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INHERITANCE OF SOME ECONOMIC CHARACTERS, REACTION TO POD ROT DISEASES AND AFLATOXEN CONTAMINATION IN PEANUT (*Arachis hypogaea* L.)

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ABSTRACT

The present study was conducted at the Experimental Farm of Ismailia Agric. Res. Station during 2010 and 2011 summer seasons to estimate general and specific combining ability, heterosis, types of gene action for yield and its components, pod rot diseases and perharvest aflatoxin contamination in peanut. In the first season, five genotypes differed in their economic characters and tolerance to diseases were crossed in a diallel crosses(without reciprocal). In the second season, the five parents *i.e* { P_1(line 85),P_2(line 367), P_3(line 284), P_4(line 205) and P_5(Giza 6)} and their ten crosses were field evaluated under artificial infection with fungi inocula *i.e*. *Rhizoctonia solani* the causal of dry brown lesion; *Fusarium moniliforme* the causal of pink discoloration as well as *Macrophomina phaseolina* and *Sclerotium rolfsii* the main causal pathogens of general breakdown pod rot, as well as aflatoxigenic fungi *i.e. Aspergillus flavus* and *A. parasiticus* in a randomized complete block design with three replications.

The most important results could be summarized as follows:

- F_1 mean values exceeded that of parents for all studied characters except plant height, number of branches and number of pods/plant.
- Specific combining ability had greater role than general combining ability for all the traits except 100-pod weight, 100-seed weight, shelling % and pod yield /fed.
- The first parent (line 85) was the best regarding general combining ability for 100-pod weight and 100-seed weight. The second parent (line 367) showed good general combining ability for most studied characters, the fifth parent (Giza 6) had good general combining ability for the traits of 100-seed weight, shelling percentage, pod yield /fed and oil percentage.
- The crosses (P_1 x P_2) and (P_3 x P_4) were superior in number of pods/plant, pod weight/plant, number of seeds/plant, seed weight/plant, shelling percentage and oil percentage, whereas, the crosses (P_1 x P_5 and P_2 x P_4) were superior in 100-pod weight and 100-seed weight, and the hybrid (P_1xP_4) was excellent in 100- pod weight and oil percentage . Positive and highly significant hetrotic effects relative to the better parent were found for most of the traits in the four crosses (P_1xP_2), (P_1xP_4),(P_2xP_4) and (P_3xP_4). Results indicated the importance of gene action due to dominance and additive effects for most characters.

-The value of heritability was moderate to low in narrow sense but it was high in broad sense.

- Parents and F_1 differed in their sensitivity to pod rots under artificial infection in the field and their contamination with aflatoxin.

-Crosses (P 1 x P 5) ,(P 2 x P 3) and Parental line 284 had the greatest resistance to all groups of pod rots followed by (P_3 x P_4) , (P_1 x P_4), (P_1 x P_3) and (P 2 x P 4).

- Parental line 284 and crosses (P_1 x P $_3$) , (P_1 x P_5),(P_2 x P_3) and (P_3 x P_4) were free of aflatoxin contamination (B_1, B_2, G_1, G_2).

Therefore, the superior of crosses (P_1 x P_3) , (P_1 x P_5) and (P_3 x P_4) in yield and its components, resistance to pod rot diseases and free of aflatoxin contamination, will be further evaluated in advanced experiments to develop new genotypes that have higher yield, disease resistance and free from aflatoxin contamination.

INTRODUCTION

Peanut, (*Arachis hypogaea* L.) is one of the world source of edible oil and protein. In Egypt, it is one of the exportal crops and locally direct human consumed.

General combining ability (GCA) is the average value of all crosses having this line as a parent, the value being expressed as a deviation from the overall mean of crosses. A particular cross, then, has an expected value, which is the sum of the general combining abilities of its two parental lines. The cross may deviate from this expected value to a greater or lesser extent. This deviation is called specific combining ability(SCA) of the two lines in combination Falconer and Mackey, (1996). This information provides guidelines for plant breeders to select parent lines to be used in breeding programs and to produce promising cross combinations for further selection procedure.

For agronomic traits, a number of reports indicated the importance of both additive and non-additive gene action. Dwivedi *et al*.,(1989) and Abd El-Aal (2008) found that pod and seed traits were largely controlled by additive gene action, whil, pod number/plant and pod weight/plant were controlled by non-additive genetic effect. Both genetic effects were equally important for shelling percentage. Wynne *et al*., (1975) also reported that estimates of both general and specific combining ability were significant for percent of mature pod, pods/kg, pod length and yield. Whereas, estimates of GCA were greater than SCA estimates in magnitude. Jogloy *et al*., (1987) found that general combining ability was highly significant for pod yield, seed yield, pod length, seed size and shelling percentage. Moreever, specific combining ability was significant for pod length and seed size. Swe and Branch (1986) found that estimates of general and specific combining abilities were significant for total pod weight, pod number, seed weight. In general, estimates of specific combining ability were more pronounced in the crosses of more diverse cultivars than in the closely related cultivars.

Since peanut is a predominately self pollinated crop and commercial product of F_1 seed is not currently feasible, it was felt that heterosis in groundnut is unstable, because tetraploid nature heterosis is unstable in groundnut. However, the magnitude of heterosis provides the basis of genetic diversity and a guide for choice of desirable parents for developing superior F_1 hybrids to exploit hybrid vigour and building gene pool which be employed in breeding programme. Heterosis in F_1 generation expressed in terms of superiority over the better, mid-parent or standard parent is of direct relevance not only for developing hybrids in cross-pollinated crops, but also in self pollinated crops because heterotic crosses help the breeder to select

appropriate crosses which would lead to desirable transgressive segregants in advanced generations Arunachalam *et al*.,(1984).

Information on variation, heritability and nature of gene action controlling the various agronomic and physiological characters of any crop plant is of crucial importance to breeders in elaborating the suitable breeding program for the improvement of this crop. The genetic components in different peanut material for some economic characters were studied. Vindhiyavarman and Raveendran (1994), Francies and Ramaling (1999), Mathure *et al*., (2000), Rudraswamy *et al*., (2001)and El-Baz *et al*., (2006) reported predominance of non-additive gene action for number of pods, pod yield, number of pods, pod yield, number of primary branches, number of secondary branches, number of nodes on main axis and oil content. However, the role of additive gene action for pods weight was reported by Varman (1998). However, epestatis also plays an important role in controlling number of mature pods/plant (Vindhiyavarman 2001). Different estimates of heritability for peanut traits were recorded by several researchers (Rudraswamy *et al*., 1999, Ayub-khan *et al*., 2000, Yogendra-Prasad 2002 and El-Baz *et al*., 2006).

Soil borne fungi can attack peanut pods, whenever environmental conditions are favorable for their growth and infection, during their development in soil after harvest and during storage (Satour *et. al.,* (1978) and Al-Ahmer *et al.,* (1989). They cause serious quantitative and qualitative losses in peanut yield in Egypt. Therefore, growing peanuts in these infested soils becomes unprofitable (Hilal *et al.,* 1994 and Hassan and Frederick, 1995).

Aflatoxigenic fungi (*Aspergillus flavus* Link and *A. parasiticus* Spear) are commonly associated with peanut pods during their development in the field. Peanut pods are a good substrate for growth of *Aspergillus flavus* and *A. parasiticus,* and for subsequent aflatoxin production (Xue *et. al.,* 2003 and Mahmoud,2004). Meanwhile preharvest aflatoxin contamination is one of the most challenges facing peanut producers in many parts of the world (Payne, 1998) including Egypt and it's the most factor attecting exportation to the world market .

Pod rot diseases are widespread on all cultivars, but cultivars differed greatly in their reaction to diseases, in both quantity and quality of peanut yield (Mehan *et. al.,* 1995). Also, no cultivars were completely resistantto aflatoxin contamination following seed infection with aflatoxigenic fungi, while there were a significant differences in their ability to allow invasion and aflatoxin production (Mahmoud *et. al.,* 2006 and Azzam *et. al.,* 2007). Plant breeding was used for improving plant characters and increasing genetic variability in a variety of crop species including peanuts (Azzam and El-Sawy, 2005 and Khalifa *et al.,* 2006).

The objectives of this study was to evaluate general and specific combining ability, gene nature, heritability, heterosis and reaction to pod rot diseases and aflatoxin contamination. These informations can support breeding programs aimed to improve peanut productivity under environmental conditions of Ismailia Governorate.

MATERIALS AND METHODS

In the first summer season 2010, five parental peanut pure lines and cultivar were chosen to represent a wide range of variability in most of the economic characters Ten F_1s were obtained by crossing five parental genotypes viz; line 85, line 367, line 284, line 205 and Giza 6 in a half diallel..

Table (1) Parents used and their origin

Parent	Name	Origin
1	Line 85	Egypt
2	Line 367	China
3	Line 284	China
4	Line 205	India
5	Giza 6	Local variety

The parental genotypes were crossed in all possible combinations excluding reciprocals to obtain 10 F_1s hybrid seeds.

15 genotypes *i.e* (ten F_1s and five parents) were grown in a randomized complete block design with three replications during 2011 summer season at the Experimental station of Ismailia. Each block contained 10 F_1 hybrids and five parents,. Each entry was planted in a single row plot, 4 m long and 60 cm apart. Plants were spaced 20 cm apart within rows. The recommended fertilizer levels and agronomical practices for the reclaimed sandy soils were applied. Data recorded on eleven characters. Viz. plant height, number of branches per plant, number of pods per plant, pod weight per plant, 100-pod weight, number of seeds per plant, seed weigh per plant, 100- seed weight, shelling percentage, pod yield/fed. and oil percentage. The general combining ability (GCA) of the parents and specific combining ability (SCA) of the crosses were computed based on Method 2 (involves parents and F_1s only) and Model1 (fixed effects) of Griffing (1956). Partitioning of genetic variance was calculated according to the procedure outlined by Hayman(1954). Heterobeltiosis percentage was determined for individual cross deviation from better parents according to Bhatt(1971).

Reaction of some peanut genotypes against pod rot pathogens and preharvest aflatoxin contamination in artificially infested soil under field conditions.

Fifteen peanut genotypes *i.e*,five parents and their ten hybrids were evaluated for their reaction against pod rot pathogens and invasion by aflatoxigenic fungi as well as aflatoxin contamination.

Fungal inocula of the main pod rot causing pathogens i.e. *Rhizoctonia solani,* the causal of dry brown lesion; *Fusarium moniliforme,* the causal of pink discoloration as well as *Macrophomina phaseolina* and *Sclerotium rolfsii* the main causal pathogens of general breakdown pod rot, as well as aflatoxigenic fungi *i.e. Aspergillus flavus* and *A. parasiticus* (which previously isolated from diseased peanut pods and confirmed their pathogenic capabilities by the authors) were prepared for artificial soil infestation under infested field conditions using sorghum - coarse sand -

water (2:1:2 v/v) media. The ingredients were mixed, bottled and autoclaved for one hour at 1.5 air pressure. The autoclaved media in glass bottles were separately inoculated using agar discs obtained from the periphery of 5 day old colony of each of the tested fungi and incubated at 26 C° for two weeks, then used for soil infestation.

At harvest plants in individual plots were dug and inverted based on an optimum maturity index. Resulted pods were threshed, air-dried for seven days. Pod rot incidence, occurrence of pathogenic and aflatoxigenic fungi as well as aflatoxin contamination were determined. Three categories for apparent symptoms of pod rots beside the apparently healthy pods were adopted according to Satour et. al., 1978): a) Rhizoctonia rot, pods with dry brown lesion, b) Fusarium rot, pods with pink discoloration and c) complex rot pod with general breakdown resulting from many fungi. Resulted pods were used for isolation and determinating the frequency of different causals of pod rots and aflatoxigenic fungi as well as for detecting aflatoxin contamination.

A-Isolation and determinating the frequency of pathogenic and aflatoxigenic fungi invasion.

Pod rot pathogens and aflatoxigenic fungi, associated with the samples of each category of pod rot symptoms, as mentioned before, beside the apparently healthy pods of peanut were isolated after harvest according to Garren and Porter (1970). Five pods were shelled and 1cm^2 pieces of shell and seeds were surface-sterilized for three minutes in 1% sodium hypochlorite and plated on potato dextrose agar (PDA) medium (3 plates in 3 replicates, 5 seeds or shell pieces per dish). Plates were examined after 7 days of incubation at 27 °C, for fungal propagates. The frequency of invasion by aflatoxigenic fungi was recorded in each pod tested samples and calculated as follow :

% invasion by pod rot pathogens and aflatoxigenic fungi =

$$\frac{\text{Number of infected samples}}{\text{Number of total samples}} \text{X} 100$$

Identification of the isolates was carried out based on taxonomic criteria for these fungi as described by Maren and Johan (1988).

B-Analysis of peanut samples for detection of aflatoxin contamination.

C-Extraction of aflatoxin

The extraction of aftatoxins was conducted according to A.O.A.C (1998). The samples were blended with 250 ml methanol -water (55:45, v/v) and 100ml hexane for 1 min. at high speed. The mixture was transferred to the centrifuge tube and centrifuged for 5 min. at 2000 rpm. An aliquot from the aqueous methanol phase (25 ml) was taken into separator contained chloroform. The separator funnel was shaken (30-60 sec.); the bottom layer (chloroform) was separated and concentrated using rotary evaporator. The residue was quantitatively transferred using small volumes of chloroform. The solvent was completely removed under nitrogen flew.

D-Determination of aflatoxin:

Aflatoxins were determined according to Singh *et al.,* (1991) using thin layer chromatographic technique as follows; the dried film representing the aflatoxins in the samples was dissolved in a known amount of chloroform. The aflatoxin standards were spotted along with the samples. The plates were developed using a mixture of acetone-chloroform (1:9, v/v), the chromatoplates were detected under UV lamp at 365nm. The concentration of aflatoxin was calculated using the formula:

µg /Kg = (S.Y.V.)/ (X.W)

Where:

S= volume of aflatoxin standard, in µL of equivalent intensity of sample.

Y= concentration of aflatoxin standard in µg/ml.

V= volume of solvent required to dilution final extract in µL.

X= volume of sample extract in µL required to give fluorescence intensity comparable to that of S µL of standard.

W= weight of original sample in gram contained in the final extract.

Statistical analysis: Data were statistically analyzed and mean were compared by Fisher's protected least significant differences (LSD) at 0.05 level (Gomez and Gomez, 1984).

RESULTS AND DISCUSSION

Analysis of variance:

The analysis of variance showed that significant genetic differences existed in all the studied characters under artificial infection hereby, the studied genotypes differed in genes controlling yield and its attributes (Table2).

The results showed that relative estimates of variance due to specific combining ability (SCA) were higher than those of general combining ability (GCA) for plant height, number of branches/plant, number of pods/plant, pod weight/plant , number of seeds/plant, seed weight/plant and oil %, indicating the predominance of non-additive gene effect in controlling characters.

The analysis of variance for general and specific combining ability was significant or highly significant for most studied traits. These results indicated the importance of both additive and non-additive components ance in the inheritance of these characters. The ratio of both estimates exceed the unity for all studied characters except plant height, number of branches, number of pods, pod weight/plant, number of seeds/plant, seed weight/plant and oil percentage. This indicates that most of the genetic variation among the investigated genotypes for these traits appears to be additive. Thus, selection could be effective for improving these characters. The importance of additive and non-additive gene action for such characters are also reported by Varman (1998), Ruraswamy *et al.,* (2001) and El-Sawy(2006).

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Mean performance of parents and F_1s:

Results showed significant differences among genotypes, parents and F_1 for all studied traits. Mean performance of the five parents and 10 F_1 hybrids were presented in Table(3). Results indicated that parents P2 and P5 and crosses (P1 x P2), (P2 x P4) and (P3 x P4) showed higher mean performance in most characters. The crosses showed higher means in most cases compared to its parent.. Besides, the upper limits of ranges for hybrids were higher than upper limits of parents for all characters except plant height, number of pods/plant, pod weight/plant, 100-pod weight and number of seeds/plant.

General combining ability effects:

The estimates of GCA for five parents are presented in Table(4). High positive and significant values were recorded for p_2 for number of pods/plant, pod weight\plant(g), 100-pod weight(g), number of seeds\plant, seed weight\plant, 100-seed weight and pod yield/fed. revealed the importance of this parent as a donor for favorable alleles for these economic charters. Also P_5 had positive and significant GCA for number of branches/plant, 100-seed weight(g), pod yield/fed. and oil percentage. However, the same parent, P_5 gave high negative and significant effect (desirable for breeding) for plant height. , but P_1 was good combiner for 100-pod weight and 100-seed weight. It could be observed that the pervious conclusion was in harmony with the mean performance of parental genotypes indicating the efficiency of phenotypic performance for detecting the potentiality of parents for inclusion in cross breeding programs. Similar results were observed by Sanun *et al*., (2005) and Naazar *et al.*, (1995).

Specific combining ability effects:

Results given in Table(5) showed the estimates of SCA for the studied characters in ten crosses.

These results indicated that cross (P_1xP_2) was positive and highly significant SCA effect for number of pods\plant, pod weight/plant, 100-pod weight, number of seeds\plant, seed weight/plant, 100-seed weight, shelling percentage and oil percentage. Only one cross (P_1 x P_3) exhibited positive and highly significant SCA effects for number of branches/plant. The cross (P_1 x P_4) exhibited highly significant SCA positive effects for 100-pod weight (g) and oil percentage. Also, both crosses (P_1xP_5) and (P_2xP_4) showed the best SCA for 100-pod weight and 100-seed weight.

Moreover, the cross (P_3xP_4) exhibited positive and highly significant SCA effects for number of pods\plant, pod weight/plant, number of seeds/plant, seed weight/plant, shelling and oil. These crosses could be of practical importance in peanut breeding programs. These results agree with those reported by Yadav *et al*., (2006)).

Heterotic effects:

In the absence of male sterile lines, the possibility of explanation of heterosis in peanut appears to be remote at present. The alternative, therefore, left to breeders is to take up these promising crosses having high heterosis, which may in turn produce desirable transgressive segregants in advanced generations Basu *et al.,* (1986).

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Estimates of heterotic effects for the F_1 crosses are shown in Table(6). Significantly positive heterobeltiosis effects relative to better parents values may be considered favorable for most characters under investigation. Highly significant negative(desirable) heterotic effects relative to the best parent were noticed for plant height in all crosses except cross (P_4xP_5). Significant or highly significant positive heterotic effects were found for number of branches\plant in the two crosses (P_1xP_3) and (P_2xP_3) and number of pods\plant and number of seeds\plant in one cross(P_3xP_4), pod weight\plant in two crosses(P_1xP_2) and (P_3xP_4). Highly significant positive heterobeltiosis was recorded for 100-pod weight in crosses(1x4), (1x5), (2x4) and (2x5). The highest heterobeltiosis effect (35.14) with respect to number of seeds/plant was shown by cross (3x4). Highly significantly positive heterotic effects were found for seed weight\plant in the(P_2xP_4) and (P_3xP_4) crosses, 100-seed weight in the(P_1xP_2), (P_1xP_4), and(P_2xP_4).

Four crosses(P_1xP_2), (P_2xP_3), (P_2xP_4) and(P_3xP_4) revealed significant and highly significant positive heterobeltiosis for shelling percentage.

For pod yield/fed. four crosses(P_1xP_2), (P_1xP_3), (P_2xP_5) and (P_3xP_5) gave significant and highly significant positive hetrotic value. All crosses except (P 1 x P 3) and(P 2 x P 4) gave the highest desirable positive and significant values for oil percentage.

In the previous combination, it can be noticed that high heterosis, involved one good general combiner and one poor combiner thereby indicating the role of inter-allelic interactions. Therefore, for exploitation such heterosis in future breeding programmes, either recurrent selection or diallel selective mating system is to be examined in such crosses. These results for most cases are in harmony with that reached by El-Sawy (2006), El-Baz (2006), Abd-El aal (2008) and K.John (2012).

Estimation of genetic component and heritability:

The estimates of genetic variation based on the approach by Hyman (1954) are shown in Table(7). The component of variation due to additive gene effects (D) was significant or highly significant for all traits studied except number of branches/plant, 100-pod weight and oil, indicating that the additive gene action was more important than the non-additive in controlling the inheritance of these characters. Genetic components due to dominant effects (H_1 and H_2) were highly significant for all studied characters except number of branches (Table 7). The magnitude of H_1 was greater than H_2 in all traits which indicated that the positive and negative alleles were not equal in proportion in the parents at any locus. It was also obvious that the magnitude of dominance (H_1) genetic component was higher than the magnitude of additive one (D) for all studied characters indicating the important role of dominance genetic variance. The h^2 values, over all dominance effect of heterozygous loci was positive and highly significant for plant height, 100-seed weight, shelling percentage and oil percentage, indicating that most of the dominant genes had positive effects. The distribution or relative frequency of dominant versus recessive genes (F) were significantly positive for plant height , number of pods /plant , pod weight / plant, number of seeds / plant , seed weight / plant and shelling percentage. Indicating a preponderance of dominant alleles controlling these characters. Also the environmental

component of variance (E) was positive and significant or highly significant for 100-pod weight, number of seeds/plant, 100-seed weight and shelling. Indicating the effect of environmental condition in this concern.

The ratio $(H_1/D)^{0.5}$ which measures the average degree of dominance was more than unity for all studied characters, indicating that over dominance is controlling these traits. To improve these characters, pedigree selection mode could be applied. Proportion of genes with asymmetry positive and negative effects as $(H_2/4H_1)$ was lower than 0.25 for all studied characters. These values indicated that positive and negative alleles among the parent.
The ratio of total number of dominance to recessive genes in all parents (KD/KR) was greater than unity for all studied characters, indicating that dominant alleles were found in all parents for these characters.

Heritability estimates in broad sense (H_b) were high for all studied traits and ranged from 77% for shelling percentage to 97% for plant height. Narrow sense heritability (h_2n) were low in most characters to moderate for 100-seed weight and pod yield/ard. and high for 100-pod weight. The low value of narrow sense heritability are mainly due to dominance components accounted for a great portion of the genetics of these characters. Different estimates of heritability in narrow sense and in the broad sense were recorded by some researchers Rudyaswamy *et al*., (1999), Ayub-Khan *et al*., (2000), Yogendra *et al*., (2002) and Abd-El-aal (2008).

Table (4): Estimates of general combining ability(gi) effects of five peanut parents for the studied traits .

Genotypes	Plant height (cm)	No. of branches /pl.	No. of pods/pl.	Pod weight /pl. (g)	100-pod weight (g)	No. of seeds/pl	Seed weight/pl (g)	100-seed weight (g)	Shelling %	Pod yield (ard/fed.)	Oil %
P1	-0.06	0.011	-0.68	-0.03	6.37**	-1.11	0.01	2.63**	-1.29	0.30	0.10
P2	0.02	-0.14*	1.02**	2.73**	6.98**	1.67*	1.45*	3.04**	0.34	0.84*	0.17
P3	1.56**	-0.04	-0.56	-1.89*	-8.62	-0.66	-2.29**	-7.67**	-3.69**	1.12**	-0.66
P4	-0.49*	0.025	-0.44	-0.73	-1.63	-0.53	0.33	-1.83	0.51	-1.06*	-0.16
P5	-1.03**	0.15*	0.64	-0.06	-3.09*	0.64	0.48	3.82**	4.13**	-1.65**	0.54*
S.E.(gi)	0.41	0.14	0.77	1.12	2.94	1.18	0.79	1.45	1.98	0.46	0.25

***,** significant at 0.05 and 0.01levels of probability, respectively.**

Table (5): Estimates of specific combining ability for ten peanut crosses.

Genotype	Plant height (cm)	No. of branches /pl.	No. of pods/pl. (g)	Pod weight /pl. (g)	100-pod weight (g)	No. of seeds/pl	Seed weight/pl (g)	100-seed weight (g)	Shelling %	Pod yield (ard/fed.)	Oil %
1x2	**-0.27**	**-0.35***	**3.77****	**9.17****	**7.17****	**4.22****	**9.56****	**17.85****	**9.46****	**1.94**	**0.73***
1x3	**-0.12**	**1.64****	**-1.38**	**-3.76****	**-9.68****	**-1.63**	**-2.77***	**-4.39***	**1.74**	**2.77****	**-2.39****
1x4	**2.47****	**-0.12**	**-3.82****	**-7.16****	**7.79****	**-6.99****	**-3.28***	**1.47**	**-6.53****	**-1.24***	**1.83****
1x5	**-4.08****	**0.05**	**-1.31**	**-0.59**	**8.88****	**-0.75**	**-1.70**	**3.93***	**-3.65**	**-0.77**	**0.51**
2x3	**-9.69****	**0.17**	**-0.62**	**-1.83**	**-2.67**	**-0.65**	**-1.07**	**-2.73**	**1.06**	**-2.63****	**1.75***
2x4	**0.16**	**0.16**	**0.16**	**2.16**	**12.60****	**2.87**	**4.71****	**10.79****	**7.75****	**0.27**	**-1.58***
2x5	**-3.52*8**	**0.10**	**-5.18****	**-10.86****	**5.17**	**-7.88****	**-7.40****	**4.19***	**2.20**	**1.41***	**2.08****
3x4	**-7.05****	**-.07**	**7.91****	**16.69****	**-5.08**	**11.56****	**13.98****	**3.01**	**5.63****	**0.77**	**1.92****
3x5	**1.39****	**0.24**	**-0.57**	**-4.70****	**-19.31****	**-3.03***	**-2.02***	**-1.38**	**3.91**	**4.94****	**2.58****
4x5	**3.74****	**-0.16**	**-0.88**	**-3.23***	**-9.11****	**-0.29**	**-3.94***	**-11.45****	**0.36**	**0.22**	**0.13**
S.E.(si-j)	**0.93**	**0.31**	**1.71**	**2.52**	**5.92**	**2.64**	**1.77**	**3.25**	**4.44**	**1.03**	**0.58**

***,** significant at 0.05 and 0.01levels of probability, respectively.**

Table (6): heterobeltiosis % of the studied traits of peanut F_1 crosses .

Character / Crosses	Plant height (cm)	No. of branches /pl.	No. of pods/pl.	Pod weight /pl. (g)	100-pod weight (g)	No. of seeds/pl	Seed weight/pl (g)	100-seed weight (g)	Shelling %	Pod yield (ard/fed.)	Oil %
1x2	**-20.9****	**-3.36**	**5.79**	**15.40****	**7.73****	**1.89**	**-2.31**	**37.99****	**18.32****	**7.25***	**2.45****
1x3	**-25.1****	**48.89****	**-15.82****	**-21.1****	**-9.14****	**-8.41****	**-50.95****	**-7.22***	**-0.22**	**22.29****	**-6.02****
1x4	**3.71***	**-4.39**	**-29.81****	**-28.1****	**3.57***	**-19.32****	**-44.59****	**9.23****	**-7.39***	**-4.52**	**4.09****
1x5	**-21.9****	**0.57**	**-30.14****	**-25.2****	**3.38***	**-21.28****	**-39.35****	**0.46**	**-10.43****	**0.39**	**2.78****
2x3	**-50.3****	**6.22***	**-15.94****	**-19.2****	**-3.76***	**-6.77****	**-8.95***	**2.34**	**12.74****	**-22.87****	**5.23****
2x4	**-20.9****	**-1.84**	**-11.36***	**-5.28**	**7.98****	**0.39**	**30.63****	**24.62****	**17.50****	**-6.30***	**-0.94**
2x5	**-33.5****	**-1.32**	**-40.03****	**-44.1****	**3.28***	**-22.20****	**-46.96****	**1.16**	**-0.22**	**15.26****	**8.60****
3x4	**-44.6****	**-4.39**	**67.49****	**77.82****	**-8.77****	**35.14****	**57.30****	**-89.4****	**7.86***	**5.02**	**5.63****
3x5	**-23.7****	**3.99**	**-26.18****	**-39.9****	**-17.1****	**-18.52****	**-41.47****	**-17.5****	**-3.40**	**29.49****	**8.86****
4x5	**10.94****	**-3.22**	**-27.09****	**-33.4****	**-7.89***	**-13.24****	**-39.12****	**-22.4****	**-2.49**	**2.31**	**4.37****

***,** significant at 0.05 and 0.01 levels of probability, respectively.**

1-Reactions to pod rot pathogens in artificially infested plots under field condition.

Data presented in Table (8) showed that tested peanut genotypes varied in their susceptibility to infection by pod rot diseases under field condition at the different three categories of pod rots diseases. In general, pods with breakdown rot had the highest disease incidence, followed by dry brown lesion, whereas pink discoloration was the least one.

The crosses (P_1 x P_5) and P_2 x P_3) and P_3 (line 284) were the highest resistant ones against all categories of pod rot diseases and gave the highest percentages of apparently healthy pods (84.8 and 87.0, 85.5 %, respectively), followed by (P_3 x P_4), (P_1 x P_4), (P_1 x P_3) and (P_2 x P_4) which recorded 79.1, 72.0, 71.4 and 69.9 %, respectively. On the other hand, the second parent (line 367), crosses (P_4 x P_5, P_3 x P_5) and P_4(line 205) appeared to be more susceptible ones for all categories of pod rots and gave the lowest percentage of apparently healthy pods (29.7, 31.5, 33.2 and 39.2%, respectively). However, the other crosses *i.e.* (P_2 x P_5, P_1 x P_2), P_1 (line 85) and P_5 (Giza 6) were intermediate in this respect recording apparently healthy pods 54.5, 52.2, 48.6 and 46.1%, respectively.

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Table (8): Evaluation of some peanut genotypes against pod rot diseases complex under artificially infested field.

Genotypes	Percentage of pod rots %			Apparently healthy pods %	Reaction
	Dry brown lesion	Pink discoloration	General breakdown		
P_1	21.3	3.3	26.8	48.6	MS
P_2	29.3	4.6	36.4	29.7	S
P_3	6.0	0.0	9.2	84.8	R
P_4	23.1	8.0	29.7	39.2	S
P_5	17.7	5.6	30.6	46.1	MS
1 x 2	20.9	0.0	26.9	52.2	MS
1 x 3	10.0	0.0	18.6	71.4	MR
1 x 4	12.0	1.7	14.3	72.0	MR
1 x 5	3.9	0.0	9.1	87.0	R
2 x 3	11.6	0.0	2.9	85.5	R
2 x 4	12.3	2.6	15.2	69.9	MR
2 x 5	22.4	3.4	19.7	54.5	MS
3 x 4	13.8	0.0	11.1	75.1	MR
3 x 5	27.3	4.5	35.0	33.2	S
4 x 5	30.5	3.9	34.1	31.5	S
Mean	17.5	2.5	21.4	58.6	-
L.S.D at 0.05	8.52	6.17	9.81	11.96	

To facilitate comparison between reactions of the tested peanutal parent lines and crosses against pod rot diseases, four categories of different varietal reactions were suggested based on percentage of apparently healthy pods. The screened peanut genotypes could be classified as follows:

1 –Resistant genotypes (R) include 3 genotypes *i.e.* (P_1xP_5), (P_2 x P_3)and P_3 which produced the highest apparently healthy pods % ranged from84.4 to 87.0.0 %.

2– Moderately resistant genotypes (MR) include 4 crosses *i.e.* (P_3xP_4), (P_1xP_4), (P_1 x P_3)and (P_2 x P_4) as they produced apparently healthy pods ranged from 75.1 to 69.9%.

3– Moderately susceptible genotypes (MS) include 4 genotypes *i.e.* (P_2x P_5), (P_1 x P_2), P_1 and P_5 which produced apparently healthy pods ranged from 46 to 54.5.1%

4 –Susceptible genotypes (S) include 4 genotypes *i.e.* P_2, crosses (P_4 x P_5), (P_3 x P_5) and P_4 which produced apparently healthy pods ranged from 29.7 to 39.2 % .

The present results concluded that all peanut genotypes which tested varied in their susceptibility to infection by all categories of pod rots of peanut genotypes under field conditions. Genotypes *i.e.* (P_1 x P_5), (P_2 x P_3) and P_3 were the highest resistant ones against all categories of pod rots diseases, followed by crosses(P_3 x P_4), (P_1 x P_4), (P_1 x P_3) and (P_2 x P_4). On the other hand, P_2, (P_4 x P_5, P_3 x P_5) and P_4 were the highest susceptible ones for all categories of pod rots However, the other genotypes *i.e.*(P_2 x P_5), (P_1 x P_2), P_1 and P_5 were intermediate in this respect. These results are in agreement with Al-Ahmer *et al.,* (1989), Hilal *et al.,* (1994) and Mehan *et al.,* (1995).

Yehan *et al.,* (1990) showed that the rotting-pod rate of F_1 was closely related to parents. If both parents were susceptible to the disease, the hybrid F_1 was also susceptible. If one parent was susceptible and the other resistant, the rotting rate of hybrid F_1 would show in the middle of parents. The heritability (h2) of resistance to rotting pod was low (range from 0.1531 to 41.77%), which revealed that rotting resistance was a quantitatively related to polygenes. In this respect, Mahmoud *et. al.,* (2006) showed that pod rot diseases were common on all cultivars and the nine cultivars tested differed greatly in their reaction to the diseases. Ismailia 1 and R 92 cvs. were the most resistant against infection by all categories of pod rot disease incidence *i.e*. dry brown lesion pods, pink discoloration and general breakdown, while Giza 4, Gorgia and Giza 5 were the highest susceptible ones. In this respect EI-Deeb and Ibrahim, (1998) and Marei (2000) found similar results since they record that, pod rot diseases were common on all tested cultivars and the highest percentages of the diseases were in Giza 4 and Giza 5. Azzam *et. al.,* (2007) reported that, mutants RT-10, RT-12 and RT-7 were the most resistance ones for pod rot diseases of peanut while Giza 5 was the highest susceptible one in this regard. Several molecular markers (positive and negative) related to pod rot resistance/susceptibility in peanut mutants and their parent variety, Giza-5 were obtained by the RAPD primers. While, ISSR didn't reveal any marker (positive or negative) associated with pod rot resistance/susceptibility in peanut mutants and their parent variety, Giza-5. (Azzam *et. al.,* 2007)

2- Reaction to aflatoxin contamination.

Data presented in Table (9) illustrate that all tested peanut genotypes varied in their susceptibility to aflatoxin contamination under field condition. Regarding aflatoxin contamination, the obtained results (Table 9) also indicated that, aflatoxin B_1 was highest aflatoxin in all detected cases of peanut genotypes followed by G_1 whereas, B_2 and G_2 were the least ones.

Table (9): Aflatoxin contamination of some peanut genotypes under artificially infested field conditions.

Genotype	Aflatoxin contamination				
	B1	**B2**	**G1**	**G2**	**Total**
P_1	8	16	9	10	43
P_2	50	40	67	63	220
P_3	ND	ND	ND	ND	ND
P_4	16	14	13	7	50
P_5	22	23	17	18	80
1x2	10	ND	15	ND	25
1x3	ND	ND	ND	ND	ND
1x4	20	ND	ND	10	30
1x5	ND	ND	ND	ND	ND
2x3	ND	ND	ND	ND	ND
2x4	35	7	16	ND	58
2x5	50	10	19	ND	79
3x4	ND	ND	ND	ND	ND
3x5	48	26	39	20	133
4x5	95	40	20	30	185

ND: Not Detected

In this respect, five genotypes *i.e.* P_3, crosses(P_1 x P_3, P_1 x P_5, P_2 x P_3 and P_3 x P_4) were free from any contamination (B_1, B_2, G_1 and G_2) while, four crosses came free from one or two aflatoxins such as (P_1 x P_2) and (P_1 x P_4) came free from (B_2 and G_2) and (B_2 and G_1), respectively, while (P_2 x P_4) and (P_2 x P_5) came free from G_2 only. On the other side, aflatoxin contamination was the lowest content in three genotypes *i.e.* P_1, crosses(P_1 x P_2) and (P_1xP_4) which contaminated with 43,25 and 30 ppb of total aflatoxin. However, three genotypes *i.e.*P_2, crosses (P_4 x P_5) and (P_3 x P_5) recorded the highest contamination with total aflatoxin (B_1 + B_2+ G_1+ G_2) (220, 185 and 133 ppb) while, the other four genotypes *i.e.* P_4, P_5, crosses (P_2 x P_4) and (P_2 x P_5) were intermediate in this respect (50,80,58 and 79 ppb, respectively). The present results coincide with Hasan *et al* (2002) and Mahmoud *et al* (2006) who found that no one of tested cultivars showed completely resistance to aflatoxin production and invasion with aflatoxigenic fungi. *Aspergillus flavus* was more invasive than *Aspergillus parasiticus* and often dominated in peanut seeds than shells. Giza 4, Gorgia and Giza 5 cvs. were the highest susceptible one to pod rot diseases and recorded at the same time the highest frequency of aflatoxigenic fungi and content of aflatoxin. While, R 92 and Ismailia 1 cvs. appeared high resistance in this respect. Anderson *et al.,* (1995) evaluate aflatoxin contamination under drought stressed conditions in potentially resistant peanut genotypes in the field plots inoculated with *Aspergillus* inoculum and found that None of the genotypes included in this study were more resistant ($P \leq 0.05$) to preharvest aflatoxin contamination than Florunner. The results of this study indicated that it would be desirable to identify higher levels of resistance to preharvest aflatoxin contamination in peanut. Liang *et al.,* (2009) summarizes research progress in peanut host resistance mechanisms to aflatoxin contamination through systematic resistance evaluations of germplasm lines resistant to *Aspergillus flavus* invasion and concluded that the resistance has been associated with testa wax and presence of cutin layer, active oxygen and membrane lipid peroxidation, phytoalexin accumulation, and antifungal proteins in the peanut kernels.

3- Determination the frequency of invasion pod rots and aflatoxigenic pathogens.

Various fungi were isolated from different samples of peanut pods, representing each type of pod rot, from fifteen peanut genotypes (Table 10-13). Eight fungi have occurred in different frequencies from either pod shells or seeds of peanut. These fungi were *Aspergillus flavus, A. parasiticus, A. niger, Fusarium moniliforme, F. solani, Macrophomina phaseolina, Rhizoctonia solani,* and *Sclerotium rolfsii.*

3.1. From pods showing dry brown lesion symptoms:

Data in Table (10) showed that generally, *Rhizoctonia solani* was the most predominantly isolated fungus from pods with dry brown lesion, followed by *Aspergillus flavus, A. niger* and *A. parasiticus*, however, *S. rolfsii* was the least frequently isolated fungus in this respect. Meanwhile, *Fusarium moniliforme*, *F. solani* and *M. phaseolina* were intermediate ones.

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Regarding genotypes, Data shown in the same Table prove that five peanut genotypes *i.e.* crosses (P_1 x P_3, P_1 x P_5, P_2 x P_3, P_3 x P_4) and P_3 were the least contaminated by the tested pathogens, while, crosses (P_3xP_5), (P_4xP_5) and P2 were the highest contaminated by the tested pathogens in this regard.

3.2. From pods showing pink discoloration symptoms:

Data shown in Table (11) illustrated that *F. moniliforme* was the main fungus isolated from pod with pink discoloration, followed by *F. solani, M. phaseolina* and *R. solani* and the other fungi were intermediate ones were intermediate ones in this respect. Also, crosses (P_1 x P_3), (P_1 x P_5), (P_2 x P_3), (P_3 x P_4) and P_3 were the least contaminated by the tested pathogens, while, crosses (P_3 x P_5), (P_4 x P_5) and P_2 were the highest contaminated by the tested pathogens in this regard.

3.3. From pods showing general breakdown symptoms:

Results in Table (12) indicated that, most tested fungi were highly frequently isolated from pods with general breakdown symptoms. *Aspergillus niger* recorded the highest frequently isolated followed by *A. flavus, Fusarium moniliforme, Macrophomina phaseolina, F. solani, Rhizoctonia solani* and *A. parasiticus,* respectively, while *S. rolfsii* recorded the lowest frequently one. At the same time, crosses (P_1x P_5, P_2 x P_3, P_3 x P_4) and P3 were the least contaminated by the tested pathogens, while, crosses (P_3 x P_5, P_4 x P_5) and P_2 were the highest contaminated by the tested pathogens in this regard.

3.4. From pods showing apparently healthy pods symptoms:

Data illustrated in Table (13) showed that the frequency of *A. flavus, A. parasiticus* and *A. niger* was higher in both seeds and shells of most genotypes while *S. rolfsii* was the least frequently one. However, other fungi recorded low occurrence in this respect. On the other hand, crosses (P_1 x P_3, P_1 x P_4, P_2 x P_3, P_3 x P_4) and P_3 were the least contaminated by the these pathogens, while, P_2, crosses (P_3 x P_5) and (P_4 x P_5) were the highest contaminated by the tested pathogens in this regard.

In general, we conclude that frequency of the tested pathogens was higher in pods showing general breakdown symptoms, followed by pods showing dry brown lesion symptoms. Meanwhile, it was lower in pods showing pink discoloration and apparently healthy pods symptoms. Also, the most resistant genotypes for pod rot diseases and aflatoxin contamination were the least contaminated ones by the target pathogens. Several workers have screened peanut genotypes for resistance to seed colonization and aflatoxin contamination of pod rot pathogens and aflatoxigenic fungi *A. flavus* and *A. parasiticus* under *in vitro* conditions (Mahmoud 2004) and in field conditions (Will *et al* 1994).

Data also showed that, under field conditions there was no clear correlation between the occurrence of of pod rot pathogens and aflatoxigenic fungi in kernels of peanut genotypes and their pod rots and aflatoxin contamination, with some exceptions. This is in agreement with Azaizeh *et al* (1989) and Will *et al* (1994) who reported no significant correlation between aflatoxin concentration and soil population densities of aflatoxigenic fungi. This may be due to that not all Egyptian isolates of *A. flavus* and *A. parasiticus* were able to produce aflatoxin in peanut pods (Mahmoud 2004).

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While peanuts grown under stress conditions will only result in extensive aflatoxigenic mould infection and subsequent aflatoxin contamination of the harvested peanuts (Azaizeh *et al* 1989).

The present study concluded that all peanut genotypes tested varied in their susceptibility to infection by peanut pod rots and aflatoxin contaminations as well as frequency of invasion pod rots and aflatoxigenic pathogens under field conditions. Genotypes *i.e.* crosses

(P_1 x P_5) , (P_2 x P_3) and P_3 were the highest resistant ones against all categories of pod rots diseases and aflatoxin contaminations, followed by crosses (P_3xP_5), (P_1x P4), (P_1 x P_3) and (P_2 x P_4). On the other hand, P_2, hybrid (P_4 x P_5), hybrid (P_3 x P_5) and P_4 were the highest susceptible ones for all categories of pod rots and aflatoxin contaminations. However, the other genotypes *i.e.* hybrid (P_2 x P_5), hybrid (P_1 x P_2), P_1 and P_5 were intermediate in this respect.

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وراثــة بعـض الصـفات الاقتصـادية ورد الفعـل لأمـراض أعفـان الثمـار والتلـوث بالأفلاتوكسين في الفول السوداني

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أجري هذاالبحث بمزرعة محطة البحوث الزراعية بالاسماعيلية خلال موسمي الزراعة ٢٠١٠-٢٠١١ بهدف دراسة القدرة العامة والخاصة علي الائتلاف وقوه الهجين وطبيعة الفعل الجيني للمحصول و مكوناتة وكذلك المقاومة لأمراض أعفان الثمار والاصابة بالأفلاتوكسين في الفول السوداني.

وقد تم في الموسم الأول اجراء التهجين بين خمسة تراكيب وراثية متباينة في صفاتها وهي سلالة ٨٥ ، سلالة ٣٦٧ ، سلالة ٢٨٤ ، سلالة ٢٠٥ وجيزه(٦) بنظام الداي أليل (بدون اجراء الهجن العكسية).

في الموسم الثاني تم تقييم الأباء والعشرة هجن الناتجة منها في الجيل الأول تحت ظروف العدوي الصناعية بالفطريات الممرضة في الحقل في تجربة في قطاعات كاملة العشوائية في ثلاث مكررات، وتمت دراسة كل من الصفات الآتية: طول الساق(بالسم)، عدد الأفرع\النبات، عدد القرون\النبات، وزن قرون النبات(بالجم)، وزن ال١٠٠ قرن(بالجم)، عدد بذور\النبات، وزن البذور\النبات(بالجم)، وزن ال١٠٠ بذرة(بالجم)، نسبة التصافي(%)، محصول القرون\إردب للفدان،نسبة الزيت(%)، الاصابة بالامراض ودرجه التلوث بالافلاتوكسين.

ويمكن تلخيص أهم النتائج المتحصل عليها في النقاط الأتية:-

- تفوقت قيم متوسطات الجيل الأول علي قيم متوسطي الأباء لجميع الصفات المدروسة ما عدا طول الساق، عدد الأفرع، عدد القرون/النبات.
- أظهرت النتائج أن القدرة الخاصة علي الائتلاف لهاالدورالأكبر من القدرة العامة علي الائتلاف لجميع الصفات المدروسة ما عدا وزن ال ١٠٠ قرن، وزن ال ١٠٠ بذرة ، نسبة التصافي و محصول الفدان بالأردب.
- أظهرت النتائج أن الأب الأول (س ٨٥) كان الأفضل في القدرة العامة علي الأئتلاف لصفات وزن الـ ١٠٠ قرن ووزن ال ١٠٠ بذرة. وقد أظهر الأب الثاني (س ٣٦٧) قدرة عامة علي الأئتلاف لمعظم الصفات المدروسة، كما أظهر الأب الخامس (جيزة ٦) قدرة عامة علي الأئتلاف لصفات وزن ال ١٠٠ بذرة، نسبة التصافي، محصول الفدان بالاردب ونسبة الزيت.
- أظهـر الهجينـين (١× ٢، ٣ ×٤) تفوقـا فـي عـدد القرون/النبـات- وزن القرون/النبـات- عـدد البـذور/النبات- وزن البذور/النبات- نسبة التصافي- نسبة الزيت. بينما أظهر الهجينين (١ × ٥، ٢× ٤) تفوقا في وزن ال ١٠٠ قرن، وزن ال ١٠٠ بذرة، بينما أظهر الهجين (١× ٤) تفوقا في صفات ال ١٠٠ قرن ونسبة الزيت.
- كانت تأثيرات قوة الهجين موجبة ومعنوية بالنسبة للأب الأفضل لمعظم الصفات في الهجن (١×٢) و (١ × ٤) و (٢ ×٤) و(٣ × ٤).
- أتضح أهمية كل من الفعل الجيني السيادي والمضيف في وراثة جميع الصفات المدروسة.
- كانت قيم معامل التوريث بمعناها الضيق منخفضة إلي متوسطة بينما كانت عالية في درجة التوريث بمعناها الواسع.
- تفاوتت التراكيب الوراثية (الأباء والهجن) في قابليتها للاصابة بأمراض أعفان الثمار تحت ظروف العدوي الصناعية بالحقل وكذلك تلوثها بسموم الأفلاتوكسين.
- وكانت الهجن (١ × ٥، ٢ × ٣) وكذلك الأب ٢٨٤ هي الأكثر مقاومة لكل مجموعات أعفان الثمار تلاها في ذلك الجن (٣ ×٤، ١ ×٤، ١ ×٣، ٢ ×٤).
- أظهرت النتائج أن الأب ٢٨٤ والهجن (١ ×٣، ٢ ×٣، ٣ ×٤) كانت خالية تماما من التلوث بالأفلاتوكسين (B_1, B_2, G_1, G_2) .

يتضح من محصلة نتائج هذه الدراسة انه يمكن ملاحظة تفوق الهجن (١×٣، ١×٥ ، ٣×٤) في صفات المحصول ومكوناتة وكذلك مقاومتها لأمراض أعفان الثمار وخلوها تماما من الاصابة بالأفلاتوكسين. ويمكن ادخال هذه الهجن في التجارب المتقدمة لامكان عزل سلالات تتفوق في المحصول والمقاومه لأمراض أعفان الثمار وتتميز بخلوها من الأفلاتوكسين.

قام بتحكيم البحث

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Table(2): Mean squares of five peanut parents and thire crosses for 11 traits.

S.O.V	d.f	Plant height (cm)	No. of branches /pl.	No. of pods/pl.	Pod weight /pl. (g)	100-pod weight (g)	No. of seeds/pl	Seed weight/pl (g)	100-seed weight (g)	Shelling %	Pod yield (ard/fed.)	Oil %
Rep .	2	2.43	0.07	8.44	28.21	58.00	12.59	10.11	37.67	3451	6.89*	0.19
Genotypes	14	70.27**	1.01**	36.22**	169.87**	592.52**	80.23*	123.30**	347.99**	139.40*	23.89**	10.76**
Parents	4	80.31**	0.84**	42.56**	156.36**	59.45	78.36*	124.36**	222.65**	181.77**	18.79**	3.80**
Crosses	9	44.87**	0.92**	37.07**	193.07**	893.47**	89.54**	132.83**	396.96**	87.75	21.92**	9.33**
Error	28	1.82	0.21	6.19	13.35	73.60	14.71	6.63	22.21	41.46	2.25	0.70
GCA	4	6.58**	0.08	4.25	20.29**	308.02**	9.10	13.43*	162.98**	57.48**	10.43**	1.41**
SCA	10	30.16**	0.44**	15.21**	71.16**	153.30**	33.79*	52.16**	97.20**	42.06*	6.68**	4.45**
GCA/SCA		0.218	0.1818	0.279	0.285	2.009	0.269	0.257	1.677	1.366	1.57	0.316

*,** significant at 0.05 and 0.01 levels of probability, respectively.

Table (3): Mean performance of five peanut parents and their crosses.

Genotype	Plant height (cm)	No. of branches /pl.	No. of pods/pl.	Pod weight /pl. (g)	100-pod weight (g)	No. of seeds/pl	Seed weight/pl (g)	100-seed weight (g)	Shelling %	Pod yield (ard/fed.)	Oil %
P1	27.77	4.50	16.67	32.20	192.40	27.67	20.37	72.90	63.47	14.80	46.81
P2	33.57	4.77	19.63	37.23	189.57	31.13	21.23	68.10	57.03	17.93	45.81
P3	37.73	4.00	12.87	24.10	187.87	22.87	12.60	64.47	53.00	11.57	43.69
P4	26.23	5.23	14.07	25.40	180.37	22.67	16.17	71.47	64.00	14.60	45.48
P5	26.03	5.27	21.90	40.67	187.73	34.33	29.73	87.07	73.43	17.17	45.39
1x2	26.57	4.60	20.77	42.97	207.27	32.10	32.27	100.60	75.10	19.23	47.96
1x3	28.27	6.70	14.03	25.40	174.80	23.90	16.20	67.63	63.33	18.10	43.99
1x4	28.80	5.00	11.70	23.17	199.27	18.67	18.30	79.33	59.27	14.13	48.72
1x5	21.70	5.30	15.30	30.40	198.90	26.10	20.03	87.47	65.77	17.33	48.11
2x3	18.77	5.07	16.50	30.10	182.43	27.67	19.33	69.70	64.40	13.83	48.21
2x4	26.57	5.13	17.40	35.27	204.70	31.33	27.73	89.07	75.20	16.80	45.38
2x5	22.33	5.20	13.13	22.90	195.80	22.27	15.77	88.13	73.27	20.67	49.75
3x4	20.90	5.00	23.57	45.17	171.40	37.67	33.27	70.57	69.03	15.33	48.04
3x5	28.80	5.43	16.17	24.43	155.70	24.27	17.40	71.83	70.93	22.23	49.41
4x5	29.10	5.23	15.97	27.07	172.90	27.13	18.10	67.60	71.60	17.57	47.47
LSD	2.26	0.78	4.18	6.14	14.42	6.45	4.33	7.92	10.83	2.52	1.40
Parental mean	30.27	4.75	17.03	31.92	187.59	27.73	20.02	72.80	62.19	15.21	45.44
Hybrids mean	25.18	5.26	16.45	30.69	186.32	27.11	21.84	79.19	68.79	17.52	47.70
Parental range	26.03-37.73	4.00-5.23	12.87-21.90	24.10-40.67	187.73-192.40	22.67-34.33	12.60-29.73	64.47-87.07	53.00-73.43	11.57-17.93	43.69-46.81
Hybrids range	18.77-29.10	4.70-6.70	11.70-23.57	22.90-45.17	155.70-207.27	18.67-37.67	15.77-33.27	67.60-100.60	59.27-75.20	13.83-22.23	43.99-49.41

Table (7): Estimates of genetic components and their derived parameters for some peanut traits.

Character	Plant height (cm)	No. of branches /pl.	No. of pods/pl.	Pod weight /pl. (g)	100-pod weight (g)	No. of seeds/pl	Seed weight/pl (g)	100- seed weight (g)	Shelling %	Pod yield (ard/fed.)	Oil %
D±S.E	26.1±12.1**	0.22±0.39	12.1±6.9**	47.3±32.5**	-4.4±50.2	32.1±18.6**	73.5±30.0**	66.5±47.7**	47.9±19.6**	5.4±3.6*	1.0±1.3
F±S.E	48.7±30.3**	0.54±0.98	23.7±17.4**	93.2±81.2**	-48.3±125.3	66.9±46.6**	124.9±75.1**	48.8±119.2	46.9±49.1*	1.9±9.1	1.4±3.3**
H1±S.E	115.6±32.8**	1.6±1.06	60.9±18.9**	296.7±87.8**	669.1±135.5**	159.3±50.3**	252.2±81.2**	397.6±128.9**	146.0±53.1**	23.3±9.8**	15.1±3.5**
H_2±S.E	91.8±29.7**	1.3±0.96	48.6±17.1**	240.4±79.6**	404.5±122.9**	117.9±45.7**	187.4±73.6**	283.9±116.9**	118.9±48.1**	20.2±8.9**	13.8±3.2**
H±S.E	65.8±20.1**	0.59±0.65	-0.5±11.5	0.83±53.8	-11.4±82.9	-2.6±30.8	-0.15±49.7	99.7±78.9**	113.1±32.5**	13.1±6.0**	13.0±2.1**
E±S.E	0.62±4.9	0.06±0.16	2.1±2.8	4.78±13.2	24.2±20.5**	4.5±7.6*	2.3±12.3	7.8±19.5**	12.7±8.0*	0.86±1.4	0.22±0.5
(H1/D)0.5	2.1±	2.8	2.24	2.50	2.34	2.22	1.85	2.44	1.74	2.07	3.80
H2/4H1	0.19	0.19	0.19	0.20	0.15	0.18	0.19	0.17	0.20	0.21	0.23
KD/KR	2.6	1.18	2.54	2.29	1.85	2.76	2.69	1.35	1.78	1.18	1.43
Hn	0.12	0.15	0.12	0.17	0.55	0.25	0.18	0.45	0.24	0.35	0.11
Hb	0.97	0.83	0.85	0.93	0.91	0.85	0.95	0.94	0.77	0.90	0.94

***,** significant at 0.05 and 0.01levels of probability, respectively.**

Table (10): Fungi associated with peanut pods of different genotypes showing dry brown lesion symptoms

Genotype	Frequency of isolation (%) *																Mean
	Aspergillus flavus		*Aspergillus parasiticus*		*Aspergillus niger*		*Fusarium moniliforme*		*Fusarium solani*		*Macrophomina phaseolina*		*Rhizoctonia solani*		*Sclerotium rolfsii*		
	Shell	seed	shell	seed	shell	seed	shell	Seed	shell	seed	Shell	seed	shell	seed	shell	seed	
P_1	25	30	10	20	10	20	0	0	10	20	10	15	25	30	10	0	14.7
P_2	40	50	45	40	30	40	20	30	20	25	15	20	40	50	10	15	30.6
P_3	0	10	10	5	0	10	10	10	5	0	5	10	0	0	0	0	4.7
P_4	20	20	15	10	20	30	15	20	0	10	20	10	30	45	0	0	16.6
P_5	25	20	20	30	10	10	10	20	10	10	10	10	20	15	0	0	13.8
1 x 2	15	10	10	15	15	20	20	25	10	5	10	10	30	20	0	0	13.4
1 x 3	0	0	0	0	10	10	20	15	0	0	0	0	5	10	0	0	4.4
1 x 4	10	15	10	10	15	10	15	15	0	10	15	10	5	15	10	5	10.6
1 x 5	0	0	0	0	5	0	5	0	0	0	5	0	0	0	5	0	1.3
2 x 3	0	0	0	0	10	5	0	0	10	0	0	0	10	10	5	0	3.1
2 x 4	15	20	10	5	15	10	0	0	10	15	20	15	15	10	10	5	10.9
2 x 5	15	25	15	20	20	30	20	10	10	10	10	20	20	10	10	10	15.9
3 x 4	10	0	0	0	10	10	0	0	0	0	0	0	5	15	0	0	3.1
3 x 5	30	25	20	30	20	35	10	10	30	30	25	30	30	50	10	20	25.3
4 x 5	40	35	35	35	25	40	30	35	40	50	30	30	50	60	20	20	35.9
Mean	16.3	17.3	13.3	14.7	14.3	18.7	11.7	12.7	10.3	12.3	11.7	12.0	19.0	22.7	6.0	5.0	13.6
	16.8		14.0		16.5		12.2		11.3		11.8		20.8		5.5		

*Each value is the mean of three replicates (3 plates / replicate, five seeds or shell pieces per dish).

Table (11): Fungi associated with peanut pods of different genotypes, showing pink discoloration symptoms

Genotype	Frequency of isolation (%) *																Mean
	Aspergillus flavus		*Aspergillus parasiticus*		*Aspergillus niger*		*Fusarium moniliforme*		*Fusarium solani*		*Macrophomina phaseolina*		*Rhizoctonia Solani*		*Sclerotium rolfsii*		
	shell	seed	shell	seed	shell	seed	shell	seed	shell	seed	Shell	Seed	shell	seed	shell	seed	
P_1	15	10	5	0	10	0	10	20	20	10	0	5	20	10	0	0	8.4
P_2	20	30	15	10	20	20	30	25	30	25	25	20	10	20	5	5	19.4
P_3	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0.6
P_4	10	0	5	0	20	30	35	30	25	20	20	20	20	10	0	10	15.9
P_5	0	0	20	20	10	20	20	10	10	10	10	20	10	10	5	0	10.9
1 x 2	5	0	10	5	10	0	5	5	0	0	10	5	10	0	0	0	4.1
1 x 3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0
1 x 4	0	5	10	10	5	0	15	15	10	5	0	0	5	0	0	0	5.0
1 x 5	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0.3
2 x 3	0	0	0	0	0	0	0	0	0	0	0	5	0	0	5	0	0.6
2 x 4	10	10	10	15	5	0	20	10	10	15	10	10	15	10	0	0	9.4
2 x 5	5	10	15	10	15	5	20	20	20	10	10	15	20	15	0	0	11.9
3 x 4	0	0	0	0	0	0	0	0	0	0	5	0	5	0	0	0	0.6
3 x 5	10	15	20	20	10	20	10	10	20	25	25	20	15	20	5	10	15.9
4 x 5	20	25	15	20	25	10	20	30	20	30	30	30	25	30	10	10	21.9
Mean	6.3	7.0	8.3	7.3	8.7	7.0	13.0	11.7	11.0	10.0	10.0	10.0	10.3	8.3	2.0	2.3	8.3
	6.7		7.8		7.8		12.3		10.5		10.0		9.3		2.2		

* Each value is the mean of three replicates (3 plates / replicate, five seeds or shell pieces per dish).

Table (12): Fungi associated with peanut pods of different genotypes showing general breakdown symptoms.

Genotypes	Frequency of isolation (%) *																Mean
	Aspergillus flavus		*Aspergillus parasiticus*		*Aspergillus niger*		*Fusarium moniliforme*		*Fusarium solani*		*Macrophomina phaseolina*		*Rhizoctonia solani*		*Sclerotium rolfsii*		
	Shell	seed	shell	seed	shell	seed	shell	seed	shell	seed	Shell	seed	shell	seed	shell	seed	
P_1	20	20	25	20	20	30	30	25	25	30	30	25	25	30	20	10	24.1
P_2	45	50	30	40	60	40	40	45	35	45	45	50	40	50	35	25	42.2
P_3	0	0	0	0	5	10	15	20	0	5	0	5	0	10	0	0	4.4
P_4	15	30	15	20	40	35	30	25	20	25	30	25	25	30	20	20	25.3
P_5	30	40	40	35	30	30	20	30	30	40	30	20	30	20	25	20	29.4
1 x 2	25	30	10	15	40	20	35	25	25	30	20	25	20	0	0	0	20.0
1 x 3	0	10	0	10	20	10	15	10	10	10	0	20	10	0	20	10	9.7
1 x 4	10	5	15	20	25	20	5	10	5	5	0	10	15	0	0	0	9.1
1 x 5	0	0	0	0	10	10	0	0	0	0	5	0	0	0	0	0	1.6
2 x 3	0	0	0	0	5	0	0	0	0	0	0	0	0	0	5	0	0.6
2 x 4	25	20	15	15	15	10	10	10	10	5	15	20	15	10	0	5	12.5
2 x 5	35	20	30	20	10	20	25	15	10	10	20	25	10	15	10	0	17.2
3 x 4	0	0	0	0	5	10	0	5	0	0	0	0	0	0	0	0	1.3
3 x 5	20	35	20	30	50	40	30	40	30	35	40	30	35	40	25	30	33.1
4 x 5	40	45	35	30	35	30	25	20	40	30	35	30	30	40	20	30	32.2
Mean	17.7	20.3	15.7	17.0	24.7	21.0	18.7	18.7	16.0	18.0	18.0	19.0	17.0	16.3	12.0	10.0	17.5
	19.0		16.3		22.8		18.7		17.0		18.5		16.7		11.0		

* Each value is the mean of three replicates (3 plates / replicate, five seeds or shell pieces per dish).

Table (13): Fungi associated with peanut pods of different genotypes showing apparently healthy pods.

Genotype	Frequency of isolation (%) *																Mean
	Aspergillus flavus		*Aspergillus parasiticus*		*Aspergillus niger*		*Fusarium moniliforme*		*Fusarium solani*		*Macrophomina phaseolina*		*Rhizoctonia solani*		*Sclerotium rolfsii*		
	shell	seed	shell	seed	shell	seed	shell	seed	shell	seed	shell	Seed	shell	seed	shell	seed	
P_1	10	10	5	10	5	10	0	0	5	10	10	15	5	10	0	0	6.6
P_2	15	25	20	20	10	20	10	15	20	15	15	20	10	20	0	5	15.0
P_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0
P_4	15	20	5	10	15	20	10	5	10	10	10	10	5	10	0	0	9.7
P_5	10	20	10	15	10	15	5	10	5	5	5	10	0	10	5	0	8.4
1 x 2	5	10	0	5	5	10	0	5	5	10	10	10	5	5	0	0	5.3
1 x 3	0	0	0	0	0	5	0	0	0	0	0	0	0	5	0	0	0.6
1 x 4	10	5	0	0	5	0	0	0	0	0	5	0	0	0	0	0	1.6
1 x 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0
2 x 3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0
2 x 4	10	15	5	15	5	10	5	0	0	5	0	5	0	5	0	0	5.0
2 x 5	15	20	10	20	0	10	0	10	5	10	0	5	10	5	0	5	7.8
3 x 4	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.3
3 x 5	20	20	10	15	10	10	10	10	10	15	5	10	15	20	10	10	12.5
4 x 5	20	15	10	20	15	10	10	15	10	10	0	5	5	10	0	10	10.3
Mean	9.0	10.7	5.0	8.7	5.3	8.0	3.3	4.7	4.7	6.0	4.0	6.0	3.7	6.7	1.0	2.0	5.5
	9.8		6.8		6.7		4.0		5.3		5.0		5.2		1.5		

*Each value is the mean of three replicates (3 plates / replicate, five seeds or shell pieces per dish).