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Evaluation of maize hybrids for grain and fodder purpose

Ramesh Kumar[1*], Pardeep Kumar[1], Yashmeet Kaur[1], G. K. Chikkappa[2], D. P. Chaudhary[1], Meenakshi Goyal[3] and U. S. Tiwana[3]

[1]ICAR-Indian Institute of Maize Research, Ludhiana-141004, India
[2]ICAR-Indian Institute of Maize Research, New Delhi-110012, India
[3] Punjab Agricultural University, Ludhiana-141004, India
*Corresponding author e-mail: rk.phagna@gmail.com

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Abstract

Total forty-eight cross combinations were evaluated along with five checks for various morphological and biochemical traits associated with green fodder quality and yield during *Kharif*, 2015 at Experimental Farm, ICAR-IIMR, Ludhiana. Based on the higher mean green fodder yield, eight promising hybrids were selected and observations were recorded for several fodder quality traits namely leaves/plant, leaf length, leaf width, stem girth, dry fodder yield, grain yield, crude protein, acid detergent fiber and neutral detergent fiber. The observations were compared with one fodder check, J1006. The results of analysis of variance (ANOVA) revealed significant differences among treatments for green fodder yield, grain yield, leaves/plant, leaf length, leaf width, crude protein, acid detergent fiber and neutral detergent fiber. Significant and positive genotypic and phenotypic correlation of green fodder yields were found with all the studied traits except for crude protein. Path analysis revealed that most of the yield components had direct positive effects on green fodder yield except leaves/plant, leaf length and acid detergent fiber. In addition, most traits showed negative indirect effects on green fodder yield except leaf width and dry fodder yield. The grain yield showed high heritability (92%) coupled with high genetic advance (24.67) along with high phenotypic (12.95) and genotypic (12.45) coefficient of variability. The phenotypic and genotypic coefficient of variability was higher for most of the traits except stem girth, acid detergent fibre, neutral detergent fibre, green fodder yield and dry fodder yield. Based on the performance of all cross combinations, WNCQPM-10390-1 × DQL-2058-2 P1 showed maximum green and dry fodder yield. In addition, the cross showed comparatively high grain yield, leaves/plant and leaf length.

Keywords: ADF, Fodder quality, Fodder yield, Maize, NDF

Introduction

Maize is one of the major crop plants having wider adaptability under varied agro-climatic conditions. Maize (*Zea mays* L.) has emerged as the most important cereal crop worldwide with the highest global production of 1060 million tonnes as compared to 749 million tonnes in wheat and 741 million tonnes in rice during 2016 (FAOSTAT, 2014; 2017). It is a dual-purpose cereal crop used as human food, livestock feed, fodder and industrial raw material for manufacturing various products (Yadav *et al.,* 2015). Maize can be grown during summer and rainy season and ideal forage crop due to its fast growth, high biomass and good palatability that help to increase body weight and milk quantity and quality in animals (Chaudhary *et al.,* 2016). In India nearly 65% of the entire maize produce is being used by feed industry, 17-20% for human consumption and 12-14% is used for manufacturing purposes (Anonymous, 2015). Maize grain has high nutritive value as it contains 72% starch, 10% protein, 4.8% oil, 9.5% fiber and 3% sugar. Whereas, its fodder has highest crude protein (9.9%) at early and at full bloom stages which decreases to 7% at milk stage and to 6% at maturity (Dahmardeh, 2011; Moreno-Reséndez *et al.,* 2017).

The economic value of maize crop has to be increased by utilising maize as dual-purpose crop. It is not only fulfilling the increasing demand of grain but also the stover for cattle (Sah *et al*., 2016). There should be a combine breeding approach for grain as well as fodder for genetic improvement in dual purpose maize (Barrière *et al*., 2006). The increase in the demand for fodder may be compensated through maize stover by developing dual-purpose maize hybrids (Erenstein *et al*., 2013). Hence, there is a need to work in a multi-disciplinary approach to develop dual-purpose maize hybrids for catering ever increasing demand of poultry and livestock.

Maize green fodder is the cheapest source of livestock food and serves as an important source of cellulose (35-40%), hemicelluloses (25.28%), crude fiber (28.70%), acid detergent fiber (ADF) (37.22%), neutral detergent fiber (NDF) (70.85%), dry matter (40.6%), ash (4%) and carbohydrates (48.86%). Besides, it also supplies 0.3% fat, 2.84% ether extract and 11% crude proteins (Maddon *et al*., 1985). The milk productivity and its quality specially depend on fatty acids per cent in forage (Khan *et al.,* 2015). Compared with a majority of other cereal crops, maize is capable in taking advantage of sunlight to grow more quickly because of the size and distribution of its foliage (Warman, 2003). It has high productivity because of the large leaf area and is quite popular among dairy farmers (Chaudhary *et al*., 2012). However, in India less attention has been given for the genetic improvement of maize crop to use as fodder (Chaudhary *et al*., 2012) and the gap still remain to be filled up through development of improved forage maize varieties. The studies on heritability, genetic advance and genotypic correlation provide a great insight to plant breeder to select genotypes on the basis of strong correlation among grain yielding and other traits which contributes for quality fodder (Ali *et al*., 2013).

The efficiency of a breeding programme depends mainly on the direction and magnitude of the association between grain yield, its components and each other factors which contributes to the forage yield. The path analysis is a statistical technique that partitions correlations into direct and indirect effects and distinguishes between correlation and causation, whereas correlation, in general, measures the extent and direction (positive or negative) of a relationship between two or more variables. The estimates of correlation and path coefficients can help us to understand the role and relative contribution of various plant traits (Shahbaz Akhtar *et al*., 2007). The present study was conducted to evaluate maize hybrids for morphological and quality traits for green fodder yield and grain yield to identify dual purpose hybrids.

Materials and Methods

Plant materials and experimental design: Forty-eight crosses were made during Rabi 2014 considering some of the fodder traits like plant height, broad and higher number of leaves. The inbred lines included in the study were composed of both quality protein maize (QPM) lines as well as normal germplasm. The 48 crosses along with 5 checks *i.e*. J-1006 (fodder), HQPM-5 (QPM), Bio 9780 (Normal), HQPM-1 (QPM) and Bio 9544 (Normal) were evaluated during *Kharif*, 2015 at Experimental Farm of ICAR-IIMR, Ludhiana in randomized complete block design (RCBD) with three replications to identify best cross combinations for fodder yield along with good grain yield based on morphological and biochemical traits. The plant to plant and row to row distance was kept 20 cm and 60 cm, respectively. Recommended agronomic practices were followed to raise a good grain crop and recommended fertilizer dose was 150 kg nitrogen, 60 kg phosphorous and 30 kg Potash per hectare. Observations were recorded on 5 randomly selected plants for 9 traits *i.e*. leaves per plant, leaf length (cm), leaf width (cm), stem girth (cm), green fodder yield (g) at flowering stage, dry fodder yield (g) after harvesting grain (oven dried), grain yield (g), crude protein, acid detergent fiber and neutral detergent fiber.

Statistical analysis: The data was subjected to descriptive statistics analysis including analysis of variance (ANOVA), correlation, GCV (genetypic co-efficient of variation), PCV (phenotypic co-efficient of variation) and path analysis using INDOSTAT Software.

Results and Discussion

Based on the higher mean yield of green fodder over the check J1006 (Table 1) eight promising hybrids were selected. The morphological and biochemical data was subjected to analysis of variance. Analysis of variance revealed significant differences among treatments for green fodder yield, grain yield, leaves per plant, leaf length, leaf width, crude protein, acid detergent fiber and neutral detergent fiber. It indicated that enough genetic variability was present among the hybrids and different traits under consideration. However, no significant differences were observed for dry fodder yield and stem girth (Table 2).

Mean performance: The mean performance of selected entries for various traits like plant height, number of leaves, stem girth, crude protein, grain yield, dry fodder and greed fodder yield etc. were recorded (Table 1). Some of the entries with highest value for different traits like green fodder, grain yield and dry fodder yield were compared to mean performance of check entry J1006. The entries selected from 48 cross combinations showed differential mean performance for studied traits. For yield traits, the hybrid combinations, WNCQPM-10390-1 × DQL-2058-2 P1, DML 1914 × DQL 2080 -1 and DML-1409 × DQL-2058-2 P2 showed maximum green fodder yield as well as dry fodder yield. Whereas the cross combination DML-1409 × DQL-2058-2 P2, DQL- 2080-1 × DML- 1409 P1 and DQL- 2080-1 × DML-1914 P1 showed maximum values for grain yield. Similarly for biochemical traits studied, the cross combinations viz., DQL-2080-1 × DML-1409 P1 and DQL 2080-1 × WNCQPM-10390-1 P1 and WNCQPM-10390-1 × DQL-2058-2 P1 had shown maximum crude protein content. Acid detergent fiber (ADF) was highest in DQL-2080-1 × DML-1914 P1 followed by DQL-2080-1 × DML-1409 P1 and DML-1409 × DQL-2058-2 P2. The genotype DML-1409 × DQL-2058-2 P2, DQL-2080-1 × DML-1914 P1 and DML-1409 × DML-1904 had maximum values for neutral detergent fiber (NDF).

Based on the mean values of important traits like dry fodder, green fodder and grain yield, WNCQPM-10390-1 × DQL-2058-2 P1 cross combination was found superior to all other crosses. It had also other desirable traits like greater number of leaves and leaf length. The higher number of leaves per plant led to the accumulation of more photosynthates in plants which resulted in production of more dry matter and thus, more green fodder yield.

Morphological traits: The association observed between different traits was also recorded (Table 3). In the present study, significant and positive genotypic as well as phenotypic correlation of leaves per plant was observed with leaf length, leaf width, dry fodder yield and neutral detergent fiber except crude protein which had negative significant correlation. Leaf length and leaves per plant were significantly correlated with each other at genotypic as well as phenotypic level. Leaf width showed positive significant genotypic and phenotypic correlation with leaves per plant, stem girth and green fodder yield. Stem girth had positive significant genotypic correlation with leaf width and green fodder yield and positive significant phenotypic correlation with leaf width, green fodder yield and dry fodder yield except grain yield.

Table 1. Mean performance of the experimental hybrids for green fodder, dry fodder and grain yield

Genotype	Green fodder yield (q/ha)	Dry fodder yield (q/ha)	Grain yield (q/ha)
DML 1409 x DQL 2080-1	444.04	133.21	80.54
DML 1409 x DML 1648-1	445.71	130.38	69.56
DML 1409 x WNCQPM 10390-1	383.80	110.47	83.29
DML 1409 x DML 1914	380.22	105.38	91.06
DML 1409 x DML 1870	177.14	54.46	58.79
DML 1409 x DML 1904	564.76	168.42	72.38
DML 1409 x HKI 1105	419.28	119.11	64.77
DML 1409 x DQL 2058-2	580.35	169.64	77.30
WNCQPM 10462-2 x DQL 2080 -1	415.95	124.78	75.51
DQL 2058-2 x WNCQPM 10390-1	458.00	156.64	65.63
DML 1648-1 x DQL 2058-2	419.76	122.59	68.27
DQL 2058-2 x DML 1409	299.61	89.87	71.72
DQL 2058-2 x DML 1870	261.42	81.12	71.80
DQL 2058-2 x DQL 2080-1	460.47	124.80	47.31
DQL 2058 -2 x DML 1869	380.47	115.80	73.72
DQL 2058 -2 x WNCQPM 10462-2	370.00	112.00	86.85
DQL 2058-2 x DML 1914	303.86	91.61	73.38
DML 1870 x DML 1904	289.74	89.03	82.83
DML 1870 x DQL 2058-2	462.04	135.30	54.88
DQL 2080-1 x DML 1904	414.28	124.28	51.71
DQL 2080-1 x DML 1409	577.14	158.45	76.72
DQL 2080-1 x DML 1914	548.33	166.56	75.08
DQL2080 -1 x DML 1648 -1	332.61	99.79	48.67
WNCQPM 10390-1 x DQL 2080-1	337.06	101.59	52.11
DML 1904 x DML 1869	250.19	76.42	59.40
DML 1904 x DML 1914	381.79	114.66	78.97
DML 1904 x DML 1648-1	329.33	98.29	66.54
DML 1904 x WNCQPM 10462-2	279.79	85.47	68.84
DML 1904 x DQL 2080-1	398.33	116.82	70.58

Genotype	Green fodder yield (q/ha)	Dry fodder yield (q/ha)	Grain yield (q/ha)
DML 1904 x DML 1409	516.42	153.06	53.78
DQL 2080-1 x WNCQPM 10390-1	533.80	156.94	55.45
WNCQPM 10390-1 x DQL 2058-2	592.38	177.71	70.55
WNCQPM 10390 - 1 x DML 1648-1	355.23	103.23	61.05
WNCQPM 10390-1 x DML 1904	305.71	91.04	71.27
WNCQPM 10390-1 x DML 1870	394.15	117.37	63.83
WNCQPM 10390-1 x DML 1409	360.17	107.07	71.07
WNCQPM 10390-1 x WNCQPM10361-1	362.61	106.78	68.25
WNCQPM 10390-1 X DML 1914	360.23	107.53	72.19
WNCQPM 10390-1 X HKI 1105	356.90	106.46	65.19
WNCQPM 10390-1 x WNCQPM 10112-1	337.27	102.42	63.70
DQL 2028 x DQL 2004	307.34	86.09	44.47
DML 1914 x DML 1869	423.57	126.15	60.91
DML 1914 x DML 1870	222.38	66.71	13.55
DML 1914 x DML 1648 -1	563.04	165.88	57.40
DML 1914 x HKI 1105	285.47	82.64	59.74
DML 1914 x DML 1409	522.61	165.27	81.85
DML 1914 x DQL 2080 -1	591.83	175.58	59.06
DML 1648-1 x DML 1870	443.33	131.88	68.84
Check J 1006	524.28	157.28	63.00
Check HQPM-5	445.13	133.72	58.89
Check Bio 9780	414.84	122.33	90.90
CheckHQPM-1	391.90	117.57	58.85
Check Bio 9544	416.81	111.77	74.96
Mean	403.64	119.80	66.55
C.V.	6.81	9.02	14.63
S.E.	15.88	6.24	5.62
C.D. (P < 0.05)	44.56	17.50	15.77
C.D. (P < 0.01)	58.96	23.15	20.86

Yield traits: Green fodder yield showed significant positive genotypic correlation with dry fodder yield (0.893), grain yield (0.351), acid detergent fiber (0.524) and neutral detergent fiber (0.644). While at phenotypic level green fodder yield had significant and positive correlation with leaf width (0.389), stem girth (3.276), dry fodder yield (0.790), grain yield (0.334), acid detergent fiber (0.520) and neutral detergent fiber (0.565). There was significant positive genotypic correlation of dry fodder yield with leaves per plant, green fodder yield, acid detergent fiber and neutral detergent fiber except crude protein. At phenotypic level, dry fodder yield showed positive significant correlation with leaves per plant, stem girth, green fodder yield, acid detergent fiber and neutral detergent fiber except crude protein. Grain yield showed positive significant correlation with green fodder yield (0.351, 0.334), acid detergent fiber (0.952, 0.869) and neutral detergent fiber (0.848, 0.771) at genotypic except stem girth (-0.694, -1.212).

Since green fodder yield was significantly correlated with several traits, thus selection of the higher green fodder yielding genotypes based on these traits may be useful. Ertiro *et al.* (2013) also showed that dry forage yield in maize plant was found to be significantly and positively associated with green fodder yield and yield components like plant height, number of leaves plant and stem diameter. Thus the improvements in characters like plant height, number of leaves plant and stem diameter were useful in improving the fodder yield in maize (Kapoor, 2017; Saiyad and Kumar, 2018).

Biochemical traits: Crude protein had significant and positive correlation with acid detergent fiber and neutral detergent fiber at genotypic and phenotypic except leaves per plant and dry fodder yield. Acid detergent fiber showed positive significant correlation with green fodder yield, dry fodder yield and grain yield except crude protein at genotypic and phenotypic level. Another biochemical trait neutral detergent fiber had positive significant correlation with leaves per plant, green fodder yield, dry fodder yield, grain yield and neutral detergent fiber at genotypic as well as phenotypic level except crude protein.

Table 2. Mean performance of eight promising cross combinations

Genotypes	Green fodder yield (q/ha)	Dry fodder yield (q/ha)	Grain yield (q/ha)	Leaves /plant (no.)	Leaf length (cm)	Leaf width (cm)	Stem girth (cm)	Crude protein (%)	Acid detergent fibre (%)	Neutral detergent fibre (%)
DML-1409 X DML-1904 P2	564.76	168.42	72.38	10.50	78.18	**8.01**	6.59	12.10	36.18	47.60
DQL-2080-1XDML-1914 P1	548.33	166.56	75.08	10.52	71.19	8.46	6.65	10.50	**37.80**	48.20
DML 1914 x DQL 2080 -1	591.83	175.58	59.06	11.00	73.52	9.75	7.10	10.90	36.32	47.29
DML-1409XDQL-2058-2 P2	580.35	169.64	**77.30**	11.74	72.26	9.23	6.75	**10.00**	37.35	**49.60**
DQL-2080-1XDML-1409 P1	577.14	158.45	76.72	10.52	76.25	9.56	7.01	**12.60**	37.45	47.00
DQL 2080-1XWNCQPM-10390-1 P1	533.80	**156.94**	**55.45**	**9.63**	**65.50**	8.04	6.60	**12.60**	**33.90**	**42.90**
WNCQPM-10390-1XDQL-2058-2 P1	**592.38**	**177.71**	70.55	11.15	81.02	8.50	**7.10**	12.40	36.11	46.30
DML-1914XDML-1648-1	563.04	165.88	57.40	**11.76**	77.60	**10.68**	6.94	11.90	34.27	45.60
CHECK J-1006	**524.28**	157.28	63.00	11.52	**81.30**	8.63	**6.46**	11.69	34.57	45.05

Table 3. Genotypic and phenotypic correlation coefficients for ten selected traits

Characters	Leaves /plant	Leaf length	Leaf width	Stem girth	Green fodder yield	Dry fodder yield	Grain yield	Crude protein	Acid detergent fibre	Neutral detergent fibre
Leaves/plant	**1.000**	0.586**	0.613**	0.009	0.284	0.493**	0.015	-0.462**	0.034	0.472**
Leaf length	0.588**	**1.000**	0.135	-0.182	0.170	0.238	0.159	0.246	-0.029	0.168
Leaf width	0.594**	0.167	**1.000**	0.570**	0.375*	0.028	-0.261	-0.163	-0.045	0.191
Stem girth	0.113	-0.073	0.502**	**1.000**	0.477**	0.203	-0.694**	0.174	-0.198	-0.211
Green fodder yield	0.268	0.198	0.389*	3.276**	**1.000**	0.893**	0.351*	-0.149	0.524**	0.644**
Dry fodder yield	0.339*	0.234	0.130	0.629**	0.790**	**1.000**	0.239	-0.463**	0.367*	0.777**
Grain yield	0.073	0.174	-0.209	-1.212**	0.334*	0.163	**1.000**	-0.287	0.952**	0.848**
Crude protein	-0.435**	0.234	-0.167	0.019	-0.142	-0.347*	-0.293	**1.000**	-0.532**	-0.764**
Acid detergent fiber	0.020	-0.024	-0.019	-0.05	0.520**	0.358*	0.869**	-0.497**	**1.000**	0.926**
Neutral detergent fiber	0.383*	0.116	0.158	-0.144	0.565**	0.518**	0.771**	-0.710**	0.868**	**1.000**

*, ** Significant at 5% and 1% level, respectively

Path coefficient analysis for effects on green fodder yield: Path analysis measures the direct and indirect effect of one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effect (Dewey and Lu, 1959). Partitioning of the total correlation coefficient into direct and indirect effects for green fodder yield showed the positive direct effects of many yield contributing traits i.e. leaf width (0.711), stem girth (0.027), dry fodder yield (0.800), grain yield (0.119), crude protein (0.576) as well as the quality trait like neutral detergent fiber (1.240) whereas the negative direct effects are contributed by traits like leaves/plant (-0.842), leaf length (-0.006) and acid detergent fiber (-0.658) towards green fodder yield (Table 4). Leaf width, dry fodder yield, crude protein and neutral detergent fiber showed high direct effects while grain yield and stem girth showed low and negligible direct effects, respectively (Lenka and Mishra, 1973).

Both the negative and positive indirect effects were contributed by different traits. Leaves/plant had negative indirect effect on green fodder yield via leaf length, leaf width, dry fodder yield and grain yield. Leaf length had also negative indirect effect on green fodder yield via leaves/plant, leaf width, dry fodder yield and grain yield whereas it showed positive indirect effect via stem girth. Leaf width showed positive indirect effect via leaves/plant, leaf length and dry fodder yield. Stem girth had negative indirect effect on green fodder yield via leaf length and grain yield. Dry fodder yield showed positive indirect effect on green fodder yield via leaves/plant, leaf length, leaf width and grain yield.

Positive and significant genotypic correlation values of traits *i.e.* leaves/plant (0.284), leaf length (0.170), leaf width (0.375), stem girth (0.477), dry fodder yield (0.893), grain yield (0.351), acid detergent fiber (0.524) and neutral detergent fiber (0.644) with green fodder yield showed the true association between these traits (Table 3). Crude protein (0.149) was found to be in negative genotypic correlation with green fodder yield. Traits like leaf width, stem girth, dry fodder yield, grain yield, and neutral detergent fiber had positive direct effects as well as significant and positive genotypic and phenotypic correlation with green fodder yield. So genetic improvement and selection of the genotypes with higher values of these traits might be helpful in development of high green fodder yielding cultivars (Kapoor, 2017).

Table 4. Path coefficient analysis for direct (bold) and indirect effects on green fodder yield

Characters	Leaves /plant	Leaf length	Leaf width	Stem girth	Dry fodder yield	Grain yield	Crude protein	Acid detergent fibre	Neutral detergent fibre	Genotypic correlation with green fodder yield
Leaves/plant	**-0.842**	-0.493	-0.516	-0.008	-0.415	-0.012	0.389	-0.028	-0.398	0.284
Leaf length	-0.003	**-0.006**	-0.000	0.001	-0.001	-0.001	-0.001	0.000	-0.001	0.170
Leaf width	0.436	0.096	**0.711**	0.407	0.020	-0.186	-0.116	-0.032	0.136	0.375
Stem girth	0.000	-0.005	0.015	**0.027**	0.005	-0.019	0.004	-0.005	-0.005	0.477
Dry fodder yield	0.394	0.191	0.022	0.163	**0.800**	0.191	-0.371	0.294	0.622	0.893
Grain yield	0.001	0.019	-0.031	-0.082	0.028	**0.119**	-0.034	0.113	0.100	0.351
Crude protein	-0.266	0.141	-0.094	0.100	-0.267	-0.165	**0.576**	-0.307	-0.440	-0.149
Acid detergent fiber	-0.022	0.019	0.029	0.130	-0.241	-0.626	0.350	**-0.658**	-0.609	0.524
Neutral detergent fiber	0.586	0.208	0.238	-0.262	0.964	1.052	-0.948	1.148	**1.240**	0.644

Table 5. Estimates of genetic parameters for studied traits in maize genotypes

Characters	Range	h^2 (%)	GA (%)	PCV	GCV
Leaves/plant	9.63-11.76	85	11.335	6.446	5.955
Leaf length	65.50-81.30	87	12.234	6.787	6.349
Leaf width	8.01-10.68	93	18.981	9.885	9.544
Stem girth	6.26-7.43	56	5.54	4.72	3.56
Green fodder yield	524.28-592.38	92	8.212	4.323	4.151
Dry fodder yield	156.94-177.71	54	5.125	4.573	3.373
Grain yield	55.45-77.30	92	24.67	12.952	12.454
Crude protein	10.00-12.60	97	16.332	8.174	8.05
Acid detergent fiber	6.46-7.10	91	7.575	4.019	3.844
Neutral detergent fiber	42.6-42.9	88	7.597	4.181	3.927

h^2: Heritability (broad sense); GA: Genetic advance as percentage of mean; PCV: Phenotypic coefficient of variability; GCV: Genotypic coefficient of variability

Genetic variability: The heritability was categorized as low (0-30%), moderate (30- 60%) and high (60% and above) following Robinson *et al.* (1949) and genetic advance as percent mean was categorized as low (0-10%), moderate (10-20% and (e"20%) as given by Johnson et al. (1955) and Falconer and Mackay (1966). Heritability for different traits was found in the range of 54-97%, while genetic advance varied from 5.12 to 24.67%. High heritability was found for crude protein, leaf width, green fodder yield, grain yield, acid detergent fiber and neutral detergent fiber, whereas genetic advance was high for grain yield, leaf width, crude protein, leaf length, and leaves/plant (Table 5). Highest heritability (97%) was recorded for crude protein whereas highest genetic advance (24.67%) was obtained for grain yield. Dry fodder yield had lowest (54%) heritability followed by stem girth (56%). The genetic parameters like higher heritability and genetic advance also showed that selection of higher green fodder yield may be helpful to improve crop yield and productivity (Ahsan *et al*., 2011; Ali *et al*., 2011; Mehdi *et al*., 2000). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as suggested by Burton and Devane (1953). Phenotypic coefficients of variation and genotypic coefficients of variation were categorized as low (0-10%), moderate (10-20%) and high (>20%) as indicated by Sivasubramanian and Madhavamenon (1973). Phenotypic coefficient of variability and genotypic coefficient of variability were low for all the traits except grain yield which showed moderate GCV and PCV values. In general, a high coefficient of variability indicates that there is a scope of selection and improvement of these traits. Low values indicate the need for creation of variability either by hybridization or mutation followed by selection (Tiwari *et al*., 2011).

The identified promising hybrids might fulfil the potential demand for dual-purpose maize to solve the problem of increasing demand of fodder. Eventually the dual purpose maize hybrids are not more widely adopted, but if dual-purpose maize is promoted as a technology it will enhance productivity per unit of land. Dual purpose maize is also important for the dry land areas, where there is strong presence of livestock against limited biomass quality and low maize yields. Hence, different types of improved dual-purpose maize hybrids can be targeted to sustain intensification processes in different environments through integrated approach.

Conclusion

The present study identified the presence of adequate genetic variability among 48 tested cross combinations and identified eight promising crosses. Hence, the information generated from this study will be helpful to the maize breeders in their future maize breeding programs. The identified eight promising hybrid combinations might help in meeting the challenges of increasing food and fodder demand. However, the stability of these hybrids in different locations needs to be confirmed.

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