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GENETIC VARIABILITY, CORRELATION COEFFICIENT AND CLUSTER ANALYSIS OF SOME QUANTITATIVE TRAITS IN SOME EXOTICS AND NEW EGYPTIAN SORGHUM GENOTYPES UNDER VARYING LOCATIONS

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ABSTRACT

Twenty grain sorghum genotypes of different geographic origin were evaluated in three locations (Shandaweel Agricultural Research Station, Sohag governorate; El-Kharga Agricultural Research Station, New valley governorate and Abo-Sombel Agricultural Research Station, Toshqi) in the summer season 2019 for assessment of the variability among the genotypes, correlation coefficient and drawing the phylogenetic tree using cluster analysis. The results indicated highly significant differences among the genotypes, environments and their interaction for all traits under investigation, suggesting that these genotypes were highly variable for almost all traits, therefore, would respond to selection. The Egyptian genotype (Dorado x LC) gave the best performance for most of studied traits under each environment and their combined data. This genotype could be released as a new Egyptian grain sorghum variety after testing in a large scale. The individual and the combined analyses indicated that most genotypes had higher genotypic and phenotypic variance components than the environmental variance, which an indicative that the environment had less effect on the expression of the studied traits; for that is these genotypes may be exploited in breeding programs. The traits which showed high genetic advance as a percentage of mean (Δg %) were plant height, panicle length, panicle width, 1000- grain weight and grain yield/plant. Moderate GCV% and PCV% were also observed for all studied traits except days to 50% flowering and number of green leaves, revealing that the genotypes have a broad base genetic background as well as good potential that will respond positively to selection. The correlation between grain yield/plant and the other studied traits was negative and highly significant for days to 50% flowering and positive and highly significant with the rest of studied traits, which mean that any improving in these traits will directly give improvement in grain yield. The lowest similarity (87.00%) was observed between genotype 5 (ICSR 89016) and genotype 15 (Dorado x LC) which are located in different groups and was located in highly diverged clusters, Therefore these genotypes were found to be a good parents for a hybridization or heterosis breading programs.

Key words: ***Sorghum bicolor (L.) Moench, Genetic parameters, Correlation and Cluster analysis.***

INTRODUCTION

Sorghum is widely grown throughout the world for food, feed and fodder. It is the fifth major cereal crop of world following wheat, rice, maize and barley in terms of production and utilization. In Egypt, grain sorghum is the fourth cereal crop ranking after wheat, maize and rice. In 2017 the cultivated area was about 147,970 hectares produced about 727660 tons of grains (FAO 2019). The success of any crop improvement program not only dependent on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress

that can be achieved through selection (Wankhede *et al* 1985). Genetic variability for agronomic characters is a key component of breeding program for broadening the gene pool of crops (Wright 1968). Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character (Narasimharao and Reche 1964). The most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (House 1985). Characters with high heritability can easily be fixed with simple selection resulting in quick progress. However, it has been accentuated that heritability alone has no practical importance without genetic advance (Mallinath *et al* 2004). Genetic advance shows the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. Therefore, availability of good knowledge of these genetic parameters existing in different yield contributing characters and the relative proportion of this genetic information in various quantitative traits are a pre-requisite for effective crop improvement.

The morphological data utilizes the computation of standard distances (*i.e.* Percent Similarity) and clustering strategies such as UPGMA (Cluster analysis by the un-weighted paired group method of arithmetic means) or neighbor joining were applied (Li and Quiros 2001). This enables genotypes to be clustered into groups that are as homogenous as possible. Phenotypic and genotypic diversity are important in genetic conservation, evaluation and utilization of genetic resources (Li *et al* 2014 and Madhusudhana *et al* 2016).

In that respect the objectives of this study were to estimate the genetic variability, the phenotypic correlation between studied traits and draw the phylogenetic grouping tree using the cluster analysis and identify the superior genotypes for grain yield.

MATERIALS AND METHODS

Twenty grain sorghum genotypes of different geographic origin were evaluated at three environments (Shandaweel Agricultural Research Station, Sohag governorate; El- Kharga Agricultural Research Station, New valley governorate and Abo-Sombel Agricultural Research Station, Toshqi) in the summer season 2019 (Table 1).

Table 1. Origin and some agronomic traits of sorghum genotypes used in this study.

No.	Genotype	Pedigree	Origin	days to 50 % flowering (days)	plant height (cm)
1	G1	ICSR-89037	India	68	144
2	G2	ICSR-89039	India	71	126
3	G3	ICSR-89028	India	73	163
4	G4	ICSR-21	India	72	141
5	G5	ICSR-89016	India	72	129
6	G6	ICSR-89025	India	71	158
7	G7	ICSR-9010	India	64	131
8	G8	ICSR-9012	India	73	149
9	G9	ICSR- 93001	India	72	169
10	G10	ICSR- 92003	India	73	174
11	G11	ICSR-93002	India	68	176
12	G12	ICSR-93004	India	63	174
13	G13	Dorado × G-113	Egypt	67	161
14	G14	Dorado × R-273	Egypt	74	151
15	G15	Dorado × L.C	Egypt	66	168
16	G16	Dorado × ICSV-112	Egypt	71	159
17	G17	NM-36565 × ICSR-92003	Egypt	72	167
18	G18	MR-812 × Zenzepar-R	Egypt	70	163
19	G19	NEB-93002 × ICSR-92003	Egypt	62	153
20	G20	Dorado	India	67	147

These genotypes involved 13 varieties introduced from ICRISAT Center (India), and 7 promising new Egyptian verities obtained from long-

term selection program by National Sorghum Research Programme at Shandaweel Agric.Res. Station, Sohag, Egypt. In each environment, the genotypes were laid out in a randomized complete blocks design with three replications. Plot size was four rows (4 meters long and 60 cm apart). Sowing was done in hills spaced 20 cm and 2 plants/hill were left after three weeks from sowing date. The other cultural practices were according to the recommendations for growing grain sorghum.

The collected data included: days to 50% flowering, plant height (cm), number of green leaves/plant, panicle length (cm), panicle width (cm), 1000-grain weight (g) and grain yield/plant (g). To estimate the extent or magnitude of variation and heritability among these genotypes, the data obtained was subjected to analysis of variance for each environment based on plot means followed by a combined analysis of the data across three environments after homogeneity of variance was detected; these were done according methods described by Senedecor and Cochran (2014). The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and Vane (1953). Genetic advance (Δg) and its percentage of the mean ($\Delta g\%$) assuming selection of superior 5% of the genotypes were estimated in accordance with the methods illustrated by Johnson *et al* (1955). Phenotypic correlation among studied traits were estimated according to Steel *et al* (1997) and the genetic similarities (Percent Similarity) among the tested genotypes were computed based on phenotypic data and UPGMA-dendrogram was performed according to Jaccard's coefficient (Jaccard 1908) using the computational package MVSP version 3.1.

RESULTS AND DISCUSSION

The individual and the combined analyses of variance for seven traits (Tables 2 and 3), indicated highly significant ($P \leq 0.01$) differences among the genotypes for all traits under investigation, indicating the existence of genotypic differences among the genotypes. Also, highly significant ($P \leq 0.01$) differences were found among the three locations for all studied traits, which indicate that the conditions in the three locations were not similar in their climatic and soil conditions.

Table 2. Analysis of variance for seven traits at three environments.

Mean squarres								
SOV	df	Days to 50% flowering (days)	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	No. of green leaves/plant	1000-grain weight (g)	Grain yield/plant (g)
Sohag								
Replication	2	2.24	28.07	6.9	1.77	2.76	4	4.54
Genotype	19	38.70**	694.64**	79.32**	3.10**	2.30*	25.26**	246.82**
Error	38	1.64	19.42	3.52	0.67	1.01	2.24	4.3
CV%		1.85	2.85	6.59	8.77	11.65	5.73	3.33
New Valley								
Replication	2	2.11	40.17	0.58	0.25	0.5	2.65	2.12
Genotype	19	24.74**	707.60**	74.26**	2.58**	2.33**	31.91**	182.60**
Error	38	1.23	16.83	2.3	0.46	0.46	1.17	2.59
CV%		1.51	2.94	6.63	10.42	11.36	4.58	2.86
Toshqi								
Replication	2	2.4	10.6	2.61	0.82	0.95	7.12	6.94
Genotype	19	14.40**	735.47**	50.07**	3.27**	2.80**	24.60**	163.58**
Error	38	1.31	3.72	2.46	0.43	0.63	4.45	5.3
CV%		1.52	1.39	6.69	11.32	13.89	10	4.23

Table 3. Analysis of variance across locations for seven studied traits across three environments.

SOV	df	Days to 50% flowering (days)	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	No. of green leaves/ plant	1000-grain weight (g)	Grain yield/plant (g)
Environments (Env.)	2	609.94**	4842.19**	465.55**	214.75**	156.16**	378.10**	1011.89**
Rep Env.	6	2.25	26.88	3.19	0.95	1.41	4.59	4.54
Genotypes (G)	19	63.08**	2071.40**	190.97**	6.86**	3.54**	72.00**	579.04**
G × Env.	38	7.38**	33.17**	6.32**	1.04**	1.94**	4.89**	6.96*
Pooled error	114	1.40	13.32	2.76	0.52	0.70	2.62	4.07
CV%		1.62	2.53	6.58	10.00	12.36	6.85	3.50

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

On the same direction, the interactions between genotypes × locations (G x Env) were highly significant ($P \leq 0.01$) for all studied traits except for grain yield/plant which was significant ($P \leq 0.05$), meaning the differential response of genotypes to environmental conditions and indicate the importance of testing the genotypes across locations to check their stability across locations and adaptability in a specific location. The individual and the combined analyses indicated that most traits had higher genotypic and phenotypic variance components than the environmental variance estimates, which indicate that, character expression in these sorghum genotypes is genetic and can be exploited in breeding programs. Similar results are reported by Ezzat *et al* (2010), Abubakar and Bubuche (2013), Ali *et al* (2013) and Zarea *et al* (2020).

Mean performances of 20 grain sorghum genotypes at three locations and across locations for seven studied traits are presented in Table (4). Most of the traits showed wide range of variability. The results revealed that the earliest genotypes at EV1 were No 7, 12, 13, 15, 19 and 20.While; the earliest genotypes at EV_2 were No. 7, 12, 15 and 19. On other hand, at EV_3 the earliest genotypes were No. 12, 13, 16 and 19. Meanwhile, the earliest genotypes across all locations were No 7, 12, 13, 15, 19 and 20. For, plant height the genotypes No 3, 9, 10, 11, 12, 15, 17 and 18 gave the tallest plants at EV_1. Also, the genotypes No. 9, 10, 11, 12, 15, 17 and 18 gave the tallest plants at EV_2. Likewise, the genotypes No. 9, 10, 11, 12, 13, 15, 16, 17 and 18 gave the tallest plants at EV_3. The genotypes 3, 9, 10, 11, 12, 13, 15, 16, 17 and 18 gave the highest plants across all locations. Panicles length of the crosses at EV_1 ranged from 21.45 to 36.70 cm for genotypes No. 9 and 15, respectively. But at EV_2 it ranged from 17.34 to 30.34 cm for genotypes No. 3 and 14, respectively. While at ENV_3 panicle length ranged from 17.67 to 30.27 cm for genotypes No 3 and 11, respectively. The combined mean of panicle length across three locations ranged from 18.92 to 31.75 cm for genotypes No. 3 and 15, respectively. Regarding to panicle width at EV_1 ranged from 6.93 to 10.63 for the genotypes No. 3 and 13, respectively. Then at EV_2 panical width ranged from 4.48 to 8.63 cm for the genotypes No. 20 and 19, respectively. While, panicle width at EV_3 ranged from 4.40 to 7.83 cm for the genotypes No. 12

and 18, respectively. For panicle width across the three locations showed that the genotypes ranged from 5.50 to 8.83 cm for the genotypes No. 3 and 19, respectively. For number of green leaves, the it ranged from 7.19 to 10.05 for the genotypes No. 1 and 12, respectively at EV_1 and it from 4.82 to 7.67 for the genotypes No 20 and 14, respectively at EV_2 but it ranged from 4.15 to 7.46 for the genotypes No. 16 and 19, respectively at EV_3 while for the combined data across the three environments it ranged from 5.77 to 8.00 for the genotypes No. 2 and 8, respectively. For 1000-grain weight, the genotypes No. 4, 15 and 16 were the heaviest at EV_1 and the genotypes No. 6, 15, 16, 18 and 19 were the heaviest at EV_2 and the genotypes No. 4, 16 and 18 were the heaviest at EV_3. Combined across all locations, the heaviest 1000-grain weight were recorded by genotypes No. 4, 10, 15, 16 and 18 which gave 28.02, 25.48, 27.33, 28.87 and 27.14 g, respectively. The grain yield /plant showed great differences among genotypes at the three locations it ranged from 45.02 to 76.28 g for the genotypes No. 5 and 15, respectively at EV_1 and it ranged from 39.34 to 67.5 g for the genotypes No. 5 and 15, respectively at EV_2 and from 40.04 to 63.96 g for the genotypes No. 5 and 14, respectively at EV_3 and across all locations it ranged from 41.47 to 68.90 g for the genotypes No. 5 and 15, respectively. The genotypes No. 4, 11, 12, 13, 14, 15, 16, 17 and 18 out-yielded all the other genotypes, at the three locations and across all the locations. Therefore, the presence of such range of variations for the studied traits indicated the presence of large amount of genetic variation among the released genotypes which is the source of variable genetic material.

In general, the Egyptian genotypes No.15 (Dorado x LC) and No.16 (Dorado x ICSV-112) gave the best performance for most of the studied traits; these genotypes could be released as a new Egyptian grain sorghum cultivars after testing at a large scale.

Table 4. Mean performances of 20 genotypes for seven traits at three locations Sohag (EV_1), New Valley (EV_2) and Toshqi (EV_3) and across the three locations.

No.	Genotype	Days to 50% flowering (days)				Plant height (cm)				Panicle length (cm)			
		EV_1	EV_2	EV_3	Mean	EV_1	EV_2	EV_3	Mean	EV_1	EV_2	EV_3	Mean
1	ICSR-89037	68.17	72.57	75.47	72.07	143.37	133.11	128.65	135.04	22.19	18.45	18.34	19.66
2	ICSR-89039	70.93	74.50	76.10	73.84	125.40	115.94	107.89	116.41	24.23	20.84	20.66	21.91
3	ICSR-89028	73.00	77.53	75.61	75.38	162.33*	146.33	136.50	148.39*	21.65	17.34	17.76	18.92
4	ICSR-21	71.33	77.15	74.83	74.44	140.37	131.39	124.56	132.11	31.67*	24.32	26.45*	27.48
5	ICSR-89016	71.85	75.77	76.50	74.71	129.00	114.89	112.56	118.82	24.08	18.13	22.37	21.53
6	ICSR-89025	70.46	74.43	78.49	74.46	157.86	143.90	139.56	147.10	25.30	20.80	19.97	22.02
7	ICSR-9010	63.65*	70.03*	74.13	69.27*	130.56	106.88	117.56	118.33	24.02	19.00	19.12	20.72
8	ICSR-9012	72.64	76.37	78.60	75.87	148.34	133.07	130.56	137.32	23.82	19.32	18.70	20.61
9	ICSR- 93001	71.51	73.47	77.65	74.21	168.19*	148.73*	155.56*	157.49*	21.45	18.23	21.23	20.30
10	ICSR- 92003	73.13	73.43	77.62	74.73	173.87*	158.82*	159.56*	164.09*	29.12	24.23	23.53	25.63
11	ICSR-93002	67.36	72.33	77.47	72.39	175.89*	161.85*	161.85*	166.53*	31.45	28.11*	30.27*	29.94*
12	ICSR-93004	63.07*	67.50*	72.57*	67.71*	173.23*	156.06*	158.56*	162.62*	27.63	21.97	24.55	24.72
13	Dorado× G-113	66.89*	74.17	72.43*	71.16*	160.60	145.93	147.56*	151.36*	32.32*	29.11*	27.40*	29.61*
14	Dorado× R-273	74.01	77.57	76.47	76.01	151.08	122.75	138.12	137.31	34.89*	30.34*	28.05*	31.09*
15	Dorado×L.C	66.26*	71.37*	74.80	70.81*	168.14*	154.84*	153.95*	158.98*	36.70*	30.08*	28.48*	31.75*
16	Dorado× ICSV-112	71.27	74.70	73.37*	73.11	159.02	144.49	143.56*	149.02*	33.59*	29.26*	25.76	29.54*
17	NM-36565×ICSR-92003	71.62	74.24	77.49	74.45	166.37*	151.21*	151.56*	156.38*	32.45*	29.65*	25.26	29.12*
18	MR812×Zenzepar-R	70.30	74.40	76.53	73.74	163.04*	147.87*	142.67*	151.19*	36.14*	29.89*	29.14*	31.73*
19	NEB-93002×ICSR-92003	61.90*	67.54*	70.57*	66.67*	152.75	137.58	136.71	142.35	32.33*	28.61*	23.83	28.26*
20	Dorado	66.47*	72.13	73.88	70.83*	147.15	135.34	132.56	138.35	24.15	19.48	17.86	20.50
Mean		69.29	73.56	75.53	72.79	154.83	139.55	139.00	144.46	28.46	23.86	23.44	25.25
$LSD_{0.05}$		2.14	1.85	1.91	1.09	7.35	6.84	3.22	3.37	3.13	2.53	2.62	1.53

Table 4. Cont.

No.	Genotype	Panicle width (cm)				No. of green leaves/plant				1000-grain weight (g)			
		EV_1	EV_2	EV_3	Mean	EV_1	EV_2	EV_3	Mean	EV_1	EV_2	EV_3	Mean
1	ICSR-89037	9.53	7.00	5.33	7.29	7.19	5.23	5.23	5.88	24.26	23.90	19.83	22.66
2	ICSR-89039	8.67	5.87	5.33	6.62	7.45	5.18	4.67	5.77	25.00	23.12	19.36	22.49
3	ICSR-89028	6.93	5.00	4.57	5.50	7.71	5.00	4.89	5.87	23.01	21.45	18.60	21.02
4	ICSR-21	9.63	6.00	5.80	7.14	8.04	5.11	7.09*	6.75	31.93*	25.03	27.09*	28.02*
5	ICSR-89016	9.67	7.00	4.93	7.20	7.90	4.88	7.19*	6.66	25.13	23.70	20.60	23.14
6	ICSR-89025	8.87	6.70	5.23	6.93	8.47	5.93	5.64	6.68	26.11	26.03*	21.60	24.58
7	ICSR-9010	9.20	6.07	5.23	6.83	8.34	5.35	4.92	6.20	24.63	21.03	16.66	20.78
8	ICSR-9012	9.30	5.87	4.97	6.71	9.42	7.56*	7.01	8.00*	22.34	16.26	17.93	18.84
9	ICSR- 93001	9.30	6.43	5.13	6.96	7.67	5.64	7.46*	6.92	23.45	20.56	17.93	20.65
10	ICSR- 92003	7.37	5.67	5.63	6.22	8.13	5.97	6.29	6.80	28.45	26.23*	21.77	25.48*
11	ICSR-93002	8.67	6.20	5.13	6.67	9.05	6.19	5.10	6.78	25.34	20.18	23.12	22.88
12	ICSR-93004	8.97	5.83	4.40	6.40	10.05*	6.83	5.27	7.38	23.01	21.03	18.96	21.00
13	Dorado× G-113	10.63	6.17	6.10	7.63	9.80	6.73	6.70	7.74*	26.98	24.36	22.06	24.47
14	Dorado× R-273	10.40	7.07	5.67	7.71	9.49	7.67*	5.22	7.46	26.28	24.83	20.99	24.04
15	Dorado×L.C	10.43	6.67	5.87	7.66	8.12	5.69	4.84	6.22	30.44*	27.03*	24.53	27.33*
16	Dorado× ICSV-112	10.14	8.12*	7.77*	8.67*	9.38	7.23*	4.15	6.92	31.31*	29.77*	25.53*	28.87*
17	NM-36565×ICSR-92003	10.60	7.30	7.58*	8.49*	9.57	6.36	5.04	6.99	27.09	24.57	20.40	24.02
18	MR812×Zenzepar-R	9.40	7.01	7.83*	8.08	8.66	5.67	6.13	6.82	28.57	27.83*	25.02*	27.14*
19	NEB-93002×ICSR-92003	10.53	8.63*	7.34*	8.83*	9.81	6.37	6.10	7.43	26.96	25.97*	22.47	25.13
20	Dorado	8.47	4.89	5.35	6.24	8.30	4.82	5.33	6.15	21.95	19.36	18.01	19.77
Mean		9.34	6.47	5.76	7.19	8.63	5.97	5.71	6.77	26.11	23.61	21.12	23.62
$LSD_{0.05}$		1.36	1.13	1.09	0.66	1.68	1.13	1.32	0.77	2.50	1.80	3.52	1.49

Table 4. Cont.

No.	Genotype	Grain yield/plant (g)			
		EV_1	EV_2	EV_3	Mean
1	ICSR-89037	52.48	48.25	46.98	49.24
2	ICSR-89039	60.09	55.56	55.17	56.94
3	ICSR-89028	52.10	49.64	47.81	49.85
4	ICSR-21	67.49*	61.23*	59.84*	62.85*
5	ICSR-89016	45.02	39.34	40.04	41.47
6	ICSR-89025	55.40	51.23	50.06	52.23
7	ICSR-9010	54.48	50.29	46.95	50.57
8	ICSR-9012	51.90	47.42	43.19	47.51
9	ICSR- 93001	57.68	54.40	51.52	54.54
10	ICSR- 92003	62.87	57.70	55.66	58.74
11	ICSR-93002	68.76*	66.07*	61.04*	65.29*
12	ICSR-93004	70.58*	65.25*	60.82*	65.55*
13	Dorado× G-113	68.44*	60.98*	59.23*	62.88*
14	Dorado× R-273	74.66*	64.70*	63.96*	67.77*
15	Dorado×L.C	76.28*	67.50*	62.92*	68.90*
16	Dorado× ICSV-112	73.06*	64.10*	61.81*	66.32*
17	NM-36565×ICSR-92003	68.41*	58.76	59.38*	62.19*
18	MR812×Zenzepar-R	68.68*	60.10*	61.05*	63.28*
19	NEB-93002×ICSR-92003	64.68	57.80	55.84	59.44
20	Dorado	52.41	45.76	44.76	47.64
Mean		62.27	56.31	54.40	57.66
LSD 0.05		3.46	2.68	3.84	1.86

*** Significant difference from the mean at 0.0 5 probability level.**

Means, phenotypic (Var.p), genotypic (Var.g) and environmental (Var.e) components of variances, phenotypic (PCV) and genotypic (GCV), coefficient of variability, expected genetic advance (Δg) and genetic advance as percentage of the mean (Δg %) for all studied traits across three environments are presented in Table (5). The genotypic variance (Var.g) was larger in magnitude than environmental variance (Var.e) for all studied traits except number of green green leaves/plant, therefore, the expression for most of the traits were less affected by the environments, which indicates that advances can be achieved in breeding programs.

Table 5. Estimaties of means, phenotypic (Var.**p), genotypic (**Var.**g) and environmental (**Var.**e) components of variances, phenotypic (PCV) and genotypic (GCV), coefficient of variability, expected genetic advance (**Δg**) and genetic advance as percentage of the mean (**Δg **%) for all studied traits across the three locations.**

Traits	Var. g	Var. gxe	Var. e	Var. p	Mean	GCV (%)	PCV (%)	Δg	Δg%
Days to 50% flowering	**6.19**	**1.99**	**1.4**	**7.01**	**72.79**	**3.42**	**3.64**	**4.82**	**6.62**
Plant Height	**226.47**	**6.62**	**13.32**	**230.15**	**144.46**	**10.42**	**10.50**	**30.80**	**21.32**
Panicle length	**20.52**	**1.19**	**2.76**	**21.22**	**25.25**	**17.94**	**18.24**	**9.19**	**36.40**
Panicle width	**0.65**	**0.18**	**0.52**	**0.76**	**7.19**	**11.21**	**12.12**	**1.54**	**21.42**
No. of green leaves/plant	**0.18**	**0.41**	**0.70**	**0.39**	**6.77**	**6.27**	**9.22**	**0.59**	**8.71**
1000-grain weight	**7.46**	**0.76**	**2.62**	**8.00**	**23.62**	**11.56**	**11.97**	**5.44**	**23.03**
Grain yield/plant	**63.57**	**0.96**	**4.07**	**64.34**	**57.66**	**13.83**	**13.91**	**16.35**	**28.36**

In general, the variance components across locations showed that all of the traits had higher genotypic variance estimates than the environmental variance estimates, suggesting that expression of the traits due to genetic variance which can be exploited by breeding. These results are in agreement with the findings of Bello *et al* (2007), Tariq *et al* (2007) Ali *et al* (2013) and Zarea *et al* (2020). The GCV is lower in value than the PCV, due to influence of environmental effect. According to Deshmukh *et al* (1986), PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are low and values between 10% and 20% to be medium. Hence moderate GCV and PCV were observed for all studied traits except days to 50% flowering and number of green leaves/plant which showed low values of PCV and GCV. These finding are in agreement with the findings of Rani and Umakanth (2012) and Endalamaw *et al* (2019).

Genetic advance as per cent of mean was categorized by Johnson *et al* (1955) as 0-10%: Low, 10-20%: Moderate and 20% and above: High; hence the high genetic advance as percentage of mean (Δg%) were observed for all studied traits except days to 50% flowering and number of green

leaves/plant. This reveals that the genotypes have abroad base genetic background as well as good potential that will respond positively to selection. Similar results were reported by Deepalakshmi and Gaenesamurthy (2007), Dhutmal *et al* (2014) and Zarea *et al* (2020). The effectiveness of selection depends upon genetic advance of the character. The characters, which showed high genetic advance as percentage of mean (Δg %) were plant height, panicle length, panicle width, 1000-grain weight and grain yield/plant. The control of additive gene effects and early selection may be effective for these characters, which is in conformity with the findings of Ali *et al* (2009) and Endalamaw *et al* (2019).

Phenotypic correlation coefficients among the seven studied traits for all genotypes across three environments are presented in Table 6. Results indicated that days to 50% flowering had negative and highly significant ($P \leq 0.01$) correlation with plant height, panicle length, panicle width, number of green leaves/plant, 1000-grain weight and grain yield/plant; meaning that, selection for earliness in genotypes would cause increasing of the means of studied traits and vice versa.

Table 6. Phenotypic correlation coefficients among seven studied traits for all genotypes across the three locations.

Traits	Days to 50% flowering	Plant height	Panicle length	Panicle width	No. of green leaves/ plant	1000-grain weight
Plant height	**-0.31****					
Panicle length	**-0.32****	**0.50****				
Panicle width	**-0.61****	**0.34****	**0.59****			
No. of green	**-0.51****	**0.41****	**0.50****	**0.67****		
1000-grain weight	**-0.32****	**0.32****	**0.68****	**0.63****	**0.38****	
Grain yield/ plant	**-0.36****	**0.59****	**0.82****	**0.48****	**0.40****	**0.58****

** **Significant at 0.01 probability level.**

Plant height had positive and highly significant correlation with each of panicle length, panicle width, and number of green leaves/plant, 1000-grain weight/plant and grain yield/plant. Positive and highly significant ($P \leq 0.01$) correlation showed between panicle length with each of panicle width, number of green leaves/plant, 1000-grain weight/ plant and grain

yield/plant. Also, positive and highly significant ($P \leq 0.01$) correlation was shown between panicle width with each of number of green leaves/plant, 1000-grain weight/ plant and grain yield/plant. Moreover, number of green leaves/plant had positive and highly significant ($P \leq 0.01$) correlation with each of 1000-grain weight/plant and grain yield/plant. Finally, the correlation between grain yield/plant with each of plant height, panicle length, panicle width, number of green leaves/ plant, 1000-grain weigh/plant was positive and highly significant, indicating that increasing of grain yield/plant for genotypes would result from selection for increasing plant height, panicle length, panicle width, no of green leaves/plant and 1000-grain weight and vice verse. These results are in the same direction with those of Potdukhe *et al* (1994) and Ali *et al* (2013) who found that grain yield was positively and significantly correlated with panicle length, panicle width and 1000-grain weight.

Based on morphological and agronomical studied traits, genetic distances were calculated between twenty sorghum genotypes and cluster analysis was performed using percent similarity. Table 7, showed that similarity coefficient values ranged from 87.00 to 98.70% with an average of 92.85%. The lowest similarity (87.00%) was observed between genotype 5 (ICSR 89016) and genotype 15 (Dorado x LC) which are located in different clusters and was located in a highly diverged group. Madhusudhana *et al* 2012, Khatab *et al* 2017 and Zarea *et al* 2019 illustrated a clear picture about classification and genetic diversity in sorghum inbred lines.

The dendrogram (Figure 1), divided the genotypes into two main clusters which were separated at 92.40% level of similarity. Nine genotypes were in the first main cluster which branched at 93.70% percent of similarity into two sub clusters, first one consisted of 3 genotypes and the second consisted of 6 genotypes. The second sub cluster was separated into two sub-sub clusters each of them three genotypes at 96.00% of similarity. The second main cluster sub-divided into two sub-groups which separated at 95.10% level of similarity. The first sub-group consists of 3 genotypes and the second consisted of 8 genotypes.

Table 7. Genetic distance among 20 genotypes of grain sorghum across three environments using seven agronomic traits based on Percent Similarity.

Genotype	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20
G1	100																			
G2	94.9	100																		
G3	96.6	92.6	100																	
G4	94.9	94.6	92.7	100																
G5	95.1	96.4	92.6	92.7	100															
G6	96.5	93.8	98.0	94.8	93.4	100														
G7	95.9	97.3	93.4	92.7	96.8	93.4	100													
G8	97.6	93.6	96.7	93.9	94.6	96.2	94.6	100												
G9	94.8	92.4	97.1	92.8	91.1	97.2	92.2	95.1	100											
G10	92.3	91.2	94.5	94.0	89.3	95.8	89.3	92.2	96.8	100										
G11	91.2	89.7	92.6	93.4	87.5	93.7	88.2	90.5	95.2	97.4	100									
G12	91.4	89.8	93.3	92.6	87.4	93.7	89.7	91.2	95.9	97.0	97.7	100								
G13	93.3	91.5	94.4	95.7	89.4	96.0	90.4	92.5	95.4	96.1	96.9	96.2	100							
G14	94.0	92.8	92.8	97.0	91.0	94.4	90.9	94.4	92.7	93.5	94.5	93.4	96.3	100						
G15	90.9	89.1	92.0	94.0	87.0	93.5	88.1	89.7	94.6	96.0	97.2	96.4	97.2	95.4	100					
G16	92.5	91.0	93.9	96.2	89.0	95.5	89.4	91.8	94.2	95.3	96.2	95.1	98.0	96.6	97.2	100				
G17	92.6	91.3	94.4	95.4	89.5	95.9	89.5	92.4	96.8	97.4	97.4	96.3	98.4	95.9	97.2	97.5	100			
G18	92.6	91.3	94.1	96.2	89.3	95.8	89.4	92.1	95.1	96.1	96.4	95.1	98.7	96.4	97.6	98.6	98.2	100		
G19	94.3	92.5	93.6	95.9	90.4	95.7	92.0	93.4	93.8	94.8	94.0	94.6	97.0	96.0	94.6	96.3	96.1	96.2	100	
G20	98.2	93.6	96.7	93.6	94.1	96.2	95.6	98.5	95.1	92.2	91.0	92.2	93.2	93.3	90.9	92.1	92.2	92.2	94.3	100

The second sub-cluster was separated into two sub-sub clusters at 96.30% of similarity, first one consisted of 5 genotypes and the second consists of 3 genotypes (Figure 1). In general, cluster analysis in cereal breeding has been used and includes identification of parental genotypes and assessing the genetic diversity. Therefore the genotypes G5 and G15 Were found to be a good parents for hybrid seed production as well as cross pollinated varieties development programs (Amelework *et al* 2015, Khatab *et al*, 2017 and Zarea *et al* 2019).

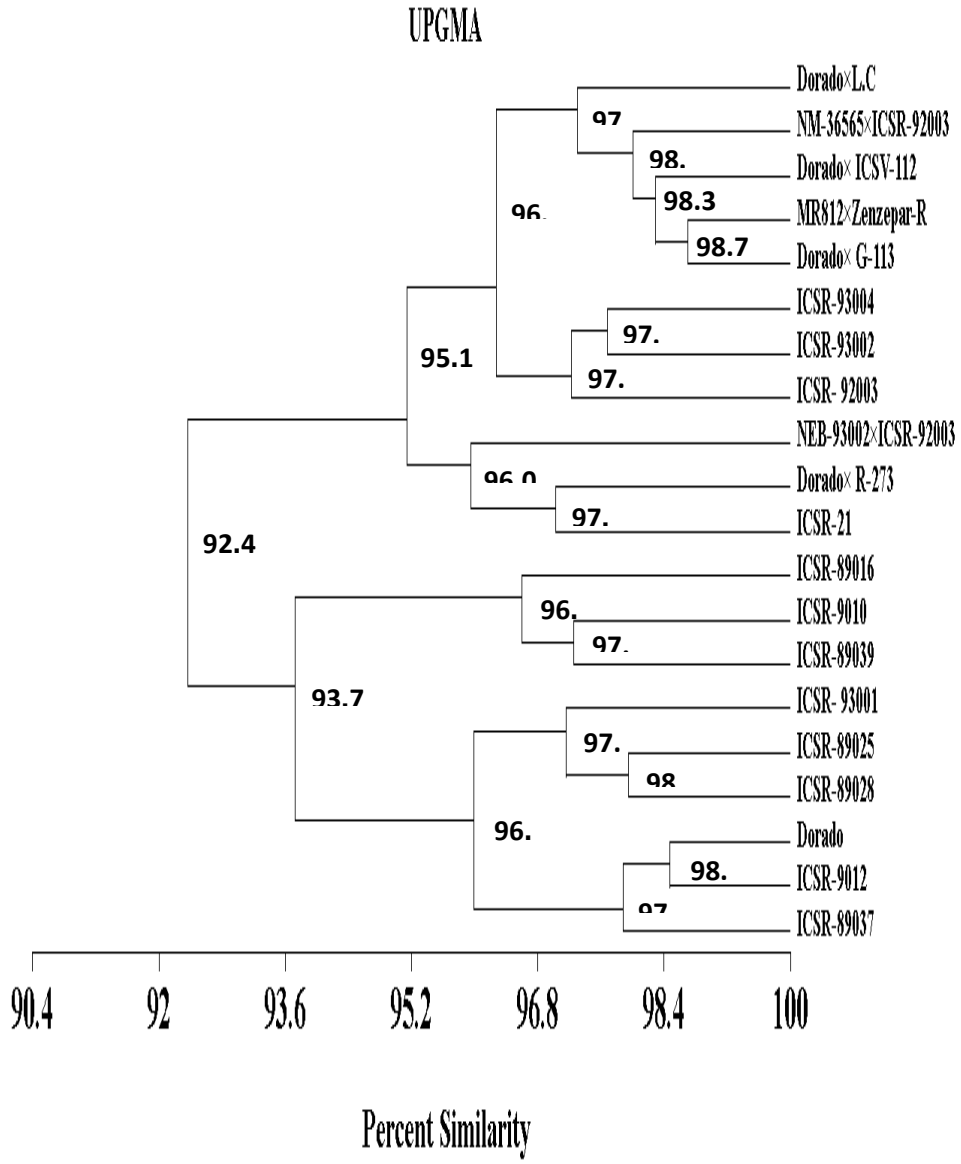

Fig. 1. UPGMA-Dendrogram of genetic similarities among tested sorghum genotypes using seven agronomic traits based on percent similarity.

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الاختلافات الوراثية ومعامل الارتباط و التحليل العنقودي لبعض لصفات الكميه في بعض المستوردات و التراكيب الوراثية المصرية الجديدة من ذرة الحبوب الرفيعة تحت مواقع مختلفة

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تم تقييم عدد ٢٠ تركيب وراثي من ذرة الحبوب الرفيعة من مناطق جغرافية مختلفة و ذلك في ثلاثة بيئات (مواقع) هي محطة البحوث الزراعية بشندويل بمحافظة سوهاج و محطة بحوث بالخارجة بالوادي الجديد و محطة بحوث أبو سمبل بتوشكي في موسم صيف ٢٠١٩م. أوضحت النتائج وجود اختلافات عالية المعنوية بين كلا من التراكيب الوراثية, المواقع (البيئات) و التفاعل بين التراكيب الوراثية و المواقع لكل الصفات محل الدراسة ممدا يدل علي أن التراكيب الوراثة كانت عالية الاختلاف فيما بينها مما يجعل استجابتها عالية في التحسين بالانتخاب فيما بين هذه التراكيب. التركيب الوراثي المصري (Dorado x LC) أعطي أفضل أداء لمعظم الصفات محل الدراسة تحت ظروف الثلاث بيئات المدروسة و كذلك للبيانات التجميعية من الثلاث بيئات. هذا التركيب الوراثي من الممكن أن يتم تسجيله كصنف ذرة حبوب رفيعة مصري جديد و ذلك بعد اختباره علي نطاق واسع في تجارب بحثية مكبرة. التحليل المفرد و التجميعي أظهروا أن التراكيب الوراثية كانت عالية الاختلافات الوراثية و المظهرية مقارنة بالاختلافات البيئية, مما يدل علي أن البيئة كان لها أقل تأثير علي التعبير المظهري للصفات المدروسة و لهذا فإن هذه التراكيب الوراثية ستكون ذات استجابة و مردود عالي في برامج التربية المختلفة. الصفات التي كان بها تقدم وراثي كنسبة من المتوسط مرتفع كانت طول النبات و طول الكوز و عرض الكوز و وزن ١٠٠٠ حبة و محصول الحبوب للنبات

الواحد. أظهرت البيانات أيضا قيم معامل اختلافات وراثية و معامل اختلافات كلية متوسطة لكل الصفات المدروسة فيما عدا صفة التزهير و عدد الأوراق الخضراء , مما يدل علي أن هذه التراكيب لها قاعدة وراثية عريضة و اختلافات وراثية واضحة تجعل استجابتها للتحسين بالانتخاب جيدة. كان التلازم بين صفة المحصول و صفة التزهير سالباً وعالي المعنوية و موجباً وعالي المعنوية مع باقي الصفات المدروسة, مما يدل علي أن أي تحسين في أي من هذه الصفات سيتبعه تحسين مباشر في صفة المحصول. كان أقل تشابه وراثي (٨٧%) بين التركيب الوراثي (ICSR 16) و التركيب الوراثي (Dorado x LC) و اللذين كانوا في مجموعتين مختلفتين علي شجرة التشابه الوراثي لذلك فإن هذين التركيبين الوراثيين يعتبروا أفضل تركيبين لتضمينهم كآباء للتهجين او لبرنامج تربية باستخدام قوة الهجين.