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GENETIC ANALYSIS OF THE PHENOTYPIC AND MOLECULAR CORRELATIONS AMONG THE RAPD-PCR MARKERS IN PEANUT (*ARACHIS HYPOGAEA* L.)

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SUMMARY

Seven peanut (*Arachis hypogaea* L.) genotypes underwent a molecular study. Using two indicators based on the PCR technique, namely, the RAPD and RE-RAPD indicators, cutting enzymes and custom prefixes from the RAPD marker determined the genetic relationship between the genotypes of the quantitative traits. The results showed that RAPD indicators could be beneficial in evaluating peanut genotypes in groups and estimating the genetic distance between them. Direct relationships to molecular genetics and the phenotype genetic distances, special uniting ability effect and the strength of the cross between the average parents, the strength of the hybrid on the best parents, and the average traits showed in parent four the maximum hereditary distance, with parent three exhibited the minimum hereditary distance based on the results of the phenotypic and RAPD indicators. The RE-RAPD indicators were also efficient in identifying 25 genetic mutations, as these mutations have become a diagnostic genetic fingerprint of most parents and an indication of the presence of specific sites, especially of parents, in their genome by using eight primers.

Keywords: Peanut (*A. hypogaea* L.), parental genotypes and hybrids, genetic analysis, genetic distance, phenotypic and molecular correlation, RAPD markers

Key findings: Peanut (*A. hypogaea* L.) genotype no. 4 and the hybrid 1 × 5 proved the leading genotypes for best performance. RAPD indicators were efficient in identifying phenotypic and genetic dimensions and mutations.

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INTRODUCTION

Peanut (*Arachis hypogaea* L.) is an important crop and a wintry annual plant grown in temperate regions globally. It is moderately cold tolerant, and cultivation has expanded outside the areas of its origin into Europe and Asia (Sardana *et al.,* 2007). The plants with high nutritional value and essential to humans as part of their diets and chief sources of plant protein reflected an increase in the global area planted the quantity of cultivated production in Iraq for 2018 at about 518.5 kg ha^{-1}.

The concept of phenotypic indicators is one of the easiest and oldest, considered the basis of indicators (Abdullah and Hasan, 2020). It has been relied upon since the scientist Mendel discovered the basics of genetics; to this day, they have become the basis for studying the genetic variation of plants (Hedrick, 2005). Environmental physiological researchers have trended toward more stable indicators unaffected by environmental influences (Li *et al.,* 2009). Selection, including molecular markers, to aid phenotypic selection makes it more effective and less expensive than traditional plant breeding methods (Sabouh *et al.,* 2010). The use of molecular indicators in plant and animal husbandry has become a new field of agriculture, called molecular breeding (Al-Skmani, 2017), with RAPD indicators used for this purpose to ensure ease and accuracy in the ability to detect the broadest area of the plant genome and lower the cost compared with other indicators (Hasan and Abdullah, 2021).

Hybridization and genetic analysis comprised prime sources for creating new genetic variations through traditional breeding. The first step for hybridization programs is to evaluate the characteristics of the genotypes used as parents in such programs. In this field, hybridization is one of the crucial methods used in breeding. The hybridization program is also one of the vital approaches in improving and selecting parents that represent the pure breeds for hybridizing in these programs' first simple step. Hybridization programs provide new unions that enable researchers to produce hybrids, and hybridization provides significant information that helps them choose the appropriate breeding method and obtain valuable genetic information about first-generation hybrids. Hybridization gives immense genetic variation and allows the selection of good genetic combinations (Hasan and Abdullah, 2020).

MATERIALS AND METHODS

The peanut genotypes came from the International Center for Agricultural Research in the Dry Areas (ICARDA), with assigned codes 1-7, and 21 individual crosses resulted from these parents. The genotypes of 28 combinations (seven parents and 21 single hybrids) (Figures 1 and 2) underwent cultivation in a farmer's field in Dhi-Qar Governorate on April 25, 2020. The chemical fertilizer NPK addition had the amount of 400 kg ha after tillage (Al-Jabouri, 2016). Collecting samples from the plants occurred two months after the planting date from the parents, taken from the hybrids 5-6 young leaves from the top, then placed in specially marked bags before taking them to the laboratory for the DNA isolation process. Analyzing measured concentration and purity of DNA proceeded in the molecular laboratory of the Faculty of Science at Al-Mustansiriyah University.

RAPD-PCR reactions

The 1.5 g of aerosol powder dissolving in 100 ml of TAE1X used a heat source, with the solution cooled down and poured in unique places to prepare an agarose gel at a concentration of 1.5%. Taking five microliters of the RAPD-PCR product for each sample continued, loading neatly into the gel pits, placing the volumetric guide Marker section 100 bp–3000 bp in a particular hole on one side of the gel. Then, switching the relay to pass the electric current had a voltage difference of 3 volts cm and afterward, adjusting the electrodes. The direction of the samples in the forward course should be

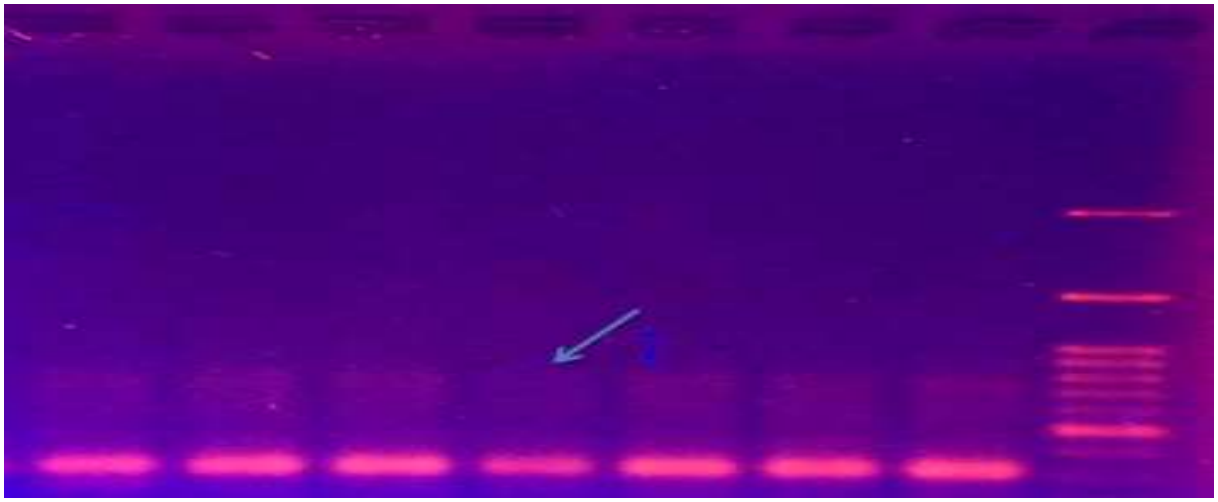

Figure 1. Primer multiplication products with the DNA of seven parents and the stage on an agarose gel at a concentration of 1.5% with the volumetric index M.

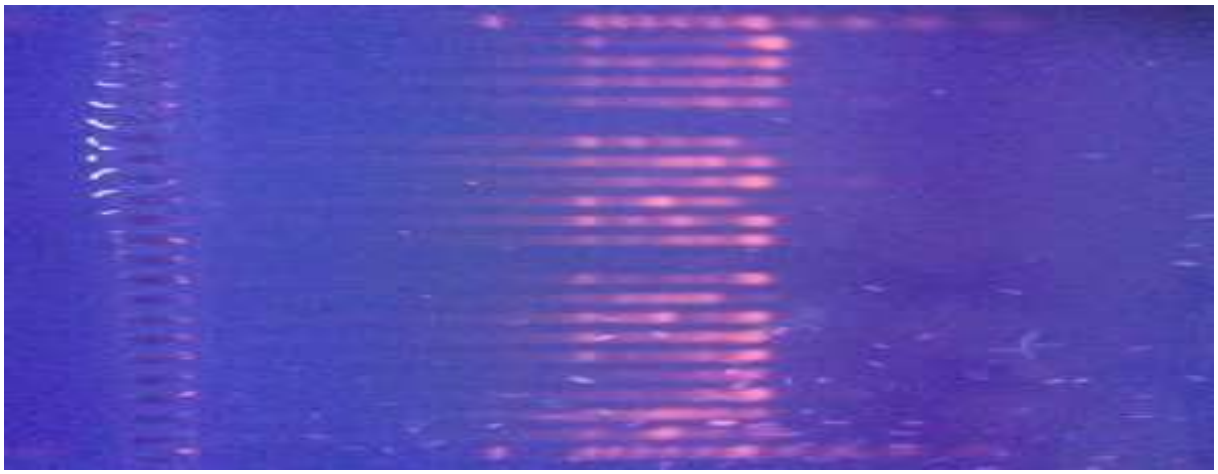

Figure 2. Primer multiplication products with 21 single hybrid DNA of the first generation and phase on an agarose gel at a concentration of 1.5% with a volumetric index M.

toward the anode to the point where samples arrive before the end, and the process takes 1.5–2.5 hours.

Performing the RE-RAPD reactions only on parents used eight prefixes to detect mutation in genotypes used in the RAPD reactions. The prefixes did not show distinct packages for the species contained in general. The prime band considered as the main goal in these interactions had the reactions done in two ways (Salman *et al.*, 2019).

DNA slicing

The solutions and materials used were the Digestion buffer x 10 buffer solution, Nuclease-free, distilled water, Clearing enzymes: EcoR1, Hind111, and Acetylated BSA Enzyme Serum supplied by Promega USA. DNA cutting ensued by preparing the reaction solutions in a 2 ml tube, with each enzyme placed separately and the samples incubated in a water bath at 37 m for four hours to confirm the completion of the

segmentation samples migrating through the appearance of DNA smeared along the gel. Performing double reactions for DNA samples upon digestion followed the same steps for parents for RAPD reactions. In transferring (separation by gel) the migration of the products of this indicator, the method used for the RAPD products was the same except for increasing the agarose gel concentration to 2%.

Slicing RAPD products

This step included model multiplication + slicing of outputs + posting and detection, needing the same materials and solutions as the first cutting method. The samples multiplied used PCR similar to RAPD reactions on parents. The cutting of PCR products employed the three enzymes (EcoR1, Hind111, and Pest1), where each enzyme had a separate eight microliters of the product placed in a new tube of 2 ml volume containing five microliters of distilled water. Two microliters of enzyme buffer solution for each enzyme had their samples incubated in a water bath for four hours, with the samples frozen until transferring. Samples placed on agarose gel had a concentration of 2%, similar to the RE-RAPD's first method, then proceeded to detect images and saved them in the computer.

Data recorded

The study included seven genotypes and their interchangeable hybrids from the bean crop introduced by ICARDA. Growing the genotypes at the Kirkuk Agriculture Directorate research station commenced on April 25, 2020, using a randomized complete block design in three replications and studying several traits. Ten random plants came from each line of the parents and hybrids and two middle lines of the experiment, and calculating their average was according to the following measurements:

The maturity time was the number of days from 50% flowering until physiological maturity. The number of branches per plant's calculation was from the crown area of each plant. Measuring the leaf area (cm^2/plant) at the end of the node stage used the gravimetric method for 20 leaflets, and their piercing was at a 1 cm diameter. The dry weight of the leaves and discs had the area of one disc calculated for the leaf area by applying the following equation (Watson, 1958):

Leaf area (cm^2/plant) = (dry weight of leaflets [g/plant]) / (dry weight of disc [g]) × area of discs (cm^2)

The leaf area per plant's computation used the following formula:

Leaf area per plant = leaf area × number of leaves.

Calculating the average number of pods per plant comprised the number of seeds per pod computed by dividing the number of seeds/plant by the number of pods/plant. Seed weight per plant (g) of 10 plants for each line incurred measuring by weighing on a sensitive balance and then averaged. Seed yield (kg/ha) on the individual plant yield materialized for 10 plants taken from each line in the experimental parental genotypes and their hybrids after correcting the weight for a moisture content of 15% (Al-Hasani, 2014). The seed yield weight received conversion from kg/m^2 to kg/ha.

Statistical analysis

The experience of parents and hybrids' statistical analysis for all studied traits continued according to the RCBD with three replications at a 5% probability level to know the differences between genotypes (Al-Rawi and Khalaf Allah, 1980). Estimates on the efficiency and discriminant power of RAPD prefixes and the efficiency of each initiator used the formula (Grudman *et al.,* 1995):

Efficiency = (No. of band per primer / total number of multiplier bands per primers) × 100

The discriminatory ability appeared based on the following formula:

Discriminant power = (number of varying bands per primer / total number of varying bands per primer) × 100 (Tables 1 and 2).

Table 1. The primers used in the RAPD-PCR study for parents + hybrids and the RE-RAPD, as the + + sign indicates the use of the primer.

Primers	The primers relay - 3 – 5	For parents only RAPD-PCR	On parents + hybrids RAPD-PCR	RE-RAPD reaction
SRA- 13	AGCTCCGTCA	+	+	
SRF-16	CTGTGCTCCA	+		
SRA-11	CGCATCGTCA	+		
SRO -06	TCTGCGATCC	+	+	
SRD -02	CACAGCGACC	+		+
SRO 12	GTGCACCCAC	+		
SRM -10	GTATAACTGG	+	+	
SRE -20	CGATCGTCGT	+		
SRA -20	GAACGGGAAG	+		
SRD -03	TGACTCAACC	+		+
SRG -13	CAGTCATGTG	+	+	
SRD -08	CATGGCGCAC	+		
SRW -13	CACAGCGACA	+	+	
SRP -01	GAAGCACTCC	+	+	
SRG -11	CGCTCAGCTC	+	+	+
SRQ -15	CAGTGCATCT	+		
SRB -20	CGACTCAACC	+	+	+
SRB -10	TTCTCATGGT	+	+	
SRH-01	CACTAGGATG	+	+	
SRD -02	CGCAAGTCGT	+		
SRJ -14	CGATGACGTG	+	+	+
SRJ -12	CCAGCATTAC	+		
SRO -04	CAGCTGGGAC	+	+	+
SRW -08	TAAAAGAGAA	+		
SRAB-12	GCTAAATCGA	+		
SRH-08	TGGACACCCC	+		+
SRN-10	ACTACTCAAG	+		
SRO-05	ATCAGTCACT	+		

Table 2. Components of segmentation of genomic DNA by cutting enzymes ECOR1, Hind111, Pest1.

No.	Solution	The final concentration	Maekerolatr / model
1	Sterile distilled water		16.80
2	Digestion buffer × 10	X1	2.00
3	Acetylated BSA		0.20
4	DNA. Genomic DNA	1 mcg	20.00
5	Enzyme shredder	10 units	1.00
6	Final volume		40.00

RESULTS AND DISCUSSION

Genetic relationship between indicators

The results revealed the level of phenotypic indicators (based on cluster analysis and average phenotypic characteristics) and parents' RAPD indicators. Parents have a high correlation based on genetic distances; the results of the genetic distance of the quantitative characteristics of the parents represented by the pooled scheme were 100% identical to the results of the genetic dimension of the parents' RAPD indicators. Although the phenotypic indicators depended on the arithmetic mean of the studied quantitative traits dividing into three groups, the RAPD indicators relied on the appearance or absence of the parents' bands on the agarose gel. It revealed the close connection between genetic

distances based on the division and genetic mean of the indicators (Al-Sakmani, 2017; Ali *et al*., 2022).

Likewise, parent no. 4 distinguished itself with the highest desirable traits (Table 4). This parent had the maximum number of distinct bands in the RAPD indicators (Table 3), supporting the use of molecular markers to classify, diagnose, and select traits with all the traits that appear on the plant. They resulted from the expression of a gene carried on the chromosomes regardless of other influences. Although the RAPD indicator is random for identifying sites, it is of high quality in evaluating the genetic distance of varieties and genotypes for being able to scan the entire genome, contrary to other indicators, which can only scan 10% of the genome. The random positioning index also plays a vital role in determining the genetic distance of varieties (Hasan and Abdullah, 2020).

Genetic relationship between phenotypic and RAPD indices

The hybrid 1 × 5 was distinct in its phenotypic traits (Table 5), having the highest value for three traits: the number of pods, weight of seeds, and seed yield. This hybrid emerged unique by having two bands distinct from all hybrids in the RAPD indicators. (Al-Zuhairi, 2014). The hybrid 2 × 6 was prominent for having the highest value of the quantity traits being the number of seeds and seed weight (Table 5), and this hybrid was remarkable for having a distinctive band in the RAPD indicators (Table 3). The results also showed a correlation between phenotypic traits and RAPD indicators that relied upon crop traits (Hasan and Abdullah, 2020).

Likewise, the hybrid 2 × 4 was noteworthy by having the highest arithmetic mean in the characteristic of paper area (Table 5), and it was significant by having a prominent band in the RAPD indicators (Table 3). It indicates the existence of a correlation between phenotypic and RAPD indicators. From the results, the distinctive bands of hybrids can be a distinguishing mark of superiority in yield traits because of the many genes governing the quantitative traits switching these sites during hybridization. The hybrid increases the possibility of obtaining variance using RAPD indicators when a correlation between it and the phenotypic indicators appears (Hasan and Abdullah, 2020).

Genetic relationship between quantitative traits

The evaluation of genotypes and their hybrids and the selection of genotype or hybrid that has desirable quantitative characteristics at the same time or the one predicted to have after following subsequent isolated generations succeeded. It was evident through the quantitative traits that parent no. 4 was distinct, having the highest means of most quantitative features (Table 4).

As for hybrids, the quantitative and qualitative traits varied in the desired direction. The fact showed that crossbreeding increases the mixing proportion, and obtaining hybrids is desirable based on quantity and quality. The hybrid 1 × 5 was notable by the highest averages of the studied quantitative traits (Table 5). It supports the correlation between the quantitative characteristics of these hybrids and helps in the success of this program. It is possible to follow the isolated generations of these hybrids only to reach the desired goal in the end. The crossbreeding process is the primary method for genetic mixing and obtaining desirable varieties with the help of molecular markers to reduce effort, cost, and time (Hasan and Abdullah, 2020).

Genetic relationship between the phenotypic and RE-RAPD indices

Parent 5 has the highest number of mutant unique packets (Table 3), while the same parent has the lowest averages in most studied quantitative traits (Table 4). It indicates that most occurring mutations were in an undesirable direction. The reason was due to mutations causing a defect in one of the genes responsible for these quantitative traits, affecting the trait's quantity (Hasan and Abdullah, 2020).

Table 3. The number of sites, molecular sizes, number of bands and distinctive bands, the contrast ratio, efficiency, discriminant ability, and polymorphism of the primers used in the study of hybrids.

No.	Primer name	Molecular size	No. of sites produced	Number of disparate sites	No. of general sites	No. of primers bands	No. of disparate bands	No. of general bands	No. of unique bands	No. of absent bands	Contrast ratio %	Primer efficiency	Discriminatory ability	Formal pluralism
1	SRf -24	175-1300bp	5.9	7.3	7.2	87	-	-	36	136	173	1	8	9
2	SRr-02	200-2500bp	6.1	7.6	7.7	90	-	1	36	140	173	-	10	12
3	SRw -01	175-2250bp	9.8	12.1	9.8	100	3	-	-	223	222	-	12	12
4	SRc -12	475-1500bp	4.5	5.5	4.5	100	-	-	-	103	106	1	8	9
5	SRF- 16	600-2500bp	3	3.7	3	71	1	-	-	69	69	-	3	7
6	SRW -08	175-950bp	4.6	5.7	8.2	60	-	-	72	105	147	2	7	10
7	SRt-14	425-1600bp	7.8	9.6	7.8	88	-	-	-	178	168	-	12	12
8	SRh -14	425-1800bp	5.8	7.2	7.4	90	-	1	36	134	160	1	9	11
9	SRv -15	450-1000bp	6.5	7.7	6.5	100	-	-	-	143	148	-	7	9
10	SRd- 13	150-1200bp	4.8	5.9	8	100	-		72	110	186	2	6	8
11	SRs -13	500-1300bp	0.9	1.1	4.1	77	-	1	72	22	95	2	4	6
12	SRy -13	350-1500bp	3.7	4.6	5.3	100	1	1	36	86	132	1	8	10
13	SRe- 11	150-900bp	4.4	5.4	4.4	100	1	-	-	101	111	-	7	7
14	SRd- 15	300-1100bp	2.1	2.6	3.6	83	-	1	36	48	94	1	5	7
15	SRm-55	200-800bp	2.7	3.4	2.7	100	1	-	-	63	66	-	6	5
16	SRg -42	350-1000bp	3.1	4.1	3.3	75	-	1	36	40	74	1	3	5
17	SRW -13	200-1000bp	4.1	5	5.6	88	1	3	36	93	129	1	9	9
Total		150-2500bp	80.9		0	88	8	10	432	1840	2253	13	124	148

Table 4. Parents' averages for the studied traits.

Traits / Parents	Maturity (days)	Branches plant^{-1}	Leaf area (cm^2/plant)	Pods plant^{-1}	Seeds pod^{-1}	Seed weight (g/plant)	Seeds yield (kg/ha)
1	143.52	7.03	1538.42	26.9	4.93	32.24	1786.7
2	131.43	5.53	1578.55	29.6	2.46	71.75	3611.5
3	143.32	7.30	1471.14	27.1	4.38	61.13	3320.8
4	145.13	7.60	1632.11	30.13	5.28	72.74	4122.6
5	141.43	5.40	1233.58	24.16	2.16	37.94	2213.6
6	129.31	7.36	1534.51	26.16	3.89	41.16	2234.5
7	137.83	7.16	1524.81	28.85	4.66	63.7	3216.2
Mean	138.85	6.92	1501.87	27.55	3.90	52.95	2943.7

Table 5. Hybrids' averages for the studied traits.

F1 Hybrids	Maturity (days)	Branches plant^{-1}	Leaf area (cm^2/plant)	Pods plant^{-1}	Seeds pod^{-1}	Seed weight (g/plant)	Seeds yield (kg/ha)
1 × 2	145.30	8.36	1540.76	31.83	4.53	50.56	3290.35
1 × 3	143.93	7.63	1558.83	27.26	4.53	57.40	3048.22
1 × 4	154.60	7.66	1574.53	26.06	3.40	53.05	3137.16
1 × 5	161.56	10.13	1850.60	35.10	5.20	72.36	4169.43
1 × 6	154.20	7.10	1475.76	28.73	4.66	53.32	2892.81
1 × 7	157.76	7.50	1746.23	26.03	4.50	49.96	3904.10
2 × 3	153.23	7.30	1681.33	30.13	4.16	63.08	3029.69
2 × 4	161.51	8.36	1593.46	28.40	4.30	59.42	2089.28
2 × 5	153.20	7.10	1376.16	28.90	4.03	65.17	3283.43
2 × 6	145.60	7.30	1522.70	31.03	3.76	65.47	3816.03
2 × 7	147.60	9.16	1630.96	31.86	4.26	48.13	3415.95
3 × 4	144.46	7.33	1577.43	29.76	4.80	70.88	3585.02
3 × 5	152.06	7.46	1737.46	31.73	3.80	65.47	3918.96
3 × 6	146.66	7.13	1735.90	32.43	5.26	46.13	3904.10
3 × 7	143.36	6.93	1759.70	33.06	3.96	61.52	3029.69
4 × 5	145.06	7.50	1723.46	31.36	4.20	55.51	2089.26
4 × 6	155.30	7.30	1254.81	37.53	3.93	71.03	4079.18
4 × 7	141.26	8.36	1478.70	39.06	4.23	64.40	3824.84
5 × 6	143.93	8.60	1723.46	31.36	4.16	61.90	4040.27
5 × 7	154.60	7.66	1254.86	27.53	4.30	55.73	4096.94
6 × 7	154.30	8.13	1574.53	29.06	4.03	61.52	3923.95
Means	150.45	7.80	1589.12	30.86	4.28	59.61	3455.65

A conclusion from the above is the possible use of RAPD indicators to evaluate genetic compositions into groups and estimate the genetic dimension between them. It has a direct link to the molecular and the phenotypic genetic dimension, affecting the unique unitary ability, the hybrid strength of the average of the two parents, and the hybrid strength of the best parents and the average trait (Abdullah and Hasan, 2020).

Correlation coefficient

Table 6 shows that the adjective maturity date of the correlation coefficient was positive and highly significant, indicating the effect values of the unit exceptional estimator on the strength of a hybrid for average parents and better parents and the average trait between the hybrid strength of average parents. A hybrid strength for the best parents and average trait and between the hybrid strength of the best parents and the average trait reached 0.781, 0.770, 0.820, 0.934, 0.913, and 0.881, respectively. The probability level of 5% was positive only between the phenotypic, genetic dimension and the effect of the unique federal estimate that reached 0.457. Note that all unmentioned correlations were positive or negative but did not reach the limits of statistical significance. The emergence of a link between the quantitative characteristics of these hybrids helps in achieving success, and, therefore, it was possible to follow up isolated generations (Al-Jubouri, 2016).

For the adjective number of branches per plant, the correlation coefficient between the effect values of the unit special estimator, the hybrid strength of the average parent, the average of the trait, and between the hybrid strength of the average parent and the average of the trait was positive and forceful, reaching 0.798, 0.731, 0.759, 0.743 and 0.782, respectively. At the 5% probability level, it was positive only between the phenotypic and genetic distance, and the effect of the distinct unit estimate was 0.434. Note that all the connections not mentioned were positive or negative but did not reach the limits of the statistical significance (Abdullah and Hasan, 2020).

Table 6. The correlation factor between the molecular genetic distance, the phenotypic distance, the effect of the unit special ability, the strength of the hybrid vigor for the average parents, the strength of the hybrid for the best parents, and the average for the traits.

Correlations	Maturity (days)	Branches plant^{-1}	Leaf area (cm^2/plant)	Pods plant^{-1}	Seeds pod^{-1}	Seed weight (g/plant)	Seeds yield (kg/ha)
$r_{x1 x 2}$	-0.172	0.072	-0.175	-0.173	-0.175	-0.069	-0.181
$r_{x1 x 3}$	-0.322	0.162	-0.025	-0.419*	0.162	-0.016	-0.108
$r_{x1 x 4}$	-0.307	0.147	0.071	-0.186	0.147	0.100	0.118
$r_{x1 x 5}$	-0.271	0.266	-0.132	-0.112	0.266	0.305	0.311
$r_{x1 x 6}$	-0.240	0.128	0.072	-0.073	0.128	-0.054	-0.027
$r_{x2 x 3}$	0.438*	0.434*	0.723*	0.141	-0.457*	-0.107	0.143
$r_{x2 x 4}$	0.024	-0.164	-0.299	0.039	-0.164	-0.021	0.239
$r_{x2 x 5}$	-0.061	-0.299	-0.005	-0.035	-0.299	-0.275	-0.031
$r_{x2 x 6}$	-0.057	-0.279	-0.325	-0.110	-0.279	-0.105	0.155
$r_{x3 x 4}$	0.781**	0.798**	0.835**	0.723**	0.710**	0.302	0.631**
$r_{x3 x 5}$	0.770**	0.731**	0.230	0.818**	0.701**	0.178	0.218*
$r_{x3 x 6}$	0.820**	0.759**	0.921**	0.501*	0.899**	0.899**	0.943**
$r_{x4 x 5}$	0.934**	0.743**	0.249	0.940**	0.923**	0.819**	0.960**
$r_{x4 x 6}$	0.913**	0.791**	0.931**	0.627**	0.711**	0.234	0.208*
$r_{x5 x 6}$	0.881**	0.782**	0.180	0.755**	0.752**	0.874**	0.361

X1 the molecular genetic distance X2 the phenotypic genetic distance X3 the effect of the special federal ability X4 the strength of the hybrid for the average of the parents X5 the power of the hybrid for the best parents X6 the average character.

The leaf area trait was the correlation coefficient indicating the effect values of the unit special estimator, the hybrid strength of the average parent, and the average trait between the hybrid strength of average parents, and the average trait was positive and active (0.795, 0.921, 0.931, and 0.423) respectively. The 5% probability level was only negative between the phenotypic and genetic distance, with the effect of the unique unit capacity amounting to -0.456. Note that all the connections not mentioned were positive or negative but did not reach the limits of statistical significance (Abdullah and Hasan, 2020).

The number of pods, seeds, pod, and seed weights per plant, the correlation coefficient was between the effect values of the unit special estimator and hybrid strength of the average parent. The hybrid strength for best parents showed the strength of the cross between the average parents, and the cross strength between the best parents and the average trait showed the strength of the hybrid for the best parents. The average of the trait is positive and highly significant (0.723, 0.818, 0.940, 0.627, and 0.755), (0.710, 0.701, 0.899, 0.923, 0.711, and 0.752), and (0.798, 0.854, 0.793, 0.793, 0.935, and 0.887) (Abdullah and Hasan, 2020). The correlation coefficient for a trait shows the weight of seeds/plant (g). The correlation was between the effect values of the special unit capability, the average trait and the hybrid strength for average parents, and a strong crossbreed for better parents and hybrid strength for the best parents, the average trait was positive and highly significant, reaching 0.899, 0.819, and 0.874, respectively. Notably, all correlations not mentioned were positive or negative but did not reach the limits of statistical significance and, thus, were nonsignificant (Hassan and Abdullah, 2020).

For seed yield, the correlation coefficient was positive and highly significant, showing the effect values of the distinct unit capacity and the hybrid strength of the average parent and average trait between the hybrid strength of average parents, the strength of the hybrid for the best parents is positive and highly significant, reaching 0.631, 0.943, and 0.960, respectively. Notably, all the unmentioned correlations and all studied traits emerged positive or negative but did not attain the limits of statistical significance (Hasan and Abdullah, 2020). These results agreed and received considerable support from past findings (Wilson and Murray, 1991; Torres *et al.*, 2006; Xuxiao *et al.*, 2009; Al-Sakmani, 2017).

CONCLUSIONS

Peanut (*A. hypogaea* L.) genotype no. 4 and the hybrid 1 × 5 proved superior in most studied traits, which can be beneficial and applicable in agriculture. RAPD indicators can help estimate the molecular phenotypic and genetic dimensions. RE-RAPD indicators were also efficient in identifying genetic mutations as these mutations are the diagnostic genetic fingerprint for most fathers and an indication of the presence of specific sites, especially for fathers in the fathers' genome, through using eight primers.

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