

Original Research Article

<https://doi.org/10.20546/ijcmas.2020.910.126>

Heterosis and Combining Ability Studies in Maize (*Zea mays* L.) for Drought Tolerance, TLB Disease Resistance and Productivity in Northern Dry Tract of Karnataka

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ABSTRACT

Maize being a cross pollinated crop has a higher yield potential compared to other cereals. In the present investigation, 30 full season hybrids (fifteen lines crossed with two testers in Line×Tester) were evaluated for their productivity, drought tolerance and turcicum leaf blight (TLB) disease resistance in the dry tract of Northern Karnataka. The line × tester analysis was carried out to determine the standard heterosis and combining ability in these hybrids with five checks namely Bio 9544, NK-6240 (National checks), CMH08-282 (Zonal check), GPMH-1101 and BRMH-1 (Local checks) under rainfed conditions during *kharif* 2018 at the Regional Agricultural Research Station, Vijayapur. Among these hybrids, GHVJP5 (GPM-26×CML-451) was found to be better performing for most of the traits followed by GHVJP23 (GPM-686×CML-451); the hybrid GHVJP13 (GPM-225×CML451) was found to be drought tolerant; GHVJP5 and GHVJP12 (GPM119×CM111) were found to be resistant to TLB and GHVJP14 (GPM-225×CM-111) and GHVJP5 were found to be early maturing. These hybrids can be further tested for their proficiency. Among parents, the lines GPM26 and GPM686 were found to be good general combiners for productivity traits. These can be used as parents in the development of superior hybrids.

Keywords

Line×tester,
Standard heterosis,
Combining ability,
TLB, Drought

Article Info

Accepted:
10 September 2020
Available Online:
10 October 2020

Introduction

Maize (*Zea mays* L.) is a versatile crop grown over a range of agro climatic zones and is an important food and forage crop with abundant natural diversity. In India, it is cultivated in 9.6 million hectares area with 27.15 million tonnes annual production and 2.83 tonnes per hectare productivity (Anon. 2018). It is one of the most important *Kharif* cereal crops of Karnataka and is cultivated in 13.7 lakh

hectares with 33.14 lakh tonnes production and 2419 kg per hectare productivity (Anon. 2017).

Maize is a highly cross-pollinated crop and scope for exploitation of hybrid-vigor depends on direction, magnitude of heterosis and type of gene action involved. The exploitation of heterosis is possible only when parents involved in crosses differ in their combining ability. In any hybridization

program, recognition of best combination of two/more parental genotypes to maximize variance within related breeding populations, and as a result the chance of recognizing superior transgressive segregants in the segregating populations are the most critical challenges to plant breeders.

Combining ability studies provide information on the genetic mechanisms controlling inheritance of quantitative traits and enable breeders to select suitable parents for further improvement or use in hybrid breeding for commercial purposes.

One of the main deterrents to high grain yield in maize is its susceptibility to several diseases. Of 112 diseases of maize reported so far from different parts of the globe, 65 are known to occur in India and in zone 3 of Karnataka, TLB (*Exerohilum turcicum*) and MLB (*Bipolaris maydis*) are found to be of common occurrence. TLB is one of the most important and widespread fungal disease infecting leaves prior to initiation of flowering and later spreading to cover entire leaves thereby affecting photosynthesis resulting in the severe reduction in grain yield. Hence resistance to TLB is one of the important criteria in development of new hybrid combinations.

Northern dry zone of Karnataka (zone-3) is where new areas of maize is expanding due to increase in command area. Hence in the present study an attempt is made to evaluate the public bred hybrids to know their combining ability, heterosis, resistance to TLB, drought tolerance and productivity traits.

Materials and Methods

The experiment was conducted at Regional Agricultural Research Station, Vijayapura in *kharif* 2018 located at 16° 49' N latitude, 75°

43' E longitude and 593 m above mean sea level with a mean annual rainfall of 590 mm. The rainfall during 2018 was 466.3 mm. June and September were the wettest months during 2018 as compared to other months. During the year 2018, maximum monthly mean temperature was the lowest in December (29.70°C), while highest was in May (39.20°C). Minimum monthly mean temperature was the highest in May (23.40°C) and the lowest in January (13.0°C).

Thirty hybrids developed by crossing 15 lines and two testers in line×tester mating design (Kempthorne 1957) were collected from AICMIP, College of Agriculture, UAS, Dharwad. These crosses were attempted in *Rabi* 2017-18 at UAS, Dharwad.

Lines: GPM-04, GPM-07, GPM-26, GPM-52, GPM-114, GPM-119, GPM-225, GPM-255, GPM-628, GPM-668, GPM-676, GPM-686, GPM-735, GPM-751 and GPM-755.

Testers: CML-451 and CM-111.

Checks: Bio 9544, NK-6240 (National checks), CMH 08-282 (Zonal Check), GPMH-1101 and BRMH-1 (local Checks).

The randomised complete block design with three replications was followed to evaluate the experimental hybrids. Each plot consisted of two rows of three meter length with inter and intra-row spacing of 60cm and 20cm, respectively and all the package of practice was followed for normal cultivation of crop. From each entry/replication, five random, competitive plants were tagged and numbered in the middle of row to observe yield and other parameters. The observations were recorded as follows. Days to 50% anthesis and days to 50% silking were recorded from date of sowing on per plot basis. Anthesis-silking interval was determined by the difference between days to 50% anthesis and

50% silking. The plant height was recorded in centimeter from the ground level to the base of the tassel and the ear height was recorded in centimeter from the ground level to the base of the uppermost ear in five selected plants in each genotype at maturity. The cob length was measured in centimeter from the base to the tip of the cob after harvest in five selected plants in each genotype. For measuring cob girth, ordinary string or thread was wrapped in the middle portion of the ear and the length of thread was measured in centimeter and noted in terms of perimeter. Then the perimeter was converted to diameter by dividing the values by 3.14.

Days to maturity, kernel row number, kernel per row, cob weight, grain weight, test weight, fodder yield and grain yield were measured as usual. The relative chlorophyll content was measured for the third leaf from the top at 60 days after sowing on five randomly selected plants in each genotype using SPAD chlorophyll meter. For measuring relative water content, fully expanded and mature leaves were selected from five randomly selected plants at 60 DAS and their fresh weight was noted down. Then the leaf samples were immersed in water for 8hrs and then the turgid weight of the samples was measured. These samples were further dried in oven at 60°C and the dry weight was determined. The relative water content was then calculated using the following formula.

$$\text{RWC (\%)} = \left(\frac{\text{Fresh weight} - \text{Dry weight}}{\text{Turgid weight} - \text{Dry weight}} \right) \times 100$$

Disease screening for TLB was done under natural conditions by following one to five disease rating scale given by Payak and Sharma (1983) at the respective stages of the crop growth. The data thus obtained was analysed statistically in TNAUSTAT software.

Results and Discussion

Analysis of variance

The analysis of variance (Table 1) for different traits revealed that, there was significant variation due to lines for all the traits studied which indicated that the lines were genetically diverse among themselves and the variation due to testers was significant for most of the traits except PH, CL, CG and SP. However, the mean sum of squares due to testers was higher than that due lines for majority of traits indicating that the testers were more genetically diverse than lines. Since there was greater diversity in the parents we can expect the crosses between them to be heterotic. There was significant variation among the crosses for all the traits studied except for plant height.

Combining ability

The identification of good general combiners for different traits and partitioning of the parents into good and poor combiners helps us in identifying and utilizing the better parents in hybridization programmes. Also identification of hybrids with good SCA helps in exploiting heterosis from such crosses.

For early maturity, the lines GPM-225, GPM-04 and tester CM-111 were found to be good general combiners (Table 2a) as they had significant negative GCA effects for DFA, DFS and DM. Thus these lines can be used as parents in the development of hybrids suitable for early maturing. The hybrids GHVJP1 (GPM-04×CML-451), GHVJP5 (GPM-26×CML-451) and GHVJP14 (GPM-225×CM-111) were found to have significant negative sca (Table 3a) for days to fifty percent flowering indicating their earliness and this may be due to the narrow sense heritability of the trait (Panda *et al.*, 2017). These hybrids showing early maturity also

had good per se performance for yield and related traits and hence can be suitable for cultivation in drought prone areas like zone 3 so that they can escape drought to considerable extent. These plants can also be used in mixed or inter cropping systems as well. Similar results were obtained by Dubey *et al.*, (2001).

For drought tolerance the traits like ASI, RWC and SPAD were taken into consideration. The line GPM-686 was found to be good general combiner for RWC and SPAD while GPM-668 was found to be good general combiner for all these traits (Table 2a) and hence can be used as source for drought tolerance. The hybrid GHVJP13 (GPM-225×CML-451) which is a cross between a good×poor combiner had significant sca effects in positive direction for relative water content (Table 3a) and also had higher yields. This indicated that the high gca of parent doesn't always assure significant sca among hybrids. This hybrid can be considered as drought tolerant and can be subjected to further evaluation in multi locations.

For TLB resistance, the lines GPM-26, GPM-119, GPM-751 and tester CM-111 were found to be good general combiners (Table 2a) and can be used as source of resistance. Among the hybrids, GHVJP5 (GPM-26×CML-451) and GHVJP12 (GPM-119×CM111) were found to be resistant to TLB. These GCA estimates indicated the possibility to select inbred lines that can be combined to generate hybrids that are resistant to the disease (Ejigu *et al.*, 2017).

With respect to productivity traits, the line GPM-26 was found to good general combiner for CL, CW, GW, SP and TW; the line GPM-686 was found to be good general combiner for CL, CG, KPR and GY (Table 2b); the lines GPM-735 and GPM-628 were found to be good general combiners for KRN (Table

2b) and the line GPM-119 was found to be good general combiner for FY (Table 2b). Among testers, CML-451 was found to be good general combiner for KRN and TW; CM-111 was found to be good general combiner for GY (Table 2b). As these traits indirectly contribute to increased yields these can be used as parents for developing elite hybrids.

The hybrids GHVJP5 (GPM-26×CML-451) and GHVJP23 (GPM-686×CML451) showed significant positive SCA for CL, KPR, CW, GW and GY (Table 3b). The hybrid GHVJP12 (GPM-119×CM111) had significant positive SCA for KPR and GY (Table 3b) and was also found to be resistant to TLB. The hybrid GHVJP13 (GPM-225×CML-451) showed significant positive SCA for KRN, GY (Table 3b) and was also found to be drought tolerant. The hybrid GHVJP25 (GPM-735×CML451) showed significant positive SCA for GY (Table 3b) with high per se values for the same. Thus these hybrids can be subjected to further evaluation for testing their proficiency.

The lines and testers were classified into good and poor general combiners, pooled gca effects for different characters was taken into consideration. This was done by assigning the value “+1” for positive gca effects and “0” for negative gca effects and then the values were summed up. If the value of a line or tester had more than average value, it was considered as good combiner or else designated as poor combiner.

In the present study, the crosses involving both good general combiner (GHVJP5 and GHVJP23) as well as one good and one poor combiner (GHVJP12, GHVJP13 and GHVJP25) showed high SCA effects which are due to additive×additive and additive×dominant gene action and confirmed by earlier reports of Amin *et al.*, (2014).

Those promising crosses that were due to additive×additive gene action were identified as overall high general combiners and could be utilized for development of either the synthetic varieties or an elite breeding

population by allowing greater recombination among them to achieve new genetic recombination and then subjecting the resultant population to recurrent selection (Izhar and Chakraborty, 2013).

Table.1 ANOVA for line x tester for yield traits

Source	MSS										
	df	PH	CL	CG	KRN	KPR	CW	GW	SP	TW	GY
Replication	2	564.49	8.34	0.91	1.99	2.33	2914.99	1051.87	29.73	16.60	0.53
Genotypes	34	282.64*	6.59**	1.57**	1.84**	24.53*	3130.35**	2243.06**	18.62*	29.35**	0.69**
Crosses	29	287.40	7.29**	1.35**	1.84**	25.01*	3549.30**	2527.22**	17.28*	31.12**	0.77**
Lines	14	382.71*	10.94**	1.29*	1.58**	27.21*	4503.66**	3321.51**	24.54**	49.06**	0.98**
Testers	1	5.98	7.74	0.80	6.83**	86.83*	4557.09*	2048.91*	19.62	100.28**	2.06**
Line x Tester	14	212.18	3.60	1.44**	1.75**	18.39	2522.97**	1767.11**	9.87	8.24	0.46**
Error	68	200.51	2.12	0.58	0.56	12.38	801.33	492.71	8.61	6.95	0.16
CV (%)		9.03	8.60	5.53	5.48	10.62	16.30	16.49	3.91	9.69	12.56
CD at 5%		22.97	2.46	1.32	1.25	5.67	46.17	36.16	4.89	4.16	0.64
CD at 1%		30.51	3.27	1.75	1.66	7.53	61.32	48.04	6.49	5.53	0.85

df: degrees of freedom, * and **: Significance at 5% and 1% probability respectively

Table.2a The GCA effects of parents for different morpho-physiological traits

Parents	DFA	DFS	ASI	EH	PH	SPAD	RWC	DM	TLB
Lines									
GPM-04	-1.84 **	-1.99 **	-0.14	3.31	6.49	-0.03	4.39 **	-1.99 **	0.56**
GPM-07	-1.68 **	-1.49 **	0.19	5.14	8.66	-2.47	1.82 **	-1.49 **	0.12
GPM-26	1.32 **	0.84 *	-0.48 **	11.31 **	17.82 **	-1.57	-1.44 **	0.84 *	-0.69**
GPM-52	1.49 **	2.01 **	0.52 **	4.98	1.16	0.30	8.26 **	2.01 **	0.19
GPM-114	2.16 **	1.84 **	-0.31	-1.52	-8.18	-3.03	4.51 **	1.84 **	0.33
GPM-119	-0.51	-0.32	0.19	-4.86	-2.18	3.07	-7.27 **	-0.32	-0.53**
GPM-225	-2.18 **	-1.99 **	0.19	-1.36	4.82	1.88	6.06 **	-1.99 **	-0.21
GPM-255	-1.01 **	-1.66 **	-0.64 **	0.48	-8.68	0.75	-8.79 **	-1.66 **	0.59**
GPM-628	-2.01 **	-1.66 **	0.36 *	-9.86 *	-7.18	-6.25 **	-9.27 **	-1.66 **	-0.46*
GPM-668	-0.84 *	-1.49 **	-0.64 **	0.14	2.99	-1.98	12.90 **	-1.49 **	0.04
GPM-676	2.16 **	2.18 **	0.02	5.48	3.32	2.68	4.32 **	2.18 **	0.02
GPM-686	-0.18	0.01	0.19	-3.36	-2.34	4.52 *	-7.92 **	0.01	0.14
GPM-735	1.99 **	2.01 **	0.02	1.48	1.99	-0.83	0.61	2.01 **	0.23
GPM-751	-2.18 **	-1.66 **	0.52 **	-4.69	-5.34	1.18	-2.91 **	-1.66 **	-0.35*
GPM-755	3.32 **	3.34 **	0.02	-6.69	-13.34 *	1.78	-5.26 **	3.34 **	0.07
SE	0.38	0.38	0.18	3.92	5.85	1.99	0.48	0.38	0.14
Testers									
CML-451	0.80 **	0.70 **	-0.10	-2.47	-0.20	-1.20	-1.99 **	0.70 **	0.45*
CM-111	-0.80 **	-0.70 **	0.10	2.47	0.20	1.20	1.99 **	-0.70 **	-0.45*
SE	0.14	0.14	0.07	1.43	2.14	0.73	0.17	0.14	0.05

* and **: Significance at 5% and 1% probability respectively

Table.2b The GCA effects of parents for yield related traits

Parents Lines	CL	CG	KRN	KPR	CW	GW	SP	TW	FY	GY
GPM-04	0.94	-0.46	-0.78 *	2.72	18.74	15.29	-1.53	-0.58	-0.36	-0.42 **
GPM-07	-0.39	-0.46	-0.28	-0.61	-30.76 *	-22.04 *	1.63	-4.41 **	-0.02	0.07
GPM-26	2.44 **	0.71 *	0.28	2.06	59.41 **	54.96 **	3.97 **	7.09 **	0.98 **	0.58 **
GPM-52	-0.22	1.04	-0.44	-1.94	-1.42	-2.38	-0.20	1.76	-0.52 *	-0.65 **
GPM-114	0.28	-0.62	-0.28	0.89	-7.4	-4.38	0.07	2.59	0.1	-0.2
GPM-119	0.06	0.54	0.06	1.72	26.74*	21.79 *	0.63	3.09 **	1.02 **	0.17
GPM-225	1.56 *	0.29	-0.11	-2.78	-9.76	-3.54	0.30	-0.91	-0.02	0.50 **
GPM-255	-1.56 *	-0.12	0.06	0.52	-7.92	-15.38	-0.37	0.09	1.31 **	-0.15
GPM-628	-2.22 **	-0.46	0.89 **	-1.94	-26.42 *	-24.38 **	-3.03 *	-1.74	-0.52 *	0.15
GPM-668	-0.72	0.24	0.06	-1.61	-27.59 *	-22.04 *	-0.37	-0.08	-0.19	0.01
GPM-676	0.78	-0.29	-0.78 *	1.72	-10.59	-0.21	-1.70	-2.24 *	0.21	-0.65 **
GPM-686	2.44 **	1.04 **	0.11	3.72 **	50.24 **	40.29 **	0.97	2.59 *	0.48 *	0.71 **
GPM-735	-0.89	-0.12	0.89 **	0.22	-15.09	-18.88 *	-4.37 **	-1.91	-0.86 **	0.01
GPM-751	0.14	0.04	0.22	-0.94	12.41	1.12	-0.70	0.76	-0.02	-0.15
GPM-755	0.28	0.38	0.32	-3.44 *	21.01	9.79	1.30	-2.58 *	0.31	0.08
SE	0.64	0.35	0.31	1.41	11.88	9.25	1.19	1.11	0.22	0.15
Testers										
CML-451	0.32	0.13	0.27 *	-0.98	7.12	4.83	-0.44	1.06 *	-0.09	-0.15 **
CM-111	-0.32	-0.13	-0.27 *	0.98	-7.12	-4.83	0.44	-1.06 *	0.09	0.15 **
SE	0.23	0.13	0.12	0.52	4.34	3.38	0.43	0.41	0.081	0.06

* and **: Significance at 5% and 1% probability respectively.

Graph 1a: Standard heterosis of better performing hybrids for morphophysiological traits

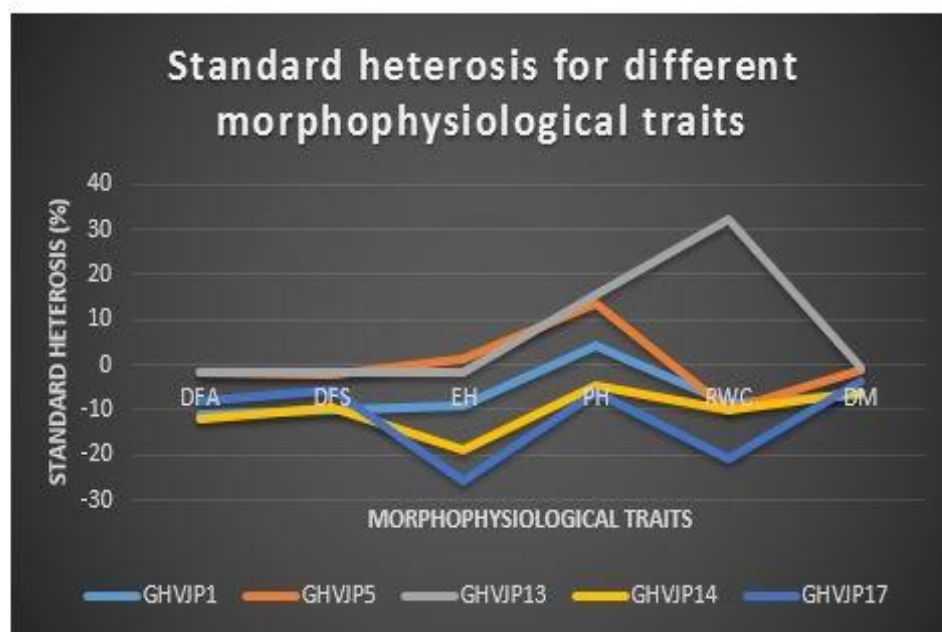


Table.3a The SCA effects of hybrids for morpho-physiological traits

Hybrids	DFA	DFS	ASI	EH	PH	SPAD	RWC	DM
GHVJP 1	-3.80 **	-3.70 **	0.10	-1.20	-3.47	4.47	-8.94 **	-3.70 **
GHVJP 2	3.80 **	3.70 **	-0.10	1.20	3.47	-4.47	8.94 **	3.70 **
GHVJP 3	0.70	1.13 *	0.43	-1.37	-2.97	-0.20	-0.03	1.13 *
GHVJP 4	-0.70	-1.13 *	-0.43	1.37	2.97	0.20	0.03	-1.13 *
GHVJP 5	-0.97	-1.20 *	-0.23	-0.20	-0.80	2.70	-4.32 **	-1.20 *
GHVJP 6	0.97	1.20 *	0.23	0.20	0.80	-2.70	4.32 **	1.20 *
GHVJP 7	-1.13 *	-1.03	0.10	1.47	0.53	-3.20	-3.01 **	-1.03
GHVJP 8	1.13 *	1.03	-0.10	-1.47	-0.53	3.20	3.01 **	1.03
GHVJP 9	-0.80	-0.87	-0.07	-1.70	-3.80	-2.26	-4.21 **	-0.87
GHVJP10	0.80	0.87	0.07	1.70	3.80	2.26	4.21 **	0.87
GHVJP11	1.53 **	0.97	-0.57 *	5.97	-1.13	4.77	14.81 **	0.97
GHVJP12	-1.53 **	-0.97	0.57 *	-5.97	1.13	-4.77	-14.81 **	-0.97
GHVJP13	2.53 **	1.97 **	-0.57 *	10.13	15.53	0.59	15.78 **	1.97 **
GHVJP14	-2.53 **	-1.97 **	0.57 *	-10.13	-15.53	-0.59	-15.78 **	-1.97 **
GHVJP15	1.70 **	1.63 **	-0.07	2.63	1.03	0.19	5.80 **	1.63 **
GHVJP16	-1.70 **	-1.63 **	0.07	-2.63	-1.03	-0.19	-5.80 **	-1.63 **
GHVJP17	-1.63 **	-1.03	0.60 *	-2.70	-5.80	-2.75	-3.23 **	-1.03
GHVJP18	1.63 **	1.03	-0.60 *	2.70	5.80	2.75	3.23 **	1.03
GHVJP19	-0.13	-0.20	-0.07	1.30	-5.97	-3.38	-4.71 **	-0.20
GHVJP20	0.13	0.20	0.07	-1.30	5.97	3.38	4.71 **	0.20
GHVJP21	3.20 **	3.13 **	-0.07	-0.70	4.37	-0.31	3.39 **	3.13 **
GHVJP22	-3.20 **	-3.13 **	0.07	0.70	-4.37	0.31	-3.39 **	-3.13 **
GHVJP23	-1.80 **	-1.70 **	0.10	-1.87	-2.97	2.19	-10.63 **	-1.70 **
GHVJP24	1.80 **	1.70 **	-0.10	1.87	2.97	-2.19	10.63 **	1.70 **
GHVJP25	-0.30	-0.37	-0.07	-0.03	9.37	-1.83	-12.11 **	-0.37
GHVJP26	0.30	0.37	0.07	0.03	-9.37	1.83	12.11 **	0.37
GHVJP27	1.20 *	1.63 **	0.43	-7.53	1.03	-1.25	10.67 **	1.63 **
GHVJP28	-1.20 *	-1.63 **	-0.43	7.53	-1.03	1.25	-10.67 **	-1.63 **
GHVJP29	-0.30	-0.37	-0.07	-4.20	-4.97	0.25	0.76	-0.37
GHVJP30	0.30	0.37	0.07	4.20	4.97	-0.25	-0.76	0.37
SE	0.53	0.54	0.25	5.54	8.27	2.82	0.68	0.54

* and **: Significance at 5% and 1% probability respectively.

Table.3b The SCA effects of hybrids for yield related traits

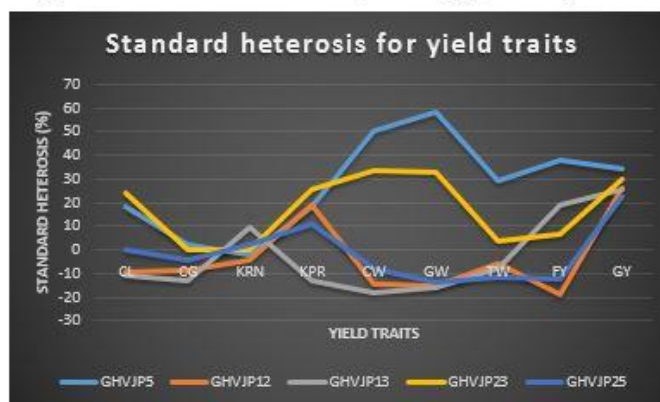
Hybrids	CL	CG	KRN	KPR	CW	GW	SP	TW	FY	GY
GHVJP 1	0.01	0.03	-0.27	-0.86	-3.46	-3.67	-0.56	0.78	-1.91**	-0.02
GHVJP 2	-0.01	-0.03	0.27	0.86	3.46	3.67	0.56	-0.78	1.91**	0.02
GHVJP 3	0.34	0.70	0.07	-1.19	-5.29	-4.67	-0.39	-0.39	0.09	0.06
GHVJP 4	-0.34	-0.70	-0.07	1.19	5.29	4.67	0.39	0.39	-0.09	-0.06
GHVJP 5	1.82*	0.53	-0.10	4.81*	35.54*	30.67*	-0.06	4.44*	0.76*	0.88**
GHVJP 6	-1.82*	-0.53	0.10	-4.81*	-35.54*	-30.67*	0.06	-4.44*	-0.76 *	-0.88**
GHVJP 7	-0.49	-0.13	-0.93 *	1.48	-11.96	-10.67	-0.56	-0.56	-0.41	-0.38
GHVJP 8	0.49	0.13	0.93 *	-1.48	11.96	10.67	0.56	0.56	0.41	0.38
GHVJP9	-0.32	-0.47	-0.10	0.31	6.04	3.67	-0.56	1.11	-0.08	-0.21
GHVJP10	0.32	0.47	0.10	-0.31	-6.04	-3.67	0.56	-1.11	0.08	0.21
GHVJP11	1.01	0.7	0.23	-4.52*	37.88 *	33.83 *	1.94	1.44	0.42	-0.68*
GHVJP12	-1.01	-0.7	-0.23	4.52*	-37.88 *	-33.83 *	-1.94	-1.44	-0.42	0.68*
GHVJP13	-0.49	-0.8	1.23**	-2.02	-12.96	-8.83	0.61	-0.22	0.76 *	0.50*
GHVJP14	0.49	0.8	-1.23**	2.02	12.96	8.83	-0.61	0.22	-0.76 *	-0.50*
GHVJP15	-0.49	-0.63	-0.77	-0.36	-21.46	-14.00	1.61	-0.56	-0.58	0.12
GHVJP16	0.49	0.63	0.77	0.36	21.46	14.00	-1.61	0.56	0.58	-0.12
GHVJP17	0.18	0.70	0.40	-0.19	11.71	11.33	1.94	-1.39	0.92 **	0.22
GHVJP18	-0.18	-0.70	-0.40	0.19	-11.71	-11.33	-1.94	1.39	-0.92 **	-0.22
GHVJP19	-0.66	-0.13	0.07	-1.19	-14.12	-12.33	-0.72	-2.06	0.92 **	-0.05
GHVJP20	0.66	0.13	-0.07	1.19	14.12	12.33	0.72	2.06	-0.92 **	0.05
GHVJP21	-0.84	-1.13*	-0.27	-1.19	-10.71	-4.67	-2.06	-0.56	-0.91 **	-0.38
GHVJP22	0.84	1.13*	0.27	1.19	10.71	4.67	2.06	0.56	0.91 **	0.38
GHVJP23	1.84 *	-0.13	0.07	5.48*	43.79*	37.17**	-1.39	-0.39	-0.41	0.72*
GHVJP24	-1.84 *	0.13	-0.07	-5.48*	-43.79*	-37.17**	1.39	0.39	0.41	-0.72*
GHVJP25	-0.16	0.37	-0.60	2.31	0.38	-0.83	-0.39	-0.22	-0.08	0.45*
GHVJP26	0.16	-0.37	0.60	-2.31	-0.38	0.83	0.39	0.22	0.08	-0.45*
GHVJP27	0.18	0.20	1.07 *	-0.52	14.88	14.83	1.61	-0.22	0.09	0.25
GHVJP28	-0.18	-0.20	-1.07 *	0.52	-14.88	-14.83	-1.61	0.22	-0.09	-0.25
GHVJP29	0.01	0.20	-0.10	-1.36	-0.12	-1.83	-1.06	0.78	0.42	-0.28
GHVJP30	-0.01	-0.20	0.10	1.36	-0.12	1.83	1.06	-0.78	-0.42	0.28
SE	0.90	0.49	0.45	1.99	16.80	13.09	1.68	1.58	0.31	0.22

* and **: Significance at 5% and 1% probability respectively

Table.4 Yield traits of good performing hybrids

Pedigree	Hybrid	CL (cm)	CG (cm)	KRN	KPR	CW (g)	GW (g)	TW (g)	GY (kg/ha)
GPM26 x CML451	GHVJP-5	21.33	16.00	14.00	37.00	271.67	220.33	37.00	10.83
GPM686 x CML451	GHVJP-23	22.33	15.77	14.43	39.33	241.67	184.67	29.67	10.36
GPM119 x CM111	GHVJP-12	16.33	14.33	13.67	37.33	155.33	118.00	27.00	10.19
GPM225 x CML 451	GHVJP-13	16.00	13.67	15.33	27.33	148.00	120.33	26.33	10.09
GPM735 x CML451	GHVJP-25	17.00	15.00	14.67	34.67	166.00	117.00	25.33	9.75
CHECK	NK6240 (NC)	17.70	15.83	14.40	31.20	181.13	138.83	28.67	8.06
	GPMH1101 (LC)	16.47	15.00	13.47	31.47	181.87	132.43	25.33	8.50
CV (%)		8.42	5.10	5.44	10.71	16.30	16.48	9.873	12.56
CD at 5%		2.43	1.22	1.25	5.75	46.46	36.38	4.227	1.79
CD at 1%		3.22	1.62	1.66	NS	61.66	48.29	5.611	2.38

Graph 1b: Standard heterosis of better performing hybrids for yield traits.



The superior crosses that were the result of good×poor general combiners may be due to the interaction between the positive alleles from good combiners and negative alleles from poor combiners as parents which under heterozygous condition resulted in high heterosis due to masking effect of favourable alleles at different loci. The high yield of such crosses would be non-fixable and thus could be exploited for heterosis breeding. The case of high SCA between good×poor combiners could produce good segregants only if the additive genetic effects are present in the good general combiners and complementary epistatic effects in the poor combiners and they act in the same direction to maximize desirable plant attributes.

In the present study it was found that the variance due to SCA was more than the variance due to GCA indicating the predominance of non-additive gene action which arises largely due to dominance and epistatic interactions (Sandesh *et al.*, 2018) and selection for such traits can be performed using recurrent selection for GCA method.

Standard Heterosis

In the present investigation standard check (NK6240) was taken into consideration for estimating heterosis as it is economically more beneficial than heterobeltiosis and mid parent heterosis. SCA is the indicative of heterosis for the evaluation of hybrids. The

SCA is due to non-additive gene interactions and the extent of heterosis depends on the magnitude of non-additive gene action and wide genetic diversity among parents.

For early maturity, the hybrids GHVJP1 (GPM-04×CML-451) and GHVJP14 (GPM-225×CM-111) showed significant negative heterosis with respect to DFA, DFS and DM. The hybrid GHVJP13 (GPM-225×CML-451) showed significant positive heterosis for PH as well as RWC (Graph 1a). It also had high SCA and per se values for yield. Hence can be considered as drought tolerant and subjected to further evaluation.

In case of yield traits, the hybrids GHVJP5 (GPM 26×CML 451) and GHVJP23 (GPM 686×CML 451) showed significant positive heterosis for CL, KPR, CW, GW, TW and GY. The hybrid GHVJP12 (GPM119×CM 111) showed significant positive heterosis for KPR and GY. The hybrid GHVJP13 (GPM-225×CML-451) showed significant positive heterosis for KRN, FY and GY (Graph 1b).

From all these observations it can be said that the hybrids GHVJP5, GHVJP23, GHVJP12, GHVJP 13 and GHVJP 25 were better performing with respect to yield and yield related traits (Table 4). These hybrids can be further evaluated in large scale and can be used for the exploitation of standard heterosis. Similar findings were obtained by Wali *et al.*, (2010).

In the present investigation, it was found that the percent contribution of lines was much greater than testers for most of the studied traits indicating that the female parent contributed maximum for total variance in hybrids followed by interaction. This is in conformity with Amin *et al.*, (2014).

Any combination among parents may produce hybrid vigour over parents which might be

due to dominant, over dominant or epistatic gene action (Moll and Stuber 1974). So, the crosses showing desirable SCA effects can be used in future breeding programmes for exploiting heterosis (GHVJP-5, GHVJP-23, GHVJP-12, GHVJP-13 and GHVJP-25). The inbred lines selected for high GCA can be used for the development of synthetic varieties or population to derive inbred lines. In the present investigation, the promising crosses were the result of good x good (GHVJP-5, GHVJP-23), good x poor (GHVJP-12) and poor x good (GHVJP13, GHVJP-25) general combiners as parents. The result, therefore, revealed that high gca value of a parent is no guarantee of high sca effect of their crosses and conforming the earlier reports of Dubey *et al.*, (2001). It was also found in some hybrids that the hybrids with high per se performance need not always reveal high SCA effect and vice versa (Peremlatha and Kalmani 2010). Hence selection must be made for such hybrids which show high per se values along with significant SCA effects for concerned traits.

Abbreviations

DFA: Days to fifty percent anthesis
DFS: Days to fifty percent silking
ASI: Anthesis silking interval
EH: Ear height (cm)
PH: Plant height (cm)
SPAD: SPAD meter reading (relative chlorophyll content)
RWC: Relative water content (percent)
DM: Days to maturity
TLB: Turicum Leaf Blight
MLB: Maydis Leaf Blight
CL: Cob length (cm)
CG: Cob girth (cm)
KRN: Kernel row number
KPR: Kernel per row
CW: Cob weight (g)
GW: Grain weight (g)
SP: Shelling percentage (percent)

TW: Test weight (g)
FY: Fodder yield (t/ha)
GY: Grain yield (t/ha)
GCA: General combining ability
SCA: Specific combining ability

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How to cite this article:

Meghashri S. Patil, B. N. Motagi and Kachapur, R. M. 2020. Heterosis and Combining Ability Studies in Maize (*Zea mays* L.) for Drought Tolerance, TLB Disease Resistance and Productivity in Northern Dry Tract of Karnataka. *Int.J.Curr.Microbiol.App.Sci.* 9(10): 1054-1064. doi: <https://doi.org/10.20546/ijcmas.2020.910.126>