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Combining Ability and Gene Action for some Traits and level of Aflatoxin Contamination in Peanut

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ABSTRACT

The aim of this investigation was to study combining ability, gene action and heterobeltiosis for some traits and determination of aflatoxin contamination in peanut. A diallel cross, without reciprocals, among five parents was done in 2013. Data revealed that the mean squares of genotypes, parents and crosses were significant for all studied traits in both of F_1 and F_2 generations. The analysis of variance for combining ability showed that mean squares due to general (GCA) and specific (SCA) combining ability were generally significant for all studied traits reflecting the importance of both additive and non- additive gene effects in the inheritance of these traits. The lines A1and 623 were good combiners for 100-pod weight, shelling percentage and pod yield feddan^{-1} in the two seasons (one ardab=75kg and one feddan=4200m^2). Genotypes 10A and 2A were good combiners for number of pods plant^{-1}, pod weight plant^{-1}, number of seeds plant^{-1} and seed weight plant^{-1} in the second season. Regression line intersects the Wr axis below the origin in shelling percentage in F_1 and F_2 generations and pod yield feddan^{-1} in F_2 generation, reflecting over- dominance. On the other hand, pod yield feddan^{-1} was controlled by partial dominance. Among these gene action partial dominance could easily be exploited through conventional breeding. Positive or negative heterosis over the better parent, i.e. heterobeltiosis was detected for all studied traits. Determination of aflatoxin contamination under normal storage conditions showed that the two crosses (P_3X P_4 and P_3X P_5) had total aflatoxins of 10.6, 20.1ppb, respectively. Meanwhile, total aflatoxins were not detected in parents and other F_2 crosses.

Keywords: Peanut, Combining ability, Gene action, Vr–Wr graph, heterobeltiosis, Aflatoxins.

INTRODACTION

Groundnut or peanut (*Arachis hypogaea* L.), is an annual legume. It is one of the world's most important oilseed crops, (Dwivedi *et al.*, 2003). Peanut ranks the 13th among the most important food crops and the 4th among the most important oilseed crops in the world (Surendranatha *et al.*, 2011). Seeds contain 45-60% oil, 25-30% protein and 20% carbohydrate (Singh and Singh, 1991). Aflatoxin contamination is one of the most obstacles facing peanut producers for exportation to the world market (Xue *et al.*, 2003). Combining ability analysis is considered the quickest method of understanding the genetic nature of quantitatively inherited traits, and gives essential information about the selection of parents which in turn throw better segregants. The knowledge of the type of gene action involved in the expression of yield and yield components is essential to choose an appropriate breeding strategy to isolate desirable segregants in the later generations, John and Reddy (2015).

Several investigators studied combining ability and gene action in peanut. Shabana *et al.* (992) in Egypt, studied yield and its contributing traits. They applied the graphical approach suggested by Hayman (1954). In Pakistan Naazar *et al.* (1995) and Naazar *et al.* (2001) reported that estimates of general combining ability were significant for 100-pod weight, pod length and shelling percentage in F_1. Meanwhile, estimates for specific combining ability were significant for 100-seed weight in F_2 generation. Sanun *et al.* (2005) showed that estimates of both general and specific combining ability were significant for number of pods, pods kg^{-1} and 100-seed weight, whereas estimates of GCA were greater than SCA estimates. In Egypt, Abd El-Aal (2008) and Abd El-Aal *et al.* (2013) found that pod and seed traits were largely controlled by additive gene action, while pod number plant^{-1} and pod weight plant^{-1} were controlled by non-additive genetic effect. Both genetic effects were equally important for shelling percentage. Alam *et al.* (2013) reported that the analysis of combining ability suggested that both additive and non-additive gene actions were involved in genetic system. The number of pods plant^{-1}, plant height, 100-pod weight and pod yield plot^{-1} were preponderant by additive gene action. Meanwhile, primary branches plant^{-1} and 100-seed weight were preponderant by non- additive gene action. Vaithiyalingan (2016) observed that additive gene action was predominant for all studied traits, except harvest index and single plant yield.

Information on variation, heritability and nature of gene action controlling the various agronomic and physiological traits in crop plants is of crucial importance to breeders in elaborating a suitable breeding program for crop improvement.

The present study was undertaken to detected the magnitude of both general and specific combining ability (GCA and SCA), heritability, gene action and heterosis for pod yield and some traits in F_1 and F_2 progenies of a five parent diallel cross (excluding reciprocals) of peanut genotypes. Aflatoxin contamination rate under storage conditions was also determined.

MATERIALS AND METHODS

The present study was carried out at Ismailia Research Station, ARC, Egypt during 2013, 2014 and 2015. Five peanut genotypes out of around 600 germblasm accessions were used in this study viz; line 329(P_1), line 10A (P_2), line 2A (P_3), line 1A (P_4) and line 623(P_5). These parents were randomly chosen, representing a wide range of variability in most traits (Table 1).

Table 1. Parents used and their origin

Parent	Name	Origin	Seed color
1	Line 329	China	Purple
2	Line 10A	Egypt	white
3	Line 2A	Egypt	Red
4	Line 1A	Egypt	pink
5	Line 623	U.S.A	pink

A diallel - mating excluding reciprocals was carried out among the five peanut genotypes in 2013season. In 2014, the parental genotypes were planted again then re-hybridized to secure more F_1 hybrid seeds and the F_2 seeds were obtained from the F_1 plants. In 2015, an experiment was conducted in open field that included five parents, 10 F_1's and 10 F_2's. A randomized complete block design with three replications was used. Each entry was represented by one row in parents and F_1's and four rows in F_2's. Seeds were planted in rows 3 m long 60 cm apart in single seeded hills spaced 20 cm apart. Cultural practices were applied as recommended. At harvest ten guarded plants were taken at random from each experimental plot in parents and F_1's and 30plants in F_2's. The data recorded were plant height (cm), number of branches plant^{-1}, number of pods plant^{-1}, pod weight plant^{-1} (g), number of seeds plant^{-1}, seed weight plant^{-1} (g), 100-pod weight (g) , 100-seed weight (g), shelling percentage (%) and pod yield ardab feddan^{-1} (one ardab of pods= 75kg and one feddan= 4200m^2).

Data were analyzed according to Griffing (1956), model 1, method 2. In this approach, the combining ability variances and effects were estimated. 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).

Aflatoxins were determined according to Roos *et al.* (1997) and A.O.A.C (2006) using monoclonal antibody columns for total aflatoxins (VCAM Science Technology, Water Town, MA, USA). Aflatoxin identification was preformed by a modified HPLC. AFLATEST procedure Agillent 1200 series USA. HPLC equipment with two pumps, column (18, Lichiospher 100RP-18, 5umX25cm) was used. The mobile phase consisted of water, methanol a cetonitrile (54:29:17, V/V/V), at flow rate 1ml/min. The excitation and emission lengths for all aflatoxins were 362 and 460nm (Fluorescence detector), respectively.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance for plant height, number of branches pl^{-1}, number of pods pl^{-1}, pod weight, number of seeds pl^{-1}, seed weight pl^{-1} ,100- pod weight, 100-seed weight, shelling percentage and pod yield feddan^{-1}are presented in Table (2). The results reflected significant differences among genotypes mean squares for all the above mentioned traits in F_1 and F_2 generations. Moreover, mean squares due to parents as well as differences among crosses were significant for studied traits. These data suggested that the parental genotypes were mostly different in their mean performance. The analysis of combining ability revealed that variance associated with general and specific combining ability reached the level of significance for all studied traits in both F_1 and F_2 (Table 2). The significant variances due to both general and specific combining abilities reflect the importance of additive and non-additive types of gene actions. However, general combining ability effects which were extremely of high magnitude for number of branches plant^{-1}, number of pods plant^{-1}, pod weight plant^{-1} and number of seeds plant^{-1} in F_2 generations suggested the predominant role of additive gene action. This result supported by the over unity of GCA and SCA values, indicating that additively play a considerable role in the inheritance of these characters. Therefore, selection in the early generation could be successfully practiced to improve these traits. The importance of additive and non-additive gene action for such traits are also reported by Shabana *et al.* (1992), Ruraswamy *et al.* (2001), El-Sawy (2006) and Abd-El-Aal *et al.* (2013).

Table 2. Mean squares of five peanut parents and their crosses for 10 traits.

S.O.V	d.f	Plant height (cm)		No. of branches pl^{-1}		No. of pods pl^{-1}		Pod weight pl^{-1} (g)		No. of seeds pl^{-1}	
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Rep.	2	5.45	0.42	0.016	0.08	0.3	1.8	6.3	8.1	4.7	1.5
Genotypes	14	2.87**	85.36**	2.2**	24.42*	114.8**	329.7**	995.6**	1697,5**	11.1**	1275.7**
Parents	4	10.1**	66.0**	2.4**	54.43*	10.9**	111.0**	855.7**	303.0**	22.2**	243.5**
Crosses	9	0.3**	90.1**	2.2**	3.62*	796.9**	303.9**	1168.2**	1809.6**	1.6	1327.2**
P vs crosses	1	19.1**	119.0**	1.4**	91.53*	75.2**	1436.8**	0.8	6266.6**	65.6**	4940.2**
Error	28	1.8	0.3	0.056	0.16	0.4	0.8	6.3	14.6	2.7	1.1
GCA	4	20.7**	16.3**	0.95	38.68	5.41**	123.08**	12.4**	583.5**	36.2	450.7**
SCA	10	54.3**	33.2**	0.64**	26.87**	52.4**	104.64**	459.6**	558.7**	275.8**	415.1**
GCA/SCA		0.38	0.49	1.48	1.43	0.10	1.17	0.02	1.04	0.13	1.08

S.O.V	d.f	Seed weight pl^{-1} (g)		100-pod weight (g)		100-seed weight (g)		Shelling percentage (%)		Pod yield ardab feddan^{-1}	
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Rep.	2	5.5	2.4	56.26	13.3	7.2	1.5	4.53	3.12	0.21	0.7
Genotypes	14	739.0**	1266.1**	1270.53**	5424.0**	78.6	1446.7**	186.03**	198.87**	67.57**	45.6**
Parents	4	623.0**	128.9**	385.25**	1842.0**	22.20	530.8	162.72**	154.05**	56.98**	16.8**
Crosses	9	816.4**	1199.6**	1642.51**	7569.3**	112.3**	1873.4**	118.82**	117.13**	53.80**	35.3**
P vs crosses	1	506.0**	6412.7	1464.1**	444.9**	1.08	1270.9**	884.23**	1113.73**	233.9**	253.8**
Error	28	4.9	16.8	19.37	31.0	11.3**	5.9	5.94	8.81	3.4	0.3
GCA	4	50.20**	245.40**	245.70**	888.53**	15.68**	568.13**	68.83**	33.65**	18.09**	7.11**
SCA	10	324.77**	492.67**	494.64**	2175.80**	30.42**	447.89**	59.28**	79.34**	24.30**	18.44**
GCA/SCA		0.15	0.49	0.49	0.40	0.52	1.26	1.16	0.42	0.74	0.38

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

Mean performance

The results of means for pod yield clearly indicated the differences among parents, F_1's and F_2's (Table 3). Significant differences between parents and F_1's and parent and F_2's were found for all traits, except for number of pods plant^{-1} among parents, F_1's and F_2's, revealed the existence of genetic variability in the materials and the possibility of estimating combining ability effects. Results indicated that parents P_1, P_2 and P_5 and crosses (P_2 x P_4), (P_3 x P_4) and (P_4 x P_5) showed higher mean performance in most traits in both of F_1 and F_2 generations. The crosses showed higher means in most cases compared to its parent.

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

Genotype	Plant height (cm)		No. of branches pl^{-1}		No. of pods pl^{-1}		Pod weight pl^{-1} (g)		No. of seeds pl^{-1}	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
P1	25.03	22.93	4.0	4.27	31.23	26.07	85.83	55.6	50.27	50.20
P2	25.27	28.60	4.0	3.47	23.23	33.20	73.33	60.4	38.80	41.27
P3	16.20	18.57	5.8	5.20	20.43	26.13	56.33	66.7	32.30	49.67
P4	22.30	26.43	5.6	6.17	27.40	20.40	67.37	42.2	44.93	33.20
P5	16.30	17.97	5.5	4.60	34.73	17.40	100.03	46.3	68.10	30.80
P1XP2	32.3	30.27	4.8	5.37	22.73	47.53	62.93	96.6	42.77	83.60
P1XP3	19.2	20.93	4.4	3.70	38.40	48.00	109.83	109.0	77.57	87.20
P1XP4	23.1	23.63	6.0	6.07	25.67	21.00	68.80	40.1	48.97	29.60
P1XP5	29.4	25.80	6.3	6.80	17.87	23.20	48.63	57.6	28.53	40.73
P2XP3	13.7	28.60	5.0	4.87	26.87	46.80	65.83	100.2	42.73	85.13
P2XP4	24.9	17.23	3.9	3.27	39.13	30.67	110.60	65.9	75.27	59.27
P2XP5	26.5	23.53	6.6	5.73	26.07	32.80	68.07	113.7	50.47	57.73
P3XP4	35.9	24.60	5.2	4.47	32.47	45.60	76.63	78.0	57.33	86.07
P3XP5	29.1	18.57	5.9	5.93	31.77	34.47	79.33	59.5	60.80	47.27
P4XP5	34.5	33.17	5.3	4.77	26.07	36.20	72.20	72.3	50.40	55.93
L.S.D at 0.05	0.92	0.99	0.67	0.64	-	-	2.64	6.4	4.10	1.78

Genotype	Seed weight pl-1 (g)		100-pod weight (g)		100-seed weight (g)		Shelling percentage (%)		Pod yield ardab feddan^{-1}	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
P1	48.83	39.20	269.13	213.60	97.20	77.40	56.83	70.50	14.83	12.93
P2	38.40	32.73	298.37	185.23	101.53	75.83	52.37	54.03	12.90	15.17
P3	30.83	45.50	275.80	252.03	95.30	94.97	54.63	68.13	17.53	16.67
P4	44.63	28.70	273.53	200.60	99.41	86.37	66.20	67.97	19.40	14.11
P5	69.10	33.27	277.93	215.90	101.47	107.93	69.03	71.90	24.17	19.03
P1XP2	38.17	79.90	263.27	203.33	89.27	97.23	60.73	82.67	26.73	22.20
P1XP3	80.63	88.83	293.30	233.83	103.90	101.83	73.37	81.43	18.03	18.83
P1XP4	50.77	31.13	265.10	199.77	103.70	107.10	73.73	77.47	23.53	20.83
P1XP5	27.23	42.43	301.37	245.13	95.60	109.03	56.00	73.60	15.17	15.87
P2XP3	44.77	69.43	238.57	201.87	104.77	72.93	67.97	68.80	18.67	18.53
P2XP4	78.43	55.33	276.43	205.50	104.17	93.37	70.93	84.03	26.60	24.23
P2XP5	46.60	89.20	265.97	346.47	91.40	154.43	68.47	78.43	23.97	19.57
P3XP4	58.17	50.60	233.43	170.93	101.50	58.73	75.83	64.87	20.60	16.20
P3XP5	57.07	46.17	243.10	172.53	93.87	97.63	71.90	77.67	27.27	25.87
P4XP5	52.90	59.00	288.00	222.07	104.93	105.43	73.23	81.63	25.47	24.07
L.S.D at 0.05	2.34	6.85	4.80	9.31	3.51	4.08	4.96	4.96	0.67	0.86

General combining ability effects

The combining ability analysis gives useful information regarding the nature and magnitude of gene action involved in the expression of quantitative traits (Dhillon, 1975) which helps in selecting appropriate breeding method for crop improvement. The estimates of GCA for five parents are presented in Table (4). High positive and significant values were recorded for p_4 and P_5 for100-pod weight (g), shelling percentage and pod yield feddan^{-1} in both seasons, revealing the importance of these parents as donors for favorable alleles for these agronomic traits. Also P_2 and P_3 had positive and significant GCA for number of pods plant^{-1}, pod weight plant^{-1}, number of pods plant^{-1}and seed weight plant^{-1} in second season. 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), El-Baz *et al.* (2006), Yadav *et al.* (2006) Vishnuvardhan *et al.* (2011) and Abd-El-Aal *et al.* (2013).

Specific combining ability effects

Specific combining ability effects can be defined as the magnitude of deviation exhibited by the parental line in the cross from its expected performance on the basis of its general combining ability (GCA) effects. A significant deviation from zero in cross would indicate specially high or low specific combining ability (SCA) according to the sign whether positive or negative. Results given in Table (5) showed the estimates of SCA for the studied characters in ten crosses in both F_1 and F_2 generations. These results indicated that the crosses (P_1xP_2, P_1xP_4 and P_2xP_5) showed significant specific combining ability effects for number of branches plant^{-1}. The crosses (P_4xP_5, P_2xP_4, P_2xP_5, P_3xP_5 and P_4xP_5) exhibited highly significant SCA positive effects for shelling percentage and pod yield feddan^{-1}. Also, both crosses (P_1xP_3 and P_3xP_4) showed the best SCA for number of pods plant^{-1} and number of seeds plant^{-1}.

Moreover, the cross P_1xP_3 exhibited positive and highly significant SCA effects for 100-pod weight and 100-seed weight. These crosses could account for the highest average performance of the respective traits. In such hybrids, desirable transgressive segregates would be expected in the subsequent genotypes.

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

Genotype	Plant height (cm)		No. of branches pl^{-1}		No. of pods pl^{-1}		Pod weight pl^{-1} (g)		No. of seeds pl^{-1}	
	2014	2015	2014	2015	2014	2015	2014	2015	2014	2015
P1	0.65**	-0.67**	-0.27**	-0.88**	-0.36	-0.56**	0.51	-1.59*	-1.33**	0.92**
P2	-0.21	0.23	-0.42**	-1.49**	-1.19**	4.06**	-0.60	10.24**	-2.69**	4.74**
P3	-2.75**	-1.83**	0.11**	-1.04**	0.11	4.48**	-2.00**	7.78**	-0.67	9.99**
P4	1.93**	2.34**	0.04	-0.82**	1.22**	-3.07**	0.67*	-12.13**	2.02	-5.40**
P5	0.37**	-0.08	0.53**	-0.60**	0.23	-4.90**	1.43**	-4.30**	2.67**	-10.26**
S.E (gi)	0.57	0.61	0.11	0.18	1.26	0.90	1.12	3.95	1.10	0.48
Genotypes	**Seed weight pl^{-1} (g)**		**100-pod weight (g)**		**100-seed weight (g)**		**Shelling percentage (%)**		**Pod yield ardab feddan^{-1}**	
	2014	2015	2014	2015	2014	2015	2014	2015	2014	2015
P1	-1.74**	0.59	5.14**	0.25	-1.19**	-0.87	-2.71**	2.13**	-1.83**	-1.43**
P2	-3.12**	6.11**	2.24**	2.87**	-0.36	-0.92	-3.38**	-2.75**	-0.60**	0.17
P3	-0.62*	4.21**	-9.33**	-3.47**	-0.08	-7.86**	0.26	-1.75**	-0.90**	-0.13
P4	3.27**	-9.02**	-2.18**	-15.44**	2.56**	-5.53**	4.23**	0.38	1.29**	-0.01
P5	2.20**	-1.89**	4.14**	15.78**	-0.92*	15.19**	1.60**	1.98**	2.04**	1.40**
S.E (gi)	0.99	1.83	1.97	2.49	2.17	2.52	1.57	3.06	0.29	0.53

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

Genotype	Plant height (cm)		No. of branches pl^{-1}		No. of pods pl^{-1}		Pod weight pl^{-1} (g)		No. of seeds pl^{-1}	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
P1XP2	6.98	5.50**	0.29*	1.64**	-3.99**	11.40**	-13.36**	17.01**	-4.49**	22.09**
P1XP3	-3.65	-1.77**	-0.64**	-0.49*	10.38**	11.45**	34.94**	31.86**	28.28**	20.44**
P1XP4	-4.43	-3.24**	0.97**	1.66**	-3.46**	-8.00**	-8.76**	-17.09**	-3.00**	-21.77**
P1XP5	3.46	1.35**	0.81**	2.18**	-10.28**	-3.97**	-29.69**	-7.45**	-24.09**	-5.78**
P2XP3	-8.25	-6.37**	0.07	1.29**	-0.32	5.63**	-7.95**	11.27**	-5.19**	14.56**
P2XP4	-1.73	-4.24**	-0.92**	-0.52*	10.84**	-2.95**	34.15**	-3.12	24.66**	4.08**
P2XP5	1.43	-0.76**	1.29**	1.72**	-1.24**	1.01**	-9.14**	36.79**	-0.79	7.40**
P3XP4	11.81	7.45**	-0.18	0.22	2.87**	11.57**	1.58	11.37**	4.70**	25.63**
P3XP5	6.53	6.64**	0.06	1.47**	3.16**	2.26**	3.52**	-14.96**	7.51**	-8.31**
P4XP5	7.29	6.93**	-0.50**	0.08	-3.65**	11.55**	-6.28**	17.75**	-5.57**	15.75**
S.E.(si-j)	0.85	0.92	0.37	0.61	1.89	1.36	3.89	5.93	3.80	1.65
Genotype	**Seed weight pl^{-1} (g)**		**100-pod weight (g)**		**100-seed weight (g)**		**Shelling percentage (%)**		**Pod yield ardab feddan^{-1}**	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
P1XP2	-8.08**	20.44**	-15.00**	-17.71**	-8.38**	3.01**	0.74	9.74**	8.17**	4.52**
P1XP3	31.88**	31.27**	26.60**	19.13**	5.97**	14.55**	9.73**	7.51**	-0.23	1.45**
P1XP4	-1.87	-13.20**	-8.74**	-2.97	3.13**	17.49**	6.13**	1.41	3.08**	3.34**
P1XP5	-24.33**	-9.03**	21.20**	11.18**	-1.49	-1.30	-8.97**	-4.06**	-6.03**	-3.04**
P2XP3	-2.60*	6.35**	-25.22**	-15.46**	6.01**	-14.30**	5.00**	-0.25	-0.83**	-0.46*
P2XP4	27.18**	5.48**	5.50**	0.14	2.77**	3.81**	4.00**	12.86**	4.91**	5.13**
P2XP5	-3.58**	32.22**	-11.30**	109.89**	-6.51**	44.15**	4.17**	5.66**	1.54**	-0.95**
P3XP4	4.41**	2.64	-25.94**	-28.08**	-0.18	-23.89**	5.25**	-7.31**	-0.78**	-2.60**
P3XP5	4.38**	-8.91**	-22.60**	-57.70**	-4.33**	-5.71**	3.96**	3.89**	5.14**	5.65**
P4XP5	-3.67**	17.14**	15.16**	3.80	4.10**	-0.24	1.32*	5.73**	1.15**	3.74**
S.E.(si-j)	0.99	1.83	6.13	8.62	3.25	3.77	2.36	4.60	1.00	0.80

Estimation of genetic component and heritability

The calculated values for the degree of dominance are listed in Table (6). This value reveals whether the different traits show an additive or non-additive gene action. In descending order, the following characteristics showed degree of dominance for pod yield and its components in peanut The component of variation due to additive gene effects (D) was significant or highly significant in F_1 and F_2 for number of branches plant^{-1}, shelling percentage and pod yield feddan^{-1}, indicating that the additive gene action was more important than the non-additive in controlling the inheritance of these traits. In contrast, Shabana *et al.* (1992) found that additive effects (D) was not significant for the number of branches plant^{-1}. This may be due to the differences in the parents used in the two researches. Genetic components due to dominant effects (H_1 and H_2) were highly significant for most studied traits in both F_1 and F_2 generations. 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 number of branches plant^{-1}, number of pods plant^{-1}, pod weight plant^{-1}, number of seeds plant-1and seed weight plant^{-1} in F_2 generation and for shelling percentage and pod yield feddan^{-1} in both F_1 and F_2, indicating that most of the dominant genes had positive effects. The ratio $(H_1/D)^{0.5}$ which measures the average degree of dominance was more than unity for all studied traits, indicating that over - dominance is controlling these

traits. To improve these traits, pedigree selection 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. The ratio of total number of dominance to recessive genes in all parents (KD/KR) was greater than unity for all studied characters in both F_1 and F_2 generations, 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 50.16% for shelling percentage to 98.75% for plant height. Narrow sense heritability (h_n) were low in most characters to moderate for pod weight plant^{-1}, seed weight plant^{-1}, shelling percentage and pod yield feddan^{-1}. 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 Shabana *et al.* (1992), Ayub-Khan *et al.* (2000), Yogendra *et al.* (2002), El-Baz *et al*, (2006), Abd-El-Aal (2008), Abd-El-Aal *et al.* (2013), Alam *et al.* (2013), John and Reddy (2015) and Vaithiyalingan (2016).

Table 6. Estimates of genetic components and their derived parameters for some peanut traits.

Genetic parameter	Plant height (cm)		No. of branches pl^{-1}		No. of pods pl^{-1}		Pod weight pl^{-1} (g)		No. of seeds pl^{-1}	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
D±S.E	20.22	20.21	0.797**	0.76**	33.04	33.34	284.38	280.37	183.87	185.47
F±S.E	34.84	34.80	0.792	0.65	87.02	88.19	693.35	677.31	406.38	412.78
H_1±S.E	212.94**	214.46	2.718**	3.28**	234.36**	238.97	2019.22**	2068.85	1181.59**	1193.07
H_2±S.E	180.59**	180.59**	2.119**	2.12**	171.72**	171.72**	1592.77**	1592.77**	934.22**	934.22**
h^2	87.04	120.38	0.345	93.07**	3.95	1468.01**	-0.34	6354.53**	110.36	5053.97**
E±S.E	0.10	0.12	0.018	0.05	0.55	0.26	0.88	4.89	1.98	0.38
(H1/D)0.5	3.25	1.63	1.847	1.04	2.66	1.34	2.66	1.36	2.53	1.27
H2/4H1	0.21	0.21	0.195	0.16	0.18	0.18	0.20	0.19	0.20	0.20
KD/KR	1.72	3.24	1.736	2.41	2.96	166.61	2.69	17.07	2.55	15.32
Hn	52.83	48.54	35.53	52.64	70.6	67.66	58.9	55.8	67.9	60.5
Hb	98.35	98.75	97.90	80.29	80.7	82.9	80.5	88.60	70.8	67.7
Genetic parameter	**Seed weight pl^{-1} (g)**		**100-pod weight (g)**		**100-seed weight (g)**		**Shelling percentage (%)**		**Pod yield ardab feddan^{-1}**	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
D±S.E	206.97	202.07	125.39	118.09	5.86	5.42	53.43**	51.31*	18.94*	18.90**
F±S.E	476.39	456.79	313.99	284.82	18.46	16.69	47.79	39.29	20.03	19.90
H_1±S.E	1406.28**	1461.82	2093.25**	2202.84	131.11**	155.94**	204.60**	235.56**	89.36**	90.42**
H_2±S.E	1089.38**	1089.38**	1626.90**	1626.90**	100.55*	100.55*	166.04**	166.04**	78.21**	78.21**
h^2	129.09	6495.06**	372.87	323.42	-0.71	1276.05	225.84**	1102.88**	59.85**	258.77**
E±S.E	0.69	5.59	3.03	10.32	1.54	1.98	0.81	2.94	0.06	0.09
(H1/D)0.5	1.46	1.34	4.09	2.16	4.73	2.68	1.96	1.07	2.17	1.09
H2/4H1	0.14	0.19	0.19	0.18	0.19	0.16	0.20	0.18	0.22	0.22
KD/KR	2.31	11.54	1.88	3.53	2.00	3.69	1.59	2.11	1.64	2.86
Hn	52.84	53.64	58.5	60.5	48.02	44.67	34.84	48.84	50.8	56.7
Hb	58.59	56.29	95.5	90.8	86.76	84.6	86.48	50.16	80.5	85.9

Graphical (wr/vr) analysis.

Graphical presentation (Vr,Wr) of different traits in both generations are given in Figures 1 and 2. The regression coefficient significantly differed from zero but not from unity for F_1 and in F_2, indicating that the genetic system could be deduced to be additive without the complication of non-allelic interaction. For the other cases, regression slope differed from unity, indicating that a complementary type of epistasis was involved.

The regression line intersected the Wr below the point of origin in shelling percentage in both generations and pod yield faddan^{-1} in the F_2, revealed the presence of over - dominance. Meanwhile, it intersects the Wr axis above the origin in pods yield in ardab faddan^{-1} in the F_1 reflecting partial dominance. However, the regression line intersected the Wr below the point of origin in the remaining cases, indicating an over - dominance in the inheritance of these cases.

This contradiction between the two types of analysis might be an expected result of the presence of complementary type of non-allelic interaction which inflated the ratios of H_1 to D and distorted the Vr,Wr (Hayman, 1954 and Mather and Jinks, 1982). However, the regression line intersected the Wr below the point of origin in the remaining cases, indicating an over-dominance in the inheritance of these cases. The array points scattered along the regression line for these traits in both generations indicating genetic diversity among the parents. The low magnitude of correlation coefficient between parental mean (Yr) and the (Wr+Vr) might be due to a presence of non- allelic interaction in some parental line.

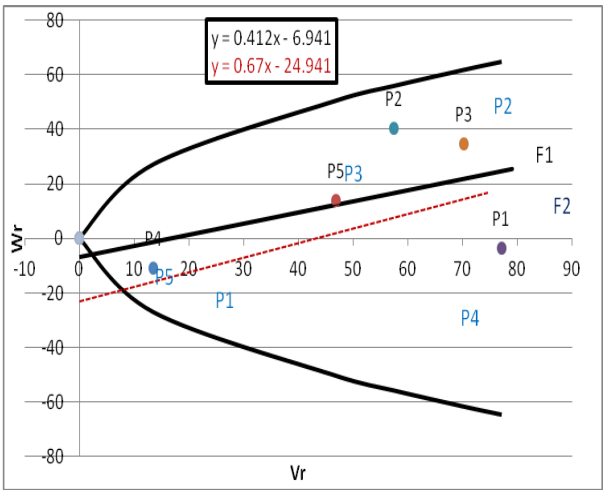

Fig 1. Wr/Vr graph for shelling percentage -1 in F_1 and F_2 generations.

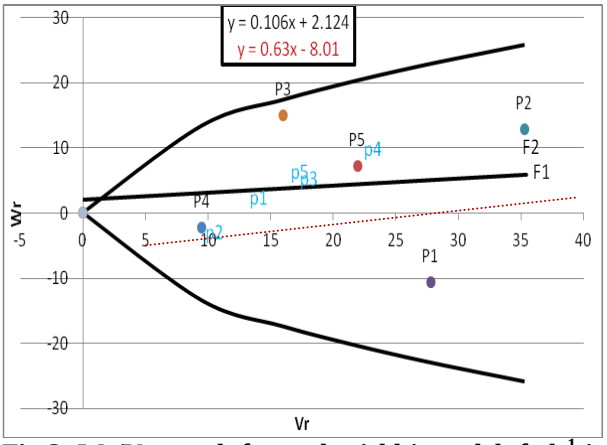

Fig 2. Wr/Vr graph for pods yield in ardab fad^{-1} in F_1 and F_2 generations.

The parental lines P_1 and P_2 for shelling percentage trait in the F_1 and the F_2 included the largest number of recessive genes. On the other hand, P_2 for pod yield faddan-^{1} in the F_1 had the highest number of recessive genes. The P_4 and P_5 were high for shelling percentage in the F_1 and the F_2 generations and P_2, P_4 in the F_1, F_2 for pod yield faddan^{-1} i.e, they contained greater number of dominant allels for those cases.

Heterobeltiosis

Physical manifestation of the beneficial effects of hybridization between diverse parents is usually termed as heterosis and is referred as heterobeltiosis and relative heterosis based on F_1 superiority over better parent and/or mid - parental value, respectively. In plant breeding programmes, useful heterosis is referred to denote the expression of increased vigor of a hybrid over its better parent. Heterosis is a complex biological phenomenon often manifested in the superiority of a hybrid over parental forms according to the rate of development of one or more complex characters (Konarev, 1974). Estimates of heterotic effects for the F_1 crosses are shown in Table (7). Significantly positive heterobeltiosis effects relative to better parent values may be considered favorable for most traits under investigation. Highly significant negative (desirable) heterotic effects relative to the best parent were noticed for plant height in crosses (P_1xP_3, P_1xP_4, P_2xP_3 and P_2xP_4). Significant or highly significant positive heterotic effects were found for number of branches plant^{-1} in the four crosses (P_1xP_2, P_1xP_4, P_1xP_5 and P_2xP_5) and number of pods plant^{-1} and number of seeds plant^{-1} in four crosses (P_1xP_3, P_2xP_3, $P_2xP_4$and P_3xP_4), pod weight plant^{-1} in two crosses ($P_1xP_3$and P_2xP_4). Highly significant positive heterobeltiosis was recorded for 100-pod weight in two crosses (P_1xP_3 and P_1xP_5). Highly significantly positive heterotic effects were found for seed weight plant^{-1} in the (P_1xP_3, P_1xP_4, P_2xP_3, P_2xP_4 and P_3xP_5) crosses, 100-seed weight in the ($P_1xP_3$and P_1xP_4). All crosses except (P_1xP_5 and P_2xP_5) revealed significant and highly significant positive heterobeltiosis for shelling percentage and pod yield feddan^{-1}. These results for most cases are in harmony with that reached by El-Sawy (2006), El-Baz *et al.* (2006), Abd-El -Aal (2008), John *et al.* (2012) and Abd-El-Aal *et al.* (2013).

Table 7. Heterobeltiosis % of the studied traits of peanut F_1 crosses.

Character crosses	Plant height (cm)	No. of branches Pl^{-1}	No. of pods pl^{-1}	Pod weight pl^{-1} (gm)	No. of seeds pl^{-1}	Seed weight pl^{-1} (gm)	100-pod weight (gm)	100- seed weight (gm)	Shelling %	Pod yield Ardab Feddan^{-1}
P1XP2	28.0**	19.8**	-27.2**	-26.6**	-14.9**	-21.8**	-11.7**	-12.0**	6.86**	80.22**
P1XP3	-23.4**	-23.6**	22.95**	27.9**	54.31**	65.1**	6.35*	6.89**	29.09**	2.85**
P1XP4	-7.9**	5.9**	-17.8**	-19.8**	-2.59	4.0**	-3.08	4.32*	11.37**	21.31**
P1XP5	17.4**	15.2**	-48.5**	-51.3**	-58.1**	-60.6**	8.43**	-5.78**	-18.88**	-37.24**
P2XP3	-45.8**	-13.8**	15.64**	-10.2**	10.14**	16.6**	-20.0**	3.18	24.40**	6.46**
P2XP4	-1.5**	-30.2**	42.82**	50.8**	67.51**	75.7**	-7.35**	2.59	7.15*	37.11**
P2XP5	4.9**	21.3**	-24.9**	-31.9**	-25.8**	-32.6**	-10.8**	-9.98**	-0.82	-0.83*
P3XP4	61.0**	-10.3**	18.49**	13.76**	27.60**	30.3**	-15.3**	2.10	14.55**	6.19**
P3XP5	78.3**	2.3	-8.54**	-20.6**	-10.7**	-17.4**	-12.5**	-7.49**	4.15**	12.83**
P4XP5	54.7**	-5.9**	-24.9**	-27.8**	-25.9**	-23.4**	3.62	3.42	6.08**	5.38**
L.S.D at 0.05	1.22	5.5	2.71	3.51	5.53	3.11	6.37	4.55	3.38	0.89

Determination of aflatoxins

Results in Table (8) showed that the two crosses (P_3X P4 and P_3X P) had a total aflatoxins 10.6, 20.1ppb, respectively. Meanwhile, total aflatoxins were not detected in all other parents and F_2 crosses. These results are in harmony with those found by Mahmoud *et al.* (2006) who found no cultivar completely resistant to aflatoxin contamination production and invasion with aflatoxigenic fungi while, there was a significant difference in genotype ability to allow invasion and aflatoxin production. The variable amount of aflatoxin in contaminate peanut genotypes and may be due to the environmental factors, nature of the fungal strains (Anderson *et al.*, 1995). Furthermore, the resistance of peanut seeds to *A. flavus* and/or *A. parasiticus* invasion might be due to genetic and/or biochemical composition of the seed or appears to be associated with certain structural and biochemical characters of the pod and seed and there is a possibility that genotypes may have differential effects up on the population of aflatoxigenic fungi in geocar posphere (Holbrook *et al.*, 2000). Also, Liang *et al.*, (2009) concluded that the resistance has been associated with testa wax and presence of cutin layer, active oxygen and membrane lipid peroxidation, phytaolexin accumulations and antifungal proteins in the peanut seeds. Sharaf *et al.*, (2011) concluded that B-1-3 glucanases enzyme has a role in the defense of peanut against the infection by *A. flavus* and the

resistant peanut mutants for *A. flavus* were identified by analyzing B-1-3 glucanases activities using polyacrylamide gel electrophoresis (PAGE). They found that these mutants have the ability to reduce the aflatoxins accumulation and RAPD-PCR showed pattern can be used as marker assisted selection (MAS) for the resistance of the fungus.

Table 8. Aflatoxin contamination of some peanut genotypes under field conditions.

Genotype	Aflatoxin contamination ppb				
	B_1	B_2	G_1	G_2	Total
P_1	ND	ND	ND	ND	ND
P_2	ND	ND	ND	ND	ND
P_3	ND	ND	ND	ND	ND
P_4	ND	ND	ND	ND	ND
P_5	ND	ND	ND	ND	ND
$P_1 \times P_2$	ND	ND	ND	ND	ND
$P_1 \times P_3$	ND	ND	ND	ND	ND
$P_1 \times P_4$	ND	ND	ND	ND	ND
$P_1 \times P_5$	ND	ND	ND	ND	ND
$P_2 \times P_3$	ND	ND	ND	ND	ND
$P_2 \times P_4$	ND	ND	ND	ND	ND
$P_2 \times P_5$	ND	ND	ND	ND	ND
$P_3 \times P_4$	5.8	1.3	2.6	0.9	10.6
$P_3 \times P_5$	11.5	2.8	4.2	1.6	20.1
$P_4 \times P_5$	ND	ND	ND	ND	ND

ND = Not detected

CONCLUSION

In light of the present findings it is evident that both additive and non-additive gene effects were important. Parental lines A1 and 623 were good combiners for 100-pod weight, shelling percentage and pod yield feddan^{-1} in both seasons revealing the importance of these parents as donors for favorable alleles for these traits. Five crosses (P_4xP_5, P_2xP_4, P_2xP_5, P_3xP_5 and P_4xP_5) showed significant and desirable SCA effects and heterobeltiosis for shelling percentage and pod yield feddan^{-1}. Meanwhile, total aflatoxins were not detected in all other parents and F_2 crosses. These results seem to be useful for peanut breeding programs in making a proper decision when initiating a crossing plan.

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القدرة علي التألف والفعل الجيني لبعض الصفات ومدي التلوث بالأفلاتوكسين في الفول السوداني

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[٢] المركز الاقليمي للاغذية والاعلاف

[٣] المعمل المركزي للتصميم والاحصاء- مركز البحوث الزراعية – مصر

يهدف هذا البحث الي دراسة القدرة علي الائتلاف وتحديد الفعل الجيني لبعض الصفات وقوة الهجين للأب الأفضل وتقدير مستوي الأفلاتوكسين في بذور الفول السوداني المخزنه تحت الظروف العادية. وقد تم التهجين بين خمسه أباء هي سلالة ٣٢٩, سلالة أ١٠, سلالة أ٢' سلالة أ١ وسلالة ٦٢٣ متباينة في صفاتها باستخدام نظام الهجن الدائرية ما عدا الهجن العكسية, وقد تمت الزراعة خلال ثلاثة مواسم صيفية هي ٢٠١٣و ٢٠١٤و٢٠١٥ بمحطة البحوث الزراعية بالاسماعيلية. وقد أظهرت النتائج تباينا معنويا لكل الصفات تحت الدراسة في كل من الجيل الأول والثاني, كما كان تحليل التباين للقدرة العامة والقدرة الخاصة علي التألف معنويا لكل الصفات المدروسه مشيرة الي أهميه كلا من الفعل الجيني المضيف وغير المضيف في وراثة الصفات. كما كان التركيبان الوراثيان A1, 623 ذات قدرة عامة علي التألف لصفات وزن ال١٠٠-قرن ونسبة التصافي ومحصول القرون بالاردب للفدان في كلا الموسمين, و كان التركيبان أ٢وأ١٠ ذات قدرة عامة علي التألف لصفات عدد القرون/النبات ووزن القرون /النبات و عدد البذور/النبات ووزن البذور/النبات. كما وقد سجلت جميع الصفات المدروسة قيم عاليه لكفاءة التوريث بمعناها العام في كلا الجيلين, واظهرت صفات ال١٠٠-بذرة ونسبة التصافي قيما منخفضة لكفاءة التوريث بمعناها الضيق كما أظهرت باقي الصفات قيما متوسطة. أظهرت قوة الهجين قيما معنوية سلبا وايجابا عن الأب الأعلي للصفات المدروسة . كما كانت السيادة الفائقة ذات التأثير الأكبر في صفتي نسبة التصافي ومحصول القرون بالاردب للفدان. أوضح تقدير مدي التلوث بالأفلاتوكسين لبذور الجيل الثاني والأباء تحت ظروف التخزين العادي أن هجينين فقط أظهرا قابلية للتلوث بالأفلاتوكسين هما الأب الثالث X الأب الرابع , الأب الثالث X الأب الخامس أما باقي الأباء والهجن خاليه من التلوث بالأفلاتوكسين.