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Assessment of Genetic Variability and Inter-Relationship for Yield Attributing Traits in Maize (*Zea mays* L.) Genotypes in White Nile State, Sudan

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Abstract

Maize is an important source of calories and protein in human lives in many countries of the world and is the main staple food in Africa, particularly in eastern Africa. In the Sudan, the low yield of maize was mainly due to the use of low yielding landraces. It is necessary to carry out breeding programs that deal with the production of high yielding, adaptable new varieties. Therefore, this study aimed to estimate genetic variability, heritability, genotypic performance and interrelationships among the traits. Ten maize genotypes evaluated at White Nile Research Station Farm, Kosti, of the Agricultural Research Corporation (ARC), Wad Medani Sudan were planted in a randomized complete block design with three replications during the two seasons of 2021 and 2022. Most evaluated genotypes exhibited a wide and significant variation in the 11 measured traits. Genotypic coefficient of variation and genetic advance were recorded for days to 50% tasseling, ear diameter (cm), number of grains per row and grain yield (t/ha) in both seasons. High heritability and genetic advance were recorded for grain yield, ear length, ear height, plant height, number of rows per ear, ear weight, days to 50% tasseling, 100-grain weight and days to 50% silking. Moreover, there was a highly significant and positive correlation of grain yield with number of rows per ear (r = 0.479), ear length (r = 0.381), 100-grain weight (r = 0.344) and days to 50% tasseling (r = 0.214). The highest yielding five genotypes across the seasons were TZCOM1/ZDPSYN (4.2 t/ha), EEPVAH-3 (4.2 t/ha), F2TWLY131228 (4.1 t/ha), PVA SYN6F2 (3.9 t/ha) and EEPVAH-9 (3.8 t/ha) these were needed to check the adaptability, stability and to test major maize growing areas to make sound recommendations for release.

Keywords

Genetic Variability, Heritability, Correlation, Maize, Yield

1. Introduction

Maize (*Zea mays* L.) is a cereal crop which is a member of the Poaceae family. It is the third most important cereal crop after wheat and rice in the world. Provides food and feeds, employment and income generation for small-holder families and raw materials for industries in Africa and the humid tropics. Also maize is an important source of calories and protein in human lives in many countries of the world and is the main staple food in Africa, particularly in Eastern Africa [1]. Maize is the fourth cereal crop in Sudan after sorghum, wheat and millet. In the Sudan, maize is of less importance than sorghum and pearl millet, but recently its importance rises as a forage and industrial crop. Grain yield is affected by genotype and environmental factors because of its quantitative properties.

Plant breeding aims to improve and enhance the genetic potential of plants, resulting in new varieties that are better than their parents [2] and [3]. The genetic variability provides useful information with regard to the possibility and extent of improvement that may be expected in the characters through breeding and selection. Breeders are interested in evaluating genetic diversity based on morphological characteristics as they are inexpensive, rapid, and simple to score. Moreover, this evaluation could be useful in developing reliable selection indices for important agronomic traits in maize. Heritability estimation is useful in breeding quantitative traits because it can be used to determine effective selection strategies and breeding methods for use in breeding programs and to predict selection progress [4]. Correlation analysis helps to focus on desirable traits. The phenotype that is observed in the field is the combination of environmental and genetic factors. Quantitative traits are badly affected by the environment so the effect of the environment cannot be neglected during the selection of superior genotypes. The best method to select the superior genotypes is to grow the maize germplasm in the open field environment. Therefore, as a result of the above facts, the present research study was undertaken to estimate genetic variability, heritability and genetic advances among yield and yield contributing traits for maize genotypes that can establish relationship in yields and their components and utilization of the available population in future maize breeding programs.

2. Materials and Methods

2.1. Study Site and Experimental Design

The experimental materials were nine maize genotypes with one check namely (**Table 1**). The genotypes introduce from International Institute of Tropical Agriculture (IITA), Nigeria and were early maturity, some have vitamin A and resistance to striga. grown for two consecutive seasons (2021 and 2022) during the rainy season under irrigated condition; at White Nile Research Station Farm (latitude 14˚24'N and longitude 33˚22'E), Kosti of the Agricultural Research Corporation (ARC) Sudan. The soil of the experimental plots was classified as vertisol with high clay content (40% to 65%), less than 1% organic carbon, low in available nitrogen (0.03% total nitrogen) and medium in available P2O5 (406 to 700 ppm total phosphorus), pH values are slightly alkaline which ranging from 7 to 8.2. The climate was semi-arid. The experimental plots were laid out in a complete randomized block design (CRBD) with three replications. Each plot consisted of three rows of 6 m long with 80 cm and 30 cm spacing between rows and plants, respectively. In both seasons, deep ploughing, harrowing and leveling were practiced preparing the experimental area. The sowing was done manually in July, 2021 and 2022 using a seed rate of 12 kg/ha, three seeds per hill and later thinned to one plant per hill. Recommended Nitrogen and phosphorus fertilizers application at the rate of 86 and 43 kg per hectare as source of N and P, respectively. Phosphorus fertilizer in the form of triple super phosphate (P_2O_5) was applied as basal dose during the final land preparation. Nitrogen, in the form of urea (46% N) was top dressed in two equal split doses at 15 days and 38 after sowing respectively. The other crop managements practices were applied following the recommendation of the location.

2.2. Data Collection

Data collected were taken on randomly selected 5 plants from each experimental plot for all the traits under consideration included, days to 50% tasseling and silking were calculated based on number of days took from date of sowing to date of 50% plants shedding pollen and plants with silk emergence respectively. plant height (cm) measured in centimeters by measuring the plant stalk from the ground level to the tip of the tassel. Ear height was expressed in centimeters by measuring the plant stalk from the ground level to the node of the attachment of the upper most ear, then ear length (cm), ear weight (g), ear diameter (cm), number of rows per ear, number of grains per row, 100-grain weight (g) and grain yield (t/ha).

2.3. Data Analysis

Analysis of variance (ANOVA) was carried out on the data to assess the genotypic effects and their interaction using the general linear model (GLM) procedure for randomized complete blocks design in [5] SAS (version 8). Then, the combined analysis of variance was done for traits in which the mean squares were homogenous. The phenotypic and genotypic variances and their coefficients, heritability in the broad sense and genetic advance were computed according to the formula described by [6]. Combined over seasons were used to compute simple linear correlation coefficients between grain yields and 11 other traits.

Table 1. Name of nine maize genotypes plus one check used in this study.

SN	Name of genotypes	Source
1	(TZEOMP5C7/TZECOMP3DTC2) C2	12A20364

Continued

2	Obatanpa/TZL Comp 4C3	
3	PVA SYN6F2	16A2030
4	F2TWL Y131228	16C25336
5	PVA SYN-14	15A20786
6	TZCOM1/ZDPSYN	
7	EEPVAH-3	
8	EEPVAH-11	
9	EEPVAH-9	
10	Hudeba-CK	

3. Results and Discussion

3.1. ANOVA Tests of Different for Quantitative Traits

The analysis of variance showed the presence of significant differences among the tested genotypes for most characters. This gives an opportunity for maize breeders to improve those traits through selection and hybridization to improve the desired traits. The range and mean of genotypes for all studied traits also indicated wide ranges of variation which also revealed possible amount of variability among the genotypes (Table 2). The genetic analysis of quantitative traits is a prerequisite for plant breeding programs, which can lead to a systemic method of design and to the appropriate planning of plant breeding strategies.

3.2. Genotypic (GCV) and Phenotypic (PCV) Coefficients of Variation Heritability (h^2B), Genetic Advance (GA), and Genetic Advance as Percent of Mean (GAPM)

The current study suggests that the PCV was higher than the GCV for all traits indicating the influence of environmental factors on all the investigated traits. This was also the case for all the traits observed in a previous study [7] which reported that the environmental effect on any trait is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation; large differences reflect a large environmental effect, whereas small differences reveal a high genetic influence. In this study, phenotypic coefficients of variation were slightly higher than the genotypic coefficients of variation for all the studied traits (Table 3). This indicated the presence of environmental influence to some degree in the phenotypic expression of the characters; this results similar to the study of [8].

The small differences between the PCV and GCV for most of the traits, such as days to 50% tasseling, ear diameter (cm), number of grains per row and grain yield (t/ha) represented some degree of environmental influence on the phenotypic expression of these characters. It also suggests that selection based on these characters would be effective for future of maize breeding programs. The other traits, which showed a higher difference between PCV and GCV, indicated that the environmental effect on the expression of those traits is higher and that selection based on these characters independently is not effective for further yield improvement. The highest PCV was recorded for plant height (68.89 - 159.6) and ear diameter (259.65 - 221.12) in both seasons were also recorded by the following researchers [8]-[10].

Table 2. Phenotypic variability for 11 traits in ten maize genotypes grown at the WNRS Farm, seasons 2021 and 2022.

Trait	Range		G.M		SE (+)		CV (%)		F Value	
	2021	2022	2021	2022	2021	2022	2021	2022	2021	2022
Days to 50% tasseling	43 - 52	653 - 58	47.9	55.4	0.40	0.29	2.31	1.00	10.74***	23.63***
Days to 50% silking	52 - 62	60 - 65	55.6	63.1	0.44	0.21	2.31	1.43	9.34***	3.17*
Plant height (cm)	169.8 - 237	178 - 222	218.6	199.4	2.86	2.18	5.09	1.84	4.16**	31.58***
Ear height (cm)	81.4 - 98.7	65.6 - 128.6	91.5	96.2	1.09	1.96	1.97	9.70	32.73***	2.14
Ear length (cm)	13 - 17.4	10.16 - 29.6	15.3	14.8	0.25	0.64	2.47	22.52	39.13***	1.29
Ear weight (g)	88.3 - 162.2	96.3 - 152.2	121.9	119.7	3.31	2.88	6.79	5.78	12.95***	14.61***
Ear diameter	3.6 - 4.4	2.9 - 3.6	4.0	3.4	0.04	0.03	2.66	4.07	14.07***	1.27
Number of rows per ear	25.3 - 37.5	26.3 - 37.2	32.5	31.0	0.60	0.40	3.41	5.66	25.78***	2.91*
Number of grains per row	12 - 20.4	12.4 - 16.2	14.5	14.2	0.27	0.19	9.73	5.13	1.07	4.31**
100-grain weight (g)	14.5 - 26.5	20.7 - 27.8	23.0	23.5	0.47	0.32	5.52	3.69	10.51***	10.79***
Grain yield (t/ha)	2.16 - 4.88	2.81 - 4.27	3.4	3.6	0.13	0.10	5.84	2.17	37.93***	145.67***

*, **, ***significant at 0.05, 0.01 and 0.001 probability levels, respectively.

Heritability assessments provide breeders with valuable insights into the share of phenotypic variation that can be attributed to genetic factors. By accurately estimating heritability, breeders can assess the potential for genetic improvement in specific traits. This gives an idea of the total variation ascribable to genotypic effects, which are an exploitable portion of the variation. The characters that showed relatively high heritability estimates (≥ 60%) grain yield (92.52 and 98.00%), ear length (92.34 and 8.85%), ear height (91.35 and 27.47%), plant height (91.07 and 37.35%), number of rows per ear (89.18 and 38.32%), ear weight (79.92 and 80.00%), days to 50% tasseling (76.42 and 67.18%), 100-grain weight (76.07 and 76.33) and days to 50% silking (73.57 and 23.23) in both seasons respectively (**Table 3**). High broad sense heritability estimates would enable plant breeders to base their selection on the phenotypic performance indicating that their improvement could be achieved by mass selection. Similar results were reported by [8] [11]-[14]. Since high heritability does not always indicate high genetic gain, The estimates of heritability combined with expected genetic advance are more useful than heritability estimates alone for predicting the ultimate effect for selecting superior varieties.

High heritability estimates with low genetic advance observed for number of grains per row, ear diameter and grain yield t/ha indicated non additive type of gene action and that genotype × environment interaction played a significant role in the expression of the traits. Similar results were reported by [15].

Table 3. Estimates of phenotypic variability, (GCV) and phenotypic (PCV), coefficients of variation, heritability in broad sense (h^2B), genetic advance, genetic advance as percentage of the mean for 11 traits in ten maize genotypes grown at the WNRS Farm seasons 2021 and 2022.

Trait	GCV		PCV		h^2B		GA		GA%	
	2021	2022	2021	2022	2021	2022	2021	2022	2021	2022
Days to 50% tasseling	8.306	4.181	10.86	4.735	76.42	67.18	8.15	3.71	17	6.69
Days to 50% silking	8.278	0.92	11.24	3.96	73.57	23.23	9.48	0.56	17.05	4.94
Plant height (cm)	59.6	68.89	159.6	75.64	91.07	37.35	14.36	23.04	18.91	11.55
Ear height (cm)	38.87	34.3	42.55	124.82	91.35	27.47	11.54	6.2	12.61	6.44
Ear length (cm)	11.83	7.29	12.81	82.36	92.34	8.85	2.66	0.63	17.38	4.55
Ear weight (g)	223.51	181.19	279.65	221.12	79.92	80.0	30.39	27.46	24.92	22.93
Ear diameter	1.21	0.058	3.99	0.614	30.32	13.84	0.25	0.035	6.2	1.02
Number of rows per ear	31.18	6.29	34.96	16.2	89.18	38.82	6.18	1.79	19.04	5.78
Number of grains per row	0.96	4.07	14.65	7.8	6.55	51.79	0.28	1.13	1.93	7.94
100-grain weight (g)	22.2	10.42	29.18	13.65	76.07	76.33	5.12	2.81	22.24	11.95
Grain yield (t/ha)	14.11	8.189	15.25	8.356	92.52	98.00	1.36	1.1	40.59	30.64

*, **, *** Significant at 0.05, 0.01 and 0.001 probability levels, respectively.

3.3. Quantitative Traits

The genetic analysis of quantitative traits is a prerequisite for plant breeding programs, which can lead to a systemic method of design and to the appropriate planning of specific plant breeding strategies to highest yielding genotypes well be considered in the national performance trials which consisting other from difference researchers and can be improvement of maize production area. The results further revealed that most of the traits exhibited wide range of variability (Table 4). The late tasseling genotypes were PVA SYN6F2, (TZEOMP5C7/TZECOMP3DTC2) C2 and EEPVAH-9 while the early tasseling genotypes were Hudeba-ck and EEPVAH-11. The late silking genotype was (TZEOMP5C7/TZECOMP3DTC2) C2 while the early silking genotypes EEPVAH-11 and EEPVAH-3. Generally, most of the genotypes showed early maturing period. This suggested the chance of selecting earliness genotypes which can escape terminal moisture and drought stress. Maximum plant height (227 cm) was observed for PVA SYN6F2, while minimum plant height (190) was recorded for Hudeba-ck. These differences for plant height might be due to genetic variations among the genotypes. Maximum ear length (17.2 cm) was recorded for EEPVAH-9 whereas minimum for EEPVAH-11 with a value of (13.2 cm). These divergences in ear length may be due to the different inherited backgrounds of the various maize genotypes. The highest 100-grain weight recorded for EEPVAH-11 (25.1 g) while the lowest 100-grain weight was recorded for (TZEOMP5C7/TZECOMP3DTC2) C2 (20.1 g). The range of ear weight was (94.8 g) to (151.9 g) for genotypes Hudeba-ck and

(TZEOMP5C7/TZECOMP3DTC2) C2 respectively. The range of ear diameter was (3.6) to (3.9) for genotypes TZCOM1/ZDPSYN, F2TWLY131228 and genotypes Hudeba-ck respectively. Number of rows per ear ranged from (27.0 to 33.9) for genotypes Obatanpa/TZL Comp 4C3 and EEPVAH-3 respectively. The range of number grains per row was (13.5 to 15.3) for genotypes Hudeba-ck and (TZEOMP5C7/TZECOMP3DTC2) C2 respectively. Grain Yield (**Table 4**) shows obtained by different genotypes in combined over two seasons. The highest yielding genotypes were; TZCOM1/ZDPSYN, EEPVAH-3, F2TWLY131228, PVA SYN6F2 and EEPVAH-9 with grain yield of (4.2, 4.2, 4.1, 3.9 and 3.8 t/ha) respectively. Particularly, the wide variability observed for grain yield as a quantitatively inherent character among the genotypes means that, there is ample opportunity for selection in the genotypes for improvement of this important economic character. The range and mean values of the studied traits suggested the existence of sufficient variability among the studied genotypes for the majority of considered traits and their considerable potential for improvement. [16] reported a wide range of variability of traits such as grain yield t/ha, number of rows per ear, number of grain per row, ear length, ear weight, ear diameter and 100-grain weight which is confirmed by the present study [17] also observed high range values for plant height and ear height in maize genotypes they studied.

Table 4. (a) Mean of growth aspects ten Maize genotypes grown at White Nile Research Station Farm (WNRSF) combined over two seasons, 2021 and 2022. (b) Mean of growth aspects ten Maize genotypes grown at White Nile Research Station Farm (WNRSF) combined over two seasons, 2021 and 2022.

(a)

Genotypes	DT	DS	PH	EH	EL
(TZEOMP5C7/TZECOMP3DTC2) C2	53.2^{A}	61.2^{A}	212.1^{BCD}	97.4^{AB}	14.8^{ABC}
Obatanpa/TZL Comp 4C3	52.0^{B}	59.8^{B}	214.7^{BC}	96.4^{ABC}	14.6^{ABC}
PVA SYN6F2	53.5^{B}	59.8^{B}	227.3^{A}	94.8^{BC}	15.7^{A}
F2TWL Y131228	50.7^{BC}	59.5^{BC}	212.3^{BC}	102.9^{AB}	16.8^{A}
PVA SYN-14	52.7^{BC}	59.7^{BC}	207.4^{CD}	93.6^{CD}	15.1^{BC}
TZCOM1/ZDPSYN	51.8^{BC}	59^{CD}	202.3^{DE}	82.2^{E}	16.2^{A}
EEPVAH-3	51.2^{CD}	58.5^{CD}	196.3^{EF}	88.8^{CDE}	15.5^{A}
EEPVAH-11	49.8^{EF}	58.0^{D}	209.2^{BCD}	96.4^{ABC}	12.1^{C}
EEPVAH-9	53.2^{A}	59.0^{CD}	218.5^{AB}	99.9^{AB}	17.2^{A}
Hudeba-CK	48.8^{F}	59^{CD}	190.2^{F}	86.3^{DE}	12.6^{BC}
Mean	51.7	59.4	209.0	93.9	15.1
CV	1.7	1.8	4.1	7.2	15.9

(b)

Genotypes	EW	ED	NRPE	NGPR	HGW	GY th
(TZEOMP5C7/TZECOMP3DTC2) C2	120.2^{D}	3.7^{BC}	32.5^{AB}	15.3^{A}	20.1^{E}	2.7^{F}
Obatanpa/TZL Comp 4C3	151.9^{A}	3.8^{AB}	27.0^{D}	14.5^{ABC}	23.2^{BCD}	2.9^{DE}
PVA SYN6F2	114.4^{DE}	3.7^{BC}	33.5^{AB}	14.1^{ABC}	21.9^{D}	3.9^{BC}
F2TWL Y131228	139.7^{B}	3.9^{A}	33.2^{AB}	14.9^{AB}	23.2^{BCD}	4.1^{AB}
PVA SYN-14	94.8^{F}	3.8^{AB}	29.7^{C}	14.0^{BC}	22.7^{CD}	3.1^{D}
TZCOM1/ZDPSYN	129.4^{C}	3.6^{BC}	33.2^{AB}	13.8^{BC}	23.8^{BC}	4.2^{A}
EEPVAH-3	108.7^{E}	3.6^{C}	33.9^{A}	14.8^{ABC}	24.8^{A}	4.2^{A}
EEPVAH-11	119.7^{D}	3.7^{C}	32.0^{B}	13.8^{BC}	25.1^{A}	3.1^{D}

Continued

EEPVAH-9	115.6^{DE}	3.8^{A}	32.5^{AB}	14.7^{ABC}	24.2^{AB}	3.8^{C}
Hudeba-CK	113.8^{DE}	3.9^{A}	29.6^{C}	13.5^{C}	23.8^{BC}	2.8F
Mean	120.8	3.8	31.7	14.3	23.3	3.5
CV	6.4	3.3	4.7	7.7	4.8	4.7

(a) *, ** significant at 0.05 and 0.01 probability respectively. Days to 50% tasseling (DT); Days to 50% silking (DS); Plant height centimeter (PH); Ear height centimeter (EH); Ear length centimeter (EL). (b) Ear diameter centimeter (ED); Means followed by the same letter(s) within a column are not significantly different at 0.05 probability level according to LSD Test; Ear weight (EW); No. of rows per ear (NRPE); No. of grains per row (NGPR); 100-grain weight (HGW); Grain yield (GY th).

3.4. Phenotypic Correlation Coefficient

The study of the correlation between different characters may help the plant breeder to know how the improvement of one character will bring simultaneous changes in other characters. The relationships existing between 11 quantitative traits represented as simple correlation coefficients are presented in (**Table 5**). Correlation of yield and other traits is important in indirect selection for high yield improvement in crop genotypes [18].

Grain yield showed positive and significant phenotypic correlation with number of row per ear (r = 0.479), ear length (r = 0.381), 100-grain weight (r = 0.344) and days to 50% tasseling (r = 0.214), respectively. Number of row per ear was the most yield attributing traits, followed by 100-grain weigh and ear length thus, simultaneous selection for these traits could boost grain production. Similar results were reported by [19] and [20]. The selection of those traits would suggest an indirect selection of genotypes for grain yield if there were a positive and high correlation between them. reported similar findings in line with [21].

Table 5. Phenotypic correlation coefficients between 11 pairs of traits in maize using (combined over two seasons 2021-2022).

Traits	DT	DS	PH	EH	EL	EW	ED	NRPE	NGPR	HGW
DS	−0.899***									
PH	−0.360**	−0.491***								
EH	−0.289*	0.297*	0.110							
EH	0.053	−0.044	0.127							
EW	−0.106	−0.040	0.171	0.120	0.084					
ED	−0.819***	−0.767***	0.573***	−0.146	0.045	0.185				
NRPE	−0.204	0.345**	0.188	0.201	−0.032	−0.132	0.128			
NGPR	−0.049	−0.047	0.210	−0.011	−0.011	0.216	0.149	0.222		
HGW	−0.046	−0.124	−0.084	−0.185	−0.185	−0.013	0.244	−0.075	0.394**	
GY	0.214*	−0.067	0.026	0.007	0.381**	0.027	−0.208	0.479***	0.069	0.344**

*, **, *** Significant at 0.05, 0.01 and 0.001 probability levels, respectively.

4. Conclusion

It could be concluded from this study that there is adequate genetic variability among ten tested genotypes. Hence, the information generated from this study can be exploited by maize breeder for future maize breeding program. The study was also carried out for one site and two seasons and will be done in next national yield trail. These qualified them to be used as selected specie, the following had the highest yield TZCOM1/ZDPSYN (4.2 t/ha), EEPVAH-3 (4.2 t/ha), F2TWLY-131228 (4.1 t/ha), PVA SYN6F2 (3.9 t/ha) and EEPVAH-9 (3.8 t/ha) these were needed to check the adaptability, stability and to test major maize growing areas to make sound recommendations for release.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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