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Strategic selection of white maize inbred lines for tropical adaptation and their utilization in developing stable, medium to long duration maize hybrids

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Abstract

White maize plays an important role in human diet, especially in traditional crop growing regions of northern hill region, north-eastern states and central-western parts of India. Breeding efforts to enhance the genetic potential of white maize was not so prominent as compared to yellow maize in the country. As a result, genetic base of the material utilized in white maize breeding program in India is very narrow and majorly contains indigenous germplasm and few introductions. Hence, efforts were made to use 365 white maize inbred lines from CIMMYT, Mexico, for breeding program. These new inbred lines were grown at winter nursery center, Indian Institute of Maize Research, New Delhi for its tropical adaptation. After preliminary evaluation, a total 47 inbred lines were selected and evaluated in randomized complete block design with two replications at Regional Maize Research and Seed Production Centre, Begusarai, Bihar, during rabi 2014. Out of this top performing 12 inbred lines viz, CML 47, CML 95, CML 314, CML 319, CML 377, CML 488, CML 494, CML 504, CML 517, CML 522, CML 531 and CML 538 were selected and were crossed in diallel manner to obtain 66 medium to long duration experimental hybrids. Stability analysis using AMMI model was done to identify adaptive hybrids with high yielding potentiality. According to the ASVi value obtained, the hybrid G38 appeared to be stable followed by G50 and G44. On the other hand, the hybrid G25 appeared as location specific hybrid suitable for high input conditions.

KeyWords *White maize, inbred lines, diallel, AMMI analysis, adaptive*

Introduction

Maize is a versatile crop having its vast adaptation across the world, ranging from tropical to temperate climatic situations. Based on the endosperm texture and structure, maize can be classified into dent corn (*Zea mays indentata* Sturt), flint corn (*Zea mays indurate* Sturt), pop corn (*Zea mays everta* Sturt), flour corn (*Zea mays amylacea* Sturt), sweet corn (*Zea mays saccharata* Sturt), pod corn (*Zea mays tunicate* Sturt) and waxy corn (*Zea mays certina* Kulesh). However, based on their endosperm color, they may be re-grouped into yellow corn, white corn, purple corn etc. Dent and flint corn are the extensively cultivated maize types worldwide. The majority of the Indian grown maize is flint, whereas dent type is preferentially cultivated in USA. Irrespectively from dent or flint type, yellow maize dominates to white maize in terms of production. In areas of the developing world, maize demand for livestock is rapidly increasing. It is one of the economy drivers of the developing countries like India where it has been utilized in the form of industrial raw material for the production of poultry feed, starch, glucose, pharmaceuticals etc (Ranum et al., 2014). Nonetheless, maize remains an important part of the human diet in many developing countries; white maize tends to assume much greater importance than yellow varieties (Anon., 1997).

Gujarat, Rajasthan, Madhya Pradesh, Bihar, Himachal Pradesh are the Indian States where white maize is prominently grown. Indian as well as world statistics about cultivation area, production and productivity of white maize are not available. Hence, the economic importance of cultivating white maize in meeting food demand is not properly reviewed; however, some estimates on the proportion of maize for human consumption are available (Anon. 2016). White maize is reported to be an important staple food for more than 1.2 billion people in sub-Saharan Africa and Latin America. It accounts for 30-50% of low–income household expenditures in Eastern and Southern Africa (Usman et al., 2015).

A series of white maize composite and hybrids were released by Indian Institute of Maize Research (IIMR), New Delhi through it's All India Co-ordinated Research Project (AICRP) Centers. Research on white maize started in India as early as 1960's which resulted in releasing of first white maize hybrid Ganga Safed-2 in 1963 by AICRP on maize, New Delhi. The efforts were continued by AICRP Centers during subsequent years; 19 composites and 8 hybrids of white maize were released (Kaul et al., 2013). Though the good number of white maize hybrids released, their adaptability is low due to the narrow genetic base of the inbred lines utilized in developing them (Kaul et al., 2013). On the other hand, the stability of the hybrids is overlooked, the average of a given genotype over years and/or locations, and its superiority over the checks is only considered for the release of hybrids under existing procedure (Rakshit et al., 2012) causing the fast breakdown of hybrids within few years of release. Breeding efforts were more prominent in yellow maize because of its nutritive value, β-carotene content, which is otherwise absent in white maize, which plays the major role in mitigating Vitamin A deficiency in resource-poor segment of the country. In this context, white maize is nearly neglected for breeding improved cultivars and also pre-breeding work on white maize is meager, narrowing the genetic base of white maize.

Hence, efforts were made to introduce available white maize inbred lines, which are released for public use in 2012 by CIMMYT, Mexico. They were evaluated for their tropical adaptation and after repeated selection, these inbred lines were utilized in breeding program. Hybrids so obtained were further analyzed for their yield stability to broad-based, stable, tropically adapted white maize hybrids.

Materials and Methods

Initial screening of genotypes

A total of 365 white maize inbred lines were received from CIMMYT, Mexico in 2012 and were grown in two consecutive *rabi* seasons, 2012-2013 at winter nursery center, Hyderabad for tropical adaptation. Twenty-two genotypes did not flower and 40 genotypes showed wide interval between anthesis and silking (ASI), hence these were selected against for the tropical conditions. Remaining 303 genotypes were grown in *Kharif* 2014 at Delhi. Based on the morpho-phenological characters *viz*., days to anthesis and silking, ASI, tassel density, cob placement, stem girth and pollen duration, a total of 47 genotypes which are suitable either for male or female parents were selected. Simple descriptive statistics *viz*., mean, range and standard deviations were used to select these genotypes.

Evaluation of inbred lines

Selected 47 genotypes were evaluated in randomized complete block design with two replications at Regional Maize Research and Seed Production Centre, Begusarai, Bihar, during rabi 2014. In the evaluation stage, data recorded included: days to 50% flowering, plant height (cm), tassel length (cm), ear height (cm), number of cobs, cob length (cm), cob diameter (cm), kernel row number, kernels per row, shelling percentage and yield (kg/ha).

Development and evaluation of experimental hybrids

Total 12 genotypes with desirable yield and yield-related traits were crossed in partial diallel manner during *rabi* 2015 obtaining 66 new experimental hybrids. These hybrids along with two each national checks of medium and late maturing categories were evaluated in *Kharif* 2016 over three locations *viz*, Ludhiana, Delhi, and Hyderabad, in randomized complete block design with two replications. Data recorded included: days to 50% flowering, plant height (cm), ear height (cm), the number of plants, cob length (cm), kernel row number, kernel per row, shelling percentage and yield (kg/ha).

All genotypes, inbred lines as well as hybrids, were grown in a 3 m row with a spacing: 75 cm between row and 20 cm between plants. All the recommended protocol for maize cultivation was followed (Parihar et al., 2011).

Statistics

Software, SAS 9.3v and NCSS11 (http://www.ncss.com) was used for data analysis. Duncan's Multiple Range Test (DMRT) given by Gomez and Gomez (1984) was adopted to compare the performance of all possible pairs of genotypes. Cluster analysis using the Ward (1963) method was performed with scores of the first five principal components (PCs) (http://stat.iasri.res.in/sscnarsportal/main.do). The correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components by using the formula given by Weber and Moorthi (1952).

The data about hybrid yield (kg/ha) over three locations were subjected to statistical analysis through Additive Main effects and Multiplicative Interaction (AMMI) model (Zobel et al., 1988) using GenStat software 17th Ed. (2014). The AMMI stability value (ASVi) was used to compare the stability of genotypes as described by Purchase (1997). The variation due to genotypes and G×E for grain yield was examined using the GGE biplot based on the principal component analysis (PCA) of environment centered data (Yan et al., 2000).

Results

Inbred lines

Based on the initial screening, only 47 inbred lines out of 365 originally received genotypes from CIMMYT were selected for genetic analysis. Analysis of variance revealed significant variations among the genotypes for various yield and yield component characters (Table 1). Upon characterization of this variability among different yield component traits, it was found that all the genotypes flowered in between 54.5 to 62.5 days with 58.48 mean days to 50% flowering. Plant height ranged from 108.83 cm to 192.5 cm and ear height from 33.33 cm to 104.17 cm; mean plant and ear height being 146.25 cm and 64.47 cm respectively. Tassel length, one of the most important male parent traits, ranged from 22.17 cm to 44.33 cm with the mean 33.96 cm. The cob length and cob diameter ranged from 10.08 cm to 15.83 cm and 11.22 cm to 16.65 cm respectively. A wide range was observed in kernel row number (9.67 to 16.67), kernel per row (12.67 to 33.50) and shelling percentage (46.09% to 89.27%). The yield of inbred lines also exhibited wide variation which ranged from 93.65 kg/ha to 3810.19 kg/ha with a mean yield 1621.45 kg/ha (Table 1).

Table 1. Some descriptive statistics for yield and yield component traits of white maize inbred lines

S.No.	Characters	Minimum	Maximum	Mean	Standard Deviation
1	Days to 50% flowering	54.5	62.5	58.48	0.26
2	Plant height (cm)	108.83	192.5	146.25	18.35
3	Tassel Length (cm)	22.17	44.33	33.96	4.570
4	Ear Height (cm)	33.33	104.17	64.47	13.75
5	No. of cobs	4.5	26.5	13.77	4.485
6	Cob Length (cm)	10.08	15.83	13.00	1.61
7	Cob diameter (cm)	11.22	16.65	13.71	1.32
8	Kernel Row Number	9.67	16.67	13.40	1.453
9	Kernel per row	12.67	33.5	24.68	4.85
10	Shelling percentage (%)	46.09	89.27	78.17	8.28
11	Yield (kg/ha)	93.65	3810.19	1621.45	877.40

As shown in Table 2, among the yield component traits, plant height (r = 0.58), tassel length (r = 0.43), ear height (r = 0.34), number of cobs (r = 0.73), cob length (r = 0.51), cob diameter (r = 0.39), kernels per row (r = 0.60) and shelling percentage (r = 0.49) showed positive and significant correlation with yield. Plant height associated positively and significantly with ear height (r = 0.78), cob length (r = 0.58), cob diameter (r = 0.49) and kernels per row (r = 0.60). The cob length recorded positive and significant correlation with cob diameter (r = 0.51) and kernel per row (r = 0.78). On the other hand there was a significant positive correlation between cob diameter and kernel row number (r = 0.54), kernel per row (r = 0.47), shelling percentage (r = 0.33). Shelling percentage was highly associated with kernel per row (r = 0.57).

Principal component analysis (PCA) was performed using the data on 11 yield and yield component traits of 47 inbred lines. Biplot between PC1 and PC2 is shown in Fig.1. The first principal component (PC1) explained 38.23% variation, followed by PC2 (16.93% variation), PC3 (14.38% variation), PC4 (9.21% variation), and PC5 (7.74% variation) (data not shown). Factor loadings of different variables which were obtained by using PCA are presented in Table 2. It indicated that all the traits under consideration contributed for the variability in

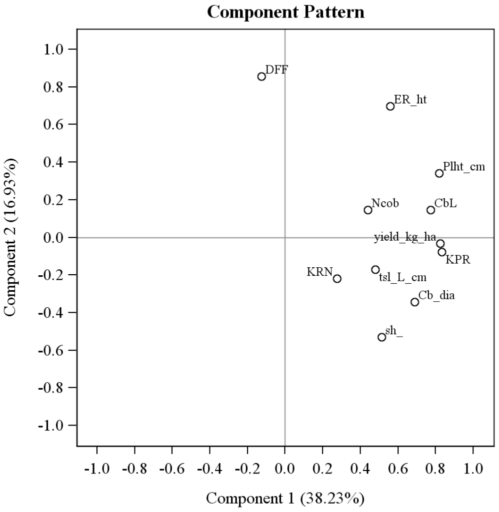

Figure 1 - Biplot between PCs 1 and 2 showing contribution of various traits in variability of white maize inbred lines. DFF-Days to 50% flowering, Er_ht- Ear height (cm), Plht-Plant height (cm), Ncob- No. of cobs, CbL-cob length (cm), KRN-Kernel row number, KPR-Kernel per row, ts_L-(Tassel length), Cb_dia-Cob diameter (cm), Sh- Shelling percentage

Table 2. Correlation between and among yield and yield components traits in white maize inbred lines, Eigen value and factors loading (Eigen vectors) of different traits with respect to different principle factors (PF) in white maize inbred lines.

S.No.	Characters	Days to 50% flowering	Plant height (cm)	Tassel Length (cm)	Ear Height (cm)	No. of cobs	Cob Length (cm)	Cob diameter (cm)	Kernel Row Number	Kernel per row	Shelling percentage (%)
1	Days to 50% flowering	1.00									
2	Plant height (cm)	0.08	1.00								
3	Tassel Length (cm)	-0.23	0.30	1.00							
4	Ear Height (cm)	0.43*	0.78*	0.13	1.00						
5	No. of cobs	0.07	0.29	0.18	0.19	1.00					
6	Cob Length (cm)	0.05	0.58*	0.27	0.45*	0.13	1.00				
7	Cob diameter (cm)	-0.37*	0.49*	0.38*	0.27	-0.01	0.51*	1.00			
8	Kernel Row Number	-0.12	0.20	-0.10	0.14	-0.13	0.19	0.54*	1.00		
9	Kernel per row	-0.10	0.60*	0.30	0.32	0.22	0.78*	0.47*	0.11	1.00	
10	Shelling percentage (%)	-0.35*	0.21	0.11	-0.10	0.28	0.21	0.33*	0.15	0.57*	1.00
11	Yield (kg/ha)	-0.13	0.58*	0.43*	0.34*	0.73*	0.51*	0.39*	0.06	0.60*	0.49*

S.No.	Characters	Eigen value	Indivi-dual Percent	Cumu-lative Percent	PF 1	PF 2	PF 3	PF 4	PF 5
1	Days to 50% flowering	4.205	38.23	38.23	38.23	0.627	0.002	0.187	-0.10
2	Plant height (cm)	1.862	16.93	55.16	55.16	0.250	0.111	-0.05	0.094
3	Tassel Length (cm)	1.582	14.38	69.55	69.55	-0.12	-0.16	-0.74	0.140
4	Ear Height (cm)	1.013	9.22	78.76	78.76	0.511	0.176	-0.04	0.153
5	No. of cobs	0.851	7.74	86.50	86.50	0.107	-0.56	0.243	0.417
6	Cob Length (cm)	0.496	4.52	91.02	91.02	0.106	0.162	-0.04	-.420
7	Cob diameter (cm)	0.418	3.80	94.82	94.82	-0.25	0.367	-0.13	0.205
8	Kernel Row Number	0.232	2.11	96.93	96.93	-0.16	0.542	0.364	0.440
9	Kernel per row	0.123	1.12	98.06	98.06	-0.06	-0.01	0.095	-0.51
10	Shelling percentage (%)	0.113	1.03	99.09	99.09	-0.38	-0.19	0.428	-0.20
11	Yield (kg/ha)	0.100	0.91	100	100	-0.02	-0.34	0.079	0.204

*Significant at the level 0.05 level of probability

the inbred lines which ultimately created variability in *per se* yield of individual inbred lines. Hence cluster analysis based on scores on five PCs (86.49%) was undertaken which delineated the accessions into three distinct clusters (Fig. 2).

Experimental hybrids

The yield data of 66 experimental hybrids derived from the partial diallel cross combinations of selected top performing 12 white maize inbred lines, were subjected to AMMI analysis. Analysis of variance indicated that there was a significant difference among tested hybrids and environments (data not shown). The variance ratio recorded for the environment (3.51) was higher than genotypes (1.62) and was significant for Genotype × Environment interaction (GEI) (1.80). The GEI was further partitioned into two principal components (PC1 and PC2). Cumulatively, these two principal components were able to explain 100% variations; PC1 accounted for 64.66% and PC2 35.34%. AMMI biplot on symmetric scaling (Fig. 3) indicated that all the three environments *viz.*,

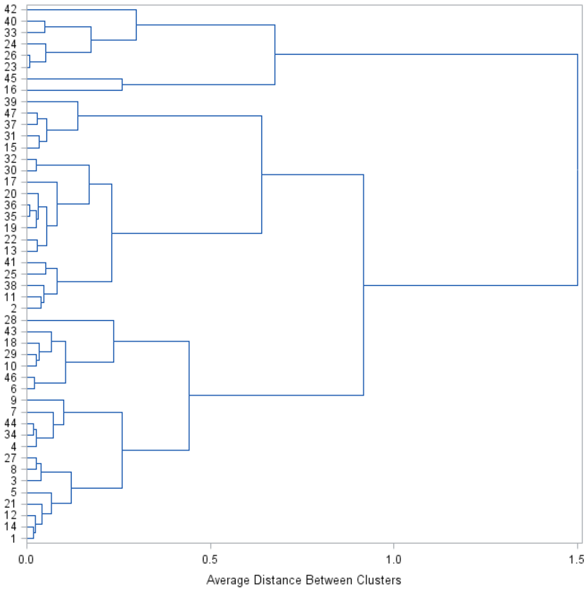

Figure 2 - Dendrogram of the 47 white maize inbred lines based on scores of first five principal component (81.49% variation).

Table 3. Mean yield, IPCA1, IPCA2 and ASVi values of white maize hybrids over threee locations

Hybrid	Pedigree	Mean	IPCA 1	IPCA 2	ASVi
G1	CML 319 X CML 531	56.44	-1.46	0.02	2.67
G2	CML 494 X CML 531	49.04	-0.44	-0.82	1.15
G3	CML 488 X CML 531	47.90	1.70	-0.19	3.12
G4	CML314 X CML 531	49.45	0.07	1.23	1.24
G5	CML 517 X CML 531	60.42	-2.18	1.34	4.21
G6	CMl 504 X CML 531	49.76	3.32	1.28	6.21
G7	CML 522 X CML 531	56.99	-2.85	1.57	5.44
G8	CML 47 X CML 531	39.70	-1.27	0.37	2.35
G9	CML 95 X CML 531	49.07	0.27	-1.17	1.27
G10	CML 538 X CML 531	31.01	1.35	0.55	2.53
G11	CML 377 X CML 531	46.00	-1.25	-0.02	2.29
G12	CML 494 X CML 319	45.79	0.72	0.21	1.33
G13	CML 488 X CML 319	44.17	0.86	-2.26	2.75
G14	CML314 X CML 319	47.04	-0.44	-0.28	0.85
G15	CML 517 X CML 319	49.80	0.24	-0.41	0.60
G16	CMl 504 X CML 319	60.46	-1.42	-0.52	2.65
G17	CML 522 X CML 319	45.39	1.06	-0.71	2.07
G18	CML 47 X CML 319	56.70	0.78	1.54	2.10
G19	CML 95 X CML 319	55.10	-0.66	-2.08	2.41
G20	CML 538 X CML 319	57.45	1.29	-0.16	2.37
G21	CML 377 X CML 319	53.59	-1.41	-1.36	2.92
G22	CML 488 X CML 494	63.29	0.90	1.28	2.09
G23	CML314 X CML 494	46.78	1.17	0.76	2.27
G24	CML 517 X CML 494	56.22	-2.43	2.16	4.94
G25	CMl 504 X CML 494	73.29	-0.96	0.52	1.83
G26	CML 522 X CML 494	51.12	1.26	1.09	2.55
G27	CML 47 X CML 494	53.75	-0.42	-1.24	1.46
G28	CML 95 X CML 494	42.99	-0.74	0.58	1.47
G29	CML 538 X CML 494	52.58	3.14	0.35	5.75
G30	CML 377 X CML 494	54.29	-2.02	0.82	3.79
G31	CML314 X CML 488	46.82	0.84	0.32	1.57
G32	CML 517 X CML 488	50.23	-0.51	1.38	1.67
G33	CMl 504 X CML 488	55.98	1.50	-1.05	2.94
G34	CML 522 X CML 488	55.40	-0.64	-0.04	1.17
G35	CML 47 X CML 488	50.48	-3.50	1.26	6.53
G36	CML 95 X CML 488	45.22	0.46	0.60	1.03
G37	CML 538 X CML 488	47.34	0.34	-1.21	1.36
G38	CML 377 X CML 488	43.73	0.02	0.02	0.04
G39	CML 517 X CML 314	53.54	0.94	-0.23	1.73
G40	CMl 504 X CML 314	46.45	0.16	-0.27	0.40
G41	CML 522 X CML 314	46.61	-0.51	-0.50	1.06
G42	CML 47 X CML 314	42.71	-0.30	-0.74	0.92
G43	CML 95 X CML 314	41.35	0.14	-0.93	0.96
G44	CML 538 X CML 314	45.03	-0.16	0.22	0.37
G45	CML 377 X CML 314	56.93	2.77	-0.91	5.15
G46	CMl 504 X CML 517	47.49	-0.89	0.51	1.71
G47	CML 522 X CML 517	57.50	-1.61	0.34	2.96
G48	CML 47 X CML 517	44.72	1.87	1.92	3.92
G49	CML 95 X CML 517	59.03	0.80	0.23	1.48
G50	CML 538 X CML 517	47.79	0.14	-0.18	0.31
G51	CML 377 X CML 517	47.28	-0.29	0.02	0.53
G52	CML 522 X CML 504	45.26	-1.38	-0.73	2.63
G53	CML 47 X CML504	41.03	-0.83	0.48	1.59
G54	CML 95 X CML 504	50.55	1.41	0.91	2.74
G55	CML 538 X CML 504	50.53	-0.01	0.45	0.45
G56	CML 377 X CML504	40.90	0.76	1.94	2.39
G57	CML 47 X CML 522	42.34	0.79	-0.26	1.47
G58	CML 95 X CML 522	45.16	-0.42	1.44	1.63
G59	CML 538 X CML 522	59.54	0.25	-0.38	0.59
G60	CML 377 X CML 522	46.55	-0.32	0.02	0.59
G61	CML 95 X CML 47	61.79	-2.16	-0.78	4.03
G62	CML 538 X CML 47	44.43	-0.21	1.10	1.17
G63	CML 377 X CML 47	63.83	-0.62	-2.68	2.91
G64	CML 538 X CML 95	51.11	0.11	1.35	1.36
G65	CML 377 X CML 95	48.77	1.33	0.90	2.59
G66	CML 377 X CML 538	39.01	1.73	-0.16	3.17
G67	PMH 1	58.45	-0.33	-3.45	3.50
G68	Bio 9637	59.03	1.94	-0.49	3.58
G69	PMH 4	55.71	-1.68	-0.16	3.08
G70	Prakash	60.20	-1.62	-2.13	3.65
G71	Vivek QPM 9	54.66	1.01	0.51	1.92
G72	Seed Tech 2324	59.96	0.48	-3.04	3.16

continue ⟶

* P ≤ 0.05, ** P ≤ 0.05, *** P ≤ 0.001

1) Ludhiana, 2) Delhi and 3) Hyderabad were able to differentiate the genotype based on their ability to adapt to the particular condition. Based on the vector distance it was found that Ludhiana is the best place for the better yield expression of the genotypes under study. The AMMI stability value was calculated as previously described by Purchase et al., (2000). The larger is absolute value of Interaction principle Component Axis (IPCA), the greater is adaptability of a specific variety for a certain environment. Conversely, lower AMMI stability values (ASV) indicate greater stability in different environments. Considering ASVi value, hybrid G38 (CML 377 × CML 488) found to be stable among all the tested genotype with lowest ASVi (0.04) value followed by hybrids G50 (CML 538 × CML 517) and G44 (CML 538 × CML 314) with ASVi value 0.31 and 0.37 respectively (Table 3). Unfortunately, mean yield of these genotypes was low compared to checks (except over PMH 4) (Table 3). Average performance of the hybrids was better in Ludhiana followed by Hyderabad as shown in Table 3 by higher mean yield (kg/ha).

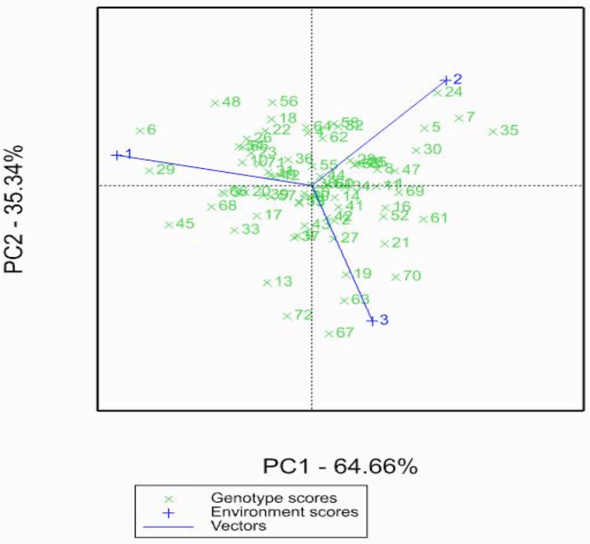

Figure 3 - GGE biplot based on environment-focused scaling

Discussion

Genetic variability is the prerequisite that enables breeders to trait-based plant selection for crop improvement. In the present study 365 white maize genotypes received from the CIMMYT, Mexico, showed a wide range of variability (data not shown), but all the inbred lines were not adapted to the tropical condition. This was evident from their flowering behavior, increased anthesis to silk interval and wide fluctuation in the yield *per se* observed in the neutral climatic situation at Winter Nursery Centre (WNC), Hyderabad. After two consecutive growing seasons at WNC, Hyderabad, selections were performed evaluating all the variability existing in the received germplasm. Finally, a representative sample of 47 inbred lines was selected based on parental traits to be considered in maize hybrid breeding program (Dass et al., 2009). Analysis of variance indicated a wide range of variability available within the selected 47 inbred lines. Our basic criteria for selection included the duration of flowering (early, medium and late) along with other yield component traits; all the selected inbred lines flowered within the range of medium to late flowering. A huge variation in traits like kernel row number, kernel per row and shelling percentage was evident, determining yielding ability of the inbred lines. Correlation between kernel row number, kernel per row, shelling percentage with yield, showed a positive and significant relationship among them. This result was useful for prioritizing the traits for selecting best genotypes among 47 inbred lines. Hence kernel row number, kernel per row and shelling percentage, cob length and cob diameter were considered as important yield component traits for selecting inbred lines for the further breeding program.

Principle component analysis was done to highlight the contribution of different variables in relation to their variability; it was evident that five components contributed to the variability for 86.49%. Graphical representation of different component traits indicated their relative contribution to the total variability. Factor loadings of different variables showed that plant height, tassel length, cob length, kernels per row and yield are the primary factor for variability while days to 50% flowering and ear height were the second factors. The cob diameter and shelling percentage were the 3rd and 4th principal factors and the number of cobs and kernel row number were the 5th principal factor responsible for variability in the test genotypes, which can be further utilized for crop improvement program (Daudo and Olakojo, 2007). Therefore, all five PCs were considered in cluster analysis for the relative grouping of inbred lines (Upadhyaya et al., 2012; Syafii et al., 2015). Three distinct clusters having high yielding genotypes in cluster I and cluster III, were formed. By combining results of cluster analysis and Duncan's Multiple Range Test (DMRT) for yield (data not shown), a total of 12 top performing inbred lines with broad genetic base were selected. Amongst them, seven inbred lines *viz.*, CML 314, CML 319, CML 488, CML 494, CML 504, CML 517 and CML 531 lie in cluster I and five inbred lines viz., CML 47, CML 95, CML 377, CML 522 and CML 538 belonged to cluster III. These inbred lines flowered within the range of medium to late duration, showing yielding ability in the range of 2120 kg/ha to 3810 kg/ha.

Selection based only on yield, may not always be adequate when genotype by environment interaction is significant (Kang et al., 1991; Zobel, 1990). The presence of genotype by environment interaction (GEI), frequently changes the hybrid ranking in different environments due to cross-interactions, making their proper selection difficult. It is essential that the genotype by environment interaction is taken into account, properly understood and analyzed. Hence to evaluate their yield stability, new hybrids were exposed to different agro-climatic condition by growing them in three distinct locations and yield data were subjected to AMMI analysis.

Several statistical techniques to identify stability of a genotype were set up (Yates and Cochran, 1938; Finlay and Wilkinson, 1963; Eberhart and Russel, 1966). But these will take into consideration only additive components of environmental interactions and consequently small portion of interaction can be accounted (Gauch,1992; Gauch and Zobel, 1992). Such approaches, however, could be useful in calculating stability statistics (Tai, 1971; Upadhyaya et al., 2012). The Additive Main Effects and Multiplicative Interaction (AMMI) model is an hybrid statistical model which incorporates both the additive and multiplicative components of the two-way data structure. In this model, the additive portion of the variance is separated from the multiplicative variance (interaction) by ANOVA. The PCA analysis is then applied to the interaction (residual) portion from the ANOVA to extract a new set of coordinate axes which account more effectively for the interaction patterns. Estimation of the PCA axes is accomplished according to the least square principle (Bradu and Gabriel, 1978).

In the present study, high environment and G×E interaction variance ratio indicated that genotype strong interaction with environments was relevant. This also may be due to the wide range of environments considered in the research for testing these newly bred hybrids. This has given the opportunity to partition the total variance into genetic component and interaction component of variance, which directed in the selection of the best stable genotype/s across the environment. According to the ASVi values, G38 hybrid appeared to be very stable followed by G50 and G44. Though they expressed stable yield potential across the tested environments, the yield of these genotypes was far below than any check hybrid tested inserted in this study. On the other hand hybrid, G25 expressed high yield potential (mean 73.29 q/ha) and stability index was higher than unity (1.83). However the ASVi value of checks ranged from 1.92-3.58 and yield ranged from 55.71 q/ha - 60.20 q/ha which was less than values observed for G25. It has been reported that genotype with stability index deviating from unity can be adapted to a specific location (Eberhart and Russel, 1966), hence, G25 can be selected as genotype adapted to specific areas. The G25 is collocated between the ordinates of Delhi and Hyderabad (Fig. 3) with yield potential 74.19 q/ha and 79.66 q/ha respectively at these specific locations, so performance of this hybrid is better expressed when targeted for the peninsular zone.

Conlusion

Adaptation of germplasm to newer environment plays an important role in plant breeding programs. Hence, newly introduced inbred lines from CIMMYT, Mexico were evaluated and were adapted to tropical Indian condition. Later, desirable, potential inbred lines were selected which could be useful in white maize improvement program. From this study 12 inbred lines were found desirable in terms of yielding ability, having desirable male and female parental characteristics for future white maize hybrid breeding program. Hybrids obtained through diallel mating among these 12 inbred lines resulted in three hybrids which are stable across the tested environments and in one location a specific hybrid reached yielding ability up to 79 q/ha. Hence, the outcome of this research may contribute to the enhancement of white maize productivity in India.

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