Correlation, Path Analysis and RAPD Markers in Sorghum (*Sorghum bicolor* L. Moench) Genotypes

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Abstract:

Genetic diversity is one of the key factors for the improvement of many crop plants including sorghum. Fifteen sorghum genotypes were planted in 2012 and 2013 seasons to compare among them for agronomic traits and molecular level. The combined analysis for agronomic traits and yield components showed significant differences among genotypes for all studied traits. The highest mean values of 1000-kernel weight (36.08g) and number of seeds/panicle traits (1315.9) were obtained from Giza-15 genotype. The lowest mean values of 1000-kernel weight (17.07g) and number of seeds/panicle traits (646.9) were obtained from local-162 and El-Kharga genotypes, respectively. Values of correlation analysis indicated that 1000-kernel weight was positive and highly significant correlation with grain weight (0.749). The path analysis showed that 1000-kernel weight had high and positive direct effect on grain weight (0.7102), also number of seeds/panicle had positive direct effect on grain weight (0.1443) but it had negative direct effect through plant height (-0.1876). Genetic diversity of sorghum genotypes detected using of Random Amplified Polymorphism DNA (RAPD) markers. 76 DNA bands were obtained from 12 primers which could detected a percentage of polymorphism ranged from 40 to 100% with an average of 73.36%. The average of polymorphic bands was 4.67 per primer. The dendrogram based on RAPD marker gave three main groups; the first group contains three genotypes, but the second group sub-divided into two sub-clusters, which contain three genotypes each. The third group contains six genotypes. The similarity percent based on agronomical traits was not significantly correlated (r = 0.07961) with the genetic distance based on RAPD markers.

Keywords: correlation; sorghum genotypes; path analysis; RAPD markers; variance analysis.

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Introduction:

Sorghum (*Sorghum bicolor* L. Moench) is fifth in worldwide economic importance among the cereal crops. It is an important food, feed, forage and provides raw material for producing of starch, fiber, dextrose syrup, biofuel and other products. The sorghum is a staple food crop of millions of the poor in semi-arid tropics of Africa and Asia (Zidenga 2004). In Egypt it is fourth most important cereal after wheat, rice and maize. Many scientists have been mostly worked to assess patterns of sorghum genetic variation based on morphological characters (Appa-Rao *et al.* 1996 and Djè *et al.* 1998) or pedigree (Jordan *et al.* 1998). However, morphological variation does not reliably reflect the real genetic variation because of genotype environment interactions and the largely unknown genetic control of poly-genetically inherited morphological and agronomical traits (Smith and Smith, 1992).

Molecular markers successfully developed during the last decades have largely overcome the problems that are associated with phenotype-based markers. One of such techniques is the use of RAPD (Williams *et al.* 1990). The advantages of RAPD is its simplicity, rapidity, requirement for only a small quantity of DNA, and the ability to generate numerous polymorphisms (Cheng *et al.* 1997) with good coverage of the entire genome (Melchinger,1993). The information obtained through germplasm characterization using RAPD is extensively used for the identification of germplasm, screening of duplicates, assessing genetic diversity and monitoring the genetic stability of conserved germplasm.

RAPD markers have been used in important crops as Barley (Hoffman *et al.* 2003), Cotton (Dongre and Parkhi, 2005), Sorghum (Jeya *et al.* 2006), Faba bean (Tanttawi *et al.* 2007), Cowpea (Abdelsabour *et al.* 2010) and wheat (khaled *et al.* 2013). Ayana *et al.* (2000) assessed the extent of genetic variation among 80 sorghum accessions from Ethopia and Eritrea using 20 RAPD primers and found limited variation among the accessions.

Yield is the final performance of any crop and conditioned by a complicated genetic system. Yield potential accompanied with desirable combination of traits has always been the major objective of sorghum breeding program. Correlation measure the level of dependence on traits and out of numerous correlation coefficients, it is often difficult to determine the actual mutual effects among traits. The estimates of correlation alone may be often misleading due to mutual cancellation of component traits. So, it becomes necessary to study path coefficient analysis, which takes in to account the casual relationship in addition to degree of relationship. The path coefficient analysis initially suggested by Wright (1960) and described by Dewey and Lu (1959) allows partitioning of correlation coefficient into direct and indirect contributions (effects) of various traits towards dependent variable and thus helps in assessing the cause-effect relationship as well as effective selection. Ikanovic *et al.* (2011) concluded that even if correlation values are similar for certain pairs of traits, direct effects for some of them and especially indirect effects via other traits can differ for some traits. Mostafa *et al.* (1992) reported that there was no significant relationship between days to 50% flowering and grain weight

while plant height was significantly positively correlated with yielded and 1000-kernel weight. Mahajan *et al.* (2011), Wankhede *et al.* (1985), Mallinath *et al.* (2004) and Ambekar *et al.* (2000) stated that panicle length, panicle width, plant height and grain weight / panicle had showed positive significant association at both levels with all characters except days to 50% flowering.

Understanding genotypes diversity is of interest in the study of evolutionary forces under domestication, and has applications in the design of programs for the conservation, management and use in breeding programs of genetic resources. Therefore, the aims of this present study were to 1) determine the traits having greater interrelationship with grain weight utilized the correlation and path analysis, 2) determine the pattern of variations among 15 Sorghum genotypes from different agro-ecological regions in Egypt using RAPD markers, and agronomical characterization and 3) determine the degree of genetic relationships among these accessions.

Materials and Methods:

Field experiments:

This experiment was conducted at Arab El-Awamer Research Station, Assiut, Egypt during two successive seasons, 2012 and 2013 seasons to study the correlation and genetic diversity in 15 sorghum genotypes. The genotypes were grown in a randomized complete block design (RCBD) with three replications under stressed soil and irrigation by spray. Each genotype was planted in one row plot, 4 meter long, and 0.6 m wide and hill to hill distance of 0.20 m apart with two plants / hill after thinning. All other cultural practices were carried out as recommended for sorghum production in both seasons. The studied traits were: plant height (cm), days to 50% flowering, panicle length (cm), panicle width (cm), 1000-kernel weight (g), number of seeds/panicle and grain weight (g).

Statistical Analysis:

Data for all traits were subjects to analysis of variance according to Steel and Torrie (1980) to evaluate the significant differences among the genotypes. Estimation of variation components and phenotypic correlations were calculated as suggested by Burton (1952), Wright (1960) and Narasimharao and Rachie (1964). The correlation coefficient was partitioned into direct and indirect causes according to Dewey and Lu (1959) and Turner and Stevens (1959). Test of significance was carried out with (n-2) degree of freedom for phenotypic correlation by referring to table given by Snedecor and Cochran (1989).

DNA extraction and PCR procedures:

Fresh young leaves were harvested and immediately ground in extraction buffer using cetyltrimethylammonium bromide (CTAB) protocol as described by Poresbski *et al.* (1997). A total of thirty varied 10-mer random primers (Metabion International AG, Germany) were scanned across the fifteen genotypes. Amplification was carried out in a DNA Thermal Cycler (Primus 25, Germany) according to the methods described by Williams *et al.* (1990). Genomic DNA was diluted 10-fold in water prior to cycles of PCR amplification with Go Taq® Green Master Mix (Promega, Madison, USA). PCR amplification was programmed for conditions with preliminary initial denaturation cycle at 95°C for five minutes. The following 35 cycles

were composed of: denaturation step at 95°C for 1 min, annealing step for 1 min at 38°C and elongation step at 72°C for 1 min 30 s. The amplified fragments were visualized and photographed using UVP Bio Doc-It imaging system (USA).

RAPD analysis:

The DNA banding patterns generated from RAPD analysis were analyzed by a computer program, Gene Profiler (version 4.03). Microsoft excel file was prepared for scoring the data as '1' for matched and '0' for the unmatched of DNA band of every genotype. In order to detect patterns of genetic relationship among sorghum genotypes based on RAPD analysis and means of all studied traits, the similarities were computed based on percent of similarity method by UPGMA (Unweighted Pair Group Method with Arithmetic Average) method using MVSP (version 3.1) program. The average of similarity matrix was used to generate a tree for cluster analysis. A cophenetic matrix was derived from each matrix to test goodness of fit of the clusters by comparing the two matrices using the Mantel test (Mantel 1967). Finally, the correlation between each distance pair using computer program NTSYS-pc version 2.2 was calculated (Rolhf 2000).

Results and Discussion:

The analysis of variance for yield and its attributes traits (Table 1) revealed that the differences among genotypes were highly significant ($p \leq 0.01$) for all the studied traits. The data regarding means of grain weight and other characters of genotypes over two years are represented in Table (2) that focused the significant ($p \leq 00.05$) variation among sorghum genotypes in all studied traits. The highest range of individual trait was registered with regard to plant height (108 - 261.8 cm), number of days to 50% flowering (70.17 - 97 day), panicle length (14.17 - 21.12 cm), panicle width (6.65 - 9.41 cm), 1000-kernel weight (17.17 - 36.08 gm), number of seeds/panicle (646.9 - 1315.9 seed) and grain weight / plant from (17.07 - 37.25 g). These variations among genotypes in all studied traits may be due to the genetic behavior combination with environmental factors, which were suitable for one genotype more than other. These finding are in agreement with these obtained by House (1985) and Mahdy *et al.* (2011). Furthermore, data in table 1 showed highly interaction between years and genotypes in studied traits expect number of seeds/panicle.

Table 1: Mean squares for combined analysis of variance for all studied traits.

S.O.V.	d.f	Plant height (cm)	Days to 50% flowering	Panicle length	Panicle width	1000-kernel weight	No. of seeds/ Panicle	Grain weight
Year	1	13.46	711.2**	4.534	1.792**	65.03*	46564.2**	75.44
Error (a)	4	53.20	7.911	7.602	0.059	5.093	1911.5	10.50
Genotypes	14	16931.8**	404.3**	26.96**	6.202**	154.7**	234239.8**	257.14**
Year x genotypes	14	516.53**	100.28**	6.424**	1.113**	3.629**	6351.3	15.233**
Error (b)	56	48.71	4.268	0.984	0.123	1.430	5951.3	3.793

*, ** significant at 5% and 1% level of probabilities, respectively.

Phenotypic correlation are presented in Table 3 showed significant ($p \leq 0.05$) and positive association of panicle width with plant height (0.563), whereas it is negative and non-significant association with days to 50% flowering (-0.385). The correlation of kernel weight trait is positive and highly significant ($p \leq 0.01$) with grain weight (0.749), but it is negative and non-significant with plant height (-0.067).

Table 2: The mean performances of the 15 sorghum genotypes for yield and its components over two years.

Genotypes	Plant height (cm)	Days to 50% flowering	Panicle length	Panicle width	1000-kernel weight (g)	No. of seeds/ Panicle	Grain weight (g)
Giza-54	208.4	73.17	15.22	9.417	29.85	957.4	25.90
Giza-114	258.8	81.17	18.55	8.050	28.28	743.5	22.98
10-1285	196.3	73.17	15.60	9.350	30.52	1274.9	35.83
Giza-113	261.8	80.50	16.27	8.200	31.12	994.9	27.37
Giza-15	259.0	78.00	20.32	9.233	36.08	1315.9	37.25
Sel.1007	108.3	97.00	17.58	6.650	27.92	794.0	32.72
CS-3541	192.7	74.00	17.95	6.933	32.15	850.5	33.30
Dorado	109.4	90.33	20.02	7.000	29.58	1029.3	36.42
El-Kharga	191.0	70.67	14.17	8.983	33.18	646.9	28.97
El-Fayom-1	193.5	79.00	15.98	7.633	30.37	1000.1	22.52
El-Fayom-2	213.9	93.17	19.57	9.283	32.70	780.0	33.22
Local-162	113.3	77.67	21.12	7.750	18.52	1169.4	17.07
Local-119	230.3	72.83	15.72	7.383	17.77	736.0	17.95
Line-c	252.8	70.17	18.95	9.400	24.18	878.5	26.05
Paris-1	220.9	81.33	16.50	9.117	28.73	968.0	33.20
L.S.D 0.05	8.30	2.45	1.17	0.415	1.42	91.30	2.31

Table 3: Phenotypic correlations for yield and yield components in 15 sorghum genotypes.

Traits	Plant height	Days to 50% flowering	Panicle length	Panicle width	1000-kernel weight	No. of seeds/ Panicle
Plant height						
Days to 50% flowering	-0.447					
Panicle length	-0.218	0.400				
Panicle width	0.563*	-0.385	-0.161			
1000-kernel weight	0.225	0.166	-0.121	0.303		
No. of seeds/ Panicle	-0.067	-0.098	0.326	0.225	0.130	
Grain weight	-0.067	0.354	0.108	0.179	0.749**	0.272

*, ** significant at 5% and 1% level of probabilities, respectively.

The path analysis (Table 4) showed that1000-kernel weight trait had high positive direct effect on grain weight (0.7102). The panicle length trait had low but positive direct effect on grain weight. Its positive indirect effect was through panicle length (0.0409), days to 50%

flowering (0.0770) and number of seeds/panicle (0.0470), whereas its indirect effect was negative through panicle width (-0.0192) and 1000-kernel weight (-0.0856). Its positive indirect effects were through days to 50% flowering (0.0320), panicle width (0.0361) and number of seeds/panicle (0.0187) traits, whereas its indirect effects were negative through plant height (-0.0421) and panicle length (-0.0058) traits. Similar results were obtained by Mahajan *et al.*, (2011) and Aml *et al.* (2012), they found that panicle length and number of grains /panicle has positive direct effect on grain weight/ panicle. Singh and Baghel (1977), El-Menshawi, (2006) and Aml *et al.* (2012) found that both number of grains per panicle and 1000-kernel weight were major components of grain weight and also has positive direct effects on grain weight.

Table 4: Direct (diagonal) and indirect effect of different traits on grain weight.

Traits	Plant height	Days to 50% flowering	Panicle length	Panicle width	1000-kernel weight	No. of seeds/ Panicle
Plant height	-0.1876	-0.0861	-0.0104	0.0670	0.1595	-0.0097
Days to 50% flowering	0.0839	0.1927	0.0191	-0.0458	0.1179	-0.0141
Panicle length	0.0409	0.0770	0.0478	-0.0192	-0.0856	0.0470
Panicle width	-0.1056	-0.0742	-0.0077	0.1189	0.2155	0.0324
1000-kernel weight	-0.0421	0.0320	-0.0058	0.0361	0.7102	0.0187
No. of seeds/ Panicle	0.0126	-0.0189	0.0156	0.0267	0.0921	0.1443

Level of polymorphism:

Fifteen sorghum genotypes in this study were differentiated using 26 RAPD primers, out of them, 12 primers were generated different degrees of genetic polymorphism (Table 5, Figure 1). A band was considered as polymorphic if the band differentiates at least any 2 of the 15 genotypes. Zhan *et al.* (2012) showed that 22 out of 100 primers were shown to have distinct amplification bands with polymorphisms. In this study, the number of amplification products per primer varied from 4 to 12, with a mean of 4.67 per primer. Zhan *et al.* (2012) obtained 3.82 an average number of polymorphic bands per primer. These primers were produced fragments varying from 97 to 1228 bp in size (Table 5). The 12 primers generated a total of 76 RAPD bands across the 15 genotypes, of these bands, only 56 (73%) were polymorphic. This level of variation is much higher than 55%, 52% and 58.33 % that observed in Sorghum genotypes by Tao *et al.* (1993); Nkongolo and Nsapato (2003) and Zhan *et al.*, (2012), respectively. Contrarily, the level of polymorphism is smaller than 85% which observed between 33 sorghum genotypes by Medraoui *et al.* (2007). Generally, in this study RAPD markers were more polymorphic than agronomical characterization, but we see that the RAPD markers combined with agronomical characterization provided the most powerful assay for discriminating genetic diversity among sorghum accessions.

Table 5: Primers used in RAPD analysis, total number of fragments detected by each primer and polymorphism among 15 sorghum genotypes.

Primer Name	Primer Sequence (5'---------3')	Amplified bands		Polymorphic bands (%)	Fragments size base pair (bp)	
		Fragments number	Polymorphic bands		Larger	Smaller
OPC-05	CACACTCCAG	8	7	87.50	380	160
OPG-09	CTGACGTCAC	6	5	83.33	392	180
OPAD-06	AAGTGCACGG	4	3	75.00	390	170
OPA-13	CAGCACCCAC	4	3	75.00	160	500
OPH-01	GGTCGGAGAA	4	4	100.00	350	250
OPAM-01	TCACGTACGG	4	2	50.00	500	340
OPA-17	GACCGCTTGT	12	9	75.00	1150	97
OPF-20	AACGGTGACC	4	3	75.00	360	240
OPW-13	GTTGTTTGCC	5	2	40.00	330	190
OPP-05	CCCCGGTAAC	11	6	54.55	1088	230
OPAT-08	TCCTCGTGGG	4	3	75.00	555	245
OPAR-05	CATACCTGCC	10	9	90.00	1228	160
Mean		6.33	4.67	73.36%		

Similarity percents analysis:

The genetic similarity percents among the 15 sorghum genotypes were calculated according to the analytical results of electrophoretic band patterns (Table 6) and means of all studied characters (Table 7), and were used UPGMA for cluster analysis. The 15 sorghum genotypes showed large differences in genetic similarity percents based on RAPD markers, which ranged from 48.8 to 91.4%. Among these genotypes, Giza-54 and Giza-114 exhibited the highest similarity (91.4%), while CS-3541 and Giza-54 showed the lowest similarity (48.8%). On the other hand, the similarities based on the means of agronomic traits were less than the similarities which observed by RAPD markers method. These similarity percents were 72.3 to 98.5% between El-Kharga and Giza-15, and between Giza-54 and Paris-1, respectively. Based on some agronomical traits, Zhan *et al.*, (2012) obtained genetic similarity coefficients which ranged from 69.4% to 89.6% among 13 sweet sorghum varieties. These results indicated that the phenotypic characterization provide less resolving power than RAPD markers for characterize the diversity between the genotypes. Agrama and Tuinstra, (2003) showed that molecular assays were much more powerful at discriminating genetic diversity than estimates based on geographical and race classification, which revealed high levels of genetic similarity (0.951) among sorghum accessions.

Table 6: Similarity values percents obtained from 67 RAPD fragments for 15 sorghum genotypes.

Genotypes	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)
Giza-54(1)	100.0													
Giza-114(2)	91.4	100.0												
10-1285(3)	88.2	85.7	100.0											
Giza-113(4)	73.7	82.1	78.9	100.0										
Giza-15(5)	70.0	78.0	75.0	72.7	100.0									
Sel.1007(6)	61.5	70.0	71.8	79.1	80.0	100.0								
CS-3541(7)	48.8	57.1	58.5	62.2	68.1	69.6	100.0							
Dorado(8)	54.5	62.2	59.1	62.5	72.0	73.5	78.4	100.0						
El-Kharga(9)	48.9	56.5	53.3	57.1	62.7	64.0	76.9	83.6	100.0					
El-Fayom-1(10)	65.1	72.7	69.8	72.3	73.5	79.2	68.0	71.7	70.4	100.0				
El-Fayom-2(11)	66.7	65.2	66.7	69.4	66.7	72.0	61.5	65.5	64.3	85.2	100.0			
Local-162(12)	56.5	63.8	60.9	72.0	69.2	74.5	67.9	64.3	63.2	87.3	87.7	100.0		
Local-119(13)	68.2	66.7	72.7	62.5	72.0	69.4	62.7	66.7	65.5	83.0	87.3	85.7	100.0	
Line-c(14)	56.5	63.8	60.9	60.0	73.1	66.7	67.9	71.4	70.2	80.0	77.2	82.8	89.3	100.0
Paris-1(15)	50.0	57.1	54.2	61.5	74.1	64.2	61.8	65.5	64.4	77.2	74.6	83.3	82.8	86.7

Table 7: Similarity values percents obtained from agronomical characterization for 15 sorghum genotypes.

Genotypes	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)
Giza-54(1)	100.0													
Giza-114(2)	88.7	100.0												
10-1285(3)	88.5	77.8	100.0											
Giza-113(4)	96.2	89.7	88.1	100.0										
Giza-15(5)	85.8	79.4	96.4	89.1	100.0									
Sel.1007(6)	87.5	89.8	77.8	84.7	75.0	100.0								
CS-3541(7)	94.5	91.7	84.6	91.2	81.5	92.6	100.0							
Dorado(8)	92.2	81.4	87.9	92.3	85.1	89.6	88.7	100.0						
El-Kharga(9)	85.4	91.1	75.4	82.0	72.3	87.0	90.0	78.3	100.0					
El-Fayom-1(10)	97.4	86.9	90.0	97.1	86.8	86.7	93.3	94.6	83.9	100.0				
El-Fayom-2(11)	91.3	95.3	80.8	89.0	79.4	94.1	95.2	85.4	91.3	89.2	100.0			
Local-162(12)	87.6	77.1	92.5	87.6	89.5	82.9	83.4	93.1	73.5	90.1	79.3	100.0		
Local-119(13)	89.0	97.2	77.8	87.2	77.0	89.4	91.9	80.7	92.4	86.7	94.9	77.7	100.0	
Line-c(14)	94.8	93.4	83.7	94.5	84.3	88.6	95.6	87.2	86.3	92.2	92.8	83.1	92.1	100.0
Paris-1(15)	98.5	89.0	88.5	97.2	87.0	87.4	93.8	92.9	84.2	97.2	91.6	87.6	88.7	94.4

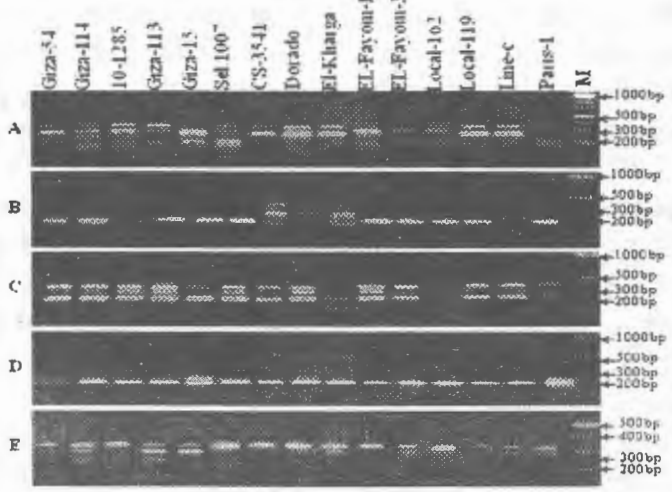

Figure 1: RAPD profiles obtained by RAPD primers A) OPC-05, B) OPG-09, C) OPAD-06, D) OPA-13 and E) OPH-01, M = 100 bp ladder.

Genetic relationship among genotypes:

Based on RAPD analysis, the dendrogram showed that the 15 sorghum genotypes separated into three distinct groups (Figure 2). The first group contains El-Kharga, Dorado and CS-3541 genotypes, but the second group sub-divided into two subclusters. The first sub cluster contains Paris-1, Line-c and Local-119 genotypes; the second sub-cluster contains Local-162 and El-Fayom-2 which clustered at 86.2 level of similarity percent with El-Fayom-1. Also, The third group sub-divided into 2 subgroups, whereas Sel.1007, Giza-15 formed the first sub-group, that clustered at 78.2 level of similarity percent with genotypes Giza-113, 10-1285, Giza-54 and Giza-114 which formed the second sub-group in dendrogram (Figure 2). Some consistency in classification was observed among clusters, whereas, the genotypes named Giza-15, Giza-54, Giza-113 and Giza-114, which originate from the same region in Egypt, were grouped together. Agrama and Tuinstra (2003) showed that sorghum genotypes SC35 and SC1158, which originate from the same region in Ethiopia, were grouped together.

Based on agronomical characterizations, the dendrogram showed that the 15 sorghum genotypes formed two big groups (Figure 3) that clustered at 84.4% level of similarity percent. Giza-54 and Paris-1 clustered at high level of similarity percent (98.5%).

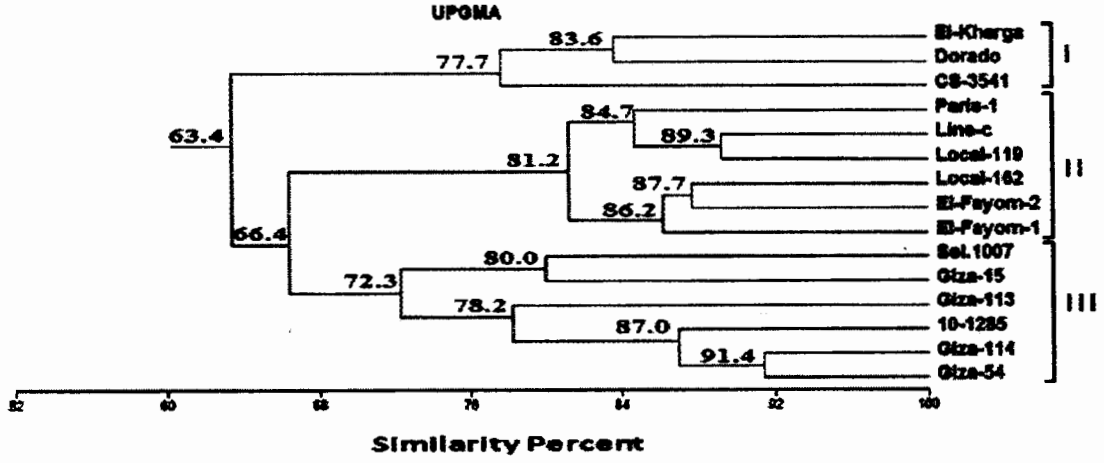

Figure 2: Dendrogram generated by UPGMA cluster analysis using similarities percents that obtained from 67 RAPD fragments.

Correlation between the two distance matrices generated by agronomical traits and RAPD marker was calculated (Figure 4), it is not significant (r = 0.07961, p = 0.7594), as shown in Figure 4. The observed relationships using molecular markers may provide information on the history and biology of cultivars but it does not necessarily reflect what may be observed with respect to agronomic traits (Metais *et al.* 2000). Genetic markers like RAPDs may accurately assay the degree of genetic change between two genomes, but they may not necessarily reflect the divergence in terms of changes in traits of agronomic importance.

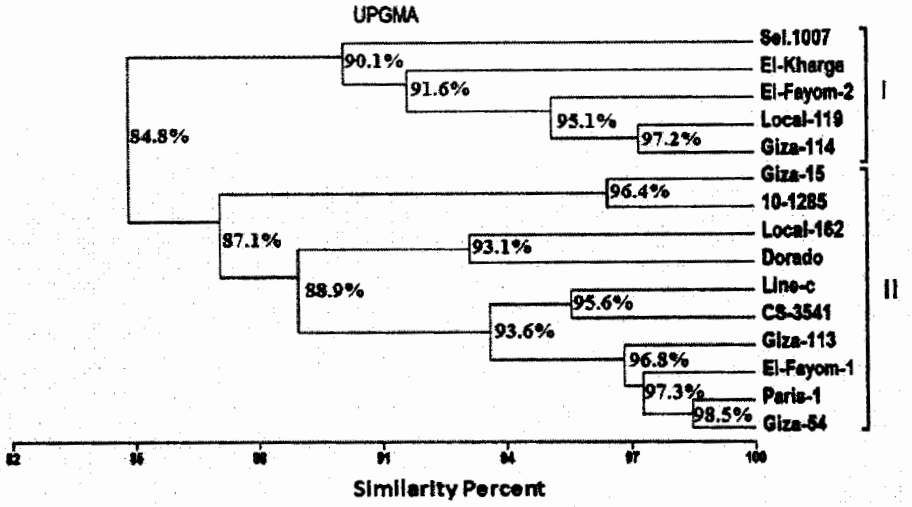

Figure 3: Dendrogram generated by UPGMA cluster analysis using similarities percents that obtained from all studied traits.

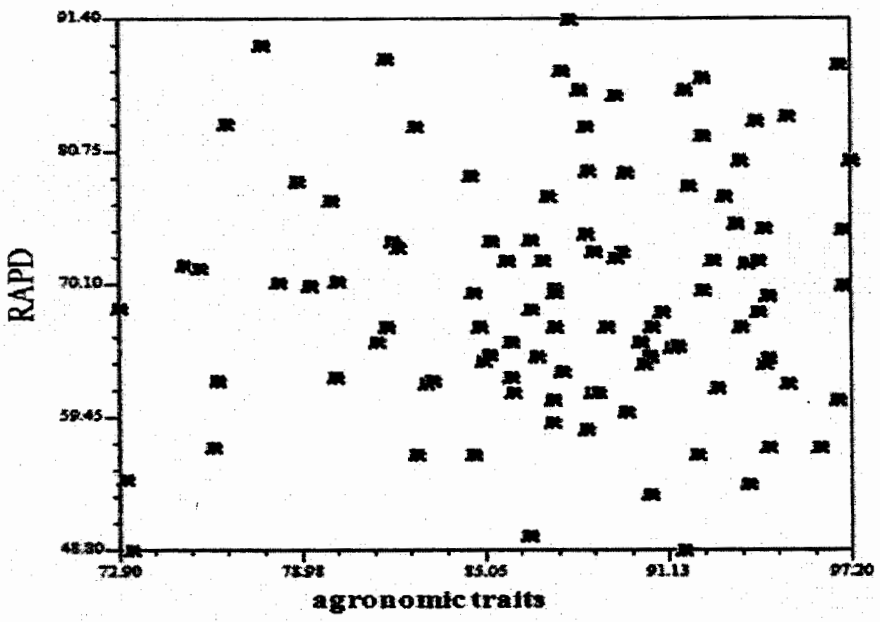

Figure 4: Correlation between similarities percents obtained from RAPD markers and agronomic traits for 15 sorghum genotypes.

Conclusion:

Our study showed the presence of broad genetic base of the investigated sorghum germplasm. The traits like number of seeds / panicle and 1000-kernel weight had greater importance. Hence, due consideration should be given to these characters, while planning a breeding strategy for increased grain yield/panicle. Finally, the agronomic traits and RAPDs markers are useful for classification of germplasm in sorghum, but a combination of different markers is preferred in studying genetic relationships among the lines of same species. It can be concluded that RAPD markers can be used for sorghum ge-

netic diversity studies and molecular characterization.

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الارتباط وتحليل معامل المرور والواسمات الجزيئيه العشوائيه لعدد من التركيب الوراثيه فى الذره الرفيعه

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الملخص:

التنوع الوراثى واحد من أهم العوامل الضروريه لتحسين العديد من المحاصيل و منها الذره الرفيعه. فى هذه الدراسه تم زراعة خمسة عشرة طراز وراثى من الذره الرفيعه فى المواسم ٢٠١٢ و٢٠١٣ للمقارنه بينها فى الصفات المحصوليه والاختلافات الجزيئيه. لقد أظهر التحليل المشترك لصفات المحصول ومكوناته وجود إختلافات معنويه بين هذه التراكيب الوراثيه وأظهرت النتائج أن الصنف جيزه-١٥ كان الأعلى بالنسبه لصفتى وزن الالف حبه (٣٦,٠٨ جرام) وعدد الحبوب فى الكوز (١٣١٥,٩). كما أتضح أنه يوجد إرتباط موجب عالى المعنويه (٠,٧٤٩) بين صفتى وزن الالف حبه و محصول الحبوب. بينما اقل قيم (g١٧,٠٧) و(٦٤٦,٩) لصفتى وزن الحبوب وعدد الحبوب فى الكوز خاصه بالصنفين محلى ١٦٥ والخارجه على التوالى. كما أوضحت النتائج المتحصل عليها بدراسة معامل المرور لمكونات المحصول أن وزن الألف حبة لها تأثير عالى موجب ومباشر على صفة المحصول (٠,٧١٠٢) وأن عدد الحبوب بالكوز لها تأثير موجب ومباشر على صفة المحصول (٠,١٤٤٣) بينما هذا التأثير كان سلبى بالنسبة لطول النبات (-٠,١٨٧٦). من ناحيه أخرى تم تقييم التنوع الوراثى فى هذه التراكيب الوراثيه بإستخدام الواسمات الجزيئيه العشوائيه. حيث، تم الحصول على ٧٦ حزمه بإستخدام ١٢ بادئ عشوائى بنسبة تعدد اشكال من ٤٠ الى ١٠٠ % بمتوسط مقداره ٧٣,٣٦%. كما أظهر تحليل الشجره الوراثيه فى تجربة البادئات العشوائيه ان الخمسة عشر تركيب وراثى تشكل ثلاثة مجاميع رئيسيه. المجموعه الأولى تحتوى على ثلاثة تراكيب وراثيه و المجموعه الثانيه انقسمت إلى تحت مجموعتين حيث تحتوى كل واحده على ثلاثة تراكيب وراثيه، بينما المجموعه الثالثه تحتوى على ٦ تراكيب وراثيه. فى هذه الدراسه اتضح أن نسبة التشابه بناءا على الصفات المحصوليه اظهرت ارتباط غير معنوى مع تحليل الواسمات الجزيئيه العشوائيه.