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Maize germplasm agro-morphological trait characterization based on heritability and expected genetic advance analysis under Ethiopian conditions

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Abstract

Abstract Germplasm characterization is essential to describe germplasms and establish germplasm diagnostic characteristics and estimate the extent of variation in the gene bank collection. In the current study, totally 94 maize genotypes including 92 accessions obtained from Ethiopian Biodiversity Institute and two standard checks were used and collected eight agronomic and morphological traits. The work was aimed to characterize maize germplasm based on genetic parameters such as heritability (h2) and genetic advance (GA) data analysis. The experiment was carried out during the main cropping season 2016 at Arsi-Negelle research site, Ethiopia. The field was laid down in augmented design without replications. The results indicated that highest heritability value was obtained from the number of cobs per plant (72.66%) and lowest heritability also observed for kernel rows per cob (26.02%). Moreover, the maximum expected genetic advance was obtained from 1000 grain weight (76.28), while the highest genetic advance value was recorded from ear height. Therefore, important characters, number of cobs per plant, and ear height were showed high to moderate heritability and genetic advance. It can be concluded that these characters may be used as a selection tool in future pre-breeding programs.

Keywords: maize germplasm, quantitative traits, heritability, genetic advance

Introduction

The food crop Maize (*Zea mays* L.) is well-thought-out as one of the most vital food crop out of the main crop species on the basis of their importance in the global economy. It brings billions of dollars worldwide to the annual income in international market for many countries across a globe.[1] It is highly produced (861 million tons), wheat (655 million tons)[2] and it is 3rd in area under cultivation among all cereal crops. The total area used for maize production throughout the world is estimated 162 million hectares with an average production of 5195 kg ha^{-1}.[3]

It is believed that maize was first introduced to Ethiopia in the 16th or 17th century.[4] Since then, it has gained a lot of acceptance as a food crop for humans and animals. Central Statistical Authority of Ethiopia indicated that during 2000/2001, the average yield of the country was estimated 1.4 million ha in area coverage and 2.52 million tons in production, that accounts for about 20.9% of the total area and 32.6% of the total annual grain production.[5] To help the field of global food security gaps of the overgrowing population and to minimize load on wheat and rice crops availability, it is very important to boost the maize cultivation, for the reason that it is not only crucial for the survival of human kind as food crop and animal fodder for cattle but also has promising bright future in the form of using it as bio-fuel, which could be another source of energy. It is hopeful that the productivity of maize has been growing for the last few years, which was estimated to be 3415 kg/ha during 2008-09 and 4268 kg/ha during 2012-13, nevertheless, there is still a big gap for its further improvement programme in its production and productivity.[6]

Ethiopia has got a lot of potential maize indigenous germplasm and traditional landraces varieties collected in the gene bank and also conserved on the hands of farmers. So, in order to offer wider genetic base population for pre-breeding programs it is mandatory to use the gene bank collection of the present day genotypes for their potentially important traits.[7] Genetic Variations always plays a key role in for emerging or evolving of a new species survival and adaptability. Whenever there is change the population, the population will have to adapt to survive by itself; the ability of the population to cope up with the changing environment will determine their ability to live with an environmental challenge. Dissimilarity in the populations' gene pool allows natural selection to act upon traits that allow the population to adapt to the changing environments. The more genetic diversity a population has the more likelihood the population will be able to adapt.[8] It can be described through different system such as morphological, biochemical and molecular markers parameters. Among these parameters, the morphological characterization parameter is well-thought-out as the initial step or the base for further breeding research work.[9,10] The degree of diversity study has been considered by scientists in other crops as well, such as in Oryzasativa L., sesame ,and in maize respectively.[7,11,12] In the current work, we aimed to calculate maize germplasms for morphological characters; depending on their phenotypic and genotypic variability, heritability and expected genetic advance along with their descriptive statistical value. Therefore, this evidence will be valuable to recognize and determine the position of germplasm collection in Ethiopia and to identify the promising accessions of Maize for further improvement work via breeding.

Materials and methods

A total of 92 maize germplasms obtained from Ethiopian Biodiversity Institute (EBI) and two standard checks were used in the study Table 1-3. The selected germplasm was grown at Arsi-Negelle farm site,1,947 m a.s.l. (meters above sea level) and astronomically located at 7°219'N latitude and 38°08'E longitude Oromia Region, Ethiopia, during main rainy season 2016. The design used was augmented design without replications of accession in each block except for the checks following.[13] The Plot size was kept at 9 m long with four rows having row to row and plant to plant distance of 75 and 30 cm respectively. Fertilizers used were Urea and DAP at the rate of 200 and 150 kg, per hectare respectively. Standard cultural practices were followed from seed bed preparation, sowing, data recording and harvesting during the entire crop season. From each plot, 20 samples were chosen randomly to score eight morphological characters such as the number of days taken to 50%flowering in days, plant height in centimeter, cob height in centimeter, number of cobs/plant in numbers, number of days taken to 50% maturity in numbers, length of cob in centimeter, number of kernels/cob and 1000-grain weight measured in gram. Hence, data on eight morphological characters were subjected to the analysis of variance (ANOVA) using Statistical Analysis System (SAS) version 9.0software. Estimation of genetic variability like genotypic coefficient of variability, phenotypic coefficient of variability, broad sense heritability, and genetic advance as percent of the mean was computed based on Singh et al.[14] calculated by using the following formulas:

PCV= $\sqrt{PV}$ Phenotypic Variance x 100/ Grand Mean

GCV= $\sqrt{GV}$ Genotypic Variance x 100/ Grand Mean

Heritability% (h2) = (GV) ÷ (PV) x 100

Genetic advance (GA)= $\sqrt{PV}$ x h2 x k

Where k is the differential selection and value for k is 2.06 (in broad sense) advance percentage of mean= Genetic advance x 100/ Grand Mean.

Table 1 List of the used maize accessions number including checks

No	Acc. no	No	Acc. No	No	Acc. No	No	Acc. No	No	Acc. No
1	9187	21	18096	41	9183	61	10000	81	16279
2	9190	22	18098	42	9188	62	15247	82	16020
3	9191	23	18100	43	9192	63	15324	83	16021
4	9993	24	18103	44	9193	64	15325	84	16559
5	9994	25	18104	45	9194	65	15326	85	16561
6	16012	26	18106	46	9195	66	15327	86	16562
7	16023	27	18108	47	9984	67	15328	87	241584
8	16025	28	18112	48	9985	68	15455	88	18113
9	16226	29	18121	49	9986	69	15456	89	18114
10	16233	30	24297	50	9987	70	15457	90	18122
11	16234	31	98098	51	9988	71	15458	91	237657
12	16236	32	228786	52	9989	72	15459	92	24308
13	16261	33	237597	53	9990	73	15460	93	**BH660**
14	16262	34	237684	54	9991	74	15461	94	**BH540**
15	16269	35	239645	55	9992	75	15462		
16	16563	36	241616	56	9995	76	15463		
17	16567	37	239620	57	9996	77	15466		
18	16570	38	239668	58	9997	78	15467		
19	16571	39	9181	59	9998	79	16276		
20	16582	40	9182	60	9999	80	16278		

Table 2 The minimum, maximum, mean value and variation coefficient of the studied quantitative variables

No	Characters	Mean	Variance	SD	Minimum	Maximum	CV%
1	Days to 50% flowering	107.68	175.91	13.26	59	134	12.32
2	Plant height (cm)	2.22	0.15	0.39	1.06	3.04	17.35
3	Ear height (cm)	1.02	0.13	0.354	0.26	1.95	34.62
4	Number of cobs/plant	2.04	0.39	0.63	0	3.25	30.57
5	Days to maturity	143.67	175.91	13.26	95	170	9.23
6	Ear length (cm)	15.33	3.33	1.83	10.65	18.95	11.91
7	Kernel rows per cob	12.33	0.7	0.84	9.8	15.6	6.8
8	1000 grain weight(g)	340.29	2782.36	52.75	196	504	15.5

Where, SD, standard deviation; CV, coefficient of variation

Table 3 Genotypic and phenotypic coefficient of variations, heritability and genetic advance for some plant traits in maize germplasm

No	Characters	Vg	Vp	GCV%	PCV%	h2	GA	GAM%
1	Days to 50% flowering	81.45	279.6	8.38	15.53	53.9	18.59	17.26
2	Plant height (cm)	0.03	0.27	7.79	23.38	33.3	0.36	16.06
3	Ear height (cm)	0	0.25	30.91	48.92	63.2	0.65	63.68
4	Number of cobs/ plant	0.28	0.53	25.87	35.6	72.7	1.09	53.29
5	Days to maturity	81.45	279.6	6.28	11.64	53.9	18.59	12.94
6	Ear length (cm)	0.75	6	5.65	15.92	35.5	1.78	11.64
7	Kernel rows per cob	0.09	1.33	2.43	9.35	26	0.62	5.01
8	1000 grain weight(g)	1371.49	4349	10.88	19.38	56.2	76.28	22.42

Where,

Vg, Genotypic variance; Vp, Phenotypic variance; GCV, Genotypic coefficient of variation; PCV, Phenotypic coefficient of variation; h^2 (bs), Heritability broad sense; GA, Genetic advance; GAM, GA as percent of mean

Results and discussion

Descriptive statistics were calculated in order to elucidate the basic traits of the data in this research study. They offer us simple pictures about the sample and the measures and they form the basis of virtually every quantitative analysis of the data, such as mean, minimum, maximum, standard deviation, coefficient of variation and variance for each quantitative character was computed among the genotypes is given in Table 2.The form of variability existed among genotypes were unlike for different morphological characters. The maximum variability in the trait was observed in 1000grain weight (2782.36) followed by number of days taken to maturity (175.91), and number of days taken to flowering (175.91). On the other hand, the statistical analysis of the quantitative variables measured on accessions in Table 1. The result showed that coefficient of variation was found between the range of 6.80 and 34.62%. Hence, the variables such as days taken to 50 % of flowering, plant height, ear height, number of cobs per plant, ear length and 1000 grain weight were recorded a high coefficient of variation (>10%). Conversely, numbers of days taken to maturity, and kernel rows per cob were found in the range low coefficient of variation (<10%).

The approximate calculation of genotypic variance, phenotypic variance, genotypic coefficient of variation and phenotypic coefficient of variation, heritability and genetic advance for 8 different variables of the maize accessions are presented in Table 3. The value of phenotypic coefficient of variation was higher than the coefficient of genotypic variance for all the characters studied revealing that the apparent variation is not totally due to the genotypes, but also the influence of environmental factors are involved.

The highest phenotypic coefficient of variation was recorded form ear height (48.92) followed by number of cobs per plant (35.60) and plant height (23.38). Likewise, the highest coefficient of genotypic variance was observed in ear height (30.91) secondly by number of cobs per plant (25.87) and thirdly by1000 grain weight (10.88). On the other hand, on an average from very high to moderate phenotypic coefficient of variation and genotypic coefficient were obtained for ear height, number of cobs/plant, plant height and 1000 grain weight providing sufficient variability and thus offers scope for genetic improvement through selection for the best or novel traits. According to Singh P[15] and Abirami S[16] reported high PCV and GCV values for grain yield per plant and ear height in maize. Moderate PCV values of ear girth, ear length, 1000-grain weight and number of grain rows per cob were reported by Singh P.[15] The estimates of the genotypic coefficient of variation reflect the total amount of genotypic variability existed in the maize germplasms which could likely to be transmitted from parents to the progeny is due to the trait heritability.

The statistical computation of heritability in a broad sense revealed that number cobs per plant trait recorded the highest value of (72.66 %) and moderate for ear height (63.20 %), 1000 grain weight (56.15 %), number of days taken to 50% of flowering is (53.97). The higher estimates results of heritability depicted that selection on the basis of phenotypic performance of genotypes would also be more efficient for further improvement of these promising characters of maize genotypes.[17] Conversely, a low heritability result was recorded for ear length (35.49 %) and plant height (33.33 %), kernel rows per cob (26.02 %). Similar studies have also reported lowest broad sense heritability estimate of 32.29% for days from planting to harvesting and highest value of 99.99% for ear weight with sheath and ear weight without a sheath. Low to high heritability values were obtained by in their research study on nine traits in maize genotypes.[18,19]

The highest estimate results of genetic advance as percent of mean (63.68) was computed and obtained for ear height followed by number of cobs/ plant (53.29), and 1000 grain weight (22.42). This indicates that selection would be highly promising for continuous improvement of such novel traits. There was also similar findings were reported by Alake et al.[19] who have recorded highest genetic advance as percent of mean for kernel row per ear (39.49) followed by grain yield/hectare (33.98) and ear length (16.54). Shelling percentage had the lowest result GA (% mean) of 6.42, followed by number of leaves/plant and days to 50% male flowering with 8.09 and 8.36 respectively.

Conclusion

Genetic variations existing in a population of a given crop plays a key role in improvement of that particular crop by using the latest technologies of plant breeding. This study was aimed at identifying and screening genetic diversity in 94 maize germplasms using agro-morphological traits. Hence, in conclusion, the highest estimated results of genotypic, and phenotypic coefficient of variation, heritability and genetic advance were observed for cob height and number of cobs/plant and suggesting sufficient genetic variability. Moreover, it also provides opportunities for maize genetic improvement through selection which is a basic research for further breeding work.

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Conflicts of interest

Authors declare no conflicts of interest.

References

1. Mabberely DJ. Mabberley's Plant–Book: A portable dictionary of plants their classifications and uses. 3rd. Cambridge University Press: VII–XVIII. 1–1021. 2008.
2. Anonymous. International Grains Council. Grain Market Report: 443. 2014
3. Anonymous. FAOSTAT Food and Agricultural commodities production. Food and Agriculture Organization of the United Nations. 2012.
4. Hffengal HP. Agriculture in Ethiopia. FAO. Rome. 1961.
5. Central Statistical Authority. Agricultural sample survey 2000/2001 on area production of major crops private peasant holdings. Meher season. Statistical bulletins 190. *Addis Ababa*. Ethiopia. 2001;3.
6. Farooq O. Agriculture In Pakistan Economic Survey. Government of Pakistan. 2013.
7. Iqbal J, ZK Shinwari, MA Rabbani. Investigation of total seed storage proteins of Pakistani and Japanese maize (Zea Mays L) through SDS–PAGE markers. *Pak J Bot*, 2014;46(3):817–822.
8. Bruford MW, Davies N, Dulloo ME, et al. Monitoring Changes in Genetic Diversity. The GEO Handbook on Biodiversity Observation Networks. Springer. Cham. 2017;107–128.
9. Smith JSC, OS Smith. The description and assessment of distance between inbred lines of maize. The utility of morphological, biochemical and genetic descriptors and a scheme for the testing of distinctiveness between inbred lines. *Maydica.* 1989;34:151–161.
10. Khan SA, J Iqbal, H Khurshid, et al. The extent of intra–specific genetic divergence in Brassica napus L. population estimated through various agro–morphological traits. *Eu. Acad Res.* 2014;2(2):2255–2275.

11. Rabbani MA, MS Masood, ZK Shinwari, et al. Genetic analysis of basmati and non–basmati Pakistani rice (*Oryza sativa L.*) cultivars using microsatellite markers. *Pak J Bot*. 2010;42: 2551–2564.
12. Akbar F, MA Rabbani, ZK, et al, Genetic divergence in sesame (Sesamumindicum L.) landraces based on qualitative and quantitative traits. *Pak. J. Bot.* 2011;43:2737–2744.
13. K Tesfay. Acta Universitatis Sapientiae Agriculture and Environment. Genetic diversity study of sorghum (Sorghum bicolor(L) Moenc) genotypes. Ethiopia. 2017;9:44–52.
14. SINGH RK, CHAUDHARY BD. Biometrical Methodsantitative Genetics Analysis. Kalyani Publishers: 1977;281–284.
15. Singh P, Dass S, Kumar Y, et al. Variability studies for grain yield and component traits in maize (Zea mays L). *Annals Agri Bio Res.* 2003;8(1):29–31.
16. Abirami S, Vanniarajan C, Armugachamy S. Genetic variability Studies in maize (Zea mays L) germplasm. *Plant Archieves.* 2005;5(1):105–108.
17. Jadhav AR, Chaudhari KN, Desai RT, et al. Variability for yield and quality traits in (single–cut) forage sorghum (Sorghum bicolor (L) Moench). *Indian J Plant Genet Resour.* 2011;24(2):205–210.
18. Ojo DK, Omikunle OA, Oduwaye OA, et al. Heritability, character correlation and path coefficient analysis among six inbred lines of maize (Zea mays L). *World J Agrl. Sci.* 2006;2(3):352–358.
19. Alake CO, Ojo DK, Oduwaye OA, et al. Genetic variability and correlation studies in yield and yield related characters of tropical maize (Zea mays L). *ASSET Series A*. 2008; 8(1):14–27.

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