-0.1751	0.0006	0.0264	-0.0175	-0.0102	-0.0488	0.4175*
PL	G	0.2463	1.0841	-0.2485	-1.2564	-1.1041	-0.1707	1.6406	-3.5840	0.5229	-0.0218	1.0737	0.1649	0.5552**
	P	0.0599	0.0360	-0.0159	0.0446	0.0055	0.5182	-0.1077	0.0011	0.0554	-0.0077	-0.0211	-0.0399	0.5284**
PW	G	0.1579	0.9313	-0.3297	-1.1787	0.6898	-0.1377	1.0187	-2.4398	0.7681	-0.0134	0.8378	0.2273	0.5316**
	P	0.0394	0.0286	-0.0130	0.0370	0.0039	0.3446	-0.0505	0.0006	0.0916	-0.0010	-0.0166	-0.0490	0.4157*
100 SW	G	-0.0518	0.7214	-0.1837	-3.2221	0.8267	-0.4352	7.4338	-8.9852	1.1779	-0.0087	0.8115	2.3767	0.4614*
	P	-0.0202	0.0066	-0.0166	0.0153	0.0013	0.2210	-0.0906	0.0002	0.0028	-0.0338	-0.0030	-0.0264	0.0565
Oil content	G	0.1193	0.4117	-0.1293	-0.9201	0.1464	-0.0810	0.4074	-1.5817	0.2645	-0.0029	2.4330	-0.6886	0.3786*
	P	0.0388	0.0135	-0.0062	0.0257	0.0007	0.2301	-0.0288	0.0004	0.0244	-0.0016	-0.0622	0.1123	0.3471*
Protein content	G	0.1174	0.2542	-0.1172	-0.5442	0.3454	-0.0854	0.7543	-0.5076	0.1500	-0.0178	-1.4392	1.1641	0.0740
	P	0.0313	0.0065	-0.0043	-0.0158	0.0019	0.1918	-0.0396	0.0002	0.0208	-0.0041	0.0323	-0.2159	0.0369
Genotypic Residual Effect = 0.5625 Phenotypic Residual Effect = 0.3958 Direct effects are shown in bold font														

DFF: Days to 50% Flowering, PH: Plant Height (cm), NPB/P: Number of Primary Branches per Plant, NSB/P: Number of Secondary Branches per Plant, NPP: Number of Pods per Plant, PY/P: Pod Yield per Plant (g), SY/P: Seed Yield per Plant (g), SH (%): Shelling outturn (%), PL: Pod Length (mm); PW: Pod Width (mm).

Fig 1. Estimates of GCV (%) and PCV (%) in backcross lines and parents



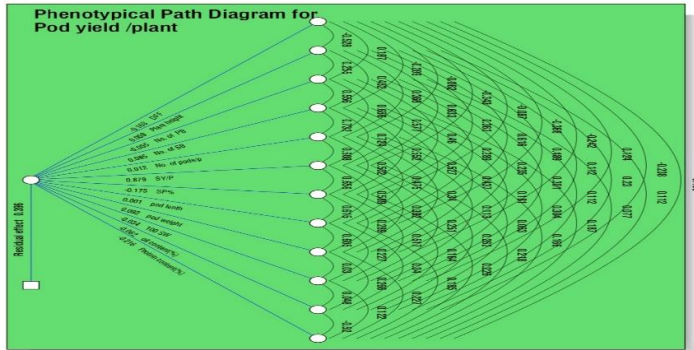
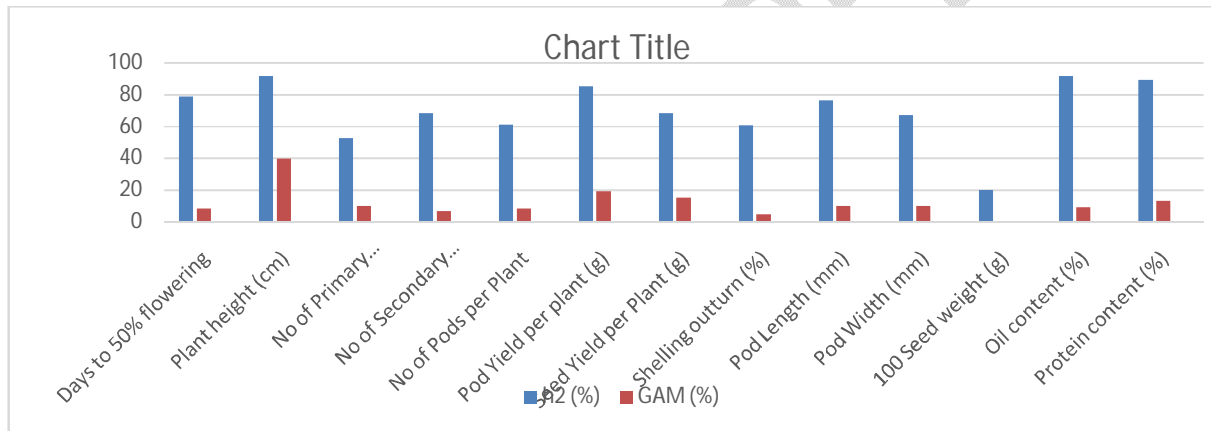


figure 2 Phenotypical path diagram for pod yield/plant

figure 3. Estimates of heritability (bs) and GAM (%) in backcross lines and parent



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