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Relationships between Hybrid Performance and Genetic Distance Revealed by Morphological and Molecular Markers in Cowpea (*Vignaunguiculata* (L.) Walp)

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ABSTRACT

The genetic diversity and relationships among six cowpea (*Vigna unguiculata*) genotypes were evaluated using 10 agro-morphological traits and two molecular marker systems ISSR and SRAP. The phenotypic distance (PD) among all genotypes was relatively high. ISSR markers were more efficient than SRAP with regards to polymorphism detection, average number of polymorphic-bands per primer (PB), resolving-power (RP), marker-index (MI) and polymorphism-information-content (PIC). ISSR and SRAP markers were generated cultivar or genotype specific unique DNA fingerprints able to identify the most diverse genotypes. The Dic genetic similarity ranged from 0.744 (P_1 and P_4) to 0.868 (P_2 and P_3). A positive correlation was found between ISSR and SRAP markers as well as between molecular markers and phenotypic markers. Based on phenotypic distance (PD) and genetic distance (GD), six parents of cowpea were crossed in half diallel fashion in order to determine combining ability to identify promising hybrids for ten traits including yield and its components. The both additive and non-additive effects of the controlling genes were involved in the inheritance of the traits studied. High broad-sense heritability estimates were obtained for all the traits as well as the narrow-sense heritability was larger than 0.60 in time to 50 % flowering, pod length, weight of pods per plant, weight of seeds per plant and total dry seed yield, so selection for these traits could be useful. The adequacy of additive-dominance model was fit for time to 50 % flowering, number of branches per plant, weight of pods per plant, weight of seeds per plant and total dry seed yield, while non-allelic gene interaction was observed for pod length, number of seeds per pod and pod diameter. The estimates of general combining effects revealed that P_5 had the highest positive and significant values for number of pods per plant, weight of pods per plant, weight of seeds per pod and total dry seed yield while P_1 exhibited the lowest negative and significant GCA for number of pods per plant, weight of pods per plant, weight of seeds per pod and total dry seed yield. The highly significant correlations were found between total dry seed yield and number of pods per plant (0.87), weight of pods per plant (0.95) and weight of seeds per plant (0.95). Mating designs used in this study were suitable for studying genetic parameters in cowpea. The high values of broad-sense and narrow-sense heritability indicated a good genetic variability for effective selection. The relationship between phenotypic and genotypic distance as well as the heterosis and SCA were estimated. Results indicated that the genetic distance was positive and/or negative and significantly correlated with some traits, while it was not significantly correlated with effects of heterosis and SCA for some other traits. Our results noted that knowledge about the genetic distance between parents can be used to predict hybrids performance.

Keywords: *Cowpea, phenotypic markers, Molecular markers, Diallel Cross, Gene action.*

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp.) is an important vegetable crop known as an important source of protein which varies from 20 - 25% as stated by Stanton (1966). Cowpea grain contains about 24.8 % protein, 1.9 % fat and 63.6 % carbohydrates and is rich source of calcium and iron (Davis *et al.*,1991).

Genetic diversity among genotypes is an important source of plant breeding program. Generally, genetic variation is estimated through measuring the diversity of phenotypic traits, but it is strongly influenced by environmental conditions, making them limited in use in genetic studies (Kameswara, 2004). In previous reports, some agro-morphological traits which affect potential yield of cowpea are mainly used as markers including pods/plants, seeds/pod and seed weight (Hedge and Mishra, 2009; Stoilova and Pereira, 2013; Mafakheri *et al.,* 2017 and Lazaridi*et al.,* 2017).

DNA markers are considered as an important approach for efficient selection of desired agronomic traits. These markers have been employed in previous research on genetic diversity and variety identification in several crops including cowpea (Franco *et al.,* 2001). Examples of DNA markers widely used in breeding studies of cowpea include simple sequence repeat (SSR) as stated by several authors such as Wamalwa *et al.* (2016) and Chen *et al.* (2017). Another example is random amplified polymorphic DNA (RAPD) (Udensi *et al.,* 2016). Many studies also employed inter-simple sequence repeat (ISSR) (Igwe *et al.,* 2017) and sequence-related amplified polymorphism (SRAP) (Salem *et al.,* 2019).

Investigations on parents and their F_1s may facilitate a selection method for assuring existence of more number of desirable characteristics in progenies. In addition, this provides a tool for planning future crossing program (Gupta and Singh, 1997). Using diallel analysis, plant breeders can evaluate heterosis and effect due to maternal, general combining ability (GCA) and specific combining ability (SCA) of parents in crosses (Glover *et al.,* 2005).

The aims of the current investigation were to (i) evaluate genetic diversity according to phenotypic, ISSR and SRAP markers of selected cowpea genotypes (ii) investigate the gene action for yield attributes (iii) study the relationship between phenotypic and genotypic distance with SCA and heterosis effects.

MATERIALS AND METHODS

The current study conducted at the Biotechnology Lab., Genetics Dept. and the Experimental Farm of Vegetable Crops Dept., Fac. Agric., Assiut Univ., Egypt, in the winter seasons of 2017/2018 and 2018/2019.

The initial plant material used in the present study consisted of six genotypes of Cowpea [*Vigna unguiculata* (L.) Walp.], quite variable in their yield performance. The field evaluations were carried out on a clay soil at the Vegetable Department Experimental Farm, Faculty of Agriculture, Assiut University, Assiut, Egypt. In 20th April 2017, the six parent's genotypes were crossed in a half diallel pattern to produce 15 F_1 crosses. The parents' names, Balady (P_1), Cream7 (P_2), Azmerly (P_3), Dokki 331(P_4), Black eye crowder (P_5) and IT82D-79 (P_6) (Table 1). In 2018 season, seeds of the parents and their F_1 hybrids (15 entries) were planted on 21st April as an optimal sowing date. The field experiments were conducted as RCBD with three replications. Each of the genotypes (parents and 15 F_1's) were depicted in each block by one row of 15 plants. The rows

were spaced at 60 cm apart and plants within a row were spaced at 50 cm. Data were recorded on 10 plants of the parents and F_1 hybrids in each row. The studied characters were: time to 50% flowering (TF), Number of branches per plant (NB), Pod length (PL) (cm), Pod diameter (PD) (mm), Number of pods per plant (NP), Weight of pods per plant (WP) (g), Number of seeds per pod (NS) (g), Weight of seeds per plant (WS) (g), 100 seed weight (100 SW) (g) and Total dry seed yield (TS) (Ton/Hectare)

Table 1. Characteristics of the tested cowpea.

Genotype	Seed color	Growth habit
Monarch Blackeye (P_1)	White with black eye	Determinate
Cream 7 (P_2)	Yellowish-white	Determinate
Azmerly (P_3)	White with black eye	Determinate
Dokii 331 (P_4)	White with black eye	Determinate
Blackeye Crowder (P_5)	White with black eye	Determinate
IT82D-799 (P_6)	Light Brown	Indeterminate

Statistical and biometrical analyses

The diallel analysis was performed according to the methods described Hayman (1954a, b) and Mather and Jinks (1971) using the DIAL98 computer software developed by Ukai (2006). Modification for the half diallel cross suggested by Jones (1965) were applied for the Hayman analysis. The adequacy of an additive-dominance model and the validity of assumptions were tested by the regression of the covariance (Wr) on the variance (Vr) as well as ANOVA of (Wr + Vr) and (Wr - Vr). The genetic and environmental components of variance were calculated according to Mather and Jinks (1971) Broad (h^2_B) and narrow-sense (h^2_N) heritability were then estimated. GCA and SCA were also estimated as measures of additive and non-additive genetic effects (Griffing, 1956).

Analysis of phenotypic traits

Average data for 10 agro-morphological traits studied in this investigation were recorded aiming at detecting patterns of genetic relationship among cowpea genotypes. Cluster analysis of the standardized the agro-morphological traits was done using NTSYS-pc version 2.11T based on the Euclidian Distance coefficient (Rolhf, 2000).

Molecular Analysis

DNA Extraction

DNA extraction from young leaves of each genotype was done following CTAB method Murray and Thompson (1980) with minor modifications by Abd El-Fatah (2018). The DNA quality was detected using gel electrophoresis (0.9% agarose).

ISSR and SRAP Genotyping

A total of 25 ISSR primers and 15 SRAP primer pairs were initially screened for polymorphism, of which only 11 ISSR and 10 SRAP primer or primer pairs gave reproducible and polymorphic bands (Table 2). The PCR reaction conditions were optimized according to Abd El-Fatah (2018).

The ISSR and SRAP amplification conditions and electrophoresis were carried out according to Abd El-Fatah (2018). DNA bands were visualized using GelDoc-It®^{2} Imager

The presence (1) or absence (0) of DNA bands for each primer was recorded in each genotype. The genetic similarity was calculated according to Dice (1945). In addition, a dendrogram was constructed based on similarity matrix using NTSYS-pc 2.11T (Rolhf, 2000). Moreover, Mantel test described by Mantel (1967) was employed to calculate the correlation between ISSR and SRAP markers and between molecular marker and phenotypic markers. Polymorphic information content (PIC) (Ghislain *et al.*, 1999), Marker index (MI) (Powell *et al.*, 1996) and Resolving power (Rp) (Prevost and Wilkinson, 1999) were calculated.

The associations between SCA, heterosis, and genetic distance (GDs) and phenotypic distance (PDs) were settled by correlation coefficient for two set of crosses together and tested at P = 0.05 and 0.01.

Table 2. Primer sequences and codes used

Primer codes		Sequence (5' to 3')
ISSR-1	UBC 807	AGAGAGAGAGAGAGAGT
ISSR-2	UBC 810	GAGAGAGAGAGAGAGAT
ISSR-3	HB09	5'-GTG TGT GTG TGT GG -3'
ISSR-4	HB10	5'-GAG AGA GAG AGA CC -3'
ISSR-5	HB12	5'-CCA CCA CCA GC-3'
ISSR-6	HB15	5'-GTG GTG GTG GC-3'
ISSR-7	UBC 823	5'-TCTCTCTCTCTCTCTCC-3'
ISSR-8	UBC840	5'–GAGAGAGAGAGAGAGATT-3'
ISSR-9	UBC826	5'–ACACACACACACACACC-3'
ISSR-10	UBC868	5'-GAAGAAGAAGAAGAAGAA-3'
ISSR-11	UBC811	5'–GAGAGAGAGAGAGAGC-3'
SRAP-1	Em 1a	5'–GAC TGC GTA CGA ATT AAT–3'
	Me1b	5'–TGA GTC CAA ACC GGA AG–3
SRAP-2	Em 2	5'–GAC TGC GTA CGA ATT TGC–3
	Me3	5'–TGA GTC CAA ACC GGA AT–3'
SRAP-3	Em 1c	5'–GAC TGC GTA CGA ATT AAC–3'
	Me4	5'–TGA GTC CAA ACC GGA CC–3
SRAP-4	Em6	5'–GACTGCGTACGAATTGCA–3
	Me5	5'–TGAGTCCAAACCGGAAG–3
SRAP-5	Em 1a	5'–GAC TGC GTA CGA ATT AAT–3'
	Me2	5'–TGA GTC CAA ACC GG AGC–3'
SRAP-6	Em11	5'–GACTGCGTACGAATTCCA–3
	Me7	5'–TGAGTCCAAACCGGACA–3'
SRAP-7	EM10	5'–GACTGCGTACGAATTCAG–3
	Me10	5'–TGAGTCCAAACCGGACG–3'
SRAP-8	EM16	5'–TGAGTCCAAACCGGATA–3
	Me16	5'–GACTGCGTACGAATTAGC–3'
SRAP-9	EM13	5'–TGAGTCCAAACCGGAGA–3
	Me13	5'–GACTGCGTACGAATTAAT–3'
SRAP-10	EM20	5'–TGAGTCCAAACCGGAGA–3
	Me20	5'–GACTGCGTACGAATTATG–3

RESULTS AND DISCUSSION

Phenotypic distances between parents

Estimated value of phenotypic distance among six cowpea genotypes for 10 agro-morphological traits ranged from 2.582 to 6.189 with a mean of 4.521. The lowest phenotypic distance was found between P_2 and P_6 (2.582) and the highest was revealed between P_1 and P_4 (6.189) followed by P_1 and P_5 (5.94).

Data illustrated in Fig. 1 represent a dendrogram constructed for the cluster analysis performed for the studied cowpea genotypes based on the standardized value of agro-morphological traits by UPGMA method. Cowpea genotypes were divided into two main clusters, where cluster I comprised of P_1, P_2 and P_6 and cluster II included P_3, P_4 and P_5.

Our study certain the presence of a high phenotypic diversity among cowpea genotypes studied in the current investigation exhibiting a good start for plant development

programs to release hybrid and new varieties. Our results are in line with those observed by Hedge and Mishra (2009), Stoilova and Pereira (2013), Mafakheri *et al.* (2017), Lazaridi*et al.* (2017), Bozokalfa *et al.* (2017) and El-Nahrawy (2018) who reported high phenotypic diversity among cowpea genotypes.

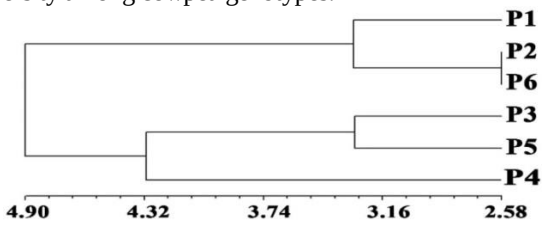

Fig. 1. Dendrogram of the genetic dissimilarities among six genotypes of cowpea, achieved by the UPGMA method based on the Euclidian coefficient from 10 agro-morphological traits. (P_1) Monarch Blackeye, (P_2) Cream 7, (P_3) Azmerly, (P_4) Dokii 331, (P_5) Blackeye Crowder and (P_6) IT82D-799

Molecular analysis

Generally, Data analysis were considered for the polymorphic and reproducible excreted by the eleven ISSR primers, and ten SRAP primer pairs. Percentage of polymorphisms as well as the total number of bands for each primer or primer pair are shown in Table 3. Distinguished differences were observed in the reproducible bands obtained from the six cowpea genotypes are shown in Figs. 2a-c, and Fig. 3a-d.

For ISSR, used primers amplified 90 fragments with a size varied from 176 to 1005 bp (ISSR-5). Out of the 90 bands, 62 were polymorphic. Polymorphism percentage ranged from 55.56% (ISSR-1) to 100% (ISSR-8), with an average of 68.67% polymorphism. PIC value ranged from 0.15 for primer ISSR-1 to 0.32 for primer ISSR-8 with an average of 0.23 (Table 3). MI was the highest (3.22) for primer ISSR-8 and lowest (0.74) for ISSR-4 with a mean value of 1.32. Highest (4.67) and lowest (1.33) Resolving power (RP) values were obtained with primers ISSR-8 and ISSR-4, respectively as shown in Table 3.

A dendrogram was constructed based on ISSR data by UPGMA and the six genotypes of cowpea were grouped into two clusters with similarity ranging from 0.692 to 0.869 (Fig. 2c). Cluster I included the genotype P_4 which separated in a single branch with genetic similarity of 0.751. Cluster II comprised of five genotypes. Genotypes within cluster II are further divided into two sub-clusters. Sub-cluster IIa consisted of P_1 which separated in a single branch from sub-cluster IIb with genetic similarity of 0.785. Sub-cluster IIb comprised of four genotypes P_2, P_3, P_5 and P_6. Within cluster II, P_2 and P_6 were closely related to each other, with a 0.869 genetic similarity.

For SRAP, the 10 primer pairs yielded a total of 116 fragments with an average of 11.6. Size range of amplified fragments varied from 175 bp (SRAP-8) to 1155 bp (SRAP-2). Out of the 116 bands, 68 were polymorphic, with an average of 6.8 per primer. Polymorphism percentage ranged from 38.46% (SRAP-7) to a maximum of 72.73% (SRAP-4), with an average of 59.36% polymorphism (Table 3). The highest values for three genetic parameters, PIC, MI and RP were recorded for SRAP-10 primer (0.28, 2.5 and 5.33, respectively). While the lowest values for three parameters, PIC (0.15), MI (0.73) and RP (2.67) were obtained with primer pair SRAP-7 (Table 3).

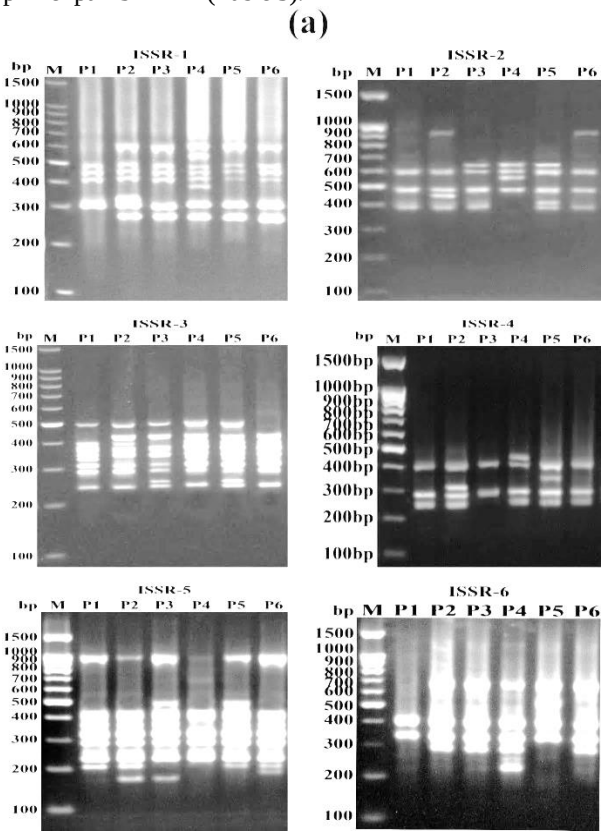

Fig. 2a. ISSR profiles of six cowpea genotypes, (P_1) Monarch Blackeye, (P_2) Cream 7, (P_3) Azmerly, (P_4) Dokii 331, (P_5) Blackeye Crowder and (P_6) IT82D-799.

A dendrogram based on SRAP data classified the six cowpea genotypes into two clusters with genetic similarity ranging from 0.774 to 0.88 (Fig. 3c). Cluster I included one genotype P_6 which separated in a single branch from the other genotypes with genetic similarity 0.796. Cluster II comprised of five genotypes. Genotypes within cluster II are further divided into two sub-clusters. Sub-cluster IIa consisted of P_1 which separated in a single branch from sub-cluster IIb with genetic similarity 0.808. Sub-cluster IIb comprised of four genotypes P_2, P_3, P_4 and P_5. Within cluster II, P_2 and P_3 were closely related to each other, with a 0.88 genetic similarity.

ISSR and SRAP combined data

Combined of ISSR and SRAP markers yielded a total of 206 bands, with an average of 9.81 bands per primer, and the average of their polymorphism was 64.23% (Table 3). The highest number of bands was recorded for P_5 (156 bands) followed by P_4 (150 bands), while the lowest number was recorded for P_1 (116 bands). The two markers were sufficient for detected the genetic diversity among six cowpea genotypes by unique bands (Table 4). Some of these unique bands may be associated with agro-morphological traits.

The Dic genetic similarity ranged from 0.744 (P_1 and P_4) to 0.868 (P_2 and P_3). The dendrogram based on genetic similarity of combined molecular markers data grouped the six cowpea genotypes into two main clusters (Fig. 3d). Cluster I included the genotype P_6 which separated from the genotypes in cluster II with genetic similarity 0.791. Cluster

II consisting of five genotypes and was further divided into two sub-clusters. Sub-cluster IIa included one genotype P_6 in a single branch from sub-cluster IIb with genetic similarity 0.796. Sub-cluster IIb comprised of four genotypes P_2, P_3, P_4 and P_5. Within cluster II, P_2 and P_3 were closely related to each other, with a 0.868 genetic similarity. The correlation between the matrices of ISSR and SRAP data using Mantel's test (Mantel, 1967) was a slight and significant (r = 0.311). ISSR and SRAP markers included in the current investigation were proved as effective tools for evaluating genetic diversity and phylogenetic relationships in various cowpea genotypes.

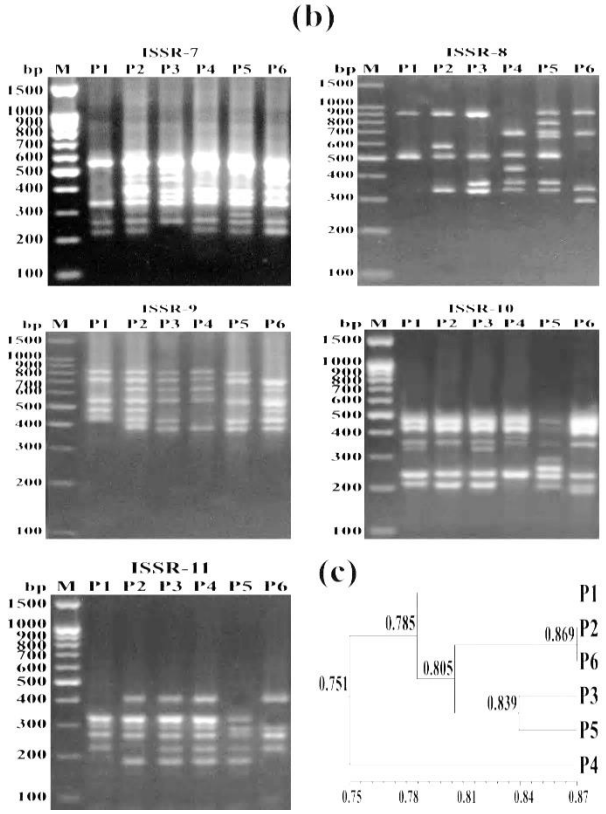

Fig. 2b, c. (b)ISSR profiles of six cowpea genotypes (c) Dendrogram showing clustering of six cowpeagenotypes constructed using UPGMA based on Dice coefficient obtained from ISSR data, (P_1) Monarch Blackeye, (P_2) Cream 7, (P_3) Azmerly, (P_4) Dokii 331, (P_5) Blackeye Crowder and (P_6) IT82D-799.

The obtained data revealed that both markers have strong differentiating potential of the cowpea genotypes as inferred from the high values of the genetic diversity indices. These results are in agreement with Igwe *et al.* (2017) who studied the genetic diversity among cowpea genotypes using SCoT and ISSR markers, they found that both marker types demonstrated high values for total number of alleles, genetic parameters (PIC, MI and RP), genetic diversity and total number of polymorphic bands.

Dias *et al.* (2015) and Araújo *et al.* (2019) found 76% polymorphism, a high value and similar to that was found in our study; also Ghalmi *et al.* (2010) studied the genetic diversity among 20 cultivars of cowpea using RAPD and ISSR markers, revealed relatively high levels of diversity which were similar to our results. Mahfouz (2015) studied the genetic diversity among cowpea genotypes and revealed that the high polymorphism attained by ISSR markers show their coverage of the genome. This is because microsatellites are abundant and well distributed in genome. Also our results in outline with Salem *et al.* (2019) who assessed the genetic diversity among seven landraces of cowpea, reporting a high genetic diversity among genotypes.

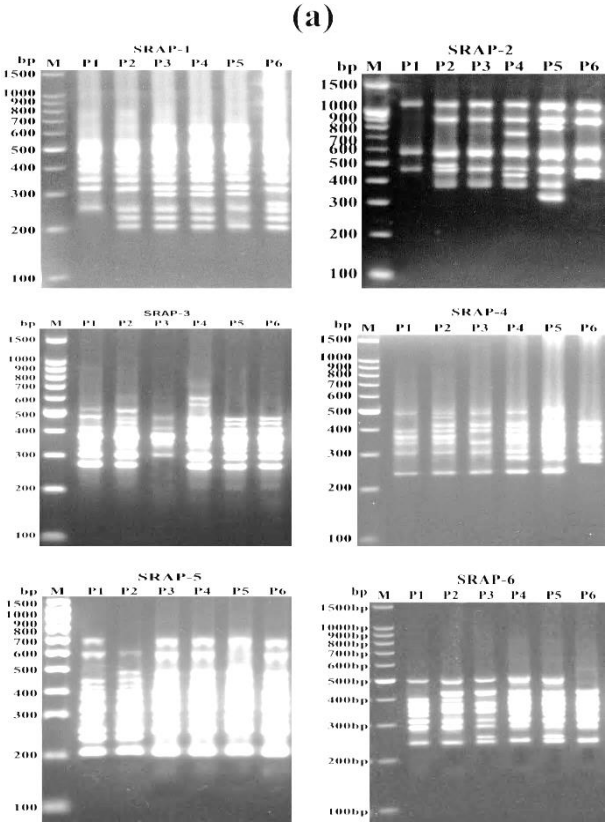

Fig. 3a. SRAP profiles of six cowpea genotypes, (P_1) Monarch Blackeye, (P_2) Cream 7, (P_3) Azmerly, (P_4) Dokii 331, (P_5) Blackeye Crowder and (P_6) IT82D-799.

The slight variations found among the dendrograms generated by ISSR and SRAP markers in our study could be interpreted by the different number of DNA fragments analyzed (90 for ISSRs and 116 for SRAPs). This fact supports the significance of allele number and their coverage of the genome, in attaining dependable approximates of genetic relationships among cowpea genotypes. Data recorded in the current research illustrates the occurrence of high genetic variation based on ISSR and SRAP analysis among cowpea genotypes which could be used to choose good parents. These parents crossed for getting appropriate populations which may be useful for genome mapping and breeding programs.

Correlation between phenotypic and molecular marker systems

The dendrogram based on genetic distance matrix of combined phenotypic and molecular marker systems data grouped the six cowpea genotypes into three main clusters (Fig. 4) with Genetic distance ranged from 13.891 (P_2 and P_3) to 19.148 (P_1 and P_4). Cluster I included the genotype P_4. Cluster II included the genotype P_6. Cluster III consisting of four genotypes P_1, P_2, P_3 and P_5.

A significant positive correlations were found between molecular markers and agro-morphological traits using Mantel test, ISSR and agro-morphological, SRAP and

agro-morphological and ISSR+SRAP and agro-morphological (r = 0.614, r = 0.464 and r = 0.656: p ≤ 0. 001, respectively). Similarly, high correlations between agro-morphological traits and molecular marker systems were reported in several studies in cowpea (Mafakheri *et al.*, 2017 and Ghalmi *et al.*, 2010).

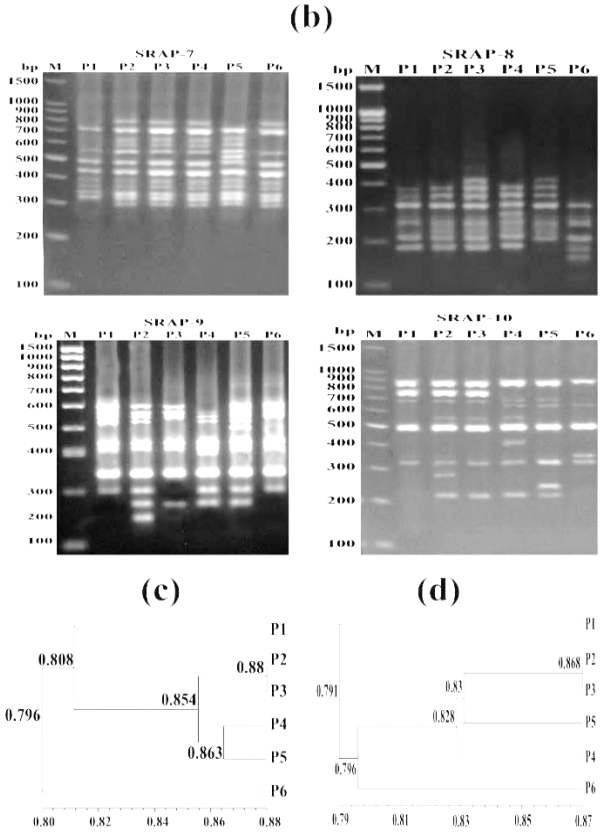

Fig. 3b, c, d. (b)SRAP profiles of six cowpea genotypes (c) Dendrogram showing clustering of six cowpeagenotypes constructed using UPGMA based on Dice coefficient obtained from SRAP data (d), Dendrogram showing clustering of six cowpea genotypes constructed using UPGMA based on Dice coefficient obtained from ISSR, SRAP and SSR combines analysis. (P_1) Monarch Blackeye, (P_2) Cream 7, (P_3) Azmerly, (P_4) Dokii 331, (P_5) Blackeye Crowder and (P_6) IT82D-799.

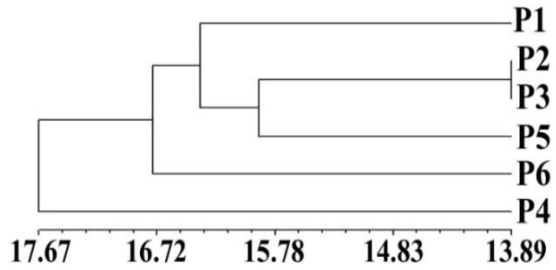

Fig. 4. Dendrogram showing clustering of six cowpea genotypes constructed using UPGMA based on Dice coefficient obtained from molecular and phenotypic markers combined dataanalysis. (P_1) Monarch Blackeye, (P_2) Cream 7, (P_3) Azmerly, (P_4) Dokii 331, (P_5) Blackeye Crowder and (P_6) IT82D-799.

Table 3. Summary of ISSR and SRAP primer combination characteristics

ISSR Primers	TB	PB	PPB	PIC	MI	RP
1	9	5	55.56	0.15	0.77	1.67
2	8	6	75.00	0.26	1.54	3.00
3	9	6	66.67	0.20	1.22	2.33
4	6	4	66.67	0.19	0.74	1.33
5	10	6	60.00	0.22	1.30	3.00
6	6	4	66.67	0.21	0.85	1.67
7	9	6	66.67	0.26	1.56	4.00
8	10	10	100.00	0.32	3.22	4.67
9	7	5	71.43	0.25	1.27	2.67
10	10	6	60.00	0.18	1.10	2.33
11	6	4	66.67	0.24	0.96	2.00
Total	90	62				
Average	8.18	5.64	68.67	0.23	1.32	2.61
SRAP Primers	TB	PB	PPB	PIC	MI	RP
1	12	6	50.00	0.19	1.14	3.67
2	10	7	70.00	0.23	1.59	3.00
3	12	7	58.33	0.22	1.56	4.00
4	11	8	72.73	0.22	1.78	3.33
5	13	6	46.15	0.17	1.00	3.00
6	11	6	54.55	0.21	1.24	3.67
7	13	5	38.46	0.15	0.73	2.67
8	10	7	70.00	0.23	1.59	3.00
9	12	7	58.33	0.19	1.33	3.00
10	12	9	75.00	0.28	2.50	5.33
Total	116	68				
Average	11.6	6.8	59.36	0.21	1.45	3.47
Total	206	130				
Average	9.81	6.19	64.23	0.22	1.38	3.02

TB total bands, PB polymorphic bands, PPB percentage of polymorphic bands, PIC polymorphic information content, MI marker index, RP resolving power.

Table 4. Unique DNA bands generated by ISSR and SRAP markers

Genotypes	Positive	Negative
P_1	----------	ISSR-$1_{605, 281}$, ISSR-3_{665}, ISSR-6_{664}, ISSR-7_{383}, ISSR-8_{350}, ISSR-9_{392}, SRAP-1_{207}, SRAP-2_{910}, SRAP-4_{435}, SRAP-5_{498}, SRAP-6_{436}, SRAP-7_{292}
P_2	ISSR-1_{325}, ISSR-2_{478}, ISSR-3_{262}, ISSR-4_{322}, ISSR-8_{590}, SRAP-2_{493}, SRAP-4_{472}, SRAP-9_{190}, SRAP-10_{280}	ISSR-11_{235}, SRAP-$5_{705, 288}$
P_3	----------	ISSR-3_{856}, ISSR-4_{258}, ISSR-7_{228}, SRAP-3_{272}, SRAP-4_{386}, SRAP-6_{396}, SRAP-9_{308}
P_4	ISSR-$1_{573, 383}$, ISSR-2_{596}, ISSR-4_{460}, ISSR-6_{236}, ISSR-8_{448}, ISSR-10_{384}, SRAP-1_{366}, SRAP-2_{762}, SRAP-$3_{605,580}$, SRAP-8_{285}, SRAP-9_{380}, SRAP-10_{405}	ISSR-3_{473}, ISSR-$5_{1005,362}$, ISSR-8_{910}, ISSR-9_{430}, ISSR-10_{208}, SRAP-9_{595}
P_5	ISSR-2_{411}, ISSR-4_{368}, ISSR-6_{518}, ISSR-7_{280}, ISSR-$8_{802,688}$, ISSR-$10_{290, 278}$, SRAP-$2_{885,335}$, SRAP-$4_{350,}$ SRAP-7_{514}, SRAP-9_{502}, SRAP-10_{248}	ISSR-2_{384}, SRAP-8_{188}
P_6	ISSR-3_{560}, ISSR-5_{195}, ISSR-8_{290}, ISSR-10_{195}, SRAP-1_{295}, SRAP-4_{271}, SRAP-8_{175}, SRAP-10_{345}	ISSR-9_{818}, ISSR-11_{325}, SRAP-$4_{495,247}$, SRAP-6_{503}, SRAP-8_{376}

Performance of cowpea genotypes:

Data presented in Table 5 showed that overall mean of time to 50 % flowering was 67.72 and 65.96 for parent and F_1s, respectively. The earlier parent was P_4 (58.33) followed by P_5 (65.33). The earlier F_1 hybrid was P_4xP_5 (58.67) followed by P_4xP_6 (60.33) with an average of 65.96. P_5 produced greater NP (64.67), WP(86.60), NS (10.67), WS (63.12) and TS (3.41). However, P_4 showed the highest 100 SW value (19.38 g), PL (15.80) and PD (8.90 mm), while the greater NB (6.33) was recorded for P_2. The means of F_1 hybrids ranged from 58.67 to 6.67for days to 50% flowering, 12.37 ($P_1 \times P_3$) to 16.67 ($P_4 \times P_6$) for PL, 7.40 ($P_1 \times P_5$) to 8.53 ($P_3 \times P_5$) for PD and 12.65 ($P_1 \times P_5$) to 20.28 ($P_3 \times P_4$) for 100 SW with an average all 5.71, 14.45, 7.94 and 16.07, respectively.

The diallel analysis of variance:

The analysis of variance indicated highly significant differences between the genotypes for all the traits studied (Table 6). Both additive and dominant effects were all significant ($p<0.01$). In F_1 the "b_1" item was significant ($P\leq0.01$), indicating directional dominance in all the studied traits except PD. Furthermore, the "b_2" item was highly significant ($P\leq0.01$) for all studied traits but significant for NP, suggesting unsymmetrical distribution of dominant and recessive genes between the parents. As well, the "b_3" item was highly significant ($P\leq0.01$) for all traits. The "b_3" item examines the part of dominance deviation for F_1 hybrid, and it is a measure of specific combining ability.

General combining ability (GCA) was significant for days to flowering and maturity ($P<0.01$) (Monininuola*et al.,* 2011; Kumar *et al.,* 2007). The magnitude of non-additive variance was higher than additive variance in most traits, indicating the importance of improving these traits by the hybrid vigor. Similar results have been reported by Kadam *et al.* (2013) and Chaudhari *et al.* (2013). Raut *et al.* (2017) found that variances due GCA were higher as compared to SCA for all the traits except PL.

Table 5. Mean performance for different studied traits in 6 cowpea parental genotypes and their F_1 crosses

Traits / Genotypes	TF	NB	PL (cm)	PD (mm)	NP	WP	NS	WS	100 SW (g)	TS (Ton/ H.)
P_1	71.33	5.33	12.37	7.40	52.33	50.60	10.33	41.32	11.75	2.27
P_2	67.33	6.33	14.37	7.87	56.33	65.70	10.67	52.70	15.32	2.79
P_3	74.67	5.67	13.60	8.67	60.33	73.35	9.33	58.30	18.30	3.14
P_4	58.33	4.33	15.80	8.90	56.67	73.72	9.33	56.38	19.38	3.05
P_5	65.33	5.33	12.43	8.10	64.67	86.60	10.67	63.12	15.03	3.41
P_6	69.33	5.33	15.33	7.23	54.67	60.60	11.67	46.30	13.38	2.63
Mean	67.72	5.39	13.98	8.03	57.50	68.43	10.33	53.02	15.53	2.88
$P_1 \times P_2$	70.67	6.67	13.50	8.17	62.67	66.60	10.67	53.37	13.75	2.94
$P_1 \times P_3$	69.33	6.33	12.37	7.47	59.33	75.52	9.67	56.70	14.43	3.21
$P_1 \times P_4$	60.67	4.67	13.40	7.63	61.33	75.30	11.67	55.47	13.37	3.20
$P_1 \times P_5$	70.33	5.33	13.30	7.40	64.67	80.23	11.33	57.80	12.65	3.47
$P_1 \times P_6$	68.33	6.67	14.13	8.30	56.33	58.60	9.67	44.30	13.35	2.50
$P_2 \times P_3$	70.67	6.33	15.60	7.63	60.67	75.50	11.00	56.52	15.58	3.28
$P_2 \times P_4$	61.33	4.67	15.60	8.00	61.67	78.80	9.33	55.28	17.50	3.26
$P_2 \times P_5$	64.67	5.33	14.70	7.48	64.33	83.30	9.67	59.38	15.10	3.54
$P_2 \times P_6$	67.67	6.33	13.50	7.99	59.33	68.18	11.33	51.68	15.73	2.86
$P_3 \times P_4$	62.33	4.67	14.13	8.10	66.67	87.60	9.67	65.93	20.28	3.50
$P_3 \times P_5$	70.67	5.67	15.97	8.53	62.33	82.92	8.67	66.40	16.70	3.72
$P_3 \times P_6$	69.33	6.67	14.33	8.10	63.67	72.50	10.00	58.95	17.18	3.26
$P_4 \times P_5$	58.67	5.67	14.47	8.17	64.67	90.12	11.67	64.40	19.50	3.53
$P_4 \times P_6$	60.33	5.33	16.67	7.87	62.67	82.03	10.33	60.05	18.45	3.24
$P_5 \times P_6$	64.33	5.33	15.13	8.27	64.67	76.50	11.33	58.92	17.42	3.26
Mean	65.96	5.71	14.45	7.94	62.33	76.91	10.40	57.68	16.07	3.25
$L.S.D_{(0.05)}$	1.74	1.27	0.31	0.22	1.25	11.85	1.43	3.81	1.94	0.029
$L.S.D_{(0.01)}$	2.33	1.71	0.42	0.31	1.67	15.06	1.95	5.10	2.59	0.038

Table 6. Computation of mean squares for ANOVA of 6 x 6 half diallel for different traits of cowpea.

Traits Parameters		TF	NB	PL(cm)	PD (mm)	NP	WP	NS	WS	100 SW(g)	TS (Ton/H.)
S.O.V	d.f	M.S	M.S	M.S	M.S	M.S	M.S	M.S	M.S	M.S	M.S
Rep	2	1.19	4.92**	0.07*	0.004	5.45**	32.00	5.86**	4.25	0.31	0.0005
Genotypes	20	106.61**	2.71**	8.13**	0.59**	61.76**	454.43**	4.42**	199.03**	18.08**	0.41**
a	5	375.3**	6.37**	21.21**	0.37**	106.30**	1425.60**	4.44**	638.9**	27.66**	0.66**
b	15	17.05**	1.49**	3.77**	0.66**	46.91**	130.70**	4.41**	52.41**	14.88**	0.32**
b_1	1	46.82**	1.55**	6.34**	0.004	350.4**	1080.10**	0.07*	325.3**	12.67**	0.01**
b_2	5	12.44**	0.99**	3.23**	0.72**	10.91**	63.37*	1.36**	21.06**	17.35**	0.30**
b_3	9	16.29**	1.77**	3.79**	0.70**	33.19**	62.68*	6.59**	39.50**	13.75**	0.37**
Error	40	0.37	0.20	0.012	0.006	0.19	17.19	0.25	1.78	0.46	0.0003

***, ** Significant differences at 0.05 and 0.01 P, respectively**

The genetic parameters

The additive genetic variance (D) was significant in all studied traits (Table 7). Also, the dominance components H_1 and H_2 were significant for all studied traits except NB and WP. The H_1 dominant component was larger than the other dominance components H_2 in all studied traits except TS, these results are in agreement with Ayo- Vaughan *et al.* (2011) and Kumar *et al.* (2007). The dominance variance (H_1) was higher than the additive variance (D) for all traits except TF, WP, WS and TS, these results are in agreement with Mohamed *et al.* (2015). The results illustrated that diallel crosses appeared the relative magnitudes of mean squares for GCA variances in F_1 hybrids and F_2 generations which were larger than those of SCA for all traits in cowpea (Ameen *et al.,* 2014). Supriyo *et al.* (2010) reported that the magnitude of non-additive gene effect was higher than that of additive gene effect for each studied trait in black gram. The positive value of (F) obtained for all traits except WP and WS indicated that the dominant alleles are more frequent in the parents than the recessive alleles. These results were in consonance with that of Ayo-Vaughan *et al.* (2011) who found that the frequency of dominance (F) was positive for days to 50% flowering and maturity indicating greater frequency of dominant increasing alleles in the parental genotypes. Therefore, the loci exhibiting positive and negative genes were equally distributed in the parents for

these characters (Mohamed *et al.,* 2015; Adeniji and Kehinde, 2007 and Amiri-Oghan *et al.,* 2009).

The heritability estimates were obtained for all the studied traits refer to high broad-sense heritability and moderate to high narrow-sense heritability. The broad-sense heritability ranged from 0.69 for NB to 0.99 for PD and TS. However, the narrow-sense heritability ranged from 0.16 for PD to 0.87 for days to 50% flowering. The narrow-sense heritability obtained for WP, NS, 100 seeds weight and TS were 0.71, 0.18, 0.31 and 0.76, respectively. The narrow sense heritability was larger than 0.60 in time to 50 % flowering, PL, WP, WS and TS, so selection for these traits could be useful.

Similar finding was reported by Ameen *et al.* (2014), who found higher values of broad-sense and narrow-sense heritability indicating good genetic variability for effective selection in cowpea. High heritability value for 100-seed weight, vegetable pod yield and pod weight were reported by Resmi (1998) and Thiyagarajana (1989). The broad sense heritability for dry pod yield was much higher (0.76) as compared to pods per plant (0.64) (Pathmanathan *et al.,* 1997).

Table 7. Genetic components Estimates for studied traits in a 6-parent half diallel cross of cowpea.

Traits / Parameters	TF	NB	PL (cm)	PD (mm)	NP	WP	NS	WS	100 SW(g)	TS (Ton/H.)
D±SE	31.21±0.43	0.216±0.17	2.07±0.04	0.12±0.02	19.05±0.42	136.6±17.2	0.55±0.11	62.89±2.88	10.23±1.19	0.22±0.003
H_1±SE	13.15±1.01	0.68±0.43	3.20±0.13	1.01±0.04	33.20±1.1	55.41±43.7	2.57±0.30	34.87±7.31	21.46±1.78	0.23±0.003
H_2±SE	10.65±0.98	0.61±0.39	2.49±0.11	0.80±0.03	30.91±0.95	53.73±39.1	2.45±0.27	31.47±6.53	16.45±1.27	0.36±0.002
F±SE	7.85±1.06	0.34±0.42	0.43±0.12	0.26±0.03	9.60±1.03	-13.4±42.1	0.27±0.29	-4.01±7.04	11.35±1.69	0.09±0.004
E±SE	0.37±0.16	0.202±0.09	0.011±0.01	0.02±0.004	0.19±0.15	17.19±6.5	0.25±0.04	1.78±1.09	0.17±0.03	0.01±0.001
uv	0.20	0.22	0.19	0.20	0.23	0.24	0.24	0.23	0.19	0.15
h^2_B	0.98	0.69	0.99	0.99	0.98	0.84	0.76	0.96	0.97	0.99
h^2_N	0.87	0.47	0.64	0.16	0.42	0.71	0.18	0.79	0.31	0.76

The Wr/Vr relationship:

The joint regression analysis (Table 8) showed the adequacy of additive-dominance model was fit for time to 50 % flowering, NB, NP, WP, WS and TS. Non-allelic gene interaction was observed for PL, NS and PD, the data obtained for these traits are in agreement with Anand Singh *et al.* (2016) who reported the additive-dominance genetic model did not fit for PL, NS and PD. However, the regression was significantly from zero and from unity for 100 SW, indicating partial adequacy of the additive-dominance model. The mean squares of the analysis of variance for (Wr + Vr) and (Wr- Vr) values (Table 8) indicated to highly significant array differences (P<0.01) for (Wr + Vr) in all the traits studied, confirming the presence of significant dominance variation. However, the analysis of variance for the (Wr – Vr) was non-significant in most the studied traits, indicating the absence of epistasis. Generation mean analysis did not fit an additive dominance model for days to 50% flowering (Adeyanju andIshiyaku, 2007). Pathmanathan *et al.* (1997) reported that the generation mean analysis showed that an additive-dominance model fitted for NP. Subsequently, Ranganatha (1986) suggested that selection for consistently high NP over environments is a good index of yield stability. Mak and Yap (1980) found that non-additive gene action was effective in the inheritance of both NP and pod yield in climber vegetable types. The partial dominance degrees were obtained for TF, PL, WP, NS, WS, 100 SW and TS (Fig. 5) whereas it was over-dominance for the remaining traits. The parent P_1 possessed a high proportion of recessive alleles for NB, NP, WP, WS and TS and a high proportion of dominant alleles for 100 SW and PL. Whereas, P_5 contained a majority of dominant alleles for NB, NP, WPand TS. The correlations between (Wr+ Vr) and the parental mean (Yp) for NP, weight of pod per plant, weight seeds per pod and TS (Fig. 6) indicated negative and significant correlation coefficient (r= -0.93, r= -0.94, r= -0.85 and r= -0.98) respectively, suggesting that recessive alleles contribute a lower for those traits. Pathmanathan *et al.* (1997) and Jean-Baptiste *et al.* (2011) reported that the degree of dominance for number and WPand 100 seeds weight were partial dominance while Ayo-Vaughan *et al.* (2011) found that the average degree of dominance for days to 50% flowering was over dominance. The coefficient of correlation between Pr and Wr+Vr was positive but non-significant for seed weight indicating the preponderance of a negative dominant gene control. Similar findings were reported by Gupta *et al.* (1984) for this trait in pea.

Table 8. Analysis of variance for (Wr + Vr) and (Wr – Vr) in a 6-parent half diallel cross as well as Joint regression.

Traits / Parameters	TF	NB	PL (cm)	PD (mm)	NP	WP	NS	WS	100 SW(g)	TS (Ton/H.)
Joint regression (b± se)	0.86± 0.15	0.76± 0.15	0.24± 0.51	1.72± 0.93	0.97± 0.13	0.93± 0.10	0.17± 0.38	0.89± 0.09	0.68± 0.11	0.85± 0.09
Test for b = 0	**	**	Ns	Ns	**	**	Ns	**	**	**
Test for b = 1	Ns	Ns	Ns	Ns	Ns	Ns	*	Ns	*	Ns
(Wr + Vr)	**	*	**	**	**	**	Ns	**	**	**
(Wr –Vr)	Ns	Ns	**	**	*	Ns	**	Ns	Ns	Ns
Fitness of the model	Fully adequate	Fully adequate	Nonadequate	Nonadequate	Partially adequate	Fully adequate	Nonadequate	Fully adequate	Partially adequate	Fully adequate

b: Regression coefficient; *, ** Significant differences at 0.05 and 0.01 P, respectively

The GCA and SCA effects

The estimates of GCA effects of the various parents for all studied traits (Table 9) revealed that P_5 had the highest values for NP, WP, weight of seeds per pod and TS; P_4 had the highest values for PD and 100 SW; P_6 presented the highest positive and significant GCA for PL and NS while P_3 and P_2 showed the highest values for TF and NB, respectively. Genotype P_1 exhibited the lowest negative significant GCA for NP, WP, weight of seeds/ pod and TS, while displaying P_4 showed the lowest negative significant values for TF, NB and NS.

Among 15 cross combinations (Table 9), the hybrids $P_1 \times P_5$ (good x poor general combiners) for NP, WPand TS; $P_4 \times P_6$ (good x poor general combiners) and $P_5 \times P_6$ (good x good general combiners) for NB and PL, respectively; $P_1 \times P_3$ (poor x poor general combiners) for PD and weight of seeds per pod, were identified as good specific combiners. The highest significant and positive SCA values for TF were found in P_4xP_5 (8.80) and P_4xP_6 (5.60). The both additive and dominance gene effects detected in the genetic control of the traits studied implies that both gene effects should be considered in developing strategies for the selection of superior lines (Skoric *et al.,* 2000). However, parents may not necessarily have high GCA during breeding because the dominance gene effects could be exploited to enhance these characters (Arunga *et al*., 2010).

Table 9. Estimates of general (GCA) and specific (SCA) combining ability effects.

Traits / Genotypes	TF	NB	PL (cm)	PD (mm)	NP	WP	NS	WS	100 SW(g)	TS (Ton/H.)
P_1	1.56**	-0.21**	-0.50**	-0.02	-3.67**	-7.53**	-0.04	-4.37**	-0.81**	-0.31**
P_2	1.51**	0.43**	-0.71**	-0.10*	-0.42**	-4.11**	0.21**	-2.59**	-1.85**	-0.12**
P_3	1.72**	0.21**	0.09**	-0.11**	-0.04	1.09	-0.17*	0.01	0.11	0.07
P_4	-2.53**	-0.50**	0.39**	0.20**	1.54**	4.62**	-0.54**	3.74**	1.66**	0.18**
P_5	-2.07**	-0.13	0.22**	-0.01	2.67**	9.24**	0.17*	5.14**	0.69**	0.31**
P_6	-0.19	0.21**	0.50**	-0.03	-0.08	-3.31**	0.38**	-1.91**	0.19	-0.13**
$SD_{(Gi)}$	0.12	0.08	0.03	0.04	0.13	0.74	0.07	0.22	0.13	0.04
$P_1 \times P_2$	-2.20**	0.51**	1.25**	0.02	-0.54*	2.85	0.12	3.32**	2.06**	0.07
$P_1 \times P_3$	4.93**	0.05	-0.32**	0.84**	3.09**	5.30**	-0.84**	6.33**	3.09**	0.23**
$P_1 \times P_4$	7.16**	-0.50*	1.59**	0.76**	-2.16**	2.13	-0.46	0.67	2.62**	0.03
$P_1 \times P_5$	-0.16	0.05	-1.61**	0.16**	4.71**	10.41**	0.16	6.03**	-0.76*	0.27**
$P_1 \times P_6$	1.51**	-0.29	1.01**	-0.74**	-2.54**	-3.04	0.95**	-3.76**	-1.91**	0.09
$P_2 \times P_3$	-0.36	0.09	-1.34**	-0.29**	-1.16**	4.05**	-0.76**	2.95**	0.26	0.12
$P_2 \times P_4$	-4.78**	-0.87**	-0.60**	-0.44**	-0.74**	0.29	1.62**	-2.03**	-2.36**	-0.01
$P_2 \times P_5$	4.43**	-0.58**	-0.53**	-0.47**	1.46**	0.62	0.58*	-1.10*	-2.11**	0.15*
$P_2 \times P_6$	0.55*	0.42*	0.02	0.40**	-4.12**	-8.47**	-1.30**	-7.54**	-0.91**	-0.40**
$P_3 \times P_4$	-4.32**	-0.66**	0.80**	-0.06	-0.79**	-1.41	-0.34	-4.79**	-0.18	-0.14
$P_3 \times P_5$	-1.44**	-0.37*	0.07	-0.37**	0.76**	-1.52	-0.71**	-2.09**	-1.61**	0.02
$P_3 \times P_6$	-0.32	0.30	-1.41**	0.11*	-1.49**	-4.08**	0.74**	-2.94**	-0.48	-0.23**
$P_4 \times P_5$	8.80**	0.67**	1.04**	0.37**	-2.83**	-5.44**	-1.34**	0.78	-1.57**	0.08
$P_4 \times P_6$	5.60**	1.34**	-0.88**	-0.10	1.26**	-3.30*	-0.22	1.10*	-0.59*	0.06
$P_5 \times P_6$	-3.86**	0.37	1.63**	-0.13*	-0.87**	1.62	-0.59*	0.48	1.65**	-0.08
$SD_{(Sij)}$	0.26	0.19	0.09	0.05	0.23	1.68	0.24	0.53	0.29	0.08

***, ** Significant differences at 0.05 and 0.01 P, respectively.**

Phenotypic correlation:

Phenotypic correlation among the studied characteristics are shown in Table 10. Correlation between TF and NB was significant (r= 0.61; P<0.01), WP (*r*= 0.49; *P*<0.05) and 100 SW (*r*= 0.51; *P*<0.05). It is also observed that NP was significantly positive correlated with WP (*r*= 0.86; *P*<0.01), WS (*r*= 0.84; *P*<0.01), 100 SW (0.61; *P*<0.01) and TS (*r*= 0.87; *P*<0.01). A highly positive significant correlations were observed between WP and WS, 100 SW and TS and a highly significant correlation was also obtained between WS and 100 SW (*r*= 0.67; *P*<0.01) and TS. However, non-significant correlation was found between TS and NB, PL and PD. These results were in agreement with those obtained by Muhammed *et al.* (2010) and Rashwan and Helaly (2015) whose observed that significant correlations between different yield and yield component traits. Several researchers have estimated the correlation between various traits associated with yield and their direct and indirect actions on yield in cowpea (El-Shainy, 2012 and Alidu *et al.* 2013). Senanayake and Wijerathne (1988) studied 17 varieties of cowpea and found that yield traits were negatively correlated with the number of primary branches (r = -0.88) and positively correlated with 100-seed weight (r = 0.98) and PL (r = 0.88).

Table 10. Phenotypic correlation coefficients among studied traits.

Traits	TF	NB	PL(cm)	PD (mm)	NP	WP	NS	WS	100 SW(g)	TS (Ton/H.)
TF	1.00									
NB	0.61**	1.00								
PL(cm)	-0.37	-0.23	1.00							
PD (mm)	-0.17	-0.05	0.27	1.00						
NP	-0.28	-0.13	0.08	0.16	1.00					
WP	-0.49*	-0.35	0.23	0.21	0.86**	1.00				
NS	-0.11	0.07	-0.19	-0.48*	0.03	-0.09	1.00			
WS	-0.33	-0.24	0.24	0.36	0.84**	0.94**	-0.20	1.00		
100 SW(g)	-0.51*	-0.30	0.51*	0.64**	0.45*	0.61**	-0.32	0.67**	1.00	
TS (Ton/H.)	-0.29	-0.26	0.25	0.19	0.87**	0.95**	-0.16	0.95**	0.51*	1.00

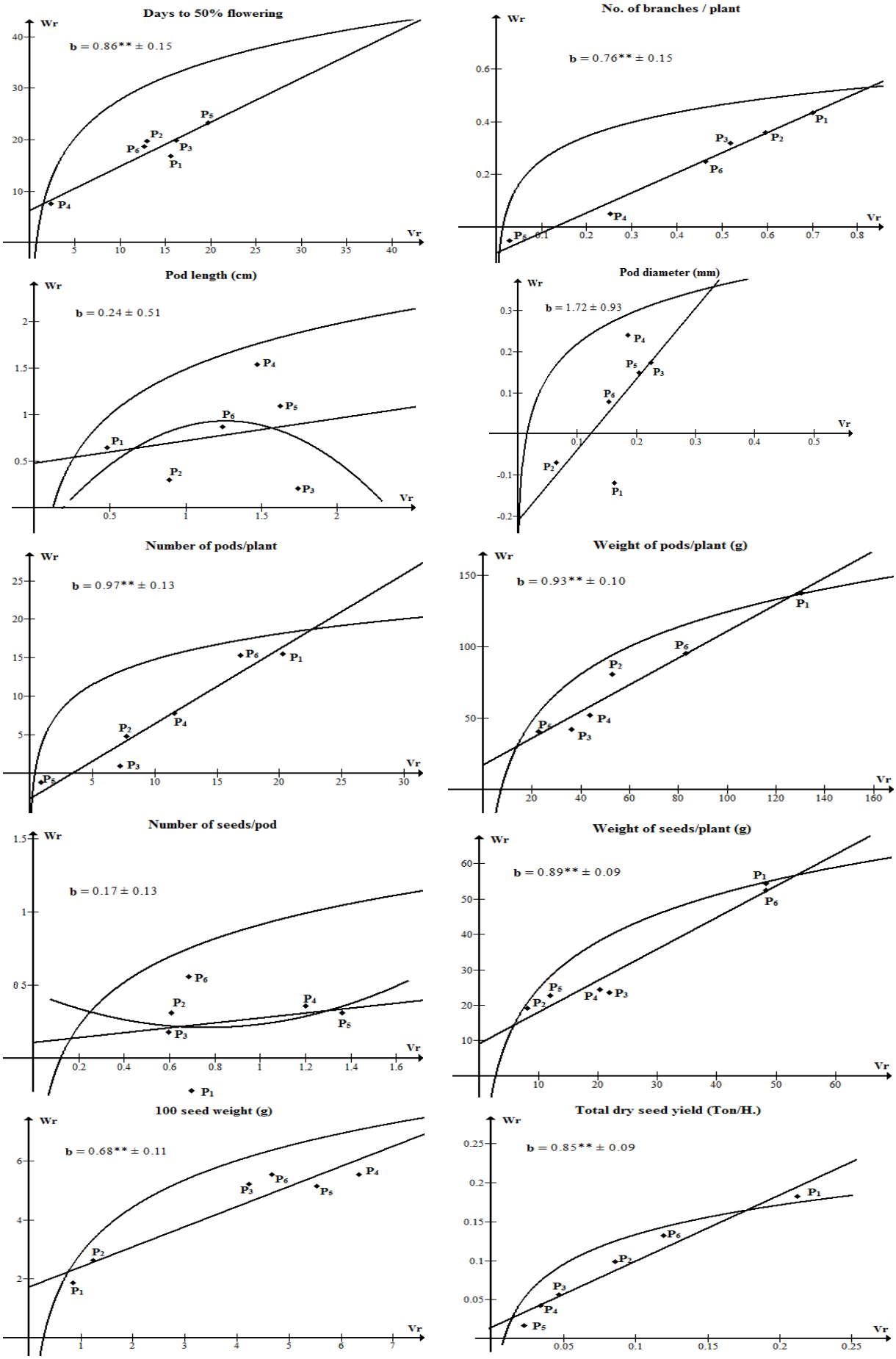

Fig. 5. The Wr/Vr graphs of the studied traits.

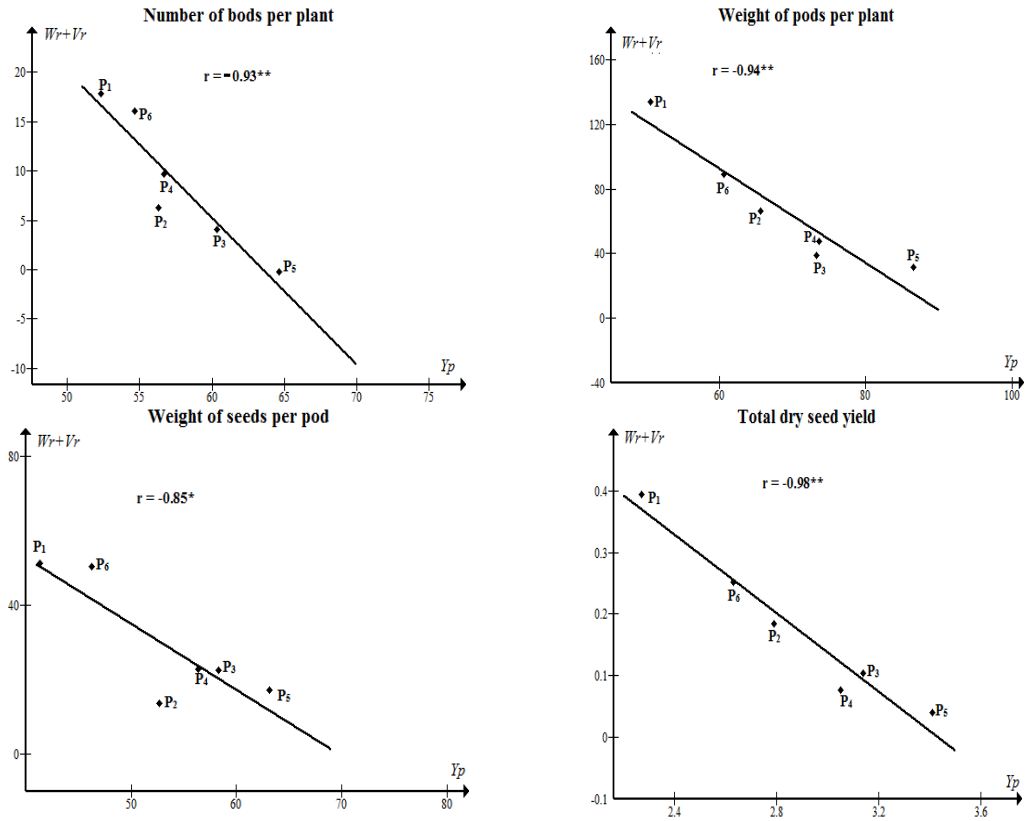

Fig. 6. Correlation between (Wr+ Vr) and the parental mean (Yp)

Correlation between phenotypic and genotypic diversity and SCA and heterosis effects

Correlations between genetic distance and SCA effects are presented in Table 11. Genetic distance based on ISSR marker was positively and/or negatively and significantly correlated with heterosis and SCA for all traits except (PL) and (100 SW) (with H M.P), WP, NS and WS (with H B.P) and NB, PD and NP (with SCA). Genetic distance based on SRAP marker was positively and/or negatively and significantly correlated with heterosis for all traits except NP, WP, NS and TS (with H M.P), TF, PD, NP and NS (with H B.P), while positively and significantly correlated was observed between genetic distance and SCA for day to TF, NB, PD and 100 SW.

Table 11. Correlation coefficients between genetic (GD) and phenotypic distances (PD) of parents and specific combining ability and heterosis effects.

	Penotypic and Genotypic distance	TF	NB	PL (cm)	PD (mm)	NP	WP	NS	WS	100 SW (g)	TS (Ton/H.)
H M.P.	ISSR	-0.517**	-0.225*	-0.164	-0.203*	0.475**	0.559**	0.224*	0.301**	-0.139	0.346**
	SRAP	-0.212*	0.326**	-0.411**	0.329**	0.196	0.125	-0.051	0.272*	0.036	0.111
	ISSR+SRAP	-0.437**	0.078	-0.350**	0.096	0.400**	0.405**	0.087	0.351**	-0.061	0.279*
	Phenotypic	-0.361**	-0.197	-0.129	-0.427**	0.436**	0.616**	0.438**	0.550**	-0.166	0.680**
H B.P	ISSR	-0.528**	-0.289*	-0.295*	-0.335**	0.369**	0.108	0.179	-0.045	-0.353*	-0.057
	SRAP	0.060	0.399**	-0.363**	0.081	0.074	-0.315**	-0.146	-0.344**	-0.205*	-0.475**
	ISSR+SRAP	-0.266*	0.092	-0.397**	-0.142	0.254*	-0.154	0.024	-0.258*	-0.342*	-0.350**
	Phenotypic	-0.422**	-0.149	-0.130	-0.605**	0.080	-0.077	0.361**	-0.164	-0.435**	-0.016
SCA	ISSR	0.372**	-0.080	0.319**	0.173	0.136	0.208*	0.327**	0.285*	0.247*	0.355**
	SRAP	0.295*	0.238*	-0.015	0.396**	0.015	-0.063	0.100	-0.022	0.294*	-0.190
	ISSR+SRAP	0.405**	0.103	0.173	0.349**	0.104	0.093	0.266*	0.162	0.337**	0.097
	Phenotypic	0.317**	0.097	-0.058	0.510**	0.459**	0.470**	0.063	0.553**	0.403**	0.353**

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

Genetic distance based on combined molecular marker systems was positively and/or negatively and significantly correlated with heterosis (H M.P and H B.P) for most agro-morphological traits, while SCA effect was positively and significantly correlated with genetic distance for TF, PD, NS and 100 SW. Phenotypic distance was positively and/or negatively and significantly correlated with heterosis (H M.P) for all agro-morphological traits except, NB, PL and 100 SW, while phenotypic distance was positively and/or negatively and significantly correlated with heterosis (H B.P) for TF, PD, NS and 100 SW. Phenotypic distance was positively and significantly correlated with SCA for all agro-morphological traits except NB, PL and NS.

In previous studies, Zhao *et al.* (2009), Krystkowiak *et al.* (2009), and Zhang *et al.* (2010) and Rajendrakumar *et al.* (2015) observed that genetic distances based on ISSR and RAPD markers were high and positively correlated with heterosis effects. Zhang *et al.* (1995) reported that the GD was more sufficient for heterosis prediction when the diversity among genotypes was high associated with hybrids performance.

CONCLUSION

In Conclusion, phenotypic and ISSR and SRAP markers were used to generate pre-breeding data that can be applied to choice of appropriate parents to introduce more genetic diversity into cowpea breeding programs and to help breeders using appropriate selection of cross combinations among large groups of parental genotypes. The molecular markers data generated in the study could also be used for variety description in the future. This study demonstrates that the ISSR and SRAP marker systems are powerful and easy methods for fingerprinting and distinguishing cowpea genotypes. Mating designs used in this study were suitable for studying genetic parameters in cowpea. The high values of broad-sense and narrow-sense heritability indicate a good genetic variability for effective selection. The yield component traits such as; WP, 100 SW and NS could be considered in breeding for improving grain yield, as they contribute significantly to its improvement. These results suggest that P_5can be used as a potential parent in hybridization programs to release new varieties of cowpea.

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العلاقة بين أداء الهجن والبعد الوراثي بواسطة الواسمات المورفولوجية والجزيئية في اللوبيا

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تم تقييم التنوع الوراثي والعلاقات بين ستة تراكيب وراثية من اللوبيا باستخدام عشرة صفات مورفولوجية ونظامين من الواسمات الجزيئية هما الـ ISSR والـ SRAP. كان البعد المورفولوجي بين جميع الطرز الوراثية عالي نسبيا. الواسم الجزيئي الـ ISSR كان أكثر فاعلية من الواسم الجزيئي الـ SRAP فيما يتعلق بتعدد الأشكال، ومتوسط عدد الحزم متعددة الأشكال وكذلك المقاييس الوراثية المختلفة للواسمات الجزيئية الـ (RP)، (MI)، (PIC). كلا الواسمين أمكنهما إكثار حزم وراثية مميزة للتراكيب الوراثية المختلفة من اللوبيا مما يظهر قدرة هذين الواسمين على تمييز التراكيب الوراثية الأكثر تنوعا. تراوح التشابه الوراثي بين التراكيب الوراثية من 0.744 بين الأب (P1) والأب (P4) إلى 0.868 بين الأب (P2) والأب (P3). كما أظهرت النتائج وجود ارتباط معنوي موجب بين الواسم الجزيئي الـ ISSR والواسم الجزيئي الـ SRAP وكذلك وجود ارتباط معنوي موجب بين كل من الواسمات الجزيئية والواسمات المورفولوجية. واعتمادا على البعد المورفولوجي والوراثي تم إجراء تهجين نصف دائري بين ستة آباء من اللوبيا لتحديد القدرة علي الإئتلاف وتحديد الهجن المتميزة لعشرة صفات تشتمل علي المحصول ومكوناتة. أظهر تحليل التباين أن كل الصفات المدروسة تقع تحت التحكم الجيني المضيف وغير المضيف كما وجد أن قيم المكافئ الوراثي بالمعني الضيق كانت أعلي من 60% في مدة الإزهار وعدد ووزن القرون للنبات ومحصول البذور الجافة مما يعني كفاءة عملية الإنتخاب في هذه الصفات وقد انطبق نموذج إضافي-سيادي للفعل الجيني في كل الصفات التالية مدة الإزهار وعدد الأفرع للنبات ووزن البذور ومحصول البذور الجافة بينما وجد تفاعل جيني في كل من طول وسمك القرن وعدد البذور بالقرن. أعطي الأب P_5 أعلي قيمة موجبة ومعنوية للقدرة العامة علي الائتلاف في عدد وزن القرون ووزن البذور للقرن ومحصول البذور الجافة بينما امتلك الأب P_1 أقل قيم سالبة ومعنوية للقدرة العامة الإئتلاف لعدد ووزن القرون للنبات ووزن البذور للقرن ومحصول البذور الجافة. وجد ارتباط عالي ومعنوي جدا بين محصول البذور الجافة وكل من عدد القرون في النبات (0.87) ووزن القرون للنبات (0.95) ووزن الحبوب للنبات (0.95). كان تصميم التزاوج المستخدم في هذه الدراسة فعالاً ومناسباً في دراسة وتقدير المكونات الوراثية المختلفة للصفات المدروسة كما أن القيم العالية للمكافئ الوراثي بالمعني الضيق مؤشر لوجود اختلافات وراثية عالية بين التراكيب الوراثية كما أنها تزيد من فاعلية الإنتخاب. كما تم تقدير العلاقة بين البعد المورفولوجي والوراثي وكذلك قوة الهجين والقدرة الخاصة للإئتلاف وقد أشارت النتائج إلى وجود ارتباطات معنوية موجبة و/أو سالبة بين البعد المورفولوجي والوراثي وكذلك قوة الهجين والقدرة الخاصة للإئتلاف لبعض الصفات وغير معنوية لصفات أخرى. وأشارت النتائج إلى أهمية معرفة العلاقة بين البعد المورفولوجي والوراثي وكذلك قوة الهجين والقدرة الخاصة للإئتلاف بين الآباء لإمكانية استخدامها للتنبؤ بأداء الهجن.