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Heterotic Grouping in Early Maturing Indian Maize Lines

Avinash Singode[1*], Manivannan A[2], Bilal Ahmad, Ekta Srivastava and Vinay Mahajan[3]
Indian Institute of Maize Research, Pusa Campus, New Delhi – 110012.
[1]ICAR-Indian Institute of Millets Research, Hyderabad- 500 030 (India).
[2]ICAR-Cental Institute for Cotton Research, Regional Station, Coimbatore – 641003.
[3]ICAR-Indian Institute of Maize Research Unit, Ludhiana – 141004.
[*]Corresponding author email id: avinash.singode@gmail.com

***Abstract* – Sixty four early maturing lines testcrossed with CML474 and V373 in Line × Tester design for heterotic grouping. All the 64 lines were derived from 'Hill Early Yellow pool'. The promising hybrids identified for yield are DE13043 × CML474 (119.4 q/ha), DE13065 × CML474 (79.1 q/ha), DE13007 × CML474 (62.9 q/ha), DE13118 × V373 (78.5 q/ha), DE13006 × V373 (73.48 q/ha), DE13060 × V373 (69.33 q/ha), and DE13057 × V373 (60.6 q/ha). L × T ANOVA revealed mean sum of squares due to lines and the L × T crosses was significant (p <0.000). GCA/SCA showed preponderance of additive gene action in the crosses for yield. GCA effects were found positive in 31 lines out of the 64 lines. GCA of CML474 was 0.04 and V373 was -0.04. Some of the lines showed high magnitude of positive GCA (> 16) for yield like DE13116, DE13073, DE13118, DE13006, DE13007, DE13065 and DE13043. The 31 lines with positive GCA for yield were classified into two heterotic groups based on SCA effect. Out of 31 lines 15 were grouped with CML474 (Heterotic group 'A') and 16 with V373 (Hetertotic Group 'B'). Biplot method of plotting GCA and SCA effect was found suitable for visualizing heterotic grouping.**

***Keywords* – Biplot, Combining Ability, GCA, Heterotic Grouping, Maize and SCA.**

I. INTRODUCTION

Heterotic grouping of germplasm lines is an important activity in hybrid breeding [1]. Heterotic response based grouping will enable development of new inbred lines with-in group and hybrid development between lines of opposite heterotic group. Hence, for systematic exploitation of heterosis characterization of populations, genetic pools and even lines for heterotic pattern and establishing heterotic groups is important. It enhances efficiency of hybrid development. Heterotic grouping in maize is done across the world. The most widely accepted pair of heterotic pools illustrated across maize breeding is the Northern flints and Southern dents of USA. Broadly four heterotic groups of US maize were illustrated as Reid, Lancaster, Iowa dents and Miscellaneous. Duvick et al., [2] described the Central and Northern American maize into Stiff stocks Synthetics (SS) and the Non-stiff stalk Synthetics (NSS). In Europe, since the germplasm was introduced from Americas there are two major groups namely American dents and European flints [3]. Chinese maize was classified into domestic group consisting of lines selfed from *Tangsipingtou* and *Ludahonggu* germplasm, and exotic group consists of Lancaster Sure Crop (LSC), Reid Yellow Dent (RYD), and germplasm derived from Pioneer hybrids (PN) [4], [5].

Legesse et al [6] grouped 23 highland transition maize inbred lines derived from three different populations (Kitale Synthetic II × N3-type lines; Ecuador-573 × SC-type lines; and Pool9A × IITA's mid-altitude streak resistant population) in two heterotic groups based on Specific Combining Ability effects. Combining ability estimates, GCA (General Combining Ability) and SCA (Specific Combining Ability) variance can be used as indicators to determine the worth of lines [7]. These genetic parameters have enabled breeder in developing populations of high breeding value. SCA effect is useful in determining the heterotic grouping of population and inbred lines for enhancing efficiency of hybrid breeding [8], [9]. Dudley et al. [10] reported higher yield, up to 21% in inter-group than intra-group hybrids between Reid Yellow Dent × Lancaster Sure Crop crosses; whereas, Dhillon et al, (1993) [11] reported 16% higher yield.

In India, grouping maize germplasm was done but, was restricted to two centres of All India Coordinated Maize Improvement Program (AICMIP), Pantnagar and Ludhiana. Early lines in AICMIP were grouped based on CM 111 and CM 202. However, Punjab Agricultural University (PAU) developed three pairs of heterotic pools [12], [13], (i) Makki Safed × Tuxpeno, (ii) Indigenous × Semi-Exotic, and (iii) Ludhiana Lancaster × Ludhiana Stiff Stalk. Among these three pairs, Makki Safed × Tuxpeno and Indigenous × Semi-Exotic are adapted to the rainy season (June to October). These heterotic groups helped in utilizing available indigenous/ local germplasm and derivatives of Makki Safed-1 at the same time keeping window open to accommodate exotic germplasm in hybrid breeding program. Although these centres have made systematic study but they do not represent whole range of Indian maize germplasm. Indian maize lines forms a complex genetic structure, coming from diverse sources, which makes heterotic grouping very difficult or may even fail. A similar kind of situation is seen in tropical CIMMYT maize germplasm where complementary heterotic patterns failed because of the complex genetic structure between populations [14]. Hence, there is need to group new inbred lines continuously developed every year based on heterotic response.

Heterotic grouping based on multi-location and over years may sometimes distort the combining ability results. This is because most of the variation is attributed to Genotype Environment Interaction (GEI). The cross-over effect is observed in multi-location trials makes the heterotic grouping difficult. Thus, lines with high GCA and SCA can be selected for developing crosses. Such crosses can evaluated in multi-location trails to identify hybrids best suited for an environment. In a hybrid breeding program the lines found inferior are rejected in the first year of testing and are not carried forward to next year of testing. Hence, in the present study heterotic grouping is done with single year one location data.

Heterotic grouping is a tedious exercise which requires great effort on field and thorough data analysis. The analysis generates huge tables and array of values; it becomes very difficult to envisage yield, heterosis, GCA and SCA effects together. In the present study we also wanted to simplify the interpretation of heterotic grouping using biplot method.

The present study was undertaken to (i) estimate the combining ability of parents and hybrids, nature and magnitude of gene action for yield and yield components in maize by adopting Line × Tester analysis [15] (ii) identify best hybrid combination of lines and testers and (iii) to group these lines into heterotic groups. The study also looks into heterotic grouping of lines derived from single population (Hill Early Yellow pool) using two diverse testers to find out how the grouping affects the selection and utilization of lines in hybrid breeding program.

II. MATERIALS AND METHODS

Plant Material

Selection of Testers: The two testers CML474 and V373 were used for making L × T crosses for heterotic grouping. CML474 (SW92145-2EV-13-1-BB) is one of the diverse lines among the highland maize germplasm of CIMMYT as revealed by SNPs. This information was generated by CIMMYT using 1.2 million SNPs data (personal communication). The line was selected to introgress water-logging tolerance genes/ QTLs. This line as one of testers will enable us to group lines from CIMMYT and other international sources. Likewise, V373 (JKMH-175-4 (O. P.) ⊗-16-7-12-1- ⊗b-#-#-⊗b-#-⊗b-⊗b) was used to harness the potential of indigenous maize germplasm adapted to hill conditions/ earliness in hybrid breeding program. V373 is good general combiner and is also parent of two commercially released hybrids in India viz. Vivek Maize Hybrid 39 and Vivek Maize Hybrid 43. It is also found resistant to Turcicum Leaf Blight (TLB) and Maydis leaf blight (MLB) [16]. The hybrid of V373, Vivek Maize Hybrid 43, was used as checks in our previous studies to identify superior early maturing hybrids [17].

Inbred Lines and Development of Crosses: A total of 118 lines developed in ICAR -Indian Institute of Maize Research (IIMR), New Delhi during 2009 to 2013 (DMR Annual Report- 12-13 and DMR Annual Report- 13-14) [18], [19]. These lines were derived from Hill Early Yellow Pool procured from ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan (VPKAS), Almora. Among these 64 lines were testcossed with CML474 and V373 in ICAR -Indian Institute of Maize Research (IIMR), New Delhi during 2013 *kharif*.

All the 128 crosses were evaluated in four trials in IIMR experimental fields, New Delhi. All the crosses were evaluated without parents. The crosses were evaluated in three trials in randomized block design in three replications.

The experimental unit consisted of two rows of 3 meters, 0.67 meters was distance between rows and plant to plant distance was 0.67 meters. Recommended cultivation practices were followed to maintain plant populations. Data was recorded on days to anthesis and silking, plant height and ear height (cm), yield (q/ha) and yield components like ear length (cm), ear girth (cm), number of kernel rows and kernels per row and hundred kernel weight (g). For heterotic grouping yield data was used.

Statistical Analysis

Data analysis was performed using Agricolae package of R software. General Combining Ability effects (GCA) and Specific Combining Ability (SCA) effects along with their standard error and ratio of GCA/SCA was estimated using 'line X tester' program of 'Agricolae' package of R-cran Software version 3.2.2.

Analysis of Variance (ANOVA) was performed to assess the total variance among the hybrids, total genetic variance was partitioned into testers (males), lines (females) and line × tester (testcrosses) as described in L × T analysis of variance [20]. The following statistical model was used for the data analysis.

$$Y_{ijk} = \mu + G + R_h + \varepsilon_{hijk}$$
$$G = \alpha_i + \beta_j + (\alpha\beta)_{ij}$$

Where,

Y_{ijk} is the observation of cross between the i^{th} female parent (Line) and the j^{th} male parent (Tester) planted in k^{th} replication;

μ is the overall mean;

G is the total genetic variance

α_i is the effect of the i^{th} female parent;

β_j is the effect of j^{th} male parent;

$(\alpha\beta)_{ij}$ is the effect of cross between i^{th} female and j^{th} male

R_k is the replication effect and εijk is the error component which remains unexplained in the experiment.

Lines with positive GCA effect for yield were retained and the rest were discarded. The lines with positive GCA (> zero) were utilized in heterotic grouping based on SCA effects. For a comprehensive assessment GCA and SCA effects on two dimensional plane biplot was generated using GGEB iplot package of R Software version 3.2.2. The GGE biplot is used for multi-location data but can also extend to generate a biplot for all types of two way data [21]. To group lines into heterotic groups we followed the procedure carried out by [8], [22]. The GCA and SCA effects bilpot was generated using GGEB iplot package of R Software version 3.2.2. The GGE biplot is used for multi-location data but can also extend to generate a biplot for all types of two way data [21].

III. RESULT AND DISCUSSION

The selected testers (CML474 and V373) were used for heterotic grouping of 64 indigenously developed maize lines. These lines were developed from the Hill Early Yellow (HEY) pool procured from VPKAS, Almora. All the lines were testcrossed with both the testers (CML474 and V373).

Analysis of Variance for L × T

The test-crosses were evaluated without parents. The variation in the testcross yield performance was significant (< 0.001 probability). Variation due to lines, testers and L × T crosses was estimated. ANOVA revealed variation in the testers was not significant/ whereas, maximum variation is attributed by lines to the total variation. The proportion of contribution of lines and line × test to total variation is 65.71 % and 34.28 %, respectively. Mean Sum of Squares (MSS) of lines, testers in ANOVA signifies GCA variance whereas, testcross MSS signifies SCA variance component. GCA due to lines was highly significant whereas, GCA due to testers was not significant. This may be because we have used only two testers. The average of yield performance of lines in the testcross with one tester did not significantly differed with other. Thereby, by definition the GCA was not significant for testers. Librando and Magulama (2008) [23] reported similar results, variance due to testers and L × T was not significant. Significant GCA and SCA variance indicated preponderance of both additive and non-additive effects genetic variation in the crosses.

Mean performance of lines along with pedigree is presented in Table 1. Among the 64 lines twelve lines viz. DE13007, DE13011, DE13019, DE13021, DE13036, DE13043, DE13056, DE13065, DE13067, DE13073, DE13074, DE13116 in combination with CML474 gave yield above 50 q/ha whereas, 14 lines (viz. DE13065, DE13007, DE13073, DE13116, DE13005, DE13057, DE13006, DE13069, DE13063, DE13060, DE13034, DE13013, DE13118 and DE13012) in combination with V373 yielded more than 50 q/ha. Most of the crosses were very promising and have out yielded the commercial checks Vivek QPM 9 and Vivek Hybrid 43 (Data not included in Table 1). The average yield of Vivek QPM 9 and Vivek Hybrid 43 was 60.06 q/ha and 63.77 q/ha, respectively. The hybrid combinations with high yielding potential identified were DE13043 × CML474 (119.4 q/ha), DE13065 × CML474 (79.1 q/ha), DE13007 × CML474 (62.9 q/ha), DE13118 × V373 (78.5 q/ha), DE13006 × V373 (73.48 q/ha), DE13060 × V373 (69.33 q/ha), and DE13057 × V373 (60.6 q/ha).

General Combining Ability (GCA) Effects

General Combining ability (GCA) effects of lines along with mean performance of lines in testcrosses is presented in Table 1. GCA effects of lines were in both positive and negative direction and ranged between -30.36 to 43.46. Among the 64 lines 31 have showed positive GCA for yield. Some of the lines like DE13116, DE13073, DE13118, DE13006, DE13007, DE13065 and DE13043 showed high magnitude of positive GCA (> 16) for yield. The lines in the study are derived from a single base population (HEY pool), it is very likely that some lines have accumulated gene block or chromosome segment which are desirable for yield during the course of inbreeding. Two lines, DE13040 (-0.54) and DE13097 (0.97) showed GCA nearing to zero. In the process of inbreeding, segregation and recombination occurs, fixation of genes or chromosome segments manifest desirable and undesirable phenotype. The lines with positive high GCA and high per-se performance can be used to develop pools. Such a pool will have accumulated desirable genes in high frequency.

Among the testers CML474 showed positive GCA whereas V373 showed negative GCA effect with magnitude of 0.044. In a situation where there are only two testers one will always have positive GCA effect and other negative and together total to zero [20]. Apart from the *per-se* performance of the lines the ability to produce productive hybrids varies which is called Specific Combining Ability (SCA)

Specific Combining Ability (Sca) Effects

Positive GCA for yield was seen in 31 lines out of 64 inbred lines. Among the 30 lines 16 in combination with CML474 and 15 with V373 showed positive SCA. V373 is productive line and is parent of two commercial hybrids released in India and is adapted to hill ecology. The line V373 and HEY pool are adapted to hill ecology. Since V373 and HEY pool derived lines are hill adapted it is possible that common set of adaptability genes were fixed in both. Hence, CML 474 could produce more number of desirable hybrids than V373. The lines DE13019, DE13021, DE13056, DE13011, DE13065 and DE13043 have shown high positive SCA with CML474 whereas DE13013, DE13060, DE13118 and DE13006 have shown positive SCA with V373. High magnitude of SCA indicates preponderance of non-additive gene action manifested by both dominance and over-dominance effect in genetically divergent lines. It is one of the methods to group lines into heterotic groups. Parentoni et al., [22] classified tropical maize germplasm into heterotic groups comparing the SCA values. Similar methodology was followed by Legesse et al., [6] to formulate heterotic groups in highland transition maize inbred lines. Combining ability based selection of tester is widely used for heterotic grouping. Akinwalea et al., [24] identified suitable testers assed by combining ability in diallel mating tested under striga infested and striga free environment. The SCA effects in striga free environment showed significant correlation SSR marker based grouping. A trait based tester specific to an environment was identified for heterotic grouping of breeding germplasm.

Heterotic Grouping of Early Maturing Inbred Lines

Melchinger and Gumber [25] defined a heterotic group "as a group of related or unrelated genotypes from the same or different populations, which display similar combining ability and heterotic response when crossed with genotypes from other genetically distinct germplasm groups. By comparison, the term heterotic pattern refers to a specific pair of two heterotic groups, which express high heterosis and consequently high hybrid performance in their cross.” The performance of testcrosses manifested in SCA effect was used to group lines in two dieverse heterotic groups. All the lines with positive GCA were selected and those shown negative GCA was discarded.

Table 1: Yield performance and combining ability estimates of lines in L×T crosses

SN	Line	Pedigree	Yield (q/ha)		GCA effects	SCA effects with		Heterotic Group
			CML474	V373		CML474	V373	
1	DE13001	HEY Pool-4-2-1-B-B	48.13	37.56	4.63	5.24	-5.24	A
2	DE13003	HEY Pool-5-2-1-B-B	31.13	25.85	-9.73	2.59	-2.59	-
3	DE13004	HEY Pool-5-2-2-B-B	35.71	19.02	-10.86	8.30	-8.30	-
4	DE13005	HEY Pool-5-3-1-B-B	43.52	58.65	12.86	-7.61	7.61	B
5	DE13006	HEY Pool-5-4-(1)1-B-B	41.48	73.48	19.26	-16.04	16.04	B
6	DE13007	HEY Pool-5-4-(1)2-B-B	62.98	56.81	21.68	3.04	-3.04	A
7	DE13008	HEY Pool-5-4-(2)3-B-B	34.23	39.77	-1.22	-2.82	2.82	-
8	DE13010	HEY Pool-5-5-2-B-B	14.48	29.94	-16.01	-7.77	7.77	-
9	DE13011	HEY Pool-6-2-1-B-B	58.88	33.25	7.84	12.77	-12.77	A
10	DE13012	HEY Pool-6-2-2-B-B	11.73	52.19	-6.26	-20.27	20.27	-
11	DE13013	HEY Pool-6-3-1-B-B	32.75	58.31	7.31	-12.82	12.82	B
12	DE13017	HEY Pool-9-1-1-B-B	44.63	40.08	4.14	2.23	-2.23	A
13	DE13018	HEY Pool-10-2-1-B-B	43.71	47.13	7.20	-1.75	1.75	B
14	DE13019	HEY Pool-11-1-1-B-B	53.04	27.73	2.17	12.61	-12.61	A
15	DE13020	HEY Pool-12-1-1-B-B	23.15	36.96	-8.17	-6.95	6.95	-
16	DE13021	HEY Pool-12-1-2-B-B	50.17	30.90	2.31	9.59	-9.59	A
17	DE13023	HEY Pool-12-3-1-B-B	31.77	20.52	-12.08	5.58	-5.58	-
18	DE13025	HEY Pool-12-4-1-B-B	30.67	35.04	-5.37	-2.23	2.23	-
19	DE13027	HEY Pool-12-5-1-B-B	17.69	19.44	-19.66	-0.92	0.92	-
20	DE13028	HEY Pool-12-5-2-B-B	44.40	9.60	-11.22	17.35	-17.35	-
21	DE13029	HEY Pool-12-6-1-B-B	40.04	29.25	-3.57	5.35	-5.35	-
22	DE13030	HEY Pool-12-6-2-B-B	29.56	36.44	-5.22	-3.48	3.48	-
23	DE13031	HEY Pool-14-1-1-B-B	11.52	4.19	-30.36	3.62	-3.62	-
24	DE13032	HEY Pool-14-2-1-B-B	35.15	48.35	3.53	-6.65	6.65	B
25	DE13033	HEY Pool-15-1-1-B-B	25.96	36.48	-7.00	-5.30	5.30	-
26	DE13034	HEY Pool-15-1-2-B-B	33.73	51.40	4.34	-8.88	8.88	B
27	DE13036	HEY Pool-15-2-1-B-B	53.42	45.50	11.24	3.91	-3.91	A
28	DE13040	HEY Pool-15-4-1-B-B	31.02	44.33	-0.54	-6.70	6.70	-
29	DE13041	HEY Pool-15-4-2-B-B	29.25	23.71	-11.74	2.73	-2.73	-
30	DE13042	HEY Pool-15-5-1WG-B-B	43.92	49.10	8.29	-2.64	2.64	B
31	DE13043	HEY Pool-15-5-2-B-B	119.40	43.96	43.46	37.67	-37.67	A
32	DE13044	HEY Pool-15-6-1-B-B	22.98	39.10	-7.18	-8.11	8.11	-
33	DE13045	HEY Pool-15-6-2-B-B	45.63	40.73	4.96	2.40	-2.40	A
34	DE13047	HEY Pool-15-9-1-B-B	22.73	29.33	-12.19	-3.34	3.34	-
35	DE13053	HEY Pool-19-6-1-B-B	29.94	26.75	-9.88	1.55	-1.55	-
36	DE13056	HEY Pool-21-2-1-B-B	55.38	31.83	5.39	11.73	-11.73	A
37	DE13057	HEY Pool-21-2-2-B-B	41.98	60.60	13.07	-9.36	9.36	B
38	DE13060	HEY Pool-24-1-2-B-B	33.94	69.33	13.42	-17.74	17.74	B
39	DE13063	HEY Pool-25-2-1-B-B	40.73	50.04	7.17	-4.70	4.70	B
40	DE13065	HEY Pool-25-4-1-B-B	79.10	56.63	29.65	11.20	-11.20	A
41	DE13067	HEY Pool-25-5-1-B-B	52.42	49.40	12.69	1.47	-1.47	A
42	DE13068	HEY Pool-25-6-1-B-B	38.19	46.52	4.14	-4.21	4.21	B
43	DE13069	HEY Pool-27-1-1-B-B	41.48	55.85	10.45	-7.23	7.23	B
44	DE13073	HEY Pool-28-1-1-B-B	56.00	53.92	16.74	1.00	-1.00	A
45	DE13074	HEY Pool-30-1-1-B-B	56.02	42.13	10.85	6.90	-6.90	A
46	DE13077	HEY Pool-30-7-1-B-B	34.67	45.50	1.86	-5.46	5.46	B
47	DE13078	HEY Pool-32-1-1-B-B	34.33	24.38	-8.87	4.94	-4.94	-
48	DE13079	HEY Pool-32-2-1-B-B	21.08	29.75	-12.81	-4.38	4.38	-
49	DE13085	HEY Pool-32-6-2-B-B	41.58	16.83	-9.01	12.33	-12.33	-
50	DE13086	HEY Pool-32-6-3-B-B	24.52	20.27	-15.82	2.08	-2.08	-
51	DE13087	HEY Pool-32-7-1-B-B	40.04	30.42	-2.99	4.77	-4.77	-
52	DE13089	HEY Pool-32-8-1-B-B	23.35	37.46	-7.81	-7.10	7.10	-
53	DE13092	HEY Pool-32-9-3-B-B	30.50	33.90	-6.02	-1.74	1.74	-
54	DE13093	HEY Pool-33-3-1-B-B	33.19	14.33	-14.46	9.38	-9.38	-
55	DE13094	HEY Pool-33-4-1-B-B	28.38	26.63	-10.72	0.83	-0.83	-
56	DE13096	HEY Pool-35-2-2-B-B	28.02	26.58	-10.92	0.68	-0.68	-
57	DE13097	HEY Pool-35-3-1-B-B	39.69	38.69	0.97	0.46	-0.46	A
58	DE13099	HEY Pool-37-1-1-B-B	46.73	43.54	6.92	1.55	-1.55	A
59	DE13108	HEY Pool-40-1-1-B-B	22.85	14.29	-19.65	4.24	-4.24	-
60	DE13109	HEY Pool-41-1-1-B-B	30.67	25.17	-10.30	2.71	-2.71	-
61	DE13114	HEY Pool-44-1-1-B-B	21.46	27.79	-13.59	-3.21	3.21	-

SN	Line	Pedigree	Yield (q/ha)		GCA effects	SCA effects with		Heterotic Group
			CML474	V373		CML474	V373	
62	DE13115	HEY Pool-44-2-1-B-B	40.96	33.33	-1.07	3.77	-3.77	-
63	DE13116	HEY Pool-44-2-2-B-B	50.92	58.75	16.62	-3.96	3.96	B
64	DE13118	HEY Pool-44-6-2-B-B	32.25	78.52	17.17	-23.18	23.18	B
		Mean	**38.26**	**38.18**				
		SE (GCA for line)	4.52					
		SE (GCA for tester)	0.80					
		SE (SCA effect)	6.40					
		SE (*gi* - *gj*) line	6.40					
		SE (*gi* - *gj*) tester	1.13					
		SE (*sij* - *skl*) tester	9.04					

The lines with SCA effect in positive direction with the tester CML474 was included in the opposite group (that is, with V373), similarly the lines showing positive SCA with V373 were included in opposite group (that is, with CML474). To visualize the heterotic pattern in the lines we used GGEBiplotGUI package of R-Cran software [26].

Based on test-cross *per se* performance and GCA effects, the testers were jointly visualized in the figure 1.

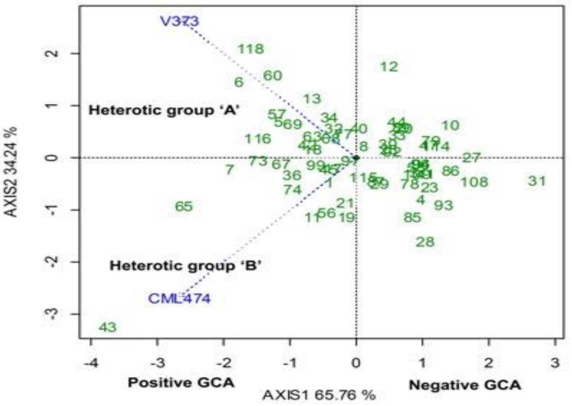

Fig. 1. Differential per se performance of lines in combination with two testers

Note: The numbers mentioned in the biplot are line names without the prefix DE13 as mentioned in the Table 1

All the 64 inbred lines along with two testers are depicted in two dimensional biplots. Here, the horizontal axis (Axis 1) is corresponding to variance due to lines and vertical axis (Axis 2) is corresponding to variance due to L×T. The principal component Axis 1 contribution is 66.08% and that of Axis 2 is 33.92% which is similar to variation in lines to the total variation 65.71% and the variation in L×T to the total variation 34.28%. Both the testers have same magnitude but in opposite direction which is corresponding to the GCA effects, one is positive and other is negative. The lines across the origin opposite to the tester have GCA in negative direction for lines. The distance from origin in horizontal direction corresponds to the magnitude of GCA.

All the lines with positive GCA were separated by origin in the plot. All the lines showing positive SCA with CML474 grouped in together in one quadrant similarly, in the other quadrant for V373. The distribution of lines falling towards a tester indicates that the line belongs to opposite heterotic group (figure 2). This indicates that the biplot captured 100% variation to explain hetrotic grouping in two dimension plot. We have found biplot are useful in visualizing the grouping as well as to identify lines with magnitude of GCA and SCA. The GGE biplot us used for multi-location data but can also extend to generate a biplot for all types of two way data [21].

The definition of heterotic group proposed by Melchinger and Gumber [25] emphasize on combining ability response of lines whether coming from same or different populations. Lines from a heterotic group will have similar combining ability and heterotic response in cross.

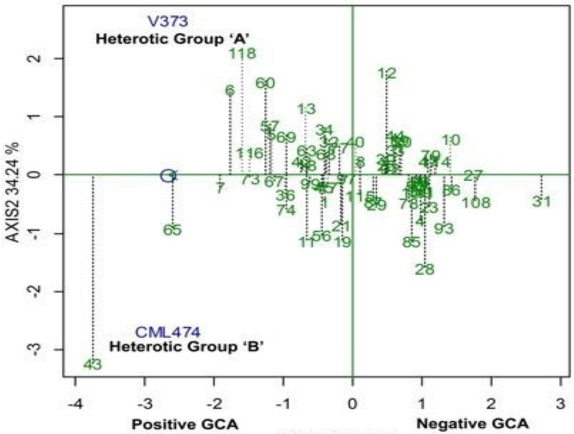

Fig. 2. Heterotic relationship and magnitude of GCA and SCA effects of inbred lines

Note: The numbers mentioned in the biplot are line names without the prefix DE13 as mentioned in the Table 1.

IV. CONCLUSION

Heterotic grouping of lines is an important activity in plant breeding. It enables the efficient selection of parents in Inbred-hybrid breeding program. A few finding that were obviously clear in the analysis are (i) there should not be any discrepancy in selection of testers. It has to be thoughtful and must render its usefulness in future also. The major hurdle of heterotic grouping is solved once the right testers are identified. In the present research we have meticulously identified the testers and have also explained in the result and discussion. (ii) The lines with positive GCA are useful and all the lines with negative GCA were discarded. (iii) heterotic grouping was based on magnitude of SCA. Heterosis in crosses of line with either of the testers depends largely on complementation and over-dominance effect. This is function of chromosomal blocks or alleles fixed during inbred line development.

In the present study all the line were derived from single pool and among them 31 lines showed positive GCA and 16 lines were grouped with V373 and 15 lines grouped with CML474. This means grouping of lines is based on testers and objective of grouping. Hence, every-time, a line derived has to undergo long process of heterotic grouping. (iv) It is better to characterize lines based on agronomic, traits and reaction to pest and diseases so that the worth of the line is assessed comprehensively. Later the lines can be used in crossing or in improvement of traits.

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AUTHORS’ PROFILES

Dr. Avinash Singode.
Scientist (Plant Breeding), ICAR-Indian Institute of Millets Research, Hyderabad.

Dr. Manivannan A.
Scientist (Genetics), ICAR - Cental Institute for Cotton Research, Regional Station, Coimbatore – 641003.

Dr. Vinay Mahajan.
Principal Scientist (Plant Breeding), ICAR-Indian Institute of Maize Research Unit, Ludhiana – 141004.