

Genetic Diversity among Maize (*Zea mays* L) Genotypes Based on Fodder Yield and Quality Parameters

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DOI: <http://doi.org/10.46382/MJBAS.2022.6202>

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Article Received: 15 January 2022

Article Accepted: 22 March 2022

Article Published: 11 April 2022

ABSTRACT

Maize (*Zea mays*) is cultivated all over the world including Pakistan for fodder and grain. Genetic diversity and environmental effects greatly affect the fodder yield and quality in maize. Therefore, it is imperative to assess the genetic diversity among 31 maize genotypes for fodder and quality related traits. Genotypes were collected from the Australian Grain Gene Bank and grown under field conditions with three replications following randomized complete block design. The morphological traits such as plant height (cm), leaf area (cm²), leaf-stem ratio (wt. basis), stem girth (cm), leaves plant⁻¹, days to 50% silking, days to 50% tasseling, leaf moisture (%), dry fodder yield plant⁻¹ (g), green fodder yield plant⁻¹ (g) and quality traits such as crude protein (%), ether extract (%), ash content (%), crude fiber (%) and nitrogen-free extract (%) were recorded.

Analysis of variance, biplot analysis and genotypic and phenotypic correlation were performed. Analysis of variance revealed significant differences with days to 50% silking, days to 50% tasseling, plant height, stem girth, leaf area, leaves plant⁻¹, moisture percentage, green and dry fodder yield, crude protein, crude fiber, ether extract, ash content and nitrogen free extract and non-significant differences with leaf stem ratio. At phenotypic and genotypic level, dry fodder yield plant⁻¹, plant height, stem diameter, leaf moisture %, No. of leaves, days to 50% silking, crude fiber and ether extract revealed significant correlation with fodder yield plant⁻¹.

Biplot analysis based on PCA for different quantitative parameters showed that first two principal components i.e F₁F₂ are contributing 23.29% and 14.53 % to the total variations respectively. Based on all the results the best genotypes were DTMA-271, DTMA-15, DTMA-281 and DTMA-295 could be used in breeding programs.

Keywords: Correlation, Fodder yield, Genetic diversity, Maize quality, PCA.

1. Introduction

Maize is cultivated for fodder and grain purposes all over the world including Pakistan. The first and the most important purpose of its cultivation is the processing of grains for food, human consumption and various industrial uses. Second, it is used as forage for livestock feed purposes.

The current population of livestock in Pakistan, cattle, buffaloes goats and sheep is 51.5, 42.4, 80.3 and 31.6 million, respectively. Fodder crops are grown over 2.038 million hectares of the total cropped area (23.3 million hectares) but it is deficient to meet the requirements of animals in Pakistan [1]. Due to the unavailability of feed for animal production, the livestock sector is not progressing at a proper rate.

As farmers become engaged in cultivating human food crops, the livestock sector faced a serious shortage of fodder. Therefore, inferior quality fodder and low production reduce the fodder availability to only 23% of feeding requirements for livestock [2]. Maize is renowned for its superior characters such as fast growth, high palatability, free from anti quality components, wider adaptability and high digestibility.

In comparison to other non-leguminous fodder crops, it has better nutritional quality due to the presence of starch (66.7%) and proteins (10%) [3]. Its fodder has highly nutritious value, palatable and succulent which is relished by animals especially milk animals. Maize is a short maturity period crop and it is cultivated for silage formation, grains and fodder. Maize fodder increases the body weight and milk quantity of animals. It contains

high nutritional value for fodder *i.e.* starch (66.7%), protein (10%), fiber (8.5%), sugar (3%) and ash (7%) [4]. In Pakistan maize is cultivated on large scale and it covers an area 1.418 million hectares and the production is 8.465 million tons annually [2].

From the total world production only two third is utilized for animal feed and commercially for oil and starch production in all over the world. No doubt maize is highly nutritional crop but its production in Pakistan is not enough to complete the human and livestock requirements. Therefore, it is necessary to modify the genetics of the traits that are responsible for quality of fodder. Genetic variations play an important role to understand the genetic variation helpful for nominating the elite genotypes for the desired traits. Wide diversity present in maize crop fruitful in breeding programs for improving the fodder quality and yield.

Association existing among different traits (genotypic and phenotypic correlation) determines the mutual relationship of traits. For developing desired genotypes it is important to estimate the relationship of various traits which are directly linked with fodder yield. Therefore, correlation analysis is effective method for selecting the traits that can be used in breeding program. Therefore, the aim of the study to elite the maize genotypes based on morphological and quality traits and that could be used in breeding programs in future.

2. Material and Methods

The experiment was planned in autumn season 2018 at MNS-University of Agriculture, Multan Pakistan. The 31 maize genotypes were collected from Australian Grain Gene Bank given in Table 1. These were sown in a randomized complete block design (RCBD) with three replications. The genotypes were sown following the dibbling method with a rate of one seed per hole on 29th of August 2019.

Each genotype was maintained with row \times row and plant \times plant distance of 75 cm and 25 cm, respectively. Before sowing recommended fertilizers *i.e.* urea (1bag, 50kg per acre) and DAP (1bag, 50kg per acre) were applied properly. At tasseling stage recommended dosage of DAP (1bag, 50kg per acre) was also applied. To control the shoot fly Trichlorofan was applied @ 250g/acre at seedling stage. A systematic insecticide Furidan was applied @ 8kg/acre against the stem borer. For imitation and establishment, the crop received seven irrigation of nine to eleven days interval. Weeding was carried out by hand hoeing.

Table 1. Maize (*Zea mays* L) germplasm collection

Sr. #	Genotype	Sr. #	Genotype	Sr. #	Genotype
1	NS(FS)L.F.W-8	12	DTMA-155	23	DTMA-289
2	TL83B-1581-11	13	DTMA-160	24	DTMA-295
3	Sel precoz C12	14	DTMA-161	25	DTMA-297
4	Rampur-8078	15	DTMA-164	26	DTMA-298
5	A 131-60	16	DTMA-195	27	DTMA-266

6	DTMA-181	17	DTMA-208	28	DTMA-254
7	DTMA-183	18	DTMA-265	29	PGH39
8	DTMA-184	19	DTMA-15	30	LH123HT
9	DTMA-187	20	DTMA-271	31	LP5
10	DTMA-119	21	DTMA-276		
11	DTMA-127	22	DTMA-281		

2.1. Morphological traits

Randomly five plants in each replication per genotype were selected for data recording of morphological traits. Following traits are considered for data recording, plant height (PH) (cm), days to 50% tasseling (DTT), days to 50% silking (DTS), leaves plant⁻¹, stem diameter (SD), leaf-stem ratio (LSR), leaf area (LA) (cm²), leaf moisture (MOS) (%), green fodder yield (GFY) and dry fodder yield (DFY) plant⁻¹.

2.2. Fodder quality traits

Five plants in each replication per genotype were collected and chopped manually for quality analysis. Ash content %, crude fiber (CF) %, ether extract (EE) %, nitrogen free extract (NFE) % and crude protein (CP) % (N x 6.25 equals crude protein content) were estimated by following the protocol of micro-kjeldahl, AOAC (1965).

3. Statistical Analysis

The Data collected on all parameters were analyzed by using analysis of variance technique and Duncan's new multiple range (DMRT) test at 1% probability level were applied to compare the means [5]. The Biplot analysis was performed for the selection of stable and adapted genotypes based on all traits along with yield by using XLSTAT software [6]. Among the traits under study genotypic and phenotypic correlation coefficient were estimated according to the statistical techniques given by [7].

4. Results and Discussion

4.1. Analysis of variance

Analysis of variance revealed significant differences with days to 50% silking, days to 50% tasseling, PH, LA, SD, MOS %, leaves plant⁻¹, GFY plant⁻¹, DFY plant⁻¹, CF %, CP %, EE %, ash content % NFE % while non-significant differences with LSR values given in Table 2. The mean values of PH, leaves plant⁻¹, DTS, SD, LA, LSR, MOS %, GFY plant⁻¹ and DFY plant⁻¹, EE (%), CF (%), NFE (%), CP (%) and ash content (%) were 156 to 46 cm, 62 to 56, 9 to 4, 14 to 9 cm, 255 to 170 cm², 0.7 to 0.2, 65 to 37%, 163 to 60 g, 79 to 24 g, 9.55 to 3.58 %, 26.43 to 15.08 %, 56.67 to 45.22 %, 10.34 to 7.82 % and 13.97 to 6.61 %, respectively given in Table 3.

The DMRT results based on morphological and quality traits revealed that the genotype DTMA-271 gave best performance for DTT, DTS, PH, number of leaves, GFY plant⁻¹, CP and SD given in Table 4. The genotype DTMA-15 gave best performance for LA, SD, MOS %, CP and number of leaves plant⁻¹ which is given in Table 2.

The genotype DTMA-281 gave best performance for MOS %, SD, CP and GFY plant⁻¹ performed better as compared to other genotypes.

Table 2. Maximum and minimum value for morphological and quality parameters of maize genotypes

Morphological Parameters	Minimum Value	Maximum Value
Days to 50% Tasseling	49	55
Days to 50% Silking	56	62
Plant height (cm)	46	156
Stem diameter (cm)	9	14
No. of leaves plant ⁻¹	56	62
Leaf: stem ratio (wt. basis)	0.26	0.74
Leaf area (cm ²)	172.73	255.95
Green fodder yield (g)	60	163
Dry fodder yield (g)	24	79
Moisture (%)	37	65
Quality Parameters		
Crude protein (%)	7.82	10.34
Crude Fiber (%)	15.08	26.43
Ash Content	6.61	13.97
Ether Extract %	3.58	9.5
Nitrogen free extract	45.22	56.67

Table 3. Mean square of absolute values for morphological and quality traits in maize genotypes

SOV	DF	DTT	DTS	PH	NOL	SD	LA	LSR	MOS	GFY	DFY	Ash	CP	CF	ETH	NFE
Replications	2	6.1	6.1	1211.1	3.1	20.1	44404.9	0.96	1626.3	3844.2	1188.9	24.2	11.5	191.8	15.3	184
Genotypes	30	13.6**	13.6**	5920.3**	8.6*	13.7*	1229.8*	0.08 ^{ns}	313.6*	2115.2**	2115.2*	6.9**	1.4**	21.9*	6.2*	32.4**
Error	296	3.4	3.4	3822.6	2.7	8.6	355.9	0.03	210.4	1962.2	624	3.1	1	17.1	5.1	19.7

SOV= Source of variation, DF= Degree of freedom, *= significant, **= highly significant, NS= non-significant

Table 4. Mean performance of morphological and quality parameters in maize genotypes

Genot ype	DTMA- 271	DTMA- 281	DTMA- 298	LP5	Rampur -8078	DTMA- 297	DTMA- 184	DTMA- 254	PGH39	DTMA- 266	Sel precoz C12	DTMA- 295	DTMA- 160	LH123HT	DTMA- 289	DTMA- 119	DTMA- 155
DTT	55.50 a	54.99 ab	54.55 b	53.63 c	53.33 cd	53.08 cde	53.00 cdef	52.92 def	52.83 defg	52.80 defgh	52.77 defgh	52.63 defghi	52.62 defghi	52.55 efghij	52.52 efghij	52.33 fghijk	52.27 fghijkl
DTS	62.61 a	60.00 efg	61.85 b	60.69 cd	59.61 fgh	61.16 c	60.33 de	59.66 efgh	59.08 hij	61.90 b	58.11 lmn	60.19 def	57.57 no	59.23 ghi	59.61 fgh	59.20 hij	59.05 hij
PH	156.76 a	86.91 l	95.62 f	67.50 t	83.91 n	96.44 e	80.66 p	100.73 c	95.45 f	94.48 g	65.72 u	91.76 i	86.38 l	49.44 w	91.44 i	98.88 d	82.11 o
NOL	9.66 a	7.85 fghi	7.30 ghijk	7.75 fghi	9.38 b	7.94 efgh	8.33 def	8.23 def	7.69 fghij	8.93 bed	7.00 jk	8.09 ef	8.34 def	4.55 l	6.97 jk	8.11 ef	9.16 bc
SD	14.56 a	14.42 a	12.76 bc	12.25 cd	11.89 de	13.10 b	10.98 f	10.87 f	11.86 de	14.06 a	9.88 gh	13.14 b	13.10 b	9.42 h	12.15 cd	14.03 a	12.79 bc
LA	237.59 E	223.96 M	219.85 q	226.25 l	211.63 s	228.48 j	219.82 q	221.23 o	231.65 h	222.94 n	208.34 t	218.84 r	233.08 h	236.19 f	221.08 o	227.14 k	220.18 pq
LSR	0.74 a	0.62 a	0.49 a	0.45 a	0.57 a	0.43 a	0.39 a	0.32 a	0.48 a	0.42 a	0.37 a	0.61 a	0.41 a	0.26 a	0.57 a	0.44 a	0.57 a
MOS	55.39 D	65.77 A	40.50 R	54.28 E	53.36 Fg	44.17 P	44.24 op	^{39.97} t	52.96 gh	47.46 n	47.53 n	39.91 s	52.37 hi	52.08 i	50.81 jk	56.08 c	53.75 ef
GFY	125.88 e	163.23 a	120.02 n	81.02 t	60.80 y	127.94 d	99.00 p	81.60 t	110.31 j	148.61 b	69.00 x	111.79 i	93.32 q	60.55 y	108.83 k	100.77 o	120.77 g
DFY	54.94 g	43.71 n	69.12 c	36.86 r	28.30 t	73.75 b	54.33 gh	53.04 i	50.80 k	79.16 a	35.83 s	69.39 c	43.52 no	24.44 u	60.75 d	43.02 o	56.66 f
Ash	9.01 kl	10.66 fgh	11.21 def	13.97 a	9.66 jk	8.18 m	9.46 jkl	10.91 efg	12.70 b	11.15 defg	9.96 hij	9.08 kl	9.71 jk	11.21 def	11.16 defg	8.89 l	11.56 de
CP	10.34 A	10.05 Ab	7.97 Jk	8.71 fghi	8.52 ghijk	9.04 defgh	9.51 bcde	7.82 K	9.34 bcdef	7.98 Jk	9.48 bcde	8.86 efghi	8.59 ghij	8.74 fghi	8.58 ghij	9.51 bcde	9.19 cdefg
CF	23.72 fg	24.35 ef	26.43 a	24.82 de	20.90 mn	22.83 hi	21.61 kl	20.32 no	19.11 p	21.63 kl	24.99 cde	23.30 gh	25.38 bcd	20.21 o	21.21 lm	23.24 gh	26.00 ab
EE	9.30 a	6.31 de	6.20 def	4.62 jk	5.12 ghijk	5.26 ghij	6.56 d	6.38 de	4.49 k	6.32 de	5.68 efg	6.77 d	7.95 bc	6.76 d	4.05 ghijk	6.59 d	5.59 fgh
NFE	56.67 a	56.05 ab	46.18 q	47.86 op	55.79 bc	54.68 de	52.83 i	54.55 ef	55.79 bc	51.54 jk	49.02 mn	49.45 m	48.36 no	53.06 hi	53.98 fg	51.74 j	47.65 p

DTMA-208	52.27 fghijkl	59.33 ghi	85.69 m	9.65 a	13.09 b	238.23 d	0.58 a	54.08 e	108.73 k	52.30 j	10.65 fgh	9.65 abcd	17.19 q	6.44 d	49.45 m
DTMA-195	52.16 ghijkl	58.00 lmn	90.63 j	8.41 def	13.17 b	223.59 n	0.54 a	55.06 d	123.13 f	52.51 ij	11.82 cd	8.89 efghi	19.05 p	4.92 hijk	55.31 cd
DTMA-161	52.08 hijkl	53.33 klm	69.13 s	8.40 def	11.26 ef	239.95 b	0.53 a	53.41 fg	76.40 u	35.26 s	11.35 def	8.83 efghi	25.60 bc	3.58 l	50.63 l
DTMA-181	52.00 ijkl	58.50 jkl	72.33 r	7.16 ijk	12.72 bc	239.49 bc	0.47 a	51.27 j	81.50 t	45.50 m	11.19 defg	9.89 Abc	24.13 f	7.66 c	45.22 r
DTMA-187	52.00 ijkl	58.66 ijkl	52.00 v	6.66 k	11.22 ef	117.73 u	0.48 a	53.34 fg	85.66 s	40.66 q	9.94 ij	8.44 Hijk	20.13 o	4.80 ijk	50.99 kl
TL33B-1581-11	51.87 jkl	57.48 no	65.44 u	7.80 fghi	10.25 g	228.96 j	0.47 a	50.63 kl	72.61 w	37.18 r	7.45 n	9.90 Abc	22.44 ij	4.45 k	55.73 bc
DTMA-265	51.71 kl	58.08 lmn	86.27 lm	7.25 hijk	12.03 d	223.58 m	0.42 a	47.41 n	104.21 m	54.80 g	11.12 defg	7.98 Jk	19.17 p	8.05 bc	53.66 gh
NS(FS)L-F.W-8	51.66 klm	56.33 p	84.33 n	8.08 ef	11.86 de	239.20 c	0.53 a	49.12 m	103.58 n	60.83 d	11.77 cd	9.21 cdefg	21.85 jkl	7.46 c	48.85 mn
DTMA-127	51.58 lmn	58.66 ijkl	77.30 q	6.80 k	11.05 f	220.60 op	0.39 a	55.09 d	110.61 j	49.30 l	11.64 cd	7.90 Jk	23.72 fg	7.65 c	49.07 m
DTMA-164	51.55 lmn	58.00 lmn	89.77 k	8.66 cde	10.94 f	230.20 i	0.56 a	43.51 q	73.55 v	41.88 p	12.28 bc	9.02 defgh	21.92 jk	6.15 def	50.61 l
DTMA-276	51.00 mn	59.25 hi	108.25 b	8.00 efg	14.20 a	230.64 i	0.35 a	46.94 n	105.00 l	58.91 e	10.47 ghi	8.27 Ijk	19.43 p	5.46 ghi	49.26 m
A 131-60	50.95 no	57.57 no	67.54 t	7.33 ghijk	13.04 b	234.02 g	0.39 a	44.86 o	90.12 r	53.77 h	11.25 def	9.33 bcdef	15.80 r	8.59 b	55.01 de
DTMA-15	50.33 o	57.26 o	93.80 h	9.86 a	14.44 a	250.95 a	0.66 a	60.53 b	110.40 j	56.60 f	10.05 hij	9.96 Ab	25.05 cd	9.55 a	56.34 ab
DTMA-183	49.66 p	57.66 mno	72.00 r	9.55 b	13.20 b	235.70 f	0.47 a	49.97 l	143.33 c	54.66 g	6.61 o	8.44 Hijk	25.33 bcd	6.53 d	53.08 hi

4.2. Correlation analysis

At genotypic and phenotypic level significant association of GFY plant⁻¹ was observed with DTS, PH, NOL plant⁻¹, SD, MOS %, DFY plant⁻¹, CF and EE %.

Significant association of PH was observed with, DTS, NOL plant⁻¹, SD, GFY plant⁻¹, DFY plant⁻¹ and CF, while significant association of NOL plant⁻¹ were observed with PH, SD, LSR at genotypic and phenotypic level, respectively. At genotypic and phenotypic level significant association of leaf area was examined with GFY plant⁻¹, DFY plant⁻¹ and NFE % given in Table 5.

Table 5. Above diagonal (phenotypic) and below diagonal (genotypic) correlation coefficient of different traits in maize genotypes

Traits	DTT	DTS	PH	NOL	SD	LA	LSR	MOS	GFY	DFY	Ash	CP	CF	ETH	NFE
DTT															
DTS	0.890*														
PH	0.623*	0.872*													
NOL	-0.066	0.522*	0.771*												
SD	0.760*	0.594*	0.413*	0.540*											
LA	-0.278	0.471*	0.628*	0.260	0.820*										
LSR	0.171	0.310*	-0.107	0.260	0.089	0.310*									
MOS	-0.093	0.2840*	-0.020	-0.067	0.005	0.2840*	0.162								
GFY	0.163	0.124	0.373*	0.464*	0.401*	0.115	0.298*	0.198*							
DFY	0.426	0.368*	0.443*	0.513*	0.596*	0.0780*	-0.407*	0.701*	0.599*						
Ash	0.216	-0.265	0.0380*	-0.111	-0.156	0.012	-0.049	-0.160	-0.116	-0.116					
CP	0.486*	-0.001	0.223	-0.036	0.0280*	-0.005	-0.046	-0.026	-0.001	-0.001	-0.205				
CF	0.365*	0.170	0.1710*	0.0480*	-0.133	0.105	0.196	0.156*	-0.017	-0.017	-0.179	0.2060*			
ETH	0.488*	-0.060	0.0760*	0.0760*	0.197	0.2630*	-0.221	0.099*	0.2360*	0.2360*	-0.109	0.033			
NFE	0.615*	-0.060	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
	-0.442*	0.0100*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
	0.777*	0.0100*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
	0.431	0.0100*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
	0.099*	0.0100*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
	0.979*	0.0100*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
	0.358*	0.0100*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
	-0.142	0.0100*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
	0.423	0.0100*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.0100*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.1710*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.0760*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.522*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.413*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		-0.009	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.067	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.477*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		-0.107	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		-0.020	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.133	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.123	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.185	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.1730*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.350*	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		0.140	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		-0.168	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			
		-0.179	0.0100*	0.0100*	0.0920*	-0.207	-0.035	-0.095	-0.036	-0.036	-0.225	-0.296			

ETH	-0.429	-0.218	0.326	-0.174	0.470*	0.550*	-0.434	-0.121	0.209*	0.731*	-0.573*	0.323*	0.855*		-0.392*
NFE	-0.248	-0.216	-0.179	-0.046	0.617*	-0.787*	-0.172	-0.185	-0.282	-0.156	-0.211	-0.486*	-0.921*	-0.599*	

4.3. Biplot analysis

Biplot analysis was performed to evaluate the genotypes based on morphological and biochemical traits. The Biplot analysis based on PCA for different quantitative parameters showed that first two principal components i.e. F_1 and F_2 are contributing 23.29% and 14.53 % to the total variations, respectively. The genotypes which were closer from the origin were considered as less similar as compared to those genotypes which were away to the origin [7]. The evaluation of the genotypes was divided into three categories which were given below.

4.3.1. Morphological traits

In the Biplot analysis the OP (origin point) length and the direction of the vectors in the given environments was considered very important for the selection of the genotypes. In the present study, the genotype DTMA-271 performed well from other genotypes in DTF, DTM, GFY and PH traits because of high OP length and positive direction of the vectors and the average values of the given traits were 52.80, 61.90, 148.61g and 94.48, respectively. The genotype DTMA-15 performed well in SD and DFY traits except the other genotypes. The OP length of this genotype for given traits was high as compared to other genotypes and the average value of these traits were 13.10cm and 73.75g, respectively. It was resulted from the Biplot analysis of the genotypes for morphological data only DTMA-271 genotype was performed well in most morphological traits as related to other genotypes.

4.3.2. Biochemical traits

In the biochemical traits the vectors were randomly scattered and the direction of the most vectors were downward but in positive manners. In the scattered vectors of the traits the genotype DTMA-298 was performed excellent in CP and Ether traits as compared to the others genotypes. The average values of given traits were 7.57% and 6.20%, respectively. While the DTMA-183, DTMA-155, DTMA-281 and DTMA-295 were also performed well for the given traits. The direction of the vectors was upward and OP length was also high for the NFE trait and in NFE trait only PGH-39 genotype performed well related to others. Based on NOL trait four genotypes NS(FS)L.F.W-8, DTMA-184, DTMA-271, DTMA-119 performed well but DTMA-271 genotype considered as an ideal genotype based on the NOL trait as related to others because the OP length of this genotype was higher than the others. It was resulted from the Biplot analysis of the genotypes for biochemical data only DTMA-298 genotype was considered as an ideal genotype for the EE and CP traits and PGH-39 for NFE trait.

4.3.3. Ideal genotypes for morphological and biochemical traits

In Biplot analysis only four genotypes were considered as ideal and best performing genotypes in the given environments. DTMA-271, DTMA-289 and DTMA-15 were screened out as best performing genotypes in both

quantitative traits. The data of these genotypes were also guided that the morphological traits are interlinked with most of the biochemical traits. As NOL, LA were interlinked with the CP and EE contents while PH, SD, DTT and DTS were linked with DFY and DGY traits. The interaction of these quantitative traits was fruitful for the breeders to develop the desire traits containing genotypes for the present and future era.

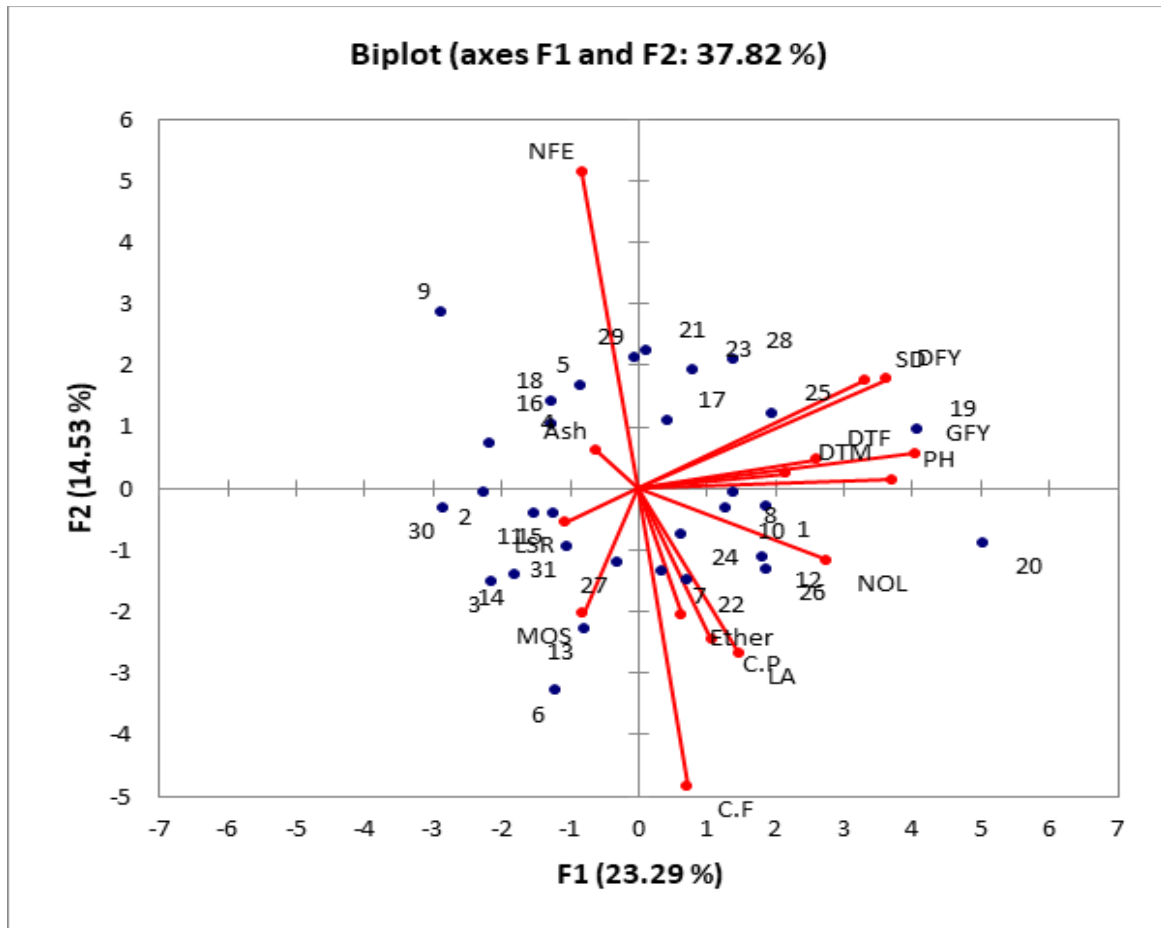


Fig.1. Biplot of different morphological and quality parameters of maize genotypes

5. Discussions

Analysis of variance revealed significant differences with DTT, DTS, PH, SD, LA, NOL plant⁻¹, MOS %, GFY plant⁻¹, DFY plant⁻¹, EE %, CF %, NFE %, CP % and ash content %. The highly significant differences indicate the presence of variability [8], studied traits which is significantly difference in genotype of maize.

Similar result were also reported in literature for days to 50 % tasseling 45 to 65 days, for days to 50 % silking 56 to 63 days, for PH 37.18 to 212.40 cm, for SD 8.6 to 12.5 cm, for NOL per plant 11 to 13, for LSR 0.27 to 0.50, for LA 157.5 to 260.9 cm² [9], for GFY 80.8 to 165.7 g, for DFY 12.71 to 34.46 g, for MOS % was recorded 25.6, for ash content 10.0% for CP 7.2 to 10 %, for average of CF 23.3 %, for EE 5.7 % and for NFE 52.3 % [10].

Association existing among different traits (genotypic and phenotypic correlation) determines the mutual relationship of traits. [11] reported the significant correlation of GFY at genotypic and phenotypic level with SD, DFY, NOL and PH. [12] studied the significant correlation of MOS % at genotypic and phenotypic level with DFY, CF and NOL. It was reported that a significant correlation of PH with SD, DTS and GFY. [13] reported the

significant relationship of NOL at phenotypic as well as at genotypic level with PH, SD and LF. [14] noticed significantly relationship of CP with CF and SD. It was studied that a positive significant correlation between ash contents and LSR.

Biplot analysis based on PCA was used to determine the genotypes which are responsive to fodder yield and quality traits. Based on PCA results, genotypes DTMA-271 and DTMA-15 performed best for the trait i.e PH, GFY, DFY and SD which enhanced the yield of fodder maize. These were most ideal genotypes. [15] showed the significant result that PH, GFY, DFY and SD were fell towards positive direction to enhanced the yield of fodder maize.

6. Conclusions

Genetic diversity is key to bring improvement in yield and fodder quality of maize. Furthermore, It was concluded that the fodder yield and quality were significantly affected by several components e.g. PH, NOL, SD, CP, MOS % and CF. The presence of variability in maize germplasm may be helpful to develop high fodder yielding cultivars. At phenotypic and genotypic level, DTS, PH, NOL, SD, MOS %, DFY plant⁻¹, CF and EE revealed significant correlation with fodder yield plant⁻¹.

Therefore, to achieve high fodder yield special attention should be given to these traits in selection. PCA for different quantitative parameters showed genotypes DTMA-271, DTMA-281 and DTMA-15 performed best for yield related parameters. Consider all the traits genotype DTMA-271, DTMA-281 and DTMA-15 performed better among the studied genotypes. These genotypes could be used in breeding programmes to enhance the fodder yield and quality.

Declarations

Source of Funding

This research did not receive any grant from funding agencies in the public, commercial, or not-for-profit sectors.

Consent for publication

Authors declare that they consented for the publication of this research work.

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