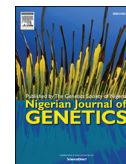


Available online at www.sciencedirect.com**ScienceDirect**

Nigerian Journal of Genetics 28 (2014) 24–28

<http://www.ajol.info/index.php/njg>

Original articles

Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.)

D.J. Ogunniyan*, S.A. Olakojo

Institute of Agricultural Research and Training, Obafemi Awolowo University, Moor Plantation, P.M.B. 5029, Ibadan, Nigeria

Received 3 December 2014; revised 10 March 2015; accepted 18 April 2015

Available online 17 July 2015

Abstract

Fifteen elite yellow maize inbred lines were evaluated in a randomized complete block design experiment with three replicates in 2014. Data were collected on days to anthesis and silking, anthesis-silking interval, plant and ear heights, number of ears per plant, leaf area, ear weight and grain yield. Mean values were used to determine characters' phenotypic and genotypic variances, phenotypic, genotypic and environmental coefficients of variation. Broad sense heritability and genetic advance percentage of mean were estimated for each trait. Significant variation existed in all the characters. The coefficients of variation were low except for ear weight and grain yield that were relatively higher. The anthesis-silking interval was highest in lines TZEI 124 and TZEI 16, but least in lines BD74-222, TZEI 11 and TZEI 13. Line BD74-222 had the height plant height and BD74-165 had the least. Line TZEI 124 produced highest maize grain yield whereas line TZEI 146 had the least. Coefficients of variation of phenotype and genotype were low for all the traits except number of ear per plant, ear and grain yield. The characters were less influenced by the environment thus the traits can be used for selection. Heritability was greater than 80% for all characters studied whereas expected genetic advance ranged from low (8.91) in days to silking to high (72.03) in number of ear per plant. Days to anthesis and silking, plant height and number of leaf per plant were positively correlated. Grain yield was positively correlated with ASI, plant and ear heights, number of leaf per plant and leaf area. High heritability and high genetic advance for ASI indicated the presence of additive genes in the trait and suggested reliable maize improvement through selection of the traits. In this study moderate genetic advance was associated with high heritability.

© 2015 The Genetics Society of Nigeria. Production and hosting by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Keywords: Correlation; Elite maize; Heritability; Genotype; Genetic advance; Phenotype

1. Introduction

Maize (*Zea mays* L.), the third most important cereal crop after wheat and rice in the world [11] provides food and feeds, employment and income generation for small-holder families and raw materials for industries in Africa and the humid tropics. The crop is widely cultivated in tropical Africa, and no other crop is more widely distributed in Nigeria. Despite the volume of improvement research and extensive heterosis exploitation in maize [3,4,13,17], the yield of maize in the

tropics is lower than that realizable in the temperate countries. This has made consistent and continuous selection for higher grain yield imperative.

Genetic improvement of a crop is pivoted on the strength of genetic diversity within the crop species. Adequate variability provides options from which selections are made for improvement and possible hybridization. Genotypic correlations had been used as an effective tool to determine the relationships among agronomic traits in genetically diverse population for enhanced progress in crop improvement [7]. Binodh et al. [8] reported that information on character association in crops is important for effective and rapid selection in crop improvement.

* Corresponding author.

E-mail address: adebayomv@yahoo.com (D.J. Ogunniyan).

Peer review under responsibility of The Genetics Society of Nigeria.

Heritability assumes that individuals more closely related are more likely to resemble one another than distant ones [10]. Estimate of heritability assists breeders to allocate resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources [23]. There are different ways to calculate heritability. It may be estimated as broad-sense or narrow-sense, on single plant, individual plot or mean of entry [16]. Smalley et al. Ref. [23] reported that parent-offspring regression analysis has been used to estimate heritability in both crops and animals. Genetic advance explains 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. It also indicates the presence of additive genes in the trait and further suggest reliable crop improvement through selection of such traits. Estimates of heritability with genetic advance are more reliable and meaningful than individual consideration of the parameters [15].

Continuous improvement of maize is imperative for the increased competition for the crop. This can be achieved through effective selection of suitable parent materials of significant genetic variability. The objective of the present study was to estimate the genetic variation, genetic associations, heritability and expected genetic advance in the elite yellow maize inbred and to evaluate suitable selection criteria for further breeding.

2. Materials and methods

Elite yellow kernel inbred lines of maize totaling 15, were obtained from International Center for Maize and Millet Improvement (CIMMYT) and International Institute of Tropical Agriculture (IITA) for the study. The pedigree, source and attribute of the inbred lines were presented in Table 1. Seeds of the inbred lines were planted in two-row plots, of 5 m long with a spacing of 0.75 m between rows and 0.50 m between plants in a row in Ibadan (forest-savanna transition agro-ecology of Nigeria). Field were sown with three seeds per hill and seedlings were thinned to two per

stand at two weeks after planting to achieve a plant density of 53,333 plants ha⁻¹. The maize lines were experimented in a randomized complete block design with three replicates. Standard cultural practices were applied for field maintenance and harvesting according to [12] package of recommendation. The experiment was carried out in the rainy and dry seasons of 2014.

Data were collected on days to anthesis (DTA) and days to silking (DTS) as number of days from planting to 50% tasseling and days from planting to 50% silking emergence respectively, plant and ear heights. Plant and ear heights were height of plant from soil surface to the base of tassel and base of uppermost ear, respectively. Anthesis-silking interval (ASI) was calculated as days to silking minus days to anthesis. Leaf area was estimated by leaf length × leaf breadth × 0.75. Number of ear per plant was counted as the number of ear with at least one fully developed grain divided by the number of harvested plant. Ears were weighed immediately after harvest. Grain yield was determined by yield components of the plants ha⁻¹ according to Bänziger et al. [5] as: grain yield = Plants ha⁻¹ × ears per plant × grains per ear × weight per grain.

Means of the data collected across seasons were subjected to Analysis of variance using SAS Ref. [24] and significant means were compared using least significant difference at $P \leq 0.05$ and 0.01. Data were transformed before subjecting to ANOVA. Phenotypic (δ^2p) and genotypic (δ^2g) variances were obtained according to [6] as: $\delta^2g = MS_p - \frac{MSe}{r}$, $\delta^2p = \frac{MSg}{r}$ and $\delta^2e = \frac{MSe}{r}$, where MS_p , MSg , MSe are mean squares of phenotypes, of genotypes, and of error, respectively; r was number of replication. The mean values were used for genetic analyses to determine phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), according to Singh and Chaudhury [21] as:

$$GCV(\%) = \frac{\sqrt{\delta^2g}}{x} \times 100$$

$$PCV(\%) = \frac{\sqrt{\delta^2p}}{x} \times 100$$

Table 1
Name, pedigree, source and attribute of the elite yellow maize inbred lines.

Inbred line	Pedigree	Source	Attribute
BD74-204	CLYN231-B	CIMMYT	High yielding
BD74-217	CLYN260-B	CIMMYT	High yielding
BD74-219	CLYN265-B	CIMMYT	High yielding
BD74-222	CLYN262-B	CIMMYT	High yielding
BD74-165	DTPYC9-F74-3-4-1-3-B-B	CIMMYT	Drought gene donor and high yielding
BD74-161	DTPYC9-F46-3-9-1-1-B-B	CIMMYT	Drought gene donor and high yielding
TZEI 8	TZE-Y Pop STR C ₀ S ₆ Inbred 62-3-3	IITA	Drought and <i>striga</i> gene donor
TZEI 16	TZE Comp5-Y C ₆ S ₆ Inbred 31	IITA	Drought and <i>striga</i> gene donor
TZEI 11	TZE Comp5-Y C ₆ S ₆ Inbred 8	IITA	Low nitrogen tolerant
TZEI 12	TZE Comp5-Y C ₆ S ₆ Inbred 8	IITA	Low nitrogen tolerant
TZEI 124	TZE-Y Pop STR C ₀ S ₆ Inbred 3-1-3	IITA	Low N and <i>striga</i> gene donor
TZEI 128	TZE-Y Pop STR C ₀ S ₆ Inbred 10-4-4	IITA	Low N and <i>striga</i> gene donor
TZEI 13	TZE Comp5-Y C ₆ S ₆ Inbred 12	IITA	Low N and <i>striga</i> gene donor
TZEI 146	TZE-Y Pop STR Co S ₇ Inbred 49-3-3	IITA	Low N and <i>striga</i> gene donor

Table 2
Mean values, coefficients of variation, ranges and mean squares of some relevant agronomic characters of 15 yellow maize inbred lines.

Character	Mean	CV (%)	Range		Mean square	
			Min	Max	Between lines	Error
Days to anthesis	52.20	0.00	49.00	57.00	20.66**	0.00
Days to silking	56.53	0.00	53.00	60.00	17.94**	0.00
Days to anthesis	4.33	0.00	3.00	6.00	2.86**	0.00
Plant height (cm)	113.57	2.21	88.40	149.07	873.73**	6.29
Ear height (cm)	46.68	6.62	26.03	65.07	273.98**	9.56
No. of leaves/plant	10.09	1.05	8.00	11.00	2.94**	0.01
Leaf area (cm ²)	361.37	6.24	282.06	508.62	18814.28**	509.99
No. of ear/plant	1.26	14.30	0.99	2.33	0.66**	0.03
Ear weight/plot (kg)	1.07	23.42	0.62	1.94	0.35**	0.06
Grain yield/plot (kg)	0.78	21.42	0.45	1.41	0.18**	0.03

**Significant at $P \leq 0.01$.

where: δ^2g = genotypic variance, δ^2p = phenotypic variance and x = sample mean. Broad sense heritability (h^2) estimate of each trait was computed according to the procedure outlined by Falconer [9] as: Heritability (h^2) = $\frac{\delta^2g}{\delta^2p}$. Where: δ^2g = genotypic variance and δ^2p = phenotypic variance. Expected genetic advance percentage of mean was calculated according to Shukla et al. [20]; as $\frac{k \cdot \delta^2p}{\mu} \times 100$, where k : standardized selection differential constant (2.06) at 5% selection intensity, δ^2p = phenotypic standard deviation and h^2 = broad sense heritability.

3. Results

3.1. Variation in agronomic characteristics of the yellow kernel inbred lines of maize

Table 2 showed the means, coefficients of variation (CV), ranges and mean squares of 10 characters of the maize lines. Significant variation existed (at $P = 0.05$) in all the characters. The coefficients of variation were low except for ear weight

and grain yield. The CVs for DTA, DTS and ASI were zero, showing high level of uniformity for these inbred lines.

3.2. Agronomic performance of the yellow inbred maize lines

Significant variation existed in all the traits studied (Table 3). Table 3 presents the mean value and the standard error for each of the traits. The ASI was highest in lines TZEI 124 and TZEI 16, but least in lines BD74-222, TZEI 11 and TZEI 13. Line BD74-222 had the highest plant height and BD74-165 had the least. Line TZEI 124 produced highest maize grain yield whereas line TZEI 146 had least.

3.3. Association between pairs of some characters of 15 yellow elite maize inbred lines

Correlation coefficients between pairs of traits are shown in Table 4. All the characters that had significant phenotypic association with each other also showed significant genotypic relationship. The DTA, DTS, plant height and number of leaf per plant were positively correlated. Grain yield positively correlated with ASI, plant and ear heights, number of leaf per plant and leaf area.

3.4. Variances, coefficients of variation, heritability and genetic advance for traits in the maize inbred lines

Phenotypic, genotypic and environmental variances as well as their coefficients of variation are presented in Table 5. Similarly, heritability and expected genetic advance are presented in the table. Both the coefficients of variation of phenotype and genotype were generally low for all the traits except the yield parameters (number of ear per plant, ear and grain yield). Heritability ranged from 81.5% to 100% whereas expected genetic advance ranged from low (8.91) in days to silking to high (72.03) in number of ear per plant.

Table 3
Mean for the agronomic characters of 15 inbred lines of elite yellow maize evaluated in Ibadan in 2014.

Inbred line	Days to anthesis	Days to silking	Athesis-silking interval	Plant height (cm)	Ear height (cm)	Number of leaf/plant	Leaf area (cm ²)	Number of ear per plant	Ear weight per plot (kg)	Grain weight per plot (kg)
BD74-165	51.00	56.00	5.00	88.40	42.23	8.43	289.07	1.00	1.24	0.90
BD74-161	49.00	53.00	4.00	122.40	51.17	10.00	455.25	1.79	0.81	0.58
BD74-204	50.00	54.00	4.00	127.07	55.70	11.00	394.04	1.00	1.12	0.81
BD74-217	55.00	59.00	4.00	98.03	26.03	8.00	457.84	2.33	0.76	0.55
BD74-219	55.00	59.00	4.00	118.90	47.17	10.00	508.62	1.87	1.26	0.91
BD74-222	50.00	53.00	3.00	149.07	55.57	10.43	455.89	2.00	1.11	0.81
TZEI 10	52.00	57.00	5.00	122.10	41.87	9.30	282.06	1.00	1.45	1.05
TZEI 11	57.00	60.00	3.00	98.00	40.43	11.00	328.00	0.99	1.07	0.77
TZEI 12	52.00	57.00	5.00	105.80	51.43	11.20	327.35	1.01	1.30	0.94
TZEI 124	51.00	57.00	6.00	137.70	65.07	11.00	372.51	1.00	1.94	1.41
TZEI 128	51.00	56.00	5.00	106.53	38.27	10.00	235.30	1.00	0.78	0.56
TZEI 13	57.00	60.00	3.00	94.70	45.00	10.80	316.13	1.00	0.98	0.71
TZEI 146	52.00	56.00	4.00	106.90	38.40	10.00	290.50	1.00	0.62	0.45
TZEI 16	52.00	58.00	6.00	125.07	55.97	11.00	376.45	1.00	1.00	0.73
TZEI 8	49.00	53.00	4.00	102.90	45.93	9.20	331.54	1.06	0.72	0.52
Mean	52.00	56.53	4.33	113.57	46.68	10.09	361.37	1.23	1.08	0.78
SE (0.05)	0.68	0.63	0.25	3.68	4.54	0.15	33.14	0.27	0.37	0.27

Table 4
Association of agronomic character of 15 yellow elite inbred lines of maize.

Character	Attribute	DTS	ASI	PH	EH	NoL	LA	EPP	GRY
DTA	P	0.88**	0.22	0.33*	0.24	0.51**	0.22	0.14	0.16
	G	0.89**	0.22	0.33*	0.25	0.51**	0.23	0.14	0.18
DTS	P		0.26	0.38*	0.28	0.59**	0.26	0.16	0.19
	G		0.26	0.39*	0.29	0.60**	0.27	0.17	0.21
ASI	P			0.75**	0.57**	0.11	0.49**	0.28	0.38*
	G			0.75**	0.56**	0.11	0.50**	0.29	0.42**
PH	P				0.86**	0.17	0.78**	0.47**	0.55**
	G				0.87**	0.17	0.80**	0.48**	0.61**
EH	P					0.12	0.57**	0.32*	0.45**
	G					0.13	0.59**	0.33*	0.48**
NoL	P						0.12	0.67**	0.83**
	G						0.12	0.69**	0.92**
LA	P							0.36*	0.37*
	G							0.37*	0.41**
EPP	P								0.20
	G								0.23

*, and **, DTA, DTS, ASI, PH, EH, NoL, LA, EPP, GRY, P and G mean significant at $P = 5\%$ and 1% , days to anthesis, days to silking, anthesis-silking interval, plant height, ear height, number of leaf/plant, leaf area, number of ear per plant, gain yield, phenotype and genotype.

4. Discussion

Coefficients of variation and ranges of 10 agronomic characters of the maize lines explained that significant variation existed in all the characters. The coefficients of variation were high for number of ear per plant, ear weight and grain yield. Ranges were very high for all the parameters. This wide range in the values of the traits was adequate to distinguish the inbred lines using these traits. The zero and low CVs in the values of the traits may be expected because the lines have undergone inbreeding depression resulting in fixation of recessive genes and thus increasing homozygosity within the lines. Besides, the lines were developed for similar characteristic. These may be responsible for minimal differences among the lines based on these traits. Collective variations in the mean value and the standard error for each of the traits showed the distinctiveness of each lines. Though the means were normally distributed around a general mean under each trait; standard errors were low across the traits indicating that the lines shared almost the same pattern of gene actions. All the same, selection can be made among the array of inbred lines for further improvement.

The genotypic variances for DTA, DTS and ASI are same as their phenotypic variances resulting in zero environmental

variances. This makes the heritability of these characters to be 100%. The offspring of these lines will be exactly like their parents because there are no visible environmental effects on the expression of these characters. The genes expressed in each of these three traits were homozygous dominant for the traits. Low coefficients of variation of phenotype and genotype for all the characters except the yield parameters encourages the use of yield parameters in selection of suitable parents for crosses or lines further improvement. Traits such as ASI, plant height, ear height and leaf area may be considered where there is need to support the yield parameters because their coefficients of variation were comparatively large. The significant difference between the phenotypic and genotypic coefficient of variation of ear and grain yield emphasizes the significant role of environment in the inheritance of the characters.

The DTA, DTS, plant height and number of leaf per plant positively correlated. Grain yield positively correlated with ASI, plant and ear heights, number of leaf per plant and leaf area. Triveni et al. [22] also found that plant and ear heights, and number of leaf per plant of maize highly significantly and positively correlated with its grain yield. This implies that maize grain yield can be indirectly selected for, by considering any of ASI, plant and ear heights, number of leaf per plant and leaf area.

Table 5
Variability, heritability and expected genetic advance of some relevant agronomic characters of elite yellow inbred lines of maize.

Trait	Phenotypic variance	Genotypic variance	Environmental variance	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability (%)	Genetic advance (%) mean
Days to anthesis	6.89	6.89	0.00	5.03	5.03	100.00	10.36
Days to silking	5.98	5.98	0.00	4.33	4.33	100.00	8.91
Days to anthesis	0.95	0.95	0.00	22.54	22.54	100.00	46.43
Plant height	291.24	289.14	2.10	15.03	14.97	99.28	30.73
Ear height	91.33	88.14	3.19	20.47	20.11	96.51	40.70
No. of leaf/plant	0.98	0.98	0.00	9.81	9.80	99.63	20.14
Leaf area	6271.43	6101.43	170.00	21.91	21.62	97.29	43.92
No. of ear/plant	0.22	0.21	0.01	36.82	35.88	94.97	72.03
Ear weight	0.12	0.09	0.02	31.48	28.42	81.50	52.86
Grain weight	0.06	0.05	0.01	31.47	28.46	81.77	53.01

Heritability is the percentage of phenotypic variance that is attributed to genetic variance. In the present study heritability, was high (greater than 80%) for all studied characters. High heritability indicates that the environmental influence is minimal on characters. Any of the characters can, therefore, be used for selection. Akbar et al. [1], Rafiq et al. [18], Rafique et al. [19] have also reported high heritability for different yield controlling traits in maize. The comparatively lower heritability for grain yield of the maize, in this study, may be due to the fact that yield is a low heritable character which that is controlled by many genes. The progress in selection for this character in maize is general slow. The expected genetic advance that was low for days to anthesis, days to silking and number of leaf per plant may be compensated for by their high heritability. Ali et al. [2], Najeeb et al. [14] found that high heritability may not always associate with large genetic advance. Since high heritability does not always indicate a high genetic gain, heritability is recommended to be considered in association with genetic advance to predict the effect of selecting superior crops varieties.

References

- [1] M. Akbar, M.S. Shakoore, A. Hussain, M. Sarwar, *J. Agric. Res.* 46 (1) (2008) 39–45.
- [2] A. Ali, S. Khan, M.A. Asad, *Asian J. Plant Sci.* 1 (2002) 420–422.
- [3] B. Badu-Apraku, A. Menkir, S. Ajala, R. Akinwale, M. Oyekunle, K. Obeng-Antwi, *Can. J. Plant Sci.* 90 (2010) 831–852.
- [4] B. Badu-Apraku, M. Oyekunle, R. Akinwale, A. Fontem Lum, *Agron. J.* 103 (2011) 544–557.
- [5] M. Bänziger, G.O. Edmeades, D. Beck, M. Bellon, *Breeding for Drought and Nitrogen Stress Tolerance in Maize: from Theory to Practice*. CIMMYT, Mexico, D.F, 2000 68.
- [6] T. Baye, *J. Agric. Sci.* 139 (2002) 161–168.
- [7] D. Bello, A.A. Sajo, D. Chubado, J.J. Jellason, *J. Sustain. Dev. Agric. Environ.* 2 (2006) 120–126.
- [8] A.K. Binodh, N. Manivannan, P.V. Varman, *Madras Agric. J.* 95 (2008) 425–428.
- [9] D.S. Falconer, *Introduction to Quantitative Genetics*, third ed. Longman Scientific and Technical, Longman House, Burnt Mill, Harlow, Essex, England, 1989.
- [10] D.S. Falconer, F.C. Mackay, *Introduction to Quantitative Genetics*, fourth ed. Longman, New York, 1996 464.
- [11] FAO (Food Agricultural Organization), *World Agriculture: Towards 2015/2030 (2002) Summary Report*, Rome.
- [12] IAR&T, Institute of Agricultural Research & Training. *Farmers' Guide Series 1. No. 4: Guide on Maize Production*. Obafemi Awolowo University, Ibadan, 2010 7.
- [13] S.K. Kim, in: B. Badu-Apraku, M.O. Akoroda, M. Ouedraogo, F.M. Quin (Eds.), *Contributing to Food Self Sufficiency in Maize Research and Development in West and Central Africa*. Proceedings of a Regional Maize Workshop, 29 May–2 June 1995, IITA Cotonou, Benin Republic (1997), pp. 42–82.
- [14] S. Najeeb, A.G. Rather, G.A. Parray, F.A. Sheikh, S.M. Razvi, *Maize Genet. Coop. Newsl.* 83 (2009) 1–8.
- [15] C.C. Nwangburuka, O.A. Denton, *Int. J. Agric. Res.* 7 (7) (2012) 367–375.
- [16] W.E. Nyquist, *Crit. Rev. Plant Sci.* 10 (1991) 235–322.
- [17] B.A. Ogunbodede, S.A. Olakojo, in: B. Badu-Apraku, M.A.B. Fakorede, M. Ouedraogo, R.J. Carsky (Eds.), *Impact, Challenges and Prospects of Maize Research and Development in West and Central Africa*. Proceedings of a Regional Maize Workshop, IITA-cotonou, Benin Republic, 4–7 May 1999 (2001), pp. 139–146.
- [18] C.M. Rafiq, M. Rafique, A. Hussain, M. Altaf, *Agric. Res.* 48 (1) (2010) 35–38.
- [19] M. Rafique, A. Hussain, T. Mahmood, A.W. Alvi, B. Alvi, *Int. J. Agric. Biol.* 6 (6) (2004) 1113–1114.
- [20] S. Shukla, A. Bhargava, A. Chatterjee, J. Sirivastava, N. Singh, S.P. Singh, *Plant Foods Hum. Nutr.* 61 (2006) 23–28.
- [21] R.K. Singh, B.D. Chaudhary, *Biometrical Methods in Quantitative Analysis*. Kalayani Publishers, New Delhi, 1985.
- [22] S. Triveni, A. Kumar, S.C. Dwivedi, R.P. Vyas, *Plant Arch.* 14 (1) (2014) 19–21.
- [23] M.D. Smalley, J.L. Daub, A.R. Hallauers, *Maydica* 49 (2004) 221–229.
- [24] SAS Institute user's guide: *Statistics, Version 9.0*. SAS Institute Incorporated, 2004 1024.