

**HETEROSIS AND COMBINING ABILITY
STUDY FOR DROUGHT TOLERANCE,
SEED YIELD AND YIELD ATTRIBUTES
IN MAIZE [*Zea mays* (L.)]**

MANASA, M.

PAL 0202

**DEPARTMENT OF GENETICS AND PLANT BREEDING
UNIVERSITY OF AGRICULTURAL SCIENCES
GKVK, BANGALORE – 560 065**

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Thesis submitted to the
University of Agricultural Sciences, Bangalore
in partial fulfillment of the requirements for the award of
the degree of

**Master of Science
(Agriculture)**
in
Genetics and Plant Breeding

BANGALORE

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Affectionately Dedicated To
My Beloved Parents

Sri. Manjuth

Smt. Savitha

My loving brother

Bharath



**UNIVERSITY OF AGRICULTURAL SCIENCES,
DEPARTMENT OF GENETICS AND PLANT
BREEDING
G.K.V.K. CAMPUS, BENGALURU-560 065**

CERTIFICATE

This is to certify that the thesis entitled “**Heterosis and combining ability study for drought tolerance, seed yield and yield attributes in Maize (*Zea mays*)**” submitted by **Ms. MANASA, M.** for the degree of **MASTER OF SCIENCE (Agriculture) in GENETICS AND PLANT BREEDING** to the University of Agricultural Sciences, Bangalore, is a record of bonafide research work done by her during the period of her study in this university under my guidance and supervision and the thesis has not previously formed the basis of the award of degree, diploma, associateship, fellowship or any other similar titles.

**Bengaluru
July, 2012**

**Dr. S. Rangaiah
Major advisor**

APPROVED BY:

Chairman:

Dr. S. Rangaiah

Co-Chairman:

Dr. Shailaja Hittalmani

Dr. K. T. Pandurange Gowda

Dr. J. Shanthala

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“Great discoveries and improvements invariably involve the co-operation of many minds. I may be given the credit for having blazed the trail but when I look at the subsequent developments I feel credit is due to others rather than myself.” - Alexander Graham Bell

The task of acknowledging the help that was rendered to me throughout this study by my teachers and friends is with hearty gratitude. I could not have completed this work without their endless support and guidance. Under this decorum I would like to recall all of them with utmost gratitude.

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Bangalore

Date:

(MANASA, M)

“Heterosis and combining ability study for drought, seed yield and yield attributes in maize [*Zea mays* (L.)]”

MANASA M

Thesis abstract

The study was conducted to assess the magnitude of combining ability and heterosis with respect to grain yield and drought tolerant traits in maize. Thirty six crosses were obtained by crossing twelve lines and three testers in line x tester mating design. Thirty six crosses along with their parents and two commercial checks were planted in RBD design in *khri* 2011 at Zonal Agricultural Research Station, Mandya.

Hybrids exhibited significant variability for three drought tolerant and twelve grain yield traits studied. The variance ratios (GCA / SCA) revealed the predominance of non-additive gene action in the inheritance of three drought tolerant traits viz., SCMR, SLA and free proline and twelve yield traits viz., days to 50 per cent tasseling, days to 50 per cent silking, days to 50 per cent anthesis, plant height, ear height, ear length, number of kernels rows per cob, shelling percentage, 100 grain weight and yield per pant.

1005, 1396, 634-2, NAI-105, 1232, 2-62-55 and 1396 among the lines and HKI-164-4-1-3 and CML-411 among the testers was showed high overall general combining ability for yield traits. The hybrids 634-2 x HKI-164-4-1-3, SKV-50 x HKI-164-4-1-3 were promising with respect to *sca* effects for drought tolerant traits. MAI-105 x CML-411 (H x H), 772-2 x CML-411 (L x H) and 1410-1 x HKI-193-2 (L x L) were promising with respect to *sca* effects for grain yield, the same crosses manifested highest standard heterosis. These crosses are best suited for exploitation of hybrid vigour.

August, 2012

Department of Genetics and Plant Breeding
UAS, GKVK, Bengaluru -65

(S. RANGAIAH)

Major Advisor

**ಮುಸುಕಿನ ಜೋಳದಲ್ಲಿ ಕಾಳಿನ ಇಳುವರಿ ಮತ್ತು ಇಳುವರಿಗೆ ಸಂಬಂಧಪಟ್ಟ ಹಾಗೂ
ಅನಾವೃಷ್ಟಿ ತಡೆಯುವ ಗುಣಗಳ ಸಂಕರಣಕಸುವು ಹಾಗೂ ಅವುಗಳ ಕೂಡಿಕೊಳ್ಳುವ
ಸಾಮರ್ಥ್ಯ**

ಮಾನಸ, ಎಮ್

ಸಾರಾಂಶ

ಮುಸುಕಿನ ಜೋಳದ ಇಳುವರಿ ಮತ್ತು ಇಳುವರಿಗೆ ಸಂಬಂಧಪಟ್ಟ ಹಾಗೂ ಅನಾವೃಷ್ಟಿ ತಡೆಯುವ ಗುಣಗಳಲ್ಲಿ ಸಂಕರಣಕಸುವು ಮತ್ತು ಕೂಡಿಕೊಳ್ಳುವ ಸಾಮರ್ಥ್ಯವನ್ನು ತಿಳಿಯಲು ವಲಯ ಸಂಶೋಧನ ಕೇಂದ್ರ, ವಿ. ಸಿ. ಫಾರಂ, ಮಂಡ್ಯದಲ್ಲಿ 2011 ರ ಮುಂಗಾರು ಋತುವಿನಲ್ಲಿ ಅಧ್ಯಯನ ಕೈಗೊಳ್ಳಲಾಯಿತು. 12 ಲೈನ್‌ಗಳು ಹಾಗೂ ಮೂರು ಟೆಸ್ಟರ್‌ಗಳನ್ನು, ಲೈನ್ x ಟೆಸ್ಟರ್ ಮಾದರಿಯನ್ನು ಉಪಯೋಗಿಸಿಕೊಂಡು 36 ಸಂಕರಣ ತಳಿಗಳನ್ನು ಪಡೆಯಲಾಗಿತ್ತು. ಅವುಗಳನ್ನು ಅವುಗಳ ಮೂಲ ಹಾಗೂ ಪ್ರತಿಪಾದಿತ ತಳಿಗಳೊಂದಿಗೆ ಮೌಲ್ಯಮಾಪನ ಮಾಡಲಾಯಿತು.

ಸಂಕರಣಗಳಲ್ಲಿ ಬೇರೆ ಬೇರೆ ಗುಣಗಳಿಗೆ ತುಂಬಾ ವ್ಯತ್ಯಾಸ ಕಂಡುಬಂದಿದೆ. ಎಲ್ಲಾ ಗುಣಗಳಿಗೆ ವಿಶೇಷ ಕೂಡಿಕೊಳ್ಳುವ ಸಾಮರ್ಥ್ಯದ ವ್ಯತ್ಯಾಸವು, ಸಾಮಾನ್ಯ ಕೂಡಿಕೊಳ್ಳುವ ಸಾಮರ್ಥ್ಯಕ್ಕಿಂತ ಹೆಚ್ಚಾಗಿದ್ದಿದ್ದು ಕಂಡುಬಂದಿದೆ. ಸಾಮಾನ್ಯ ಕೂಡಿಕೊಳ್ಳುವ ಸಾಮರ್ಥ್ಯದ ಅಧ್ಯಯನ ತಿಳಿಸುವುದೇನೆಂದರೆ 1005, 1396, 634-2, ಎನ್‌ಎಐ-105, 1232, 2-62-55 ಮತ್ತು 1396 ಹೆಣ್ಣು ಅಂತಪ್ರಜನಗಳು ಬಹಳಷ್ಟು ಗುಣಗಳಿಗೆ ಉತ್ತಮವೆಂದು ತಿಳಿದುಬಂದಿದೆ. ಹೆಚ್‌ಕೆಐ-164-4-1-3 ಮತ್ತು ಸಿಎಮ್‌ಎಲ್-411 ಗಂಡು ತಳಿಗಳು ಉತ್ತಮವೆಂದು ತಿಳಿದುಬಂದಿದೆ.

ಸಂಕರಣಗಳಾದ 634-2 x ಹೆಚ್‌ಕೆಐ-164-4-1-3, ಎಸ್‌ಕೆವಿ-50 x ಹೆಚ್‌ಕೆಐ-164-4-1-3 ಗಳು ಬಹಳಷ್ಟು ಅನಾವೃಷ್ಟಿ ತಡೆಯುವ ಗುಣಗಳಿಗೆ ವಿಶೇಷ ಕೂಡಿಕೊಳ್ಳುವ ಸಾಮರ್ಥ್ಯದ ಪರಿಮಾಣ ಹೊಂದಿದ್ದವು. ಎಮ್‌ಎಐ-105 x ಸಿಎಮ್‌ಎಲ್-411, 772-2 x ಸಿಎಮ್‌ಎಲ್-411 ಮತ್ತು 1410-1 x ಹೆಚ್‌ಕೆಐ-193-2 ಸಂಕರಣಗಳು ಕಾಳಿನ ಇಳುವರಿಗೆ ಹೆಚ್ಚು ವಿಶೇಷ ಕೂಡಿಕೊಳ್ಳುವ ಸಾಮರ್ಥ್ಯದ ಪರಿಮಾಣ ಮತ್ತು ಹೆಚ್ಚು ಸಂಕರಣಕಸುವನ್ನು ಹೊಂದಿದ್ದವು.

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ಕೃ.ವಿ.ವಿ., ಜಿ.ಕೆ.ವಿ.ಕೆ.

ಬೆಂಗಳೂರು-65

ಡಾ|| ಎಸ್. ರಂಗಯ್ಯ

(ಪ್ರಧಾನಸಲಹೆಗಾರರು)

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I. INTRODUCTION

Maize (*Zea mays* L.) the “queen of cereals” is one of the most important crops in world agricultural economy and ranks third next to wheat and rice in production. By origin, maize is native to South America and has well to adapted magnificently to temperate regions with much higher productivity. It is grown in a latitude of 58° N to 40° S, from sea level to higher than 3000 m altitudes and in areas receiving yearly rainfall of 250 mm to 5000 mm (Dowswell *et al.*, 1996). Most of the area under this crop is in the warmer parts of temperate regions and in humid-subtropical climate. Highest production is in areas having the warmest temperature ranging from 21°C to 27°C and a frost free season of 120 to 180 day duration.

Maize was introduced to India in the beginning of 17th century. It is now one of the important crops in India ranks fifth in area and fourth in production. The total area in the country during 2010-2011 under maize was 8.26 m ha and registered a record production of 16.72 mt and productivity of 2029 Kg ha⁻¹. (Anon., 2010). Maize is cultivated in the states of Gujarat, Bihar, Andra Pradesh, Madhya Pradesh, Rajasthan, Chattisgarh, Karnataka, Maharashtra, Tamil Nadu and Uttar Pradesh. It is also widely believed that, in the very near future maize may become a staple food for human consumption, if the demand for rice and wheat is not fulfilled through increased production. Some estimates indicate that India may have to produce 20 million tonnes of maize to meet its requirement for human consumption, poultry, piggery, pharma industry and fodder by 2020.

Karnataka is one of the major maize producing states in the country and it ranks first in production. During 2009-10 a total of 13.31 lakh hectares of maize was grown with a production of 30.13 lakh tonnes

and average productivity of 2430 kg per hectare was realized with almost cent percent adoption of modern maize production technology. Karnataka state ranked first in yield realization till 1996-97 now lagging behind to Andhra Pradesh. The average productivity of state is much higher than the national productivity. Area under maize is increasing rapidly in the state, because of better environment (Anon., 2009).

Maize has occupied an important place due to its potential and greater demand for food, feed and industrial utilization. The kernel contains about seventy-seven per cent starch, two per cent sugar, nine per cent protein, five per cent oil and two per cent ash on a water free basis. Maize is used for live stock feeds in a variety of forage. About 50-55 per cent of maize production in India is consumed directly as food, 30-35 per cent goes for poultry, piggery and fish meal and 10-12 per cent in wet milling industry. Hence, increasing the grain production, productivity and grain quality in maize is of paramount importance in order to cater to the needs of ever growing human and livestock population and also to provide raw material for maize based industries. In this direction, plant breeders are intensifying their research efforts to evolve superior and higher yielding hybrids.

The invention of heterosis phenomenon, the development of hybrid breeding technology and exploitation of heterosis in maize are the landmarks in the biological sciences during the present century. A number of genotypes e.g., single crosses, double crosses, varietal hybrids, multiple hybrids, composites, synthetics, pools, populations *etc.* are feasible to maize growing farmers for commercial cultivation by virtue of the crop being a highly cross pollinated, Maize.

Throughout the tropics, periodic drought caused by uncertain and ill distributed rainfall and soil with low water holding capacities and

increased incidence of insect pests and diseases are major factors causing sizeable reduction in the maize yield.

Evaluation of genotypes for relative drought tolerance is a tough task, since it is difficult to predict the stage at which the moisture stress is encountered under rainfed conditions. Field screening of genotypes for relative drought tolerance, although important and results are directly applicable, is not always feasible as the number of genotypes that could be handled would be limited. Thus, it is important to realise that the effect of moisture stress on growth and yield is not a direct one, but is manifested through its effect on various physiological processes. Though maize in general, is considered to be the most drought susceptible crop, genotypic differences in tolerance to moisture stress have been noticed. Several workers have attributed this to various morphological, anatomical, physiological and biochemical characters of the plant. Physiological changes due to moisture stress, which reflect an adaptive mechanism in genotype, are worth measuring for relative assessment of differences. Plant scientists are making concerted efforts in identifying genotypes with higher yield coupled with relatively better drought tolerance. But drought tolerance is a complex trait, expression of which depend on action and interaction of different morphological (*viz.*, earliness, reduced leaf area, leaf rolling, efficient rooting system and stability of yield) and biochemical (*viz.*, accumulation of proline, betaine) parameters. Accumulation of very high quantity (10 to 100 times than in normal leaves) of free proline under stress is an adaptive mechanism to moisture stress. Several scientists are of the opinion that extent of proline accumulation under stress is directly correlated with drought tolerance.

Among the various maize diseases in South and Southeast Asia and other maize growing areas, downy mildews (DM) is considered to be

a major disease. Sorghum downy mildew is emerging as a destructive systemic disease of major economic importance to maize. Worldwide, the percentage of area with reported economic losses to downy mildew is 30 per cent, both in tropical lowland maize and in subtropical, mid-altitude, transition zone and highland maize (Jeffers *et al.*, 2000). Sorghum downy mildew was found in 17 of 34 counties surveyed in south central and southeastern Nebraska in 1987 (Jensen *et al.* 1989). In the Asian region, downy mildews are considered as the top priority biotic constraints, where yield losses of 50 per cent or more are common (Pingali, 2001). Sorghum downy mildew (SDM) in maize, caused by *Peronosclerospora sorghi*, is one of the most important among the DM diseases prevalent in India. Sorghum downy mildew (SDM) causes considerable yield losses in several maize growing states, particularly Karnataka, Tamil Nadu and Rajasthan. A survey conducted in Karnataka revealed that the incidence of disease ranged from 10 to 90% and yield loss from 30-40%. Very few genetic resources with resistance to SDM and better combining ability are available in the country necessitating introgression of resistance genes into different genetic backgrounds (heterotic groups). Hence, incorporation of disease resistance in high combiners and various germplasm using DNA markers assisted breeding that eventually aid in development of high yielding disease resistant hybrids suited to specific environments, needs to be given utmost importance.

Hence, there is an immediate need to evolve new hybrids which are having tolerance for both disease and drought. Combining ability analysis through line $\times$ tester mating system is one such method to select parents and single cross hybrids in maize. In this context, the present investigation was undertaken to identify hybrids for drought and disease tolerance through line $\times$ tester approach using twelve elite inbreds with the following objectives.

1. To assess the parental gca and hybrids sca effects for seed yield and its component traits
2. To assess the heterosis for seed yield and its component traits
3. To identify superior maize hybrids.

II. REVIEW OF LITERATURE

The literature pertaining to present study entitled “Heterosis and Combining ability study for drought, seed yield and yield attributes in Maize” are reviewed under following headings.

2.1 Drought and drought tolerant traits

2.2 Sorghum downy mildew resistance

2.3 Heterosis for yield and yield attributes

2.4 Combining ability and gene action

2.5 Heterosis and its relationship with combining ability

2.1 Drought and drought tolerant traits

There are many biotic and abiotic stresses responsible for losses in crop yield worldwide. Abiotic stresses like drought, heat, excessive rain, water logging soil, wind and extensive cold etc. Drought is one of the major challenges in plant production in present scenario for agricultural scientists, which affects 26% of arable area. Among them drought strongly affects the crop yield especially that of cereals and possesses a serious threat to the food security of entire subcontinents.

Bennet and Hammond (1983) reported two maize varieties having possible drought tolerance mechanisms. Hopi Indian maize has been grown in near desert regions where better known varieties fail due to lack of water. ‘Michuhacuan-21’ has high endogenous levels of ABA and might have been associated with drought tolerance.

Chen *et al.* (1990) concluded that cv. Yuyu No. 3 was highly drought tolerant maize while cv. Yuyu No. 1 was moderately drought tolerant and cv. Xiahuangdam 85-1 was drought susceptible.

Grazesiak (1991) reported a wide range of variability in maize genotypes grown under water stress, with inbreds being more drought sensitive than hybrids. Photosynthetic rate was more depressed by drought in inbreds than in hybrids.

Tawat (1992) studied proline accumulation, growth and yield components under various water regimes for evaluation of drought resistance in maize genotypes. At soil moisture of 25 per cent AWC, all maize genotypes accumulated higher concentration of proline even though there were differences among genotypes which were classified into three groups, high, medium and low proline accumulators.

Camacho and Caraballo (1994) studied ten maize cultivars and concluded that cultivars differed significantly in all growth parameters except the length of longest roots. The cv. Cargill-163 was the most sensitive and cv. Danac-3006 was the least sensitive to water deficit.

Mitu *et al.* (1994) studied the behaviour of 22 Romanian maize hybrids under drought. The hybrids Fundulea 322, Fundulea 340, Fundulea 365, Fundulea 376, Fundulea 410, Fundulea 412, exhibited good tolerance to drought.

Saneoka *et al.* (1996) indicated that mid day leaf water potential was higher in drought tolerant cultivars (3358, FFR-915c and K-8388) than in drought susceptible cultivars (Choko, P-3424 and JX-77). The degree of leaf rolling in drought tolerant cultivars was lower than in drought susceptible cultivars in Japan.

Aleksov (1998) released a new hybrid of maize INSC-730, tolerant to drought, and characterized by high genetic potential for grain yield.

In Thailand, Kingkarn (1998) studied the effect of water deficit at different growth stages on development and yield of three maize cultivars such as DK 888 (Strongly drought tolerant), Suwan 3 (moderately drought tolerant) and Suwan 1 (drought sensitive) in dry season.

Mugo *et al.* (1998) evaluated two widely used open pollinated maize cultivars from East Africa Katumani and Kito composites for drought tolerance at seedling and flowering stage. The early maturing cultivar was the most drought tolerant with large biomass accumulation in both stress and non-stress environments.

Mufuru *et al.* (1999) reported that in low rainfall zones of Tanzania, farmers' preferred composite varieties like Kilima (60%) and Katumani (10.9%) for their high yield and drought tolerance. In intermediate rainfall zones, farmers preferred Tuxpeno (44.4%) for its drought tolerance. Farmers in high rainfall zone mainly preferred hybrid varieties (92.9%) for their high yield.

Liu *et al.* (2000) compared the drought tolerance of Nongda-60 and Jifeng-58 with Yedon-19 and opined that they were suitable to the arid and semi-arid region in Hebei province.

Saindas *et al.* (2001) subjected 160 lines of maize including inbreds, hybrids and composites to water stress at Uchani (Haryana) by limiting irrigation at different plant growth stages (knee-high, flowering, grain filling). Dependence of vertical expansion of roots was positively associated with the drought tolerating ability of the genotypes. While, the horizontal expansion of roots may play an important role under moderate stress conditions in the field with lesser plant populations. Inbreds 1342 and 1324 and hybrids 1007 x 295, 610-2 x 295 and 610 x 295 were identified as some of the best drought tolerant genotypes.

Li *et al.* (2002) reported the physiological differences between the drought tolerant variety Dango no. 13 and drought sensitive variety Shannong No. 3 of maize during soil drought and following re-watering.

Wang *et al.* (2002) reported physiological response of two hybrids (ZD-14 and DY-13) to water stress. Hybrid ZD-14 (higher yield potential), was a water consuming hybrid due to its sensitivity to water, whereas DY-13 (lower yield potential) was a water saving hybrid due to its insensitivity to water.

Zhao *et al.* (2003) compared the drought resistance of eight maize hybrids with two widespread maize hybrids (Jidon 156 and Zhongdhan 2). The hybrids 9612, 9610 and 9672 were highly drought resistant and hybrids 9652, 9643, 9609 and 9682 were moderately drought resistant.

2.1.1 Drought tolerant traits

2.1.1.1 SPAD chlorophyll meter reading

Schepers *et al.* (1992) reported that N concentration and SPAD 502 chlorophyll meter readings were compared at silking. Chlorophyll meter readings correlated well with leaf N concentrations for a given hybrid and location, but it was suggested that the calibration of chlorophyll meters to determine crop N status may not be practical because of the unique greenness characteristics of different hybrids.

Blackmer and Schepers (1995) reported that, the SPAD 502 chlorophyll meter was successfully used to identify photosynthetic efficient maize genotypes.

Sunderman *et al.* (1997) conducted the experiment with 45 maize cultivars, irrigated and given recommended fertilizer rate, determined: how much variability was present for leaf chlorophyll concentration (LCC)

in a large sample of commercially available, fully-fertilized maize hybrids; and if results suggested alternatives to the normalization method. The SPAD meter was used to measure LCC twice during the vegetative phase and twice during the reproductive phase. Results indicated that genetic potential for maximum LCC was achieved.

Shapiro *et al.* (1999) reviewed that, the chlorophyll meter is a useful tool for scheduling N applications when irrigation water is contaminated with nitrate, since use of the chlorophyll meter prevented any yield limiting N deficiencies.

Tumbo *et al.* (2000) reported that chlorophyll levels, which are strong indicators of nitrogen status and photosynthetic status in plants which were measured using SPAD chlorophyll meter.

Costa *et al.* (2001) showed that, the SPAD chlorophyll meter was found to be reliable, quick and non-destructive tool used for directly measuring leaf chlorophyll and indirectly assessing the proportional parameter of leaf, and by extension, plant nitrogen (N) status.

Zebarth *et al.* (2002) conducted experiments in British Columbia, Canada, to evaluate the potential to use leaf chlorophyll index (LCI), measured using a Minolta SPAD-502 meter, for making fertilizer nitrogen (n) recommendations for silage maize in a high N fertility environment. Results showed nitrogen concentration of the above ground plant increased with increasing soil inorganic N content.

2.1.1.2 Specific leaf area

Milla and Reich (2007) noticed that for leaves, the light capturing surface area per unit dry mass investment (specific leaf area, SLA) is a key trait from physiological, ecological and biophysical perspectives. The generally greater mass per unit leaf area of larger than smaller leaves

directly translates into a greater cost to build and maintain a unit of leaf area.

2.1.1.3 Proline content

Palfi *et al.* (1973) reported that the content of proline increases markedly in water deficit plants and can be used to estimate their water retaining ability and drought resistance. After 3 days of wilting, the contents of proline increased by 235-1170 per cent depending on the species, where as the total content of other amino acids increased by 329-431 per cent.

Navari Izzo *et al.* (1990) reported the accumulation of free proline in maize under water stress condition.

Wang *et al.* (1990) tested drought adaptability and physiological characteristics of three different maize hybrids at different growth periods under field and plastic shed from 1987-1988. The hybrid with high drought resistance had higher root activities. Physiologically, the drought tolerance was mainly due to greater amount of free proline accumulation.

Accumulation of free proline due to drought was more rapid during leaf elongation than at the 10-leaf stage. Free proline content increased during stress (Bao *et al.*, 1991).

Grazesaik (1991) suggested that proline level in the leaves is a reliable index of resistance to drought.

Voetburg and Sharp (1991) mentioned that the maize cv. WF-9 x MO. 17 seedlings grown at low water potentials (0.03, -0.2, -0.8 and -1.6 MPa) were known to contain high concentration of proline in the primary root meristem at -1.6 MPa.

Two maize cultivars from each group of proline accumulation were grown in field under four water stress regimes. Water stress caused grain yield reduction with a pronounced effect when stress occurred during 3-6 and 9-12 weeks after emergence. The maize cultivars, which were in the high proline accumulation group, gave higher grain yield in contrast to the maize cultivars that were in the low proline accumulation group (Tawat, 1992).

Maize inbred line K-13 and hybrid DK-888 were stressed in the vegetative, tasselling and silking stage. Water stress at tasselling had most effect in increasing proline accumulation (Udomprasert and Thiraporn, 1994).

Nayer Mohammadkhani and Reza (2008) studied drought-induced accumulation of soluble sugars and proline in two maize varieties. A higher amount of soluble sugars and a lower amount of starch were accumulated under stress in two maize cultivars -704 and 301. Soluble sugars concentration increased (from 1.18 to 1.90 times) in roots and shoots in both the varieties, but starch content were significantly ($p < 0.05$) decreased (from 16 to 84%) in both varieties. The free proline level also increased (from 1.56 to 3.13 times) in response to drought stress and the increase in 704 var. was higher than 301 var.

2.2 Sorghum Downy mildew resistance

2.2.1 Inoculation technique

The success of any programme of finding and using genetic characters depends primarily on the effectiveness of the screening technique being used for identification of resistance. Various workers have evolved several methods, which is reviewed below.

Weston and Uppal (1932) and Uppal and Desai (1932) used the powdered leaves of infected plants containing oospores. Safeulla and

Thirumalachar (1984) used host seeds coated with oospores prior to sowing. They also used conidial suspension in the unfurling leaves of seedling, to bring about infection.

Jones (1970) placed leaves of infected sorghum and corn plants, in direct contact with the seedling leaves; covered over night and removed them in the next morning. Sporulation was observed in six days after exposed to the inoculum.

Siradhana *et al.* (1976) reported that conidial inoculation technique was very useful for evaluation of large number of maize germplasm under field condition. In this technique, conidia were collected from the infected leaves at about 0300 hr, and were adjusted to approximately $2.5-3.00 \times 10^6$ conidia/ml. Two to three drops of conidial suspension was placed in the whorl of each seedling (2-3 leaves stage) for three consecutive days between 0400 and 0600 hr.

Anahosur and Hegde (1979) reported that “Infector row method” was most reliable technique for assured screening. In this technique, plants were exposed to both oospores and conidial inoculation. The spreader rows were generally inoculated to ensure a uniform and high level of infection.

2.2.2 Recording of observations

Rao *et al.* (1984) found out the response of 21 cultivars to downy mildew evaluated by inoculation with conidia. Reactions were categorized into highly resistant (0 %), resistant (1-10 %), moderately resistant (31-50 %) and highly susceptible (51-100 %) based on percentage of systematically infected plants.

Lal and Singh (1984) indicated a simple procedure for finding disease intensity as the ratio of infected plants over total number of plants and expressed as percentage. This should be observed 35th day after planting. Pandurange Gowda, *et al.*, (1987) have also followed the same for their study on epidemiology of sorghum downy mildew.

2.2.3 Molecular characterization

Butler (1907) in Tamil Nadu and Maharashtra states of India as *Sclerospora graminicola*. Later Melechers (1931) reported the downy mildew of maize and sorghum in June in Egypt. The sorghum downy mildew disease of maize caused by *Peronosclerospora sorghi* (Weston and Uppal, 1932) is widely distributed all over the world and attacks all kinds of maize.

Renfro (1970) reported losses from South East Asia to be as high as 40-60%. Only India and Nepal had significant losses in maize yield, usually located to late planted areas.

Kaneko and Aday (1980) showed that the mode of inheritance of resistance to downy mildew changes from complete to partial dominance.

Susceptibility to SDM is generally inherited as a dominant characteristic (Narong and Renfro, 1982). Both additive and non additive gene actions were detected by a portioning gene effects by generation means. They found that reaction of maize to downy mildew was governed by several genes and that the inheritance of resistance is complex. They identified an inbred line Mexico, Gpo.48 var.168-1 as a promising general source of resistance to downy mildew.

Craig (1982) indicated resistance to *Peronosclerospora sorghi* was conditioned by two linked genes with susceptibility being partially dominant. Singh (1984) pointed out that for *Peronosclerospora* downy mildew, most of the resistant sources were yellow flint types from

Philippines. But they concluded that no single material released or experimental had shown resistance to downy mildew.

Bhat *et al.* (1982) indicated from their study on *Peronosclerospora sorghi* on sorghum that resistance was dominant and controlled by six genes.

Nair *et al.* (2001) studied responses of Indian maize inbred lines to sorghum downy mildew (SDM, caused by *P.sorghi*) and Rajasthan downy mildew (*P.heteropogonis*), and analysed simple sequence repeat polymorphism among SDM-resistant and susceptible lines.

Maria Luz George *et al.* (2004) studied a total of 102 inbred lines, including lines from Asian breeding programs, Mexico, USA and Germany, were analyzed with 76 SSR markers to measure diversity and investigate the effect of selection for downy mildew resistance. A mean polymorphism information content of 0.59, with range of 0.14 to 0.83, was observed. Diversity at the gene level showed an average of 5.4 alleles per locus and range of two to 16 alleles per locus, with a total of 409 alleles. About half of the alleles in the Asian lines had frequencies of 0.10 or less, and only 2% had frequencies > 0.80, indicating the presence of many alleles, and thus a high level of diversity. Some of the high-frequency alleles were in chromosomal regions associated with disease resistance.

Sabry *et al.* (2006), identified quantitative trait loci (QTLs) for downy mildew resistance in maize based on co-segregation with linked restriction fragment length polymorphism or simple sequence repeats in 220 F₂ progeny from a cross between susceptible and resistant parents. Disease response was assessed on F₃ families in nurseries in Egypt, Thailand and South Texas and after inoculation in a controlled greenhouse test. Heritability of the disease reaction was high (around 93

percent in Thailand). One hundred and thirty polymorphic markers were assigned to the ten chromosomes of maize with LOD scores exceeding 4.9 and covering about 1,265 cM with an average of interval length between markers of 9.5 cM. about 90 percent of the genome is located within 10 cM of the nearest marker. Three putative QTLs were detected in association with resistance to downy mildew.

Premlatha *et al.* (2010) screened 100 maize inbreds against downy mildew and Diallel analysis was adopted using eight inbreds to understand the inheritance of downy mildew resistance in maize. Parents, UMI 57, UMI 62, UMI 39 and UMI 743 recorded positive *gca* effects, of which the effects of UMI 57 and UMI 743 were significant. Among the hybrids, UMI 57 × CM 500, UMI 13 × CM 500 and UMI 62 × UMI 118 recorded highly significant and positive *sca* effects. The hybrids UMI 743 × CM 500, UMI 13 × UMI 57 and UMI 13 × UMI 97 recorded highly significant positive reciprocal effects. Two hybrids *viz.*, CM 500 × UMI 39, CM 500 × UMI 57 were found to be highly resistant (100%) to downy mildew with high grain yield.

2.3 Heterosis

Heterosis of varying magnitude has been observed in almost all the crop plants. Any of a multitude of genetic phenomena known to influence qualitative or quantitative characters is expected to influence heterosis but over the years that dispersion of completely or incompletely dominant genes and over-dominance along with some contribution of non-allelic interactions have been considered to be the main causes of heterosis.

Heterosis breeding has received more attention than other branches of plant breeding in several crop plants and maize is one such cross fertilized crop in which has an array of hybrids have been realized

over decades. Heterosis is the deviation of F1 from the reference for the particular character.

Shull (1908) coined the term heterosis to provide a term to describe the phenomenon but it did not include a description of genetic mechanism involved in its expression. Bruce (1910) and Keeble and Pellow (1910) put-forth the support for dominance hypothesis, which suggested that increase in vigour after crossing resulted from the combination of various dominant alleles by each parent. Shull (1911), East and Hays (1912) objected the dominance theory and proposed overdominance hypothesis indicating heterosis as the result of heterozygosis.

Jones (1917) stated that heterosis was due to complementary action of linked dominant growth favourable genes brought from both parents.

Ashby (1930 and 1932) suggested that heterosis resulted from the maintenance of the initial advantage in embryo size and not from an acceleration of metabolic process. East (1936) concluded that seed size or the size of any part of the seed cannot be the cause of heterosis. Hull (1945, 1946 and 1948) reported the evidence of overdominance in the expression of heterosis.

Griffing and Zsiros (1971) viewed heterosis as not entirely the result of genetic stimuli but rather as a result of the interaction between genetic and environmental stimuli and implicated that the environment was a significant factor in the manifestation of heterosis.

Annenkova (1973) stated that selecting suitable pollen parents with 21.8 to 41.2 per cent higher yield than standard check could produce hybrids with superior heterotic vigour.

Mabo (1977) noticed encouraging results by selecting parents with a large number of grain rows per cob, since the degrees of heterosis for the number of grains per ear, number of grains per row, plant height and grain yield depended on the number of grain rows per ear in the parents. Petrenko (1980) observed high positive heterosis for yield and yield components *viz.*, plant height, ear height and length of growth period.

Debnath (1984) obtained heterosis over mid parental value and better parent for grain yield components in 36 F1 hybrids from a diallel cross among nine elite diverse inbreds. The heterosis for grain yield ranged from 21.07 to 123.58 per cent over the mid parental value and from -2.96 to 95.07 per cent over the better parent. Heterosis was high for grains per row and ear length. Mukherjee and Saha (1984) observed positive heterosis for grains per ear in seven crosses, ear length in ten crosses and 100-grain weight in eight cross combinations.

According to Prasad and Singh (1986), the magnitude of heterosis for grain yield per plant and six of its components were greater when the parents were moderately diverse than when they were highly diverse. Shakoor (1988) observed positive heterosis for number of leaves (13.4% to 20.0%) and leaf area per plant (-0.01 to 54.8) over better parent. Muthiah (1989) obtained significant positive heterosis for grain yield per plant and other 15 yield related characters in several cross combinations from 9 × 9 diallel analysis.

Masikevich *et al.* (1989) presented evidence that the increased yield of heterotic hybrids is the result of competitive interaction between photorespiration and photosynthesis. They have shown that heterotic organisms have a more economical utilization of energy and nutrient resources than non-heterotic ones and greater autonomy of the protein

synthesizing system of the chloroplasts in relation to the ribonuclease function.

Muthiah (1989) studied 72 hybrids in maize and reported significant positive heterosis with many cross combinations for grain yield per plant and other fifteen yield related characters.

Malhi *et al.* (1993) in their study of relative performance of the single crosses and double crosses observed that the single cross hybrids had a significantly higher ranking than the double cross hybrids for yield on average over all crosses and over the five best crosses. Comparison of yield performance indicated that the single cross hybrids were more stable than the double cross hybrids.

Gupta *et al.* (1994) studied twenty three double cross hybrids of which sixteen out of twenty three double cross hybrids showed high degree of heterosis for grain yield than the best standard variety “Shweta”.

Abdul (1995) noticed heterotic effects in plant height and leaf area per plant. Kumar (1995) observed high degree of heterosis for grain yield per plant and earliness in eight hybrids. Nagda *et al.* (1995) obtained significant positive heterosis for grain yield per plant over the best check in 15 crosses and significant relative heterosis for days to silking, plant height and ear height in 14 hybrid combinations.

Ling *et al.* (1996) noticed that mean heterotic effects were highest for grain yield per plant followed by grain weight and ear thickness. Saha and Mukherjee (1996) observed significant positive heterosis for grains per ear and the crosses with highest heterosis for 100- grain weight and

grain yield per plant and negative heterosis for percentage grain conversion.

Verma and Singh (1996) reported that dominance $\times$ dominance gene interactions were important for improving heterosis for yield. Yurankova *et al.* (1996) obtained considerable instability in heterosis for ear width, ear length and number of grains per row. Heterosis was slight or absent for number of rows per ear.

Stojokovic *et al.* (1999) reported that partial or complete dominance of dominant alleles with additive effects were the main contributors to heterosis in maize. Over dominance may exist at some loci but of minor importance. Saindass and Pawan Arora (1999) reported that negative heterosis will be considered as desirable for the phenological traits as it contributed favourable genes for earliness.

Netaji *et al.* (2000) obtained significant and positive heterosis and heterobeltiosis for grain and moreover the expression of heterobeltiosis was most evident for grain yield per plot followed by test weight, ear length, plant height and number of grain rows per ear. Rosa *et al.* (2000) noticed the highest values of heterosis over the mid-parental value in the hybrid PP- 9539 $\times$ AN-453 (11.35%) and PP-9603 $\times$ PP-9539 (11.13%).

Geetha (2001) obtained maximum heterosis for grain yield per plant, ear weight and number of grains per ear. They also reported that significant positive heterosis in grain yield which was associated with the heterosis for plant height, number of grains per row, 100grain weight and number of rows per ear.

Han Li Jun *et al.* (2001) made crosses using North Carolina Design II. The results showed that all the F1 hybrids exhibited positive heterosis in some degrees and the highest heterosis was in crosses in which MO-17 was the male parent. Kara (2001) observed positive heterosis for all characters studied except for days to tasseling with the average hybrid yield being 79.89 per cent above that of the parents. Shahwani *et al.* (2001) noticed positive and significant heterosis in 17 hybrids, while 11 hybrids showed heterobeltiosis for ears per plant.

Vidal Martinez *et al.* (2001) observed negative heterotic values in pollen yield components and reported heterotic values upto 300 per cent for pollen yield in Corn belt genotypes and upto 200 per cent for grain yield in exotic genotypes.

Saleh *et al.* (2002) reported high estimates of heterosis for grain yield, ear weight, grain weight per ear, moderate estimates for plant and ear height, shelling percentage, ear circumference, number of kernel rows per ear, number of kernels per ear row and grain weight.

Aydyn Nay *et al.* (2003) while studying Inheritance of grain yield in a half-diallel maize population by using 9 inbred parental lines observed midparent heterosis values ranging from 46.10% (H.96 x DNB) to 573.12% (ALKD 222 x A 632) whereas the useful heterosis values varied between -46.47% (A 619 x A 632) and 10.78% (N 7A x ALKD 90-1), and only 9 crosses showed higher grain yields than that of the check variety. Of these crosses, N 7A x ALKD 90-1, N 7A x DNB and N 7A x IDRN Cornell, were considered as promising hybrids.

Srivastava and Singh (2003) studied heterosis and combining ability for yield and maturity by using exotic and indigenous inbred lines of maize. Eighty single crosses along with parental lines were evaluated

in three environments *viz.*, Uttaranchal, Uttarpradesh and Punjab, during *kharif* 2000. The mean square due to interaction of lines and lines x testers with environments were significant for all characters, while testers with environments was significant for days to 50 per cent silking.

Betran *et al.* (2003) conducted experiment on genetic diversity and heterosis in tropical maize under stress environment. They observed that SCA had the strongest correlation with genetic diversity. Environment significantly affected the correlation between F1, SCA, MPH and HPH, with lower values of gd revealed in most stress condition

Kabdal *et al.* (2003) in their studies on combining ability and heterosis analysis for grain yield and its components in maize by using 7 inbred lines derived from half-diallel mating, along with 4 control cultivars were determined in a field experiment conducted in Pantnagar, during the *kharif* season of 1999. the general combining ability for all the characters examined was higher than the specific combining ability except for ear height.

Li-Jizhu *et al.* (2004) reported highest heterosis for ear grain weight and lowest for ear row number. All characters studied were controlled by additive gene action. Ear length had significant additive and dominance effects, whereas, ear row number and ear grain weight had dominant and epistatic effects, respectively

Parvez sofi *et al.* (2007) in their study used fifteen phenotypically diverse white maize inbred lines and crossed them to three testers namely W3, W5 and W6 in line x tester fashion to obtain 45 test cross progenies and evaluated them in two diverse locations and recorded heterosis upto 78.83% for grain yield. The mean heterosis estimates for

component traits was found to be highest in case of ear diameter (25%) followed by ear height (23%), 100-seed weight (21%) whereas, it was lowest in case of harvest index (7%).

Saidesh *et al.* (2008) obtained a set of 40 F₁'s by crossing 10 inbred lines with four testers in maize through Line $\times$ Tester approach. Out of 40 crosses, 23 crosses over better parent and 11 crosses over standard check significantly out yielded for grain yield. The crosses DMR 274 $\times$ HOL 34, DMR 201 $\times$ EI 34 and DMR 156 $\times$ EI 34 showed high heterosis over better parent and standard check (DHM 103) for grain yield per plant as well as 100 seed weight, ear length, chlorophyll content at 50 per cent flowering and plant height.

Amiruzzaman *et al.* (2011) studied 7 $\times$ 7 diallel cross in maize for grain yield and yield contributing characters and reported that the Standard heterosis ranged from -17.60 to 9.71%; -20.41 to 8.04%; -13.89 to 7.54% and -6.17 to 14.48% for yield per plant, number of kernels per ear, length of ear, ear diameter and 1000-kernel weight, respectively.

2.4 Combining ability and gene action

For a systematic breeding programme, it is essential to identify the parents as well as crosses which could be exploited in order to bring about further genetic improvement in yield. Combining ability of parents give useful information regarding the selection of parents based on the performance of their hybrids.

In relation to single cross of corn, Sprague and Tatum (1942) formulated the concept of combining abilities. General combining ability is the average performance of a strain in a series of cross combinations, estimated from the performance of F₁s from the crosses, whereas specific combining ability is used to designate those cases in which certain

combinations do relatively better or worse than would be expected on the basis of average performance of lines involved.

Griffing (1956) has shown relationship between various heritable variance components and GCA and SCA variances. GCA variance is due to additive variance and additive $\times$ additive interaction variance while, SCA variance is due to dominance variance, additive $\times$ additive variance, additive $\times$ dominance variance and dominance $\times$ dominance variance components. Estimates of the variances due to GCA and SCA provide an appropriate diagnosis of the predominant role of additive or non-additive variances of gene.

The concepts of combining ability in terms of genetic variation were further elaborated by Sprague and Federer (1951), Kempthorne (1957) and Carnahan *et al.*, (1960).

Ratio of additive to non-additive gene action is to be considered in order to decide the predominance of the kind of genetic variation for a given character. If the ratio of additive to non-additive gene action is more than unity indicates the major role of additive variance in controlling the expression of a character, whereas, less than unity indicates the importance of non-additive variance (Gardner, 1963).

Martin and Hallauer (1976) studied diallel analysis for ear length, ear width, 100-grain weight, number of grain rows and yield and concluded that epistasis was more frequent for all characters except for 100-grain weight. Epistasis was most common for ear width and number of grain rows and least common for yield.

Muthiah (1989) reported that the proportion of GCA variance was higher than the SCA variance showing preponderance of additive genetic effects for all the characters studied. According to Debnath and Sarkar (1990) non-additive gene action was preponderant in the inheritance of

grain yield, ear width, whereas equal importance of both additive and non-additive effects were observed for ear length, kernel rows per ear and kernels per row.

Vasal *et al.* (1992) reported significant GCA variances for grain yield, days to tasseling and plant height. The SCA variances or effects were significant for days to silking and ear length.

According to Packiaraj (1995) GCA variance was greater in magnitude than SCA for shelling percentage, number of leaves, leaf breadth, 100-grain weight, days to 50 per cent silking, number of grains per row and plant height. SCA variance was high for ear weight, grain weight per plant and number of grain rows per ear indicating that dominance and epistatic played a major role in the expression of these traits.

Dass *et al.* (1997) reported that non-additive gene action played major role in the inheritance of grain yield and majority of ear traits. Geetha (1997) observed that additive gene effects controlled the inheritance of grain yield per plant and also added that proportion of GCA variance was higher than the SCA variance having preponderance of additive genetic effects for characters such as plant height, number of grain rows per cob, number of grains per row, ear weight, days to 50 per cent silking, 100-grain weight and starch content.

Geetha (1997) reported that additive and dominance components were significant for plant height, number of kernel rows per cob, number of kernels per row, ear weight, 100-grain weight and grain yield.

Dehghanapour *et al.* (1997) and Paul and Duara (1991) found predominant of non-additive genetic variance for days to 50 per cent silking.

Mathur *et al.* (1998) reported that significant GCA variance for shelling percentage in both normal and stress environments. SCA variance was significant for shelling percentage in the normal environment. A preponderance of additive gene effects was observed in the expression of this character.

Mathur *et al.* (1998), Paul and Debanath (1999) and Tallei and Kochaksaraei (1999), reported predominance of additive genetic variance for days to 50 per cent silking.

According to Altinbas and Tosum (1998) GCA and SCA variances for grain yield per plant and other yield components indicated that screening the parental lines and crosses based on combining ability effects for 100-grain weight and ear length should be effective.

Kumar *et al.* (1999) noticed that predominance of non additive gene action for grain yield and yield component characters. Mani *et al.* (1999) indicated that ear weight, grain yield per plant, ear height and hundred grain weight were the most variable characters, whereas days to silking showed lowest levels of variability.

Paul and Debnath (1999) obtained significant gca and sca effects for all characters studied *viz.*, days to 50% silking, plant height and ear height. Tallei and Kochaksaraei (1999) observed significant gca effects for plant height, ear height, kernel length and yield per plant.

Rosa *et al.* (2000) obtained highest SCA values in 13 × 13 diallel crosses *viz.*, AS- 910 × AS-4450 and PP-9538 × AS-948. Suneetha *et al.* (2000) noticed significant variances for GCA and SCA for days to 50 per cent tasseling, plant height and neutral detergent fiber content. Zelleka (2000) had derived an information from data on grain yield, plant height, ear length, days to maturity and 1000-grain weight from a diallel mating that both gca and sca effects were significant for all traits.

Nass *et al.* (2000) studied the combining ability analysis of diallel data across environments results showed that highly significant effects for both GCA and SCA. Considering the thirteen hybrids that showed higher yield than the commercial checks, contributions by GCA and SCA effects were 56% and 44%, respectively. On the other hand, SCA effects were always more important than GCA effects for each environment and over all environments.

Desai and Singh (2001) conducted experiment with material from 7 x 7 half diallel cross involving relatively drought tolerant inbreds of maize which were grown under rain fed condition. Analysis of variance revealed that significant differences in gca and sca effects for 10 traits studied *viz.*, days to 50% tasselling, days to 50% silking, anthesis-silking interval, plant height, ear height, number of leaves per plant, canopy air temperature difference, relative water content, proline content and grain yield per plot.

Konak *et al.* (2001) obtained non-additive gene effects for ear length and number of kernel rows on ear and additive gene effect for yield, 1000-kernel weight, plant height, ear height and days to silking. Mandal *et al.* (2001) noticed significant GCA and SCA variances for most of the traits studied. Mahto and Ganguly (2001) observed both additive and nonadditive genetic components for 100-grain weight and shelling percentage in CML 85 and CML 79. The crosses showed positive and highly significant specific combining ability effect for grain yield.

Vacaro *et al.* (2002) reported that mean square for gca effects was greater than that for sca effects for the traits like plant height, point of insertion of the first ear, number of ears per plant, number of grains per ear, root and stalk lodging and grain yield indicating the predominance of additive effects.

Amer *et al.* (2002) evaluated the combining ability of 8 inbred lines of maize and their top crosses by line x tester analysis. Non-additive genetic variance was observed in the inheritance of grain yield, number of kernels per row. Whereas, additive genetic variance was observed in the inheritance of silking date, plant height and ear height, ear diameter, number of rows per cob and 100 kernel weight.

Barakat *et al.* (2003) evaluate 9 maize inbred lines in half diallel fashion for studying combining ability for yield and yield components under different location. Results showed that both general and specific combining abilities were significant for all the traits. Non additive genetic variance (dominance and epistasis) played important role in the inheritance of these traits. The interaction of GCA and locations was significant for grain yield, plant height and silking date. The interaction between SCA and locations was significant for silking date, plant height and ear height, and grain yield. Inbred lines Gm-112, Gm-117 and Gm-118 showed positive and significant GCA effects for grain yield and ears/plant. Twenty-four crosses showed significant SCA effects for grain yield.

Singh and Jha (2004) studied the combining ability in maize involving 10 diverse parents and their 45 F1s under moisture non-stress and stress environments. Result indicated significant differences due to (GCA) of parents and (SCA) of crosses for all the characters except the SCA for anthesis silking interval (ASI). Interaction was significant for tassel vigour index, plant height, ear girth and kernel rows per ear, whereas due to SCA x environments was non-significant for ASI, tassel condensation and harvest index.

The general combining ability (GCA) variance was larger than the specific combining ability (SCA) variance, indicating the predominance of additive gene action. Further a strong association between grain yield of

populations *per se* and their GCA for harvest at grain moisture was also observed. The population CGSS (S1–S2) C5 was the earliest among the 10 populations studied which had the best GCA value for grain moisture (Melani and Carena, 2005).

Thanda *et al.* (2009) reported that GCA was more important than SCA for grain yield, indicating that yield was controlled mainly by additive gene action among 14 southern African maize inbred lines, while Srdic *et al.* (2006) reported high significant values for both GCA and SCA for grain yield of ten maize inbred lines

Hee *et al.* (2006) compared the results obtained by two methods *viz.*, Griffing method and Gardner and Eberhart method by using diallel mating design. Hybrids and parents averaged over hybrids differed significantly for plant and ear height. Relative ear position over plant height (REPH) was also calculated from plant and ear heights. By Griffing Method, general combining ability (GCA) was significant for plant height. Specific combining ability (SCA) was highly significant in all three measurements. The traits with low heterosis showed higher ratios of GCA/SCA variance.

Mean squares for GCA-males, GCA-females and SCA effects were significant for grain yield under both low and high N, whereas their interactions with year was significant only for GCA-male effects under low N (Meseka *et al.* 2006). Non-additive gene action was slightly higher than additive gene action for grain yield under low N. Five of the 12 drought tolerant lines and two of the 12 susceptible inbred lines had significant positive *gca* effects for grain yield under low N and hence, they concluded that use of inbred lines, such as KU1409, 4058, 1824 and 9432 with consistently positive *gca* effects for grain yield under low-N in a breeding program would be desirable for further improvement of grain yield and associated traits for low N environments.

Asif *et al.* (2007) observed higher contribution of lines towards GCA variance for six traits. Inbred lines *viz.*, KDM 334, KDM 342 and KDM 347 were good combiners for yield and yield attributing characters. Tester C6 was a good combiner for grain yield, number of kernel rows per ear and number of kernels per row. Among the hybrids, KDM 331 × Super-1; KDM-333 × KDM-34; KDM 342 × C6; KDM331 × KDM-346 and KDM 336 × KDM-346 exhibited highest significant sca effects for yield and yield attributing traits.

Alam *et al.* (2008) carried out combining ability analysis for grain yield and its contributing characters in maize in 5 x 5 diallel cross. The highest percentage of heterosis for grain per ear over mid parent⁵ and better parent were observed by the cross P2 x P3. Crosses P1 x P3 and P1 x P5 showed significant negative heterosis for days to maturity. Significant general and specific combining ability variances were observed for all the characters except ear height. Almost equal role of additive and non-additive gene actions was observed for days to maturity.

Rather *et al.* (2009) used half diallel design in maize to evaluate 45 cross combinations along with parents in 2 locations and 3 replications to assess variability, gca and sca effects. The pooled mean squares due to combining ability indicated high significance of both GCA and SCA variances for all of the traits was being relatively more in magnitude than the later for turcicum resistance and for six other quantitative traits. Both gca and sca interacted significantly with location for all the traits except grain yield, plant height and ear placement for sca interaction.

Reddy *et al.* (2009) the effects of selection for yield and ears per plant were assessed. Results showed that selection for yield tended to delay silking and husk senescence, and increase plant height and ear length. Selection for ears per plant increased yield but did not result in any undesirable correlated effects.

Genetic distances were not significantly associated with hybrid performance, specific combining ability effects, or midparent heterosis for grain yield, but they effectively grouped the lines according to known pedigree relationships and approximately according to heterotic patterns used by CIMMYT and IITA (Thanda *et al.* 2009).

Muhammad Akbar *et al.* (2009) evaluated F1 generation obtained from a 6×6 diallel for combining ability effects at normal and high temperature regimes. The mean squares due to genotypes, general combining ability (GCA), specific combining ability (SCA) and reciprocal effects were highly significant for all the traits at both temperature regimes. The GCA: SCA variance ratio exhibited that all traits were controlled by the non-additive genes except for growing degree-days to 50% maturity that was predominantly under the control of additive genes at both temperature regimes. The inbred line 935006 was found to be the best general combiner with better mean performance for grain yield plant⁻¹ with lesser growing degree days to 50% silking growing degree days to 50% physiological maturity and higher turgor potential at normal and high temperature regimes.

Muhammad Irshad-Ul-Haq *et al.* (2010) carried out to determine the type of gene action, genetic parameters of yield and other quantitative traits by crossing 8 diverse maize inbred lines in complete diallel fashion. The estimates of components of genetic variation revealed that non additive genetic effects were more pronounced in the inheritance of plant height, days to 50% tasseling, days to 50% silking, ear height and grain yield per plant.

Combining ability analysis was conducted using line x tester design in late maturity inbred lines of maize (*Zea mays* L.) for yield and yield contributing traits. Three lines viz., KML-2, KML-30 and KML-181

were good general combiners for grain yield. Among the hybrids, KML-225 x KML-226 recorded high *per se* performance for grain yield followed by KML-2 x KML-226. The hybrid, KML-227 x KML-161 was found to be superior in terms of days to 75 per cent dry husk and KML-181 x KML-75 for ear length, ear girth, number of ears per plant and number of kernel rows (Sumalini and Shobha Rani (2010)).

Premlatha *et al.* (2010) studied combining ability and heterosis of nine lines and four testers for grain yield components using Line X Tester mating design. Combining ability analysis showed the predominant role of non-additive gene action for all the characters studied. The line UMI 199 was good general combiner for number of grains per row, hundred grain weight, grain yield per plant, protein content and oil content. The line UMI 235 was good general combiner for number of grains per row, hundred grain weight, grain yield per plant, protein content and oil content and the line UMI 278 was identified as better combiner for number of rows per cob, number of grains per row, hundred grain weight, grain yield per plant, protein content and oil content. The line UMI 348 showed high *gca* for grain yield per plant. In case of testers UMI 217 was identified for high *gca* effects for number of rows per cob, number of grains per row, hundred grain weight, grain yield per plant and oil content. The tester UMI 330 recorded high *gca* effect for protein content.

2.5 Heterosis and its relationship with combining ability

Heterosis breeding has received more attention than other branches of plant breeding in several crop plants and maize is one such cross fertilized crop which has paid rich dividend since an array of hybrids have been realized over decades. Heterosis is the deviation of F1 from the reference for the particular character.

The information on heterosis and combining ability considered together will be more meaningful. If the heterotic hybrids involve both the parents with high general combining ability effects, then it implies that the parental contribution to heterosis is mainly through additive gene action.

Johnson and Hayes (1940) found that low $\times$ low crosses yielded less than low $\times$ high or high $\times$ high, although the F1 crosses between low $\times$ high yielded as well, on the average, as F1 crosses between high $\times$ high. Hull (1952) believed that while the mean of the high $\times$ high combination may be best, the highest specific combination is more likely to occur in high $\times$ low crosses. Leng (1954) reported that if over dominance is present, the highest degree of heterosis should be found in high $\times$ low crosses.

Vaidya (1986) reported that the crosses showing heterosis over check for yield and yield components had at least one good general combiner in their parentage.

Giridharan *et al.* (1996) in their study on gene action and combining ability in grain yield, found that yield was controlled by additive and non-additive gene action in diallel crosses and dominant gene action in triallel and quadriallel crosses, suggesting that grain yield could be improved by heterosis breeding. Rana and Vinod Kumar (2001) reported that the non-additive gene action was important for grain yield and its components, while additive gene effects were important for phenological traits. San-Vicente *et al.* (2001) reported that the combined analysis of variance detected highly significant differences among genotypes, parents and crosses for all traits. The test for average heterosis, parents versus crosses, was significant for grain yield and time to silk. General combining ability (GCA) was significant or highly significant for all traits, whereas specific combining ability (SCA) was highly significant for grain yield and time to silk.

Dodiya and Joshi (2003) reported that the combining ability analysis showed the predominant role of non-additive type of genetic component in the inheritance of all characters. Single cross Pop-30-25-1-1-1 x X1 W-1076-1 had positive significant specific combining ability effects all characters except for starch content, with the highest estimates of economic heterosis for oil content.

Yousif *et al.* (2003) reported that highly significant variation was observed among genotypes (parents and their crosses) and in genotype x environment interaction. These results indicated significant heterosis for all traits except leaf area, and the presence of partial-, complete and overdominance gene effects. Maximum heterosis was recorded for grain yield.

Abdel Hady *et al.* (2004) reported that highly significant heterosis relative to better parent and mid parents were found for callus growth in vitro and also for grain yield in the field. There were highly significant differences due to general and specific combining ability for callus growth and also for grain yield.

Abdolhamid *et al.* (2004) reported that the additive gene effects were more important than non additive gene effects for all traits. General combining ability effects were significant for most of the parents and all the traits. Specific combining ability effects were significant in a few crosses for all traits. Yield and plant height were significant in more than 50% of the crosses. High heterosis was observed in more than 50% of the crosses for all studied characteristics. The highest and lowest amounts of heterosis were observed for grain yield and number of ears per row, respectively.

Katna *et al.* (2005) reported that both the general and specific combining ability effects were significant for all traits at both locations.

Preponderance of additive gene effects was important in the expression of all the traits studied.

Amit-Dadheech and Joshi (2007) reported that the ratio of non additive/additive gene effect revealed that there was preponderance of non additive gene action in the expression of all the traits under study. Single cross L15 x T1 had positive significant sca effects for oil content along with starch content with highest estimate of heterobeltiosis for oil content.

III. MATERIAL AND METHODS

The experimental material for present investigation, method of recording of observations on various trait and method of statistical analysis are briefly presented under the following headings.

3.1 Location of the experiment

3.2 Material used layout of the for the experiment

3.3 Field plot technique used in the experiment

3.4 Crossing programme

3.5 Recording of the observations

3.6 Screening of hybrids for sorghum downy mildew

3.7 Screening of hybrids for drought tolerance

3.8 Statistical analysis

3.1 Location of the experiment

The experiment was conducted in Zonal Agricultural Research Station, V.C. Farm, Mandya district, University of Agricultural Sciences, Bengaluru, during *kharif* 2011 and *rabi* 2011. The experiment station is located in Southern Dry Zone of Karnataka at 12° N latitude, 76° E longitude and an altitude of 695 m above mean sea level.

3.2 Material used for the experiment

The base material for the present study comprised of twelve inbred lines, three testers and two standard checks as listed in Table 1, which were maintained at the AICRP on Maize, Zonal Agricultural Research

Station, Mandya. Using these twelve inbred lines and three testers as parents, thirty six hybrids were obtained by crossing them in a Line x Tester design during *Rabi* 2010.

3.3 Field plot technique used in the experiment

Evaluation of F₁ hybrids was done by sowing thirty six hybrids along with fifteen parents(12 lines and 3 testers) during *kharif* 2011-12. The summary of experimental lay out is given below

1. Experimental design	: RCBD
2. Number of replications	: 2
3. Number of total entries per replication	: 53
4. Row length	: 4 m
5. Number of rows per plot	: 2
6. Spacing between rows	: 75 cm
7. Spacing between plants within the row	: 30 cm
8. Plot size	: 4.0 m X 4.0 m

After thorough land preparation, sowing was carried out by hand dibbling of seeds with one seed per hill and the plot was irrigated. The recommended doses of fertilizers (150 N, 75 P₂O₅ and 37.5 K₂O kg/ha) was given to the crop. The entire dose of P₂O₅, K₂O and one third of nitrogen was applied as basal dose and remaining two third nitrogen was top dressed in two equal splits at fourth and seventh week after planting. Weeding, irrigation and other recommended cultural practices were followed to raise a healthy crop.

3.4 Crossing programme

The male and female parents were raised during *rabi* 2010 in three staggered sowings at five days interval in order to achieve synchrony in flowering and to complete the programmed pollination. All the cultural operations were carried out similar to the normal maize crop. Tassel bag method was used for hybridization. Ear shoot of maize emerging from leaf sheath was bagged with butter paper cover to protect the silk from cross pollination. Ear shoots were covered two days before silk emergence. Kraft bag cover was placed over the tassel of the male parent on the previous day of pollination to collect pollen. The pollen collected in the tassel bag was dusted over the silk after removing the butter paper cover and it was replaced immediately to avoid contamination. A Kraft cover was tightly fastened over the pollinated ear for protection. Hand pollination was carried out between 9 to 10 am for twenty to thirty days. Simultaneously, parents were selfed by tassel bag method to get the parental seeds for further evaluation. The resultant thirty six hybrids, parents were harvested at maturity.

3.5 Recording of the observations

Observations on different quantitative characters were recorded on five randomly selected competitive plants. The average was taken as the mean of the treatment. The way in which observations were recorded is described below.

3.4.1 Days to 50 per cent tasselling

The number of days taken from the date of sowing to the day on which 50 per cent of plants in a treatment showed full tassel emergence was recorded as days to 50 per cent tasseling.

3.4.2 Days to 50 per cent silking

The number of days taken from the date of sowing to the day on which 50 per cent of the plants in a treatment showed complete silk emergence was recorded as days to 50 per cent of silking.

3.4.3 Days to 50 % anthesis

The number of days taken from the day of sowing to the day on which 50 % of the plants in treatment showed anthesis the anthesis starts is recorded as days to anthesis.

3.4.4 Plant height (cm)

Plant height was expressed in centimeters by measuring the plant stalk from the ground level to the base of the last leaf sheath of the matured plant.

3.4.5 Ear height (cm)

Ear height was measured and recorded in centimeter as the length of plant from the ground level to the upper most ear bearing node.

3.4.6 Ear length (cm)

Length of the ear was measured and recorded in centimeters at the time of harvest (from the base to the tip of the ear).

3.4.7 Number of kernel rows per cob

The number of kernel rows per cob was counted and recorded.

3.4.8 100-seed weight (gm)

Weight of 100 seeds randomly drawn from a random sun dried sample of each plot was recorded in grams.

3.4.9 Shelling percentage

Average pith weight and average grain weight of the randomly selected plants per plot were used to compute the shelling percentage by using the following formula.

$$\text{Shelling percentage} = \frac{\text{Grain weight}}{\text{Ear weight}} \times 100$$

3.4.10 Grain yield per plot (kg)

$$f = \frac{e \times (100-d)}{100}$$

Where,

e = corrected fresh ear weight

$$e = ab/c$$

a = average stand per plot of the trial

b = fresh ear weight (g)

c = stand at harvest of the respective plot

d = average moisture (%)

f = corrected fresh ear weight at zero per cent moisture

At the time of harvesting, fresh ear weight was recorded in grams per plant. Moisture determinations were made from shelled samples of five random ears of each plot with the help of electronic moisture meter. The fresh weight of ear data was used to work out the dry weight grain yield per plant at 15 per cent moisture level.

Corrected fresh ear weight at 0 per cent moisture to be multiplied by correction factor (0.9412) for calculation of plot yield at 15 per cent moisture content.

3.6 SCREENING OF HYBRIDS FOR SORGHUM DOWNY MILDEW

Maize hybrids were screened for sorghum downy mildew by artificial inoculation.

3.6.1 Spraying inoculum

Artificial inoculation was carried out when the plants were at two leaf stage (Lal and Singh, 1984). The diseased plants were sprayed with water at 6 pm so as to create congenial environment for good sporulation and thus enable to draw adequate quantities of inoculum at around 2 am through cleaned sprayers, torches and buckests. The leaves with good sporulation were selected and washed in the bucket of water at the rate of 15 liters of water. Then collected spore suspension in different buckets was thoroughly mixed and made up to 25 liters. The 25 liters of conidial inoculum collected from 375 diseased leaves. The inoculation completed by 4 am with hand compression sprayer. Further this inoculated plots was sprayed with water between 6 am and 6 pm so as to artificially create the required humidity. Hundred percent disease incidence was ensured through this methodology.

3.6.2 Spreader row technique

Spreader rows were sown 15-20 days prior to the sowing of the entries in 2.5 meter bands with a row spacing of 60 cm and plant to plant spacing of 30 cm. Each band consisted of four rows surrounding on all four directions. Highly susceptible variety CM-500 was used for this purpose. Inoculation of these spreader rows was done by following the above artificial inoculation procedure. Test entries were sown as mentioned above. Disease incidence was recorded at 35th day after sowing (Anahosur and Hegde, 1979).

3.6.3 Recording of observation

Disease incidence: systematically infected plants were taken into consideration while recording the disease incidence. Observations were recorded in only two classes, viz., (i) Downy mildew infected plants and (ii) Healthy plants. The observations were made at 35 days after sowing and at full bloom stage. The total number of plants and the number of plants showing systematic infection in a genotype were counted and the disease percentage was calculated. The reactions of the genotypes were classified into six different classes given Rao *et al.*, (1984).

Percent disease	Reaction category
0.0	Immune
1-10	Resistant
11-15	Moderately resistant
16-30	Moderately susceptible
31-50	Susceptible
Above 51	Highly susceptible

3.6.4 Validation of SSR markers for disease resistance

DNA isolation: CTAB

DNA from the parental inbred lines was isolated by using appropriate method. Quantification of DNA was done by running DNA in 0.8 percent agarose gel. Reported SSR markers for disease resistance were screened for validating those markers.

3.6.4.1 Total DNA extraction

Leaf samples of twenty-five days old seedlings were used for DNA extraction. DNA was isolated as per modified CTAB (Cetyl Trimethyl Ammonium Bromide) method.

- a) The leaves were cut into pieces and homogenized completely with liquid nitrogen using pestle and mortar and leaf powder(2g) was transferred to 50 ml Falcon tube containing 5 ml extraction buffer (100mM TrisCl pH 8, 25mM EDTA, 1.5M NaCl, 2.5% CTAB, 0.2% β Mercaptoethanol, 1% PVP).
- b) The samples were incubated for 30 min. at 65°C. During incubation, the samples were shaken well at regular intervals.
- c) Equal volume of chloroform: isoamyl alcohol (24:1) was added to the mixture and mixed through gentle inversion for 5 min. and then centrifuged for 10 min. at 4000 RPM.
- d) The upper aqueous layer was carefully taken and 1/10th volume of sodium acetate pH 5.2 was added, and double volume 100% chilled ethanol was added and kept at room temperature for 30 min.
- e) The DNA was spooled out or alternatively centrifuged at 10000 RPM for 15 min
- f) The supernatant was discarded and the pellet was washed with 70 per cent ethanol and the pellet was dried for 15 min at room

temperature and dried DNA pellet was dissolved in 200-400 µl TE buffer depending on size of the pellet and then dissolved DNA was transferred to 2.2 ml centrifuge tube and kept for incubation for 30 min. at 37°C after adding 8 µl RNase and mixing.

- g) The mixture was extracted with equal volume of phenol:chloroform.
- h) The upper aqueous layer was taken out and transferred to 1.5 ml centrifuge tube and added double volume of chilled ethanol and kept at -20°C for 20 min. and centrifuged at 10000 RPM for 15 min. at 25-30°C.
- i) The pellet was dried for 15 min. and dissolved in 200 µl TE buffer and quantified using UV spectrophotometer.

3.6.4.2 PCR reaction mixture

PCR reaction mixture consisted of 1µl of template DNA (50ng), 1µl each of forward and reverse primers (Sigma-Aldrich), 1µl of dNTPs, 0.25 µl of Taq polymerase (Sigma-Aldrich) and 1µl of 1x PCR buffer (10 mM Tris pH 8.0, 50 mM KCL, 1.8mM MgCl₂ and 0.01 mg/ml gelatin) in a volume of 20µl. one drop of mineral oil (Sigma) was put on reaction mixture.

The amplification profile was as follows

Initial denaturation temperature	: 94°C	- 5 min
Denaturation	: 94°C	-1 min
Primer annealing	: 58°C	- 45 sec
Later three steps were repeated 35 times		
Complete primer extension	: 72°C	- 7min.
Holding temperature	: 4°C	- until removed

3.6.4.3 Gel electrophoresis

The frame of the gel casting unit was cleaned, dried and sealed with a tape to form a mold. The frame was placed on a flat platform to ensure a flat and level base. The comb was then positioned parallel to the open edge of the frame about 2 mm above the surface.

1. Sufficient 1x electrophoresis buffer was prepared from 50x stock.
2. Agarose powder was added (1%) to TAE buffer (1x) and dissolved by melting at 100°C. The solution was cooled to 50°C and ethidium bromide added (0.5 µg/ml) and the comb positioned above the base of the plate. Then agarose solution was poured into the gel frame and allowed to set. After setting, the gel was transferred to the gel tank such that the wells were towards the negative pole. The gel tank was filled with TAE buffer (1x) just enough to cover the surface of the gel.
3. The DNA sample was mixed with gel loading buffer and slowly loaded into the wells of the submerged gel using a disposable micropipette tip.
4. The electrodes were connected to the power supply and electrophoresis was carried out at 100 volts for 1 hr or till the dye migrated to the end of the gel.
5. The DNA was visualized on a UV transilluminator and documented in a gel documentation system.

3.7 Screening of hybrids for drought tolerance

3.7.1 Estimation of free proline (µg /g dry weight)

Proline content in leaf tissue of maize genotypes was estimated by the method as suggested by Bates *et al.* (1973) and it was estimated

when crop was 45 days old and there is no rain and irrigation for 20 days.

Reagents

The reagents used were 3 per cent sulphosalicylic acid, toluene and acid ninhydrin. Acid ninhydrin was prepared by dissolving 2.5 g of ninhydrin in 100 ml of glacial acetic acid and orthophosphoric acid (6 M) mixed in the ratio of 3:2.

Procedure

The leaf sample of 0.5 gramme was homogenized in 10 ml of 3 per cent sulphosalicylic acid. The homogenate was filtered through a double-layered filter paper. A 2.0 ml of the filtrate was taken in a test tube to which 2 ml of acid ninhydrin reagent (2.5 g of ninhydrin was dissolved in 40 ml of 6 M orthophosphoric acid and 60 ml of glacial acetic acid) and 2 ml of glacial acetic acid were added. The test tubes containing the mixture were placed in boiling water bath for one hour. The test tubes were then cooled by keeping them in a ice bath. The contents were transferred to a separating funnel and 4 ml of toluene was added and mixed vigorously. The coloured toluene fraction was separated and measured at 520 nm in a spectrophotometer. A blank was maintained with all the reactants except the leaf extract. Proline content in leaf tissue was calculated by using the formula.

$$\text{Proline } (\mu\text{g /g dry weight}) = \frac{34.11 \times \text{OD}_{520} \times V}{2 \times f}$$

Where,

V = Total volume of extract

f = Grammes of fresh leaf

2 = Volume of extract taken

3.7.2 SPAD chlorophyll meter reading

Amongst several leaf characters, chlorophyll content determines the leaf transmittance characters. Leaf nitrogen content normally influences the leaf chlorophyll content. A device has been developed by Minolta company, New Jersey USA (SPAD-502) which measures the light attenuation at 430 nm (the peak wavelength for chlorophyll a and chlorophyll b) and at 750 nm (near infrared) with transmittance. The unit value measured by the chlorophyll meter is termed as SCMR (SPAD chlorophyll meter reading) which provides information on the relative amount of leaf chlorophyll. The SPAD meter (Soil Plant Analytical Development) is a simple hand held instrument, which operates with DC power of three Volts.

The third leaf from the apex was selected to record the SCMR. Selected leaf was clamped avoiding the midrib region into the sensor head SPAD meter. A gentle stroke was given to record the SPAD reading and the average such four strokes was considered. The SCMR was recorded under normal sunlight between 9 am to 4 pm.

3.7.3 Specific leaf area (cm²/g)

Fully expanded leaf of the middle region was collected and the leaf area was measured using leaf area meter. Then the leaves were kept in an oven at 70⁰ C for 3 days. The dry weight of the leaf was accurately measured using a sensitive balance. SLA computed using the formula.

$$\text{SLA} = \frac{\text{Leaf area (cm}^2\text{)}}{\text{Leaf dry weight (g)}}$$

3.8 STATISTICAL ANALYSIS

Mean values of the five plants selected at random in all the entries and in each replication were subjected to statistical analysis. The following statistical methods were adopted in the present study.

3.8.1 Analysis of variance for parents and hybrids

Analysis of variance was performed following the linear model given below,

$$X_{ij} = \mu + g_i + g_j + s_{ij} + e_{ijk}$$

Where,

X_{ij} = value of ij^{th} observation

μ = population mean

g_i = gca effect of i^{th} line

g_j = gca effect of j^{th} tester

s_{ij} = sca effect of ij^{th} cross

e_{ijk} = error associated with $(ijk)^{\text{th}}$ observation

Mean values of the 14 characters recorded for the hybrids and parents were subjected to statistical analysis and variances due to different sources were estimated. The method as suggested by Panse and Sukhatme (1961) was followed for analysis of variance. The ANOVA structure is given below.

ANOVA for Parents and Hybrids

Sl.No.	Source of Variance	df	MSS	Variance ratio
1	Replication	(r-1)	Mr	Mr/Me
2	Genotypes	(t-1)	Mt	Mt/Me
	a) Parents	(f+m-1)	Mp	Mp/Me
	i) Females	(f-1)	Mf	Mf/Me
	ii) Males	(m-1)	Mm	Mm/Me
	iii) Females vs. Males	1	Mf vs Mm	Mf vs Mm/Me
	b) Hybrids	(fm-1)	Mh	Mh/Me
	c) Parents Vs hybrids	1	Mp vs Mh	Mp vs Mh/Me
3.	Error	(t-1) (r-1)	Me	-
4.	Total	(mfr-1)		

Where,

r = Number of replications

t = Number of treatments

f = Number of females (lines)

m = Number of males (testers)

P = Parents

h = Hybrids

e= Error

M = Mean sum of squares

3.8.2 Combining Ability Analysis

3.8.2.1 Analysis of Variance

The mean of each character for each entry was subjected to line x tester analysis and the variance of combining ability was estimated as per the procedure developed by Kempthorne (1957). The form of analysis is given in the table below.

Source	Degree of freedom	Mean sum of squares	Expected mean sum of square
Replication	(r-1)		
Hybrids	(fm-1)		
Females	(f-1)	M ₁	$\sigma^2 + r [\text{COV (FS)} - 2 \text{ COV (HS)}] + [\text{mr COV (HS)}]$
Males	(m-1)	M ₂	$\sigma^2 + r [\text{COV (FS)} - 2 \text{ COV (HS)}] + [\text{fr cov (HS)}]$
Female x Male	(f-1) (m-1)	M ₃	$\sigma^2 + r [\text{COV (FS)} - 2 \text{ COV (HS)}]$
Error	(r-1)(fm-1)	M ₄	σ^2

Where,

r = Number of replications

f = Number of females (lines)

m = Number of males (testers)

COV (FS) = Covariance of full sibs

COV (HS) = Covariance of half sibs

M_1 = Mean sum of squares due to females (lines)

M_2 = Mean sum of squares due to males (testers)

M_3 = Mean sum of squares due to female x male

M_4 = Mean sum of square due to error.

3.8.4 Estimation of variance components

From the expectation of mean squares, the co-variance of half sibs (COV (HS)) and Co-variance of full-sibs (COV (FS)) were estimated as below.

$$\text{COV (HS)} = (M_1 + M_2 - 2M_3) / r (f+m)$$

$$\text{COV (FS)} = (1/3r) [M_1 + M_2 + M_3 - 3M_4] + 2r \text{ COV (HS)} - r (f+m) \text{ COV (HS)}$$

The estimates of COV (H.S) and COV (F.S) were used to estimate the variance due to general combining ability (GCA) and variance due to specific combining ability (SCA) as below.

$$\sigma^2_{\text{gca}} = \text{COV (HS)}$$

$$\sigma^2_{\text{sca}} = \text{COV (FS)} - 2 \text{ COV (HS)}$$

The estimates of variance component due to females, males and hybrids were obtained as shown below.

$$\sigma^2_f = \text{COV (HS) line} = \frac{M_1 - M_3}{r \times m}$$

$$\sigma^2_m = \text{COV (HS) tester} = \frac{M_2 - M_3}{r \times f}$$

$$\text{Covariance (HS) average} = \frac{M_1 + M_2 - 2M_3}{r(f+m)}$$

$$\sigma^2_{mf} = \sigma^2_{\text{SCA}} = \frac{M_3 - M_4}{r}$$

After estimating the GCA and SCA variances, the GCA/SCA ratio was computed to predict the type of gene action involved.

3.8.5 Proportional contribution of lines, testers and line x tester interaction to total variance

$$\text{a) Contribution of lines (\%)} = \frac{\text{SS (f)}}{\text{SS (C)}} \times 100$$

$$\text{b) Contribution of testers (\%)} = \frac{\text{SS (m)}}{\text{SS (C)}} \times 100$$

$$\text{c) Contribution of line} \times \text{testers (\%)} = \frac{\text{SS (f} \times \text{m)}}{\text{SS (C)}} \times 100$$

Where,

SS (c) = sum of squares due to crosses

SS (f) = sum of squares due to lines

SS (m) = sum of squares due to testers

SS (f x m) = sum of squares due to line × tester interaction

3.8.6 Estimation of combining ability effects

The model used to estimate gca and sca effect of ijk observations was as follows.

$$X_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$$

Where,

μ = population mean

g_i = gca effects of the i^{th} female parent

g_j = gca effects of the j^{th} male parent

s_{ij} = sca effects of the ij^{th} cross combination

i = number of female parents involved

j = number of male parents involved

k = number of replications

e_{ijk} = error associated with the observation X_{ijk}

3.8.7 General combining ability (gca) effects

a) Lines:

$$g_i = \frac{X_{i..}}{tr} - \frac{X_{...}}{ltr}$$

Where,

$\hat{g}_i$ = General combining ability effect of i^{th} line.

$X_{i..}$ = Total of i^{th} line over t testers and r replications.

$X_{...}$ = Total of all hybrids over r replications

b) Testers:

$$g_j = \frac{X_{j.}}{lr} - \frac{X_{...}}{ltr}$$

Where,

$\hat{g}_j$ = General combining ability effect of j^{th} tester

$X_{j.}$ = Total of j^{th} tester over l lines and r replications.

$X_{...}$ = Total of all hybrids over r replications.

3.8.8 Specific combining ability (sca) effects ($\hat{s}_{ij}$)

$$s_{ij} = \frac{X_{ij.}}{r} - \frac{X_{i..}}{tr} - \frac{X_{.j.}}{lr} + \frac{X_{...}}{ltr}$$

Where,

$\hat{s}_{ij}$ = sca effect of ij^{th} combination

$X_{ij.}$ = ij^{th} combinations total over all the replications

$X_{i.}$ = Total of i^{th} line over male parent and r replications

$X_{.j.}$ = Total of j^{th} tester over female and r replications

$X_{...}$ = Total of all hybrids over r replications.

3.8.9 Standard error (SE) pertaining to gca effects of males and females and sca effects of different crosses were calculated as under.

Standard error (SE) of $g_i = (Me/tr)^{1/2}$

Standard error (SE) of $g_j = (Me/lr)^{1/2}$

Standard error (SE) of $s_{ij} = (Me/r)^{1/2}$

The estimates of g_i and s_{ij} were tested for their statistical significance by 't' test. For testing the significance of difference between gca effects of two lines (or two testers) and sca effects of two hybrids, the standard error is as follows.

Standard error of $(g_i - g_j)$ for lines = $(2M_e / tr)^{1/2}$

Standard error of $(g_i - g_j)$ for testers = $(2M_e / lr)^{1/2}$

Standard error of $(s_{ij} - s_{kl})$ for crosses = $(2M_e / r)^{1/2}$

3.8.10 Critical difference (CD)

The critical difference values in each case were computed by multiplying their corresponding SE values with Table 't' value at error degrees of freedom at 5 and 1 per cent level of significance.

3.8.11 Estimation of Heterosis

Heterosis expressed as per cent increase or decrease of F_1 hybrid over mid-parent (average or relative heterosis), better parent (heterobeltiosis) and the best commercial check (standard heterosis) were computed as per the method of Hayes *et al.*, (1955). Out of the two checks, the mean performance of the best check for a given character was considered to work out the standard heterosis.

$$\text{Heterosis per cent over mid parent (\%)} = \frac{F_1 - MP}{MP} \times 100$$

$$\text{Heterosis per cent over better parent (\%)} = \frac{F_1 - BP}{BP} \times 100$$

$$\text{Heterosis per cent over standard check (\%)} = \frac{F_1 - SC}{SC} \times 100$$

Where,

$\overline{F_1}$ = mean performance of F_1

$\overline{MP}$ = mean mid-parental value = $(P_1 + P_2)/2$

P_1 = mean performance of parent one

P_2 = mean performance of parent two

$\overline{BP}$ = mean performance of better parent

$\overline{CC}$ = mean performance of the best commercial check

To compute the standard error (SE) of estimates of heterosis, mean squares due to error (M_e) was considered.

$$\text{SE for heterosis over mid parent (MP)} = (3 M_e / 2 r)^{1/2}$$

$$\text{SE for heterosis over better parent (BP)} = (2 M_e / r)^{1/2}$$

$$\text{SE for heterosis over standard check (SC)} = (2 M_e / r)^{1/2}$$

Where,

M_e = Error MSS in general ANOVA table

r = Number of replications

$\bar{1}$ = Mean value of hybrid over two replication

$\overline{MP}$ = Mean value of mid parent over two replication

$\overline{BP}$ = Mean value of better parent over two replication

SC = Mean value of standard check over two replication

Further 't' value is calculated to test the significance for heterosis

$$\text{'t' value for mid parent heterosis} = \frac{F_1 - MP}{SE(MP)}$$

$$\text{'t' value for better parent heterosis} = \frac{F_1 - BP}{SE(BP)}$$

$$\text{'t' value for standard heterosis} = \frac{F_1 - SC}{SE(SC)}$$

The calculated 't' value was compared with table 't' value at error degrees of freedom

3.8.12 Overall gca status of parents, sca and heterotic status of crosses

Since yield and its component characters are correlated either positively or negatively, it is usual to find *gca* status of parents and *sca*/heterosis for crosses in the desirable direction for some characters and undesirable direction for the others. The problem of ascertaining the status of a parent with respect to *gca* and *sca*/heterosis for crosses over a number of characters assumes importance under present context. Therefore, overall status of a parent or cross with respect to *gca* and *sca*/heterosis, respectively was determined following a method suggested by Arunachalam and Bandopadhyaya (1979) and modified by Mohan Rao

et al. (2004). General combining ability effects of parents, *sca* effects and estimates of mid parent heterosis (MPH) of crosses were ranked by giving highest rank for the parent or a cross which manifested highest *gca* effects and *sca* effects or heterosis, respectively. The lowest rank was given for parents or the cross with lowest *gca* effects and *sca* effects or heterosis, for a character, respectively. The ranks obtained by parents/crosses were summed up across all characters to arrive at total score for each of the parent or a cross. Further, the mean of the total scores thus obtained was used as the final norm to ascertain the status of a parent or a cross for their *gca* and *sca*/heterosis. The parents and crosses whose total rank exceeded the final norm were given as high (H) overall *gca* and *sca*/heterotic status, respectively. On the other hand, the parents or crosses which secured a total rank less than the final norm were given as low (L) overall *gca* and *sca*/heterotic status, respectively.

Table 3.1 List of Maize genotypes used in the present investigation.

Sl. No	Genotypes	Source
Lines		
1	1232	ZARS Mandya
2	1005	ZARS Mandya
3	1201	ZARS Mandya
4	1396	ZARS Mandya
5	772-2	ZARS Mandya
6	1410-1	ZARS Mandya
7	2422	ZARS Mandya
8	2-62-55	ZARS Mandya
9	634-2	ZARS Mandya
10	NAI-137-2	ZARS Mandya
11	MAI-105	ZARS Mandya
12	SKV-50	ZARS Mandya
Testers		
1	HKI-164-4-1-3	ZARS Mandya
2	HKI-193-2	ZARS Mandya
3	CML-411	ZARS Mandya
Checks		
1	NAH-2049 (Nithyashree)	ZARS Mandya
2	NAH-1137 (Hema)	ZARS Mandya

IV. EXPERIMENTAL RESULTS

The present investigation was carried out to identify drought and disease tolerant inbred lines, hybrids and to study combining ability, gene action and heterosis. The results obtained in the present investigation are presented under the following sub headings.

4.1.1 Mean performances of parents, crosses and checks

4.1.2 Analysis of variance

4.1.3 Variance due to *gca* and *sca* effects

4.1.4 Combining ability analysis

4.1.5 Proportional contribution of lines and testers

4.1.6 Heterosis

4.7 Reaction to Sorghum downy mildew

4.1 Mean performances of parents, crosses and checks

The character wise mean performance of parents (lines and testers), crosses and commercial checks are presented in Table 4.1, 4.2, 4.3, 4.4, respectively.

4.1.1 Drought tolerant traits

4.1.1.1 SPAD chlorophyll meter reading (SCMR)

Mean SCMR ranged from 23.65 (1201) to 36.35 (SKV-50) among lines with an average of 28.24. While, it ranged from 22.80 (HKI-193-2) to 30.70 (HKI-164-4-1-3) among testers.

Among the hybrids it varied from 11.25 (772-2 x HKI-164-4-1-3) to 34.45 (2422 x HKI-164-4-1-3). Among checks, it was 29.95 (NAH-2049) and 31.05 (NAH-1137).

Table 4.1: Mean performance of lines for drought tolerant, yield and yield attributing traits in maize

LINES	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
1232	29.75	46.0	138.46	50.0	53.50	52.0	140.0	84.50	16.50	15.50	47.14	28.50	3.75
1005	27.30	19.10	158.57	53.0	56.50	56.50	189.50	89.50	16.30	15.50	45.90	28.50	0.80
1201	23.65	37.90	168.07	48.0	53.0	50.0	191.0	83.0	15.50	13.20	57.72	33.50	2.30
1396	23.95	41.45	158.79	51.50	54.50	53.50	190.0	85.0	16.10	16.70	43.58	28.50	3.0
772-2	30.85	50.90	128.75	51.0	55.0	53.0	207.50	97.50	17.50	14.85	47.82	29.50	4.25
1410-1	29.90	46.35	185.90	49.0	53.0	51.0	179.50	79.50	17.30	15.80	49.83	33.50	3.95
2422	25.50	50.55	112.74	49.0	53.0	51.0	194.0	98.50	15.60	15.20	46.44	30.50	4.10
2-62-55	30.60	44.20	110.42	53.50	56.50	55.50	196.0	101.50	15.40	16.25	46.28	26.50	3.90
634-2	30.05	39.45	146.01	52.0	55.0	54.0	184.50	84.50	16.30	13.80	44.64	35.50	3.15
NAI-137-2	25.50	55.540	142.89	52.0	55.0	53.0	194.50	94.50	17.20	14.15	46.60	35.50	5.15
MAI-105	25.50	46.45	125.31	49.0	53.50	51.0	179.50	80.0	16.25	15.30	45.58	33.50	3.45
SKV-50	36.35	49.0	144.39	53.50	57.0	56.0	206.0	101.50	16.05	14.75	48.14	30.50	4.10
Mean	28.24	43.91	143.36	50.96	54.63	53.04	187.67	89.96	16.33	15.08	47.47	31.17	3.49
S.Em.±	0.82	0.83	10.29	0.70	0.69	0.52	10.89	5.41	0.27	0.22	0.77	0.54	0.18
CD (P=0.05)	2.33	2.36	29.27	2.01	1.97	1.48	30.97	15.39	0.77	0.63	2.21	1.54	0.53
CD (P=0.01)	3.10	3.14	39.03	2.69	2.63	1.98	41.29	20.53	1.03	0.85	2.94	2.06	0.71

Drought tolerant traits

X1: SCMR values

X2: Proline content (µg /g dry weight)

X3: Specific leaf area (cm²/g)

Yield and yield attributing traits

X4: Days to 50% tasselling

X5: Days to 50% silking

X6: Days to 50% anthesis

X7: Plant height (cm)

X8: Ear height (cm)

X9: Ear length (cm)

X10: Number of kernel rows per cob

X11: Shelling percentage

X12: 100- grain weight

X13: Yield per plot (kg)

Table 4.2: Mean performance of testers for drought tolerant, yield and yield attributing traits in maize

TESTERS	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
HKI-164-4-1-3	30.70	40.15	165.92	50.0	53.0	52.0	189.0	83.50	16.25	14.0	46.75	30.50	3.20
HKI-193-2	22.80	42.65	161.33	47.50	52.50	49.50	195.50	89.50	15.60	12.20	47.26	27.50	3.60
CML-411	23.45	38.90	137.30	52.0	55.0	54.0	200.0	98.0	17.0	11.40	44.12	31.50	2.40
Mean	25.65	40.57	154.85	49.83	53.50	51.83	194.83	90.33	16.28	12.53	46.04	29.83	3.07
S.Em.±	0.36	0.33	4.52	0.33	0.27	0.21	3.96	2.47	0.09	0.07	0.29	0.23	0.07
CD (P=0.05)	0.71	0.65	8.86	0.65	0.53	0.41	7.76	4.84	0.18	0.14	0.57	0.45	0.14
CD (P=0.01)	0.93	0.85	11.64	0.85	0.70	0.54	10.20	6.36	0.23	0.18	0.75	0.59	0.18

Drought tolerant traits

X1: SCMR values

X2: Proline content (µg /g dry weight)

X3: Specific leaf area (cm²/g)

Yield and yield attributing traits

X4: Days to 50% tasselling

X5: Days to 50% silking

X6: Days to 50% anthesis

X7: Plant height (cm)

X8: Ear height (cm)

X9: Ear length (cm)

X10: Number of kernel rows per cob

X11: Shelling percentage

X12: 100- grain weight

X13: Yield per plot (kg)

Table 4.3: Mean performance of hybrids for drought tolerant, yield and yield attributing traits in maize

HYBRIDS	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
1232 x HKI-164-4-1-3	16.20	28.80	140.71	58.50	63.50	61.50	149.0	62.0	15.0	14.70	46.37	30.50	2.10
1232 xHKI-193-2	11.80	26.40	143.38	56.50	62.0	59.50	148.0	58.0	18.20	12.75	45.46	34.50	1.75
1232xCML411	19.15	24.35	140.85	58.0	63.50	61.50	128.50	59.0	15.15	10.85	46.52	27.50	2.10
1005x HKI-164-4-1-3	18.80	34.70	144.26	56.0	61.0	58.0	180.50	83.50	14.20	13.50	45.98	31.0	2.45
1005x HKI-193-2	16.30	25.05	117.81	62.0	66.0	64.0	168.50	76.50	17.10	18.05	45.6	28.50	1.80
1005x CML411	14.90	22.0	139.43	56.50	62.50	60.0	144.0	65.0	12.75	14.60	44.32	23.50	1.30
1201x HKI-164-4-1-3	16.65	23.15	170.40	56.0	63.50	60.50	161.0	69.50	10.60	12.50	44.14	29.50	1.80
1201x HKI-193-2	18.40	12.95	129.59	58.0	64.0	61.50	130.50	53.0	13.30	15.35	43.15	21.0	0.75
1201x CML411	13.30	15.60	150.65	56.0	62.0	60.0	145.0	58.0	15.55	16.45	44.01	29.50	1.50
1396x HKI-164-4-1-3	14.90	12.40	131.01	56.50	63.0	60.50	162.50	70.50	15.85	13.65	43.28	20.50	0.85
1396x HKI-193-2	16.05	15.55	131.91	56.50	63.50	60.0	131.0	46.50	14.10	14.15	44.31	21.50	0.95
1396x CML411	11.45	16.45	165.35	56.50	62.50	59.50	147.0	53.0	12.55	10.05	49.81	34.50	1.10
772-2x HKI-164-4-1-3	11.25	13.30	156.93	53.50	61.50	58.0	138.50	49.50	14.10	13.10	44.40	24.50	5.63
772-2x HKI-193-2	18.05	20.95	130.87	55.50	63.50	59.50	141.0	53.0	14.55	12.45	44.75	21.50	1.35
772-2x CML411	15.65	38.40	121.30	58.50	67.0	64.0	150.50	69.50	17.05	14.35	45.19	35.50	3.05
1410-1x HKI-164-4-1-3	32.10	45.05	120.90	51.50	58.0	56.0	181.0	90.0	17.10	16.10	47.27	28.50	3.65
1410-1x HKI-193-2	32.15	49.15	126.69	51.0	56.50	55.0	195.0	92.50	15.80	14.30	46.99	35.0	3.80
1410-1x CML411	31.40	20.80	137.55	49.0	54.0	52.0	183.50	90.50	14.85	14.25	32.31	31.50	1.50
2422x HKI-164-4-1-3	34.45	37.10	166.12	48.0	54.0	51.50	177.50	73.0	16.30	15.30	40.33	34.50	2.25

HYBRIDS	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
2422x HKI-193-2	29.40	42.65	133.58	51.0	56.50	54.0	181.50	93.50	17.0	15.30	46.0	33.50	3.70
2422x CML411	25.25	43.10	119.56	50.0	55.0	52.50	181.0	89.50	18.45	16.30	44.06	32.50	3.85
262-55x HKI-164-4-1-3	29.40	46.60	144.49	48.50	55.50	52.0	193.50	91.50	16.10	14.40	44.22	31.50	3.55
262-55x HKI-193-2	23.45	51.40	148.64	50.50	55.0	53.50	195.0	92.50	16.40	15.10	44.04	33.50	4.05
262-55x CML411	23.35	43.40	124.51	51.0	56.50	54.50	189.0	84.0	16.60	14.30	45.58	35.50	3.30
634-2x HKI-164-4-1-3	25.90	53.20	111.17	53.0	57.0	56.0	200.0	92.0	19.60	15.80	45.10	36.50	4.25
634-2x HKI-193-2	24.95	36.70	151.42	53.0	57.50	56.0	176.0	78.0	17.10	14.0	45.02	31.50	2.25
634-2x CML411	27.25	46.05	141.76	53.0	57.0	56.0	207.50	93.50	18.40	14.40	44.70	32.50	3.80
NAI-137-2x HKI-164-4-1-3	33.25	52.35	110.35	50.0	54.0	54.0	202.0	84.50	17.45	14.75	44.19	30.50	4.30
NAI-137-2x HKI-193-2	26.50	52.05	115.63	50.50	55.50	53.50	202.0	89.50	16.65	17.90	44.85	32.50	6.31
NAI-137-2x CML411	25.35	51.25	104.92	51.50	56.0	55.0	212.0	106.50	14.60	17.20	44.90	30.50	4.20
MAI-105x HKI-164-4-1-3	23.55	37.45	140.32	52.0	56.50	55.50	182.50	90.50	17.40	15.20	44.34	25.50	2.70
MAI-105x HKI-193-2	32.25	22.70	128.81	51.50	56.0	55.0	196.0	87.0	18.70	14.0	44.60	34.50	1.65
MAI-105x CML411	29.25	53.65	122.59	49.50	56.50	52.0	203.0	102.50	16.50	14.20	47.74	33.50	5.7
SKV-50x HKI-164-4-1-3	33.90	50.95	120.11	54.0	56.50	55.50	205.50	101.50	15.60	14.20	44.92	38.50	3.95
SKV-50x HKI-193-2	25.50	41.35	148.0	50.0	54.50	52.0	197.0	98.0	15.50	13.60	44.65	31.50	3.05
SKV-50x CML411	28.85	43.15	126.20	52.50	55.50	54.50	210.50	103.50	17.70	16.20	44.70	33.50	3.35
Mean	23.06	34.73	134.93	53.49	58.96	56.78	174.90	79.18	15.94	14.54	44.66	30.57	2.66
S.Em.±	1.24	1.16	15.67	1.15	0.94	0.74	13.72	8.57	0.32	0.26	1.02	0.79	0.25
CD (P=0.05)	2.43	2.27	30.71	2.25	1.84	1.45	26.89	16.80	0.63	0.51	2.00	1.55	0.49
CD (P=0.01)	3.19	2.99	40.37	2.96	2.42	1.91	35.34	22.08	0.82	0.67	2.63	2.04	0.64

Drought tolerant traits

X1: SCMR values

X2: Proline content (µg /g dry weight)

X3: Specific leaf area (cm²/g)

Yield and yield attributing traits

X4: Days to 50% tasselling

X5: Days to 50% silking

X6: Days to 50% anthesis

X7: Plant height (cm)

X8: Ear height (cm)

X9: Ear length (cm)

X10: Number of kernel rows per cob

X11: Shelling percentage

X12: 100- grain weight

X13: Yield per plot (kg)

Table 4.4: Mean performance of checks for drought tolerant, yield and yield attributing traits in maize

CHECKS	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
NAH-2049	29.95	55.85	123.20	49	52	51	191	98.5	15.4	16.65	44.64	32.5	5.6
NAH-1137	31.05	52.05	130.75	56	59.5	58.5	185.5	80.5	18.5	13.9	43.52	37	4.5
Mean	30.5	53.95	126.98	52.5	55.75	54.75	188.25	89.5	16.95	15.28	44.08	34.75	5.05
S.Em.±	0.36	0.33	4.52	0.33	0.27	0.21	3.96	2.47	0.09	0.07	0.29	0.23	0.72
CD (P=0.05)	0.72	0.67	9.09	0.66	0.54	0.43	7.96	4.97	0.19	0.15	0.59	0.46	0.14
CD (P=0.01)	0.96	0.89	12.12	0.89	0.73	0.57	10.61	6.63	0.25	0.20	0.79	0.61	0.19

Drought tolerant traits

X1: SCMR values

X2: Proline content (µg /g dry weight)

X3: Specific leaf area (cm²/g)

Yield and yield attributing traits

X4: Days to 50% tasselling

X5: Days to 50% silking

X6: Days to 50% anthesis

X7: Plant height (cm)

X8: Ear height (cm)

X9: Ear length (cm)

X10: Number of kernel rows per cob

X11: Shelling percentage

X12: 100- grain weight

X13: Yield per plot (kg)

4.1.1.2 Specific leaf area (cm²/g)

Specific leaf area ranged from 110.42 cm²/g (2-62-55) to 185.90 cm²/g (1410-1) in females, whereas, it ranged from 137.30 cm²/g (CML-411) to 165.92 cm²/g (HKI-164-4-1-3) in males. Among the crosses, it varied from 104.92 (NAI-137-2 × CML-411) to 170.40 cm²/g (1201 × HKI-164-4-1-3) and 123.20 cm²/g (NAH-2049) to 130.75 cm²/g (NAH-1137) in checks.

4.1.1.3 Proline content (µg g dry weight⁻¹)

The range for proline content is from 19.10 µg g dry weight⁻¹ (1005) to 50.90 µg g dry weight⁻¹ (772-2) among lines and 38.90 µg g dry weight⁻¹ (CML-411) to 42.65 µg g dry weight⁻¹ (HKI-193-2) among testers. In case of hybrids it ranged from 12.40 µg g dry weight⁻¹ (1396 × HKI-164-4-1-3) to 53.65 µg g dry weight⁻¹ (MAI-105 × CML-411) and 52.05 µg g dry weight⁻¹ (NAH-1137) to 55.85 µg g dry weight⁻¹ (NAH-2049) in checks.

4.1.2 Yield and yield attributing traits

4.1.2.1 Days to 50 per cent tasseling

Among the lines, mean ranged from 48 days (1201) to 53.50 days (SKV-50 and 2-62-55) with an average of 50.96 days, which ranged from 47.50 (HKI-193-2) to 52 days (CML-411) among testers.

Whereas, among the hybrids it varied from 48 (2422 × HKI-164-4-1-3) to 62 days (1005 × HKI-193-2). In checks, it was 49 (NAH-2049) and 56 days (NAH-1137).

4.1.2.2 Days to 50 per cent silking

Days to 50 per cent silking ranged from 53 days (1201, 1410-1, 2422) to 57 days (SKV-50) among the females, whereas, it ranged from 52.5 (HKI-193-2) to 55 days (CML-411) among the males. Among the crosses, it varied from 54 (1410-1 x CML-411, 2422 x HKI-164-4-1-3, NAI-137-2 x HKI-164-4-1-3) to 67 days (772-2 x CML-411) and 52 (NAH-2049) to 59.5 days (NAH-1137) in checks.

4.1.2.3 Days to 50 per cent anthesis

The range for days to 50 per cent anthesis was from 51 days (1410-1, 2422, MAI-105) to 56.50 days (1005) among lines and 49.50 (HKI-193-2) to 54 days (CML-411) in testers. Among hybrids, it varied from 51.50 (2422 x HKI-164-4-1-3) to 64 days (772-2 x CML-411). While, in checks it was 51 (NAH-2049) and 58.5 days (NAH-1137).

4.1.2.4 Plant height (cm)

Mean plant height ranged from 140 cm (1232) to 207.50 cm (772-2) among lines, whereas in testers, it was ranged from 189 (HKI-164-4-1-3) to 200 cm (CML-411). Among the hybrids it varied from 128.50 (1232 x CML-411) to 212 cm (NAI-137-2 x CML-411) and from 185.5 cm (NAH-1137) to 191 cm (NAH-2049) among checks.

4.1.2.5 Ear height (cm)

Ear height ranged from 83 cm (1201) to 101.5 cm (SKV-50) among lines and from 83.5 cm (HKI-164-4-1-3) to 98 cm (CML-411) among testers. Among the hybrids, the mean ear height ranged from 46.50 (1396 x HKI-193-2) to 106.50 cm (NAI-137-2 x CML-411), while in checks, it was 80.5 cm (NAH-1137) and 98.5 cm (NAH-2049).

4.1.2.6 Ear length (cm)

The range for mean ear length was from 16.05 cm (SKV-50) to 17.50 cm (772-2) in lines. Among testers, it varied from 15.60 (HKI-193-2) to 17 cm (CML-411). Among crosses and checks, it varied from 10.60 cm (1201 x HKI-164-4-1-3) to 19.60 cm (634-2 x HKI-164-4-1-3) and 15.4 cm (NAH-2049) to 18.5 cm (NAH-1137), respectively.

4.1.2.7 Number of kernel rows per cob

The number of kernel rows per cob ranged from 13.2 (1201) to 16.70 (1396) among lines. Among testers, it varied from 11.40 (CML-411) to 14 (HKI-164-4-1-3). Among crosses, it varied from 10.05 (1396 x CML-411) to 18.05 (1005 x HKI-193-2) and in checks, it was 13.9 (NAH-1137) and 16.65 (NAH-2049).

4.1.2.8 Shelling percentage

The range for shelling percentage was from 43.58 (1396) to 57.72 per cent (1201) among lines. Among the testers, it varied from 44.12 (CML-411) to 47.26 per cent (HKI-193-2). Among the crosses, it ranged from 32.31 (1410-1 x CML-411) to 49.81 per cent (1396 x CML-411), while in checks it was 43.52 (NAH-1137) and per cent (NAH-2049).

4.1.2.9 Test weight (g)

The mean test weight ranged from 28.50 g (1005 and 1232) to 35.50 g (NAI-137-2 and 634-2) among lines. Among the testers, it varied from 27.50 g (HKI-193-2) to 31.50 g (CML-411). Among the crosses, it varied from 20.5 g (1396 x HKI-164-4-1-3) to 38.50 g (SKV-50 x HKI-164-4-1-3), while it was 32.5 g (NAH-2049) and 37 g (NAH-1137) in checks.

4.1.2.10 Grain yield per plot (Kg)

Grain yield per plot ranged from 0.80 kg (1005) to 5.15 kg (NAI-137-2) among lines and from 2.40 kg (CML-411) to 3.60 kg (HKI-193-2) among testers. In case of hybrids, grain yield ranged from 0.75 kg (1201 x HKI-193-2) to 6.31 kg (NAI-137-2x HKI-193-2). In checks, it was 4.5 kg (NAH-1137) to 5.6 kg (NAH-2049).

4.2 Analysis of variance

The analysis of variance in respect to three drought tolerant and ten yield and yield attributing characters (Table 4.5) indicated highly significant differences among the genotypes as revealed by 'F' test.

The variance due to genotypes was further partitioned into variance due to parents, crosses and parent's v/s crosses. The parents and hybrids exhibited highly significant differences for all the characters. The mean sum of squares for parent's v/s hybrids was also significant for all the traits. Superiority of hybrids indicating presence of heterosis for all the traits studied.

4. 3 Variance due to combining ability effects

The variances due to general and specific combining ability effects for the thirteen different attributes are presented in Table 4.6.

The data showed that, all the three drought tolerant and ten yield and yield attributing characters manifested higher degree of SCA variance as compared to GCA variance.

Table 4.5: Analysis of variance for drought tolerant, grain yield and its contributing characters in maize

Sources of variation	Mean Sum of Squares						
	d.f	SCMR values	Specific leaf area (SLA)	Free Proline	Days to 50% tasseling	Days to 50% silking	Days to 50% anthesis
Replication	1	34.70	1945.17	1.101	6.12	8.24	0.62
Genotypes	50	90.42**	660.63**	337.43**	21.83**	31.55**	27.48**
Parents	14	29.13**	896.21**	139.88**	7.7**	4.3**	9.2**
Hybrids	35	104.38**	515.77**	382.34**	23.52**	30.78**	26.01**
Parents vs. Crosses	1	459.75**	2432.82**	1531.3**	160.47**	440.01**	335.06**
Lines	11	284.03**	581.14**	909.78**	63.19**	88.88**	69.61**
Testers	2	26.94**	181.41	60.91**	3.01**	1.79	0.84
Line x Testers	22	21.6**	513.47	147.84**	5.55**	4.36**	6.49**
Error	50	1.34	212.11	1.38	1.007	0.96	0.54

Table 4.5 contd.....

Sources of variation	Mean Sum of Squares							
	d.f	Plant height (cm)	Ear height (cm)	Ear length (cm)	No of kernel rows per cob	Shelling percentage	Test weight (g)	Yield per plot (g)
Replication	1	518.62	69.17	0.0	0.24	11.97	0.35	0.106
Genotypes	50	1172.14**	510.39**	5.42**	5.14**	18.42**	35.29**	2.84**
Parents	14	500.8**	123.53**	0.9**	4.32**	22.01**	16.22**	2.1**
Hybrids	35	1352.69**	608.46**	7.3**	5.62**	13.64**	43.86**	2.88**
Parents vs. Crosses	1	4251.66**	2494.22**	3.1**	0.029	135.8**	2.31	11.9**
Lines	11	3746.65**	1625.95**	12.84**	8.09**	7.08**	56.8**	6.41**
Testers	2	214.01	140.68	1.24**	0.79**	1.4	21.93**	0.75**
Line x Testers	22	259.22	142.24**	5.08**	31.21**	18.03**	39.38**	2.1**
Error	50	237.42	58.69	0.14	0.10	1.20	0.59	0.07

Table 4.6: Estimates of variance components for drought tolerant, yield and yield contributing characters in maize

Sl. No.	Characters	Variance due to GCA	Variance due to SCA	SCA:GCA ratio	VA	VD
1.	SCMR values	1.95	10.02	5.14	7.82	40.09
2.	Specific leaf area (cm ² /g)	0.05	133.91	2678.20	0.21	535.66
3.	Free Proline (µg /g dry weight)	5.53	73.24	13.24	22.15	292.97
4.	Days to 50% tasselling	0.42	2.11	5.02	1.69	8.46
5.	Days to 50% silking	0.62	1.73	2.79	2.49	6.94
6.	Days to 50% anthesis	0.46	2.97	6.46	1.84	11.89
7.	Plant height (cm)	25.82	35.40	1.37	103.29	141.63
8.	Ear height (cm)	11.01	34.33	3.12	44.04	137.34
9.	Ear length (cm)	0.05	2.48	49.60	0.20	9.95
10.	Number of kernel rows per cob	0.01	2.37	237.00	0.07	9.51
11.	Shelling percentage	-0.10	8.49	-84.90	-0.41	33.96
12.	100-grain weight	0.10	19.37	193.70	0.42	77.49
13.	Yield per plot (kg)	0.03	0.62	20.67	0.14	2.48

4.4 Combining ability analysis

4.4.1 General combining ability effects

The estimates of general combining ability (gca) effects of parents (lines and testers) of maize for thirteen different traits are presented in Table 4.7 and 4.8. The character wise results are presented below.

4.4.1.1 Drought tolerant traits

4.4.1.1.1 SPAD chlorophyll meter reading (SCMR)

The magnitude of gca effects varied from -8.93 to 8.82 among lines and -0.97 to 1.13 in testers. Among the lines, 1410-1, 2422, 2-62-55, 634-2, NAI-137-2, MAI-105 and SKV-50 registered significant gca effects in positive direction, while 1232, 1005, 1201, 1396 and 772-2 lines registered significant gca effects in negative direction. Among testers HKI-164-4-1-3 registered significant gca effects in positive direction and CML-411 exhibited significant gca effect in the negative direction.

4.4.1.1.2 Specific leaf area (cm²/g)

The line 1201 exhibited significant gca effects in positive direction, whereas the line NAI-137-2 registered significant gca effect in negative direction. No testers have been registered significant gca effect both in positive and negative direction.

4.4.1.1.3 Proline content (µg g dry weight⁻¹)

The magnitude of gca effects varied from -19.93 to 17.16 among lines and -1.65 to 1.53 among testers. Five lines exhibited significance in negative direction *viz.*, 1232, 1005, 1201, 1396 and 772-2 and seven lines exhibited significance in positive direction *viz.*, 1410-1, 2422, 2-62-55, 634-2, NAI-137-2, MAI-105 and SKV-50. Among the testers (males) HKI-164-4-1-3 exhibited significant gca effects in positive direction and HKI-193-2 exhibited significant gca effects in negative direction.

Table 4.7: General combining ability effects of lines for drought tolerance, yield and yield contributing characters in maize

Lines	SCMR values	Specific leaf area (SLA)	Free proline	Days to 50% tasseling	Days to 50% silking	Days to 50% anthesis	Plant height (cm)
1232	-7.35**	6.71	-8.21**	4.18**	4.04**	4.06**	-33.10**
1005	-6.40**	-1.11	-7.48**	4.68**	4.21**	3.89**	-10.60
1201	-6.95**	15.28*	-17.49**	3.18**	4.21**	3.89**	-29.43**
1396	-8.93**	7.81	-19.93**	3.01**	4.04**	3.22**	-28.10**
772-2	-8.08**	1.43	-10.51**	2.35**	5.04**	3.72**	-31.60**
1410-1	8.82**	-6.56	3.61**	-2.99**	-2.79**	-2.44**	11.74*
2422	6.64**	4.81	6.22**	-3.82**	-3.79**	-4.11**	5.07
2-62-55	2.34**	4.28	12.41**	-3.49**	-3.29**	-3.44**	17.74**
634-2	2.97**	-0.15	10.59**	-0.49	-1.79**	-0.78*	19.57**
NAI-137-2	5.30**	-24.64**	17.16**	-2.82**	-3.79**	-2.61**	30.40**
MAI-105	5.29**	-4.36	3.21**	-2.49**	-2.63**	-2.61**	18.90**
SKV-50	6.35**	-3.50	10.42**	-1.32**	-3.46**	-2.78**	29.40**
S.Em.±	0.50	6.39	0.47	0.46	0.38	0.30	5.60
CD (P=0.05)	0.98	12.52	0.92	0.90	0.74	0.59	10.98
CD (P=0.01)	1.29	16.46	1.21	1.18	0.98	0.77	14.43

Table 4.7 contd.....

Lines	Ear height (cm)	Ear length (cm)	Number of kernel rows per cob	Shelling percentage	Test weight (g)	Yield per plot (kg)
1232	-19.51**	0.18	-1.77**	1.46**	0.26	-0.67**
1005	-4.18	-1.26**	0.85**	0.56	-2.90**	-0.81**
1201	-19.01**	-2.79**	0.23*	-0.89*	-3.90**	-1.31**
1396	-22.51**	-1.77**	-1.92**	1.14**	-5.07**	-1.69**
772-2	-21.85**	-0.71**	-1.24**	0.13	-3.40**	-0.86**
1410-1	11.82**	-0.02	0.35**	-2.47**	1.10**	0.33**
2422	6.15	1.31**	1.10**	-1.19**	2.93**	0.61**
2-62-55	10.15**	0.43**	0.06	-0.04	2.93**	0.98**
634-2	8.65*	2.43**	0.20	0.28	2.93**	0.78**
NAI-137-2	14.32**	0.29*	2.08**	-0.01	0.60	1.63**
MAI-105	14.15**	1.59**	-0.07	0.91*	0.60	0.23**
SKV-50	21.82**	0.33**	0.13	0.10	3.93**	0.79**
S.Em.±	3.50	0.13	0.10	0.41	0.32	0.10
CD (P=0.05)	6.86	0.25	0.20	0.80	0.63	0.20
CD (P=0.01)	9.02	0.33	0.26	1.06	0.82	0.26

* Significant at P = 0.05

** Significant at P = 0.01

Table 4.8: General combining ability effects of testers for drought tolerance, yield and yield contributing characters in maize

Males	SCMR values	Specific leaf area(SLA)	Free proline	Days to 50% tasseling	Days to 50% silking	Days to 50% anthesis	Plant height (cm)
HKI-164-4-1-3	1.13**	3.12	1.53**	-0.36	-0.29	-0.19	2.86
HKI-193-2	-0.16	-1.08	-1.65**	0.35	0.25	0.18	-3.10
CML-411	-0.97**	-2.05	0.12	0.01	0.04	0.01	0.24
S.Em±	0.25	3.19	0.23	0.23	0.19	0.15	2.80
CD at 5%	0.49	6.25	0.45	0.45	0.37	0.29	5.49
CD at 1%	0.64	8.22	0.59	0.59	0.49	0.39	7.21

Table 4.8 Contd....

Males	Ear height (cm)	Ear length (cm)	Number of kernel rows per cob	Shelling percentage	Test weight (g)	Yield per plot(kg)
HKI-164-4-1-3	0.65	-0.17*	-0.10	-0.11	-0.44**	0.08
HKI-193-2	-2.68	0.26**	0.21**	0.28	-0.65**	-0.20**
CML-411	2.03	-0.09	-0.11	-0.17	1.10**	0.12*
S.Em±	1.75	0.06	0.05	0.20	0.16	0.05
CD at 5%	3.43	0.12	0.10	0.39	0.31	0.10
CD at 1%	4.51	0.15	0.13	0.52	0.41	0.13

4.4.1.2 Yield and yield attributing traits

4.4.1.2.1 Days to 50 per cent tasseling

The magnitude of gca effects varied from -3.82 to 4.68 among lines and -0.36 to 0.35 in testers. The lines, 1232, 1005, 1201, 1396 and 772-2 exhibited significant gca effects in positive direction and seven lines 1410-1, 2422, 2-62-55, 634-2, NAI-137-2, MAI-105 and SKV-50 exhibited significant gca effect in negative direction. Among testers none has registered significant gca effect both in positive and negative direction.

4.4.1.2.2 Days to 50 per cent silking

For this trait, the magnitude of gca effects varied from -3.79 to 5.04 among lines and -0.36 to 0.25 among testers. All the females registered significant gca effects in which 1232, 1005, 1201, 1396 and 772-2 were in negative direction and 1410-1, 2422, 2-62-55, 634-2, NAI-137-2, MAI-105 and SKV-50 in positive direction. None of the testers has registered significant gca effect.

4.4.1.2.3 Days to 50 per cent anthesis

The lines *viz.*, 1232, 1005, 1201, 1396 and 772-2 showed significant gca effects in positive direction, whereas lines 1410-1, 2422, 2-62-55, 634-2, NAI-137-2, MAI-105 and SKV-50 registered significant gca effect in negative direction. Among testers no single individuals expressed either positive or negative significant gca effect.

4.4.1.2.4 Plant height (cm)

For this trait, the magnitude of gca effects varied from -33.10 to 30.40 among lines and -3.10 to 2.86 among testers. Out of twelve females, 1410-1, 2-62-55, 634-2, NAI-137-2, MAI-105 and SKV-50

registered significant gca effect in positive direction. Whereas 1232, 1201, 1396 and 772-2 registered significant gca effects in the negative direction.

No single tester expressed significant gca effect with respect to plant height.

4.4.1.2.5 Ear height (cm)

Among the lines, the magnitude of gca effects varied from -22.51 to 21.82 and -2.68 to 2.03 among testers for this trait.

Out of twelve lines, six lines *viz.*, 1410-1, 2-62-55, 634-2, NAI-137-2, MAI-105 and SKV-50 registered significant gca effects in positive direction. Whereas, the lines *viz.*, 1232, 1201, 1396 and 772-2 exhibited significant gca effects in negative direction. Among testers none has expressed significant gca effect.

4.4.1.2.6 Ear length (cm)

The magnitude of gca effects for this trait varied from -2.79 to 2.43 in females and -0.17 to 0.26 among testers.

Lines *viz.*, 1005, 1201, 1396 and 772-2 registered significant effects in negative direction, whereas 2422, 2-62-55, 634-2, NAI-137-2, MAI-105 and SKV-50 registered significant gca effects in positive direction. Among the testers HKI-164-4-1-3 exhibited significant gca effects in negative direction and HKI-193-2 exhibited significant gca effects in positive direction.

4.4.1.2.7 Number of kernel rows per cob

Among 8 lines which registered significant gca effects, 1232, 1396 and 772-2 had significant effect gca effects in negative direction, whereas

gca effects of 1005, 1201, 1410-1, 2422 and NAI-137-2 were in positive direction. Among three testers HKI-193-2 had registered significant gca effects in positive direction.

4.4.1.2.8 Shelling percentage

The magnitude of gca effects range from -2.47 to 1.46 in females and from -0.17 to 0.28 among males. Out of twelve lines two lines *viz.*, 1232 and MAI-105 registered significant gca effects positive direction, and three lines *viz.*, 1201, 1410-1 and 2422 exhibited significant gca effects in negative direction. No single tester has expressed significant gca effects in desirable direction.

4.4.1.2.9 Test weight (g)

For test weight, the magnitude of gca effects varied from -5.07 to 3.93 among females and -0.65 to 1.10 among males. Nine out of twelve lines registered significant gca effects of which 1005, 1201, 1396 and 772-2 were in the negative direction and 1410-1, 2422, 2-62-55, 634-2 and SKV-50 were in the positive direction. Among testers, CML-411 registered significant gca effects in positive direction. While HKI-164-4-1-3 and HKI-193-2 registered significant gca effects in negative direction.

4.4.1.2.10 Grain yield per plant (kg)

The magnitude of gca effects ranged from -1.69 to 1.63 among females and from -0.20 to 0.12 among males. All twelve lines registered significant gca effect of which 1232, 1005, 1201, 1396 and 772-2 registered significant gca effects in negative direction and 1410-1, 2422, 2-62-55, 634-2, NAI-137-2, MAI-105 and SKV-50 exhibited significant gca effects in positive direction.

Among the testers HKI-193-2 registered significant gca effects in negative and HKI-164-4-1-3 in positive direction.

4.4.2 Overall general combining ability status

The overall general combining ability status of lines and testers for their gca effects across the traits estimated according to method suggested by Arunachalam and Bandopadhyay (1979) and modified by Mohan Rao *et al.* (2004) is presented in Table 4.9.

From the Table 4.9, it is evident that the lines 1232, 1005, 1396, 2-62-55, 634-2 and MAI-105 were grouped under overall high general combiners (H) category and 1201, 772-2, 1410-1, 2422, NAI-137-2 and SKV-50 were grouped as low overall general combiners (L).

Among the testers HKI-164-4-1-3 and CML-411 were overall high general combiners (H) and HKI-193-2 was low overall general combiner (L).

4.4.3 Specific combining ability effects

The estimates of specific combining ability effects of 36 crosses in respect of 13 traits are presented in the Table 4.10 and results are presented under character wise.

4.4.3.1 Drought tolerant traits

4.4.3.1.1 SPAD chlorophyll meter reading (SCMR)

Among 36 crosses, 19 crosses registered significant sca effects, which ranged from -5.93 to 4.4. Eleven Crosses recorded significant sca effects in positive direction. The cross 1231 x CML-411 registered the highest significant positive sca effects for SCMR (4.40) followed by MAI-105 x HKI-193-2 (4.06) and NAI-137-2 x HKI-164-4-1-3 (3.75). whereas eight crosses recorded significant sca effects in negative direction of which MAI-105 x HKI-164-4-1-3 (-5.93) followed by 772-2 x HKI-164-4-1-3 (-4.87), 1232 x HKI-193-2 (-3.75) and SKV-50 x HKI-193-2 (-3.75).

Table 4.9: Overall general combining ability status of parents in maize

Lines

Lines	Total rank	Overall gca status
1232	85	(H)
1005	110	(H)
1201	82	(L)
1396	100	(H)
772-2	62	(L)
1410-1	57	(L)
2422	76	(L)
2-62-55	99	(H)
634-2	100	(H)
NAI-137-2	70	(L)
MAI-105	93	(H)
SKV-50	80	(L)

FINAL NORM : **84.5**

H: OVERALL HIGH COMBINER

L: OVERALL LOW COMBINER

Testers

Lines	Total rank	Overall gca status
HKI-164-4-1-3	27	(H)
HKI-193-2	23	(L)
CML-411	28	(H)

FINAL NORM : **26**

H: OVERALL HIGH COMBINER

L: OVERALL LOW COMBINER

Table 4.10: Specific combining ability effects of single cross hybrids for drought tolerant, yield and yield contributing characters in maize

Single cross hybrids	SCMR values	Specific leaf area(SLA)	Free proline	Days to 50% tasseling	Days to 50% silking	Days to 50% anthesis
1232xHKI-164-4-1-3	-0.65	-4.06	0.76	1.19	0.79	0.86
1232xHKI-193-2	-3.75**	2.81	1.53	-1.51	-1.25	-1.51**
1232xCML411	4.40**	1.25	-2.29**	0.32	0.46	0.65
1005x HKI-164-4-1-3	1.00	7.30	5.92**	-1.81*	-1.88**	-2.47**
1005x HKI-193-2	-0.20	-14.94	-0.55	3.49**	2.58**	3.15**
1005x CML411	-0.80	7.64	-5.37**	-1.68*	-0.71	-0.68
1201x HKI-164-4-1-3	-0.60	17.06	4.39**	-0.31	0.62	0.03
1201x HKI-193-2	2.45**	-19.55	-2.63**	0.99	0.58	0.65
1201x CML411	-1.85*	2.49	-1.76*	-0.68	-1.21	-0.68
1396x HKI-164-4-1-3	-0.37	-14.87	-3.93**	0.36	0.29	0.69
1396x HKI-193-2	2.08*	-9.77	-2.40**	-0.35	0.25	-0.18
1396x CML411	-1.72	24.64*	1.53	-0.01	-0.54	-0.51
772-2x HKI-164-4-1-3	-4.87**	17.44	-12.44**	-1.97*	-2.21**	-2.31**
772-2x HKI-193-2	3.23**	-4.42	-1.62	-0.68	-0.75	-1.18*
772-2x CML411	1.63	-13.01	14.06**	2.65**	2.96**	3.49**
1410-1x HKI-164-4-1-3	-0.92	-10.60	5.19**	1.36	2.13**	1.86**
1410-1x HKI-193-2	0.43	-0.61	12.47**	0.15	0.08	0.49
1410-1x CML411	0.48	11.22	-17.66**	-1.51	-2.21**	-2.35**
2422x HKI-164-4-1-3	3.62**	23.24*	-5.38**	-1.31	-0.87	-0.97
2422x HKI-193-2	-0.14	-5.09	3.35**	0.99	1.08	1.15*
2422x CML411	-3.48**	-18.15	2.03*	0.32	-0.21	-0.18
262-55x HKI-164-4-1-3	2.87**	2.15	-2.06*	-1.14	0.13	-1.14*
262-55x HKI-193-2	-1.79*	10.50	5.92**	0.15	-0.92	-0.01
262-55x CML411	-1.08	-12.65	-3.86**	0.99	0.79	1.15*
634-2x HKI-164-4-1-3	-1.27	-26.74*	6.36**	0.36	0.12	0.19
634-2x HKI-193-2	-0.92	17.71	-6.97**	-0.35	0.08	-0.18
634-2x CML411	2.18*	9.03	0.61	-0.01	-0.21	-0.01

Single cross hybrids	SCMR values	Specific leaf area(SLA)	Free proline	Days to 50% tasseling	Days to 50% silking	Days to 50% anthesis
NAI-137-2x HKI-164-4-1-3	3.75**	-3.07	-1.06	-0.31	-0.87	0.03
NAI-137-2x HKI-193-2	-1.70	6.41	1.82*	-0.51	0.08	-0.85
NAI-137-2x CML411	-2.05*	-3.34	-0.76	0.82	0.79	0.82
MAI-105x HKI-164-4-1-3	-5.93**	6.62	-2.01*	1.36	0.46	1.53**
MAI-105x HKI-193-2	4.06**	-0.68	-13.58**	0.15	-0.58	0.65
MAI-105x CML411	1.87*	-5.94	15.59**	-1.51	0.13	-2.18**
SKV-50x HKI-164-4-1-3	3.35**	-14.46	4.27**	2.19**	1.29	1.69**
SKV-50x HKI-193-2	-3.75**	17.64	-2.15*	-2.51**	-1.25	-2.18**
SKV-50x CML411	0.40	-3.18	-2.12*	0.32	-0.04	0.49

Table 4.10 contd.....

Single cross hybrids	Plant height(cm)	Ear height(cm)	Ear length(cm)	Number of kernel rows per cob	Shelling percentage	Test weight (g)	Yield per plot(kg)
1232xHKI-164-4-1-3	4.31	1.68	-0.95**	2.04**	0.36	0.11	0.04
1232xHKI-193-2	9.26	1.01	1.82**	-0.23	-0.93	4.32**	-0.03
1232xCML411	-13.57	-2.69	-0.87**	-1.81**	0.57	-4.43**	-0.01
1005x HKI-164-4-1-3	13.31	7.85	-0.32	-1.78**	0.87	3.78**	0.52**
1005x HKI-193-2	7.26	4.18	2.16**	2.46**	-0.14	1.49*	0.15
1005x CML411	-20.57*	-12.03	-1.84**	-0.68**	-0.73	-5.26**	-0.67**
1201x HKI-164-4-1-3	12.64	8.68	-2.38**	-2.16**	0.48	3.28**	0.37*
1201x HKI-193-2	-11.90	-4.49	-0.11	0.37	-0.89	-5.01**	-0.40
1201x CML411	-0.74	-4.19	2.49**	1.79**	0.42	1.74**	0.03
1396x HKI-164-4-1-3	12.81	13.18*	1.85**	1.14**	-2.41**	-4.56**	-0.20
1396x HKI-193-2	-12.74	-7.49	-0.33	1.32**	-1.77*	-3.35**	0.19
1396x CML411	-0.07	-5.69	-1.52**	-2.46**	4.17**	-7.90**	0.01
772-2x HKI-164-4-1-3	-7.69	-8.49	-0.97**	-0.10	-0.27	-2.22	-0.88**
772-2x HKI-193-2	0.76	-1.65	-0.94**	-1.06**	-0.31	-5.01**	-.25
772-2x CML411	6.93	10.14	1.91**	1.16**	0.58	7.24**	1.13**
1410-1x HKI-164-4-1-3	-8.53	-1.65	1.35**	1.32**	5.19**	-2.72**	0.59**
1410-1x HKI-193-2	11.93	4.18	-0.38	-0.79**	4.53**	3.99**	1.02**
1410-1x CML411	-3.40	-2.53	-0.97**	-0.53**	-9.72**	-1.26*	-1.61**
2422x HKI-164-4-1-3	-5.36	-12.99*	-0.78**	-0.23	3.02**	1.44*	-1.10**
2422x HKI-193-2	4.60	10.85	-0.51**	-0.54**	2.26**	0.65	0.64**
2422x CML411	0.76	2.14	1.29**	0.77**	0.76	-2.10**	0.46*
262-55x HKI-164-4-1-3	-2.03	1.51	-0.10	-0.10	-0.29	-1.56**	-0.16
262-55x HKI-193-2	5.43	5.85	-0.23	0.29	-0.85	0.65	0.62**
262-55x CML411	-3.40	-7.36	0.33	-0.19	1.14	0.90	-0.46*
634-2x HKI-164-4-1-3	2.64	3.51	1.10**	1.17**	0.27	3.44**	0.74**
634-2x HKI-193-2	-15.40	-7.15	-1.53**	-0.94**	-0.20	-1.35*	-0.98**
634-2x CML411	12.76	3.64	0.13	-0.23	-0.07	-2.10**	0.24
NAI-137-2x HKI-164-4-1-3	-6.19	-9.65	1.38**	-1.76**	-0.35	-0.22	-0.06

Single cross hybrids	Plant height (cm)	Ear height(cm)	Ear length(cm)	Number of kernel rows per cob	Shelling percentage	Test weight (g)	Yield per plot(kg)
NAI-137-2x HKI-193-2	-0.24	-1.32	0.16	1.07**	-0.08	1.99**	0.27
NAI-137-2x CML411	6.43	10.97	-1.54**	0.69**	0.42	-1.76**	-0.21
MAI-105x HKI-164-4-1-3	-14.19	-3.49	0.03	0.84**	-1.11	-5.22**	-0.26
MAI-105x HKI-193-2	5.26	-3.65	0.91**	-0.68**	-1.24	3.99**	-0.13**
MAI-105x CML411	8.93	7.14	-0.94**	-0.16	2.35**	1.24**	1.29**
SKV-50x HKI-164-4-1-3	-1.69	-0.15	-0.50*	-0.36	0.27	4.44**	0.42*
SKV-50x HKI-193-2	-4.24	0.32	-1.03**	-1.28**	-0.38	-2.35**	-0.20
SKV-50x CML411	5.93	0.47	1.53**	1.64**	0.11	-2.10**	-0.22

* Significant at P = 0.05

**Significant at P = 0.01

4.4.3.1.2 Specific leaf area (cm²/g)

The magnitude of sca effects ranged from -26.74 to 24.64. Among the crosses, 3 crosses recorded significant sca effects of which the cross 634-2 x HKI-164-4-1-3 exhibited highest negative sca effect (-26.74). Whereas, 2 crosses exhibited high significant sca effects in positive direction in that 1396 x CML-411 recorded highest positive sca effect (24.64) followed by 2422 x HKI-164-4-1-3.

4.4.3.1.3 Proline content (µg g dry weight⁻¹)

The sca effects of crosses was ranged from was -17.66 to 15.59. sixteen crosses recorded significant sca effects in negative direction and twelve in positive direction. The cross 1410- x CML-411 recorded highest sca effect in negative direction (-17.66) followed by MAI-105 x HKI-193-2 (-13.58). and the cross MAI-105 x CML-411 recorded highest sca effect in positive direction (15.59) followed by 772-2 x CML-411 (14.06).

4.4.3.2 Yield and yield attributing traits

4.4.3.2.1 Days to 50 per cent tasseling

The magnitude of sca effects ranged from -2.51 to 3.49. Among the crosses, 7 crosses recorded significant sca effects in which 1005 x HKI-164-4-1-3, 1005 x CML-411, 772-2 x HKI-164-4-1-3 and SKV-50 x HKI-193-2 exhibited negative sca effects and 772-2 x CML-411 and SKV-50 x HKI-164-4-1-3 were with positive sca effects.

4.4.3.2.2 Days to 50 per cent silking

The magnitude of sca effects ranged from -2.21 to 2.96. Among the crosses, three crosses exhibited highly significant sca effects in positive direction (1005 x HKI-193-2, 772-2 x CML-411 and 1410-1 x HKI-164-4-1-3) and three crosses registered significant sca effect in negative

direction (1005 x HKI-164-4-1-3, 772-2 x HKI-164-4-1-3 and 1410-1 x CML-411).

4.4.3.2.3 Days to 50 per cent anthesis

The magnitude of sca effects for this trait was ranged from -2.47 to 3.49. Fifteen crosses recorded significant sca effects of which six crosses registered significant effects in positive direction. The cross 1005 x HKI-164-4-1-3 expressed higher sca effects (-2.47) in negative direction followed by 1410-1 x CML-411 (-2.35) and 772-2 x HKI-164-4-1-3(-2.31). Nine crosses exhibited significant sca effects in positive direction in that 772-2 x CML-411 registered highest sca effect (3.49) followed by 1005 x HKI-193-2 (3.15) and 1410-1 x HKI-164-4-1-3 (1.86).

4.4.3.2.4 Plant height (cm)

The range of sca effects for this trait ranged from -20.57 to 13.31. Only the cross, 1005 x CML-411 has registered significant sca effect in negative direction (-20.57).

4.4.3.2.5 Ear height (cm)

The sca effects for ear height was ranged from -12.99 to 13.18. Two crosses were expressed significant sca effect in which the cross 1396 x HKI-164-4-1-3 exhibited in positive direction (13.18) and 2422 x HKI-164-4-1-3 in negative direction (-12.99).

4.4.3.2.6 Ear length (cm)

For ear length, the magnitude of sca effects was ranged from -2.38 to 2.49. Among 36 crosses, eleven and fifteen crosses were with significant positive and negative sca effects, respectively. The top three crosses which showed positive significant sca effects were 1201 x HKI-164-4-1-3, 1005 x CML-411 and NAI-137-2 x CML-411 and significant

negative sca effects were shown by the crosses 1201 x CML-411, 1005 x HKI-193-2 and 772-2 x CML-411.

4.4.3.2.7 Number of kernel rows per cob

The range of sca effects for this trait was from -2.46 to 2.04. Among the crosses, thirteen crosses manifested significant negative sca effects. The cross 1396 x CML-411 registered the highest significant negative sca effects for kernels rows per cob (-2.46) followed by 1201 x HKI-164-4-1-3 (-2.16) and 1232 x CML-411 (-1.81) and twelve crosses recorded positive sca effects of which 1232 x HKI-164-4-1-3 exhibited highest sca effects (2.04) followed by 1201 x CML-411 (1.79) and SKV-50 x CML-411 (1.64).

4.4.3.2.8 Shelling percentage

The magnitude of sca effects for this trait was from -9.72 to 5.19. Among 70 crosses, six and three crosses manifested significant positive and negative sca effects, respectively. Three crosses *viz.*, 1410-1 x HKI-164-4-1-3 (5.19) followed by 1410-1 x HKI-193-2 (4.53) and 1396 x CML-411 (4.17) showed highest significant positive sca effects for shelling percentage and 1410-1 x CML-411 (-9.72) followed by 1396 x HKI-164-4-1-3 (-2.41) and 1396 x HKI-193-2 (-1.77) showed highest significant negative sca effects for shelling percentage.

4.4.3.2.9 Test weight (g)

For test weight, the magnitude of sca effects was from -7.9 to 7.24. Among 36 crosses, thirteen crosses expressed significant positive sca effects. The cross 772-2 x CML-411 registered the highest significant positive sca effects for test weight (7.24) followed by SKV-50 x HKI-164-4-1-3 (4.44) and 1232 x HKI-193-2 (4.32). and thirteen crosses registered the significantly higher negative sca effects. The cross 1396 x CML-411

expressed higher significant negative sca effect (-7.9) followed by 1005 x CML-411 (-5.26) and MAI-105 x HKI-164-4-1-3 (-5.22).

4.4.3.2.10 Grain yield per plot (kg)

For grain yield per plant, the magnitude of sca effects was from -1.61 to 1.29. Eleven crosses manifested significant positive sca effects of which MAI-105 x CML-411 (1.29) was highest followed by 772-2 x CML-411 (1.13) and 1410-1 x HKI-193-2 (1.02) and seven crosses registered negative sca effects of which 1410-1 x CML-411 (-1.61) expressed highest followed by 2422 x HKI-164-4-1-3 (-1.10) and 634-2 x HKI-193-2 (-0.98).

4.4.4 Overall specific combining ability status

It becomes important to determine whether the cross possess good sca values across the traits. Hence, using the method explained in chapter three, the overall sca status of each hybrid was determined. The results of the same are presented in Table 4.11. From the results, it was found that forty four per cent of the crosses showed overall high sca status. Out of sixteen crosses which showed higher overall sca status, five were of H × H, three with H × L, five with L × H and three with L × L combinations.

4.5 Proportional contribution of lines, testers and line × tester interaction for the performance of hybrids

Per cent contribution of line × tester interaction towards variation in hybrids was higher for the characters specific leaf area, number of kernel rows per cob, shelling percentage and test weight and for remaining characters proportion of contribution of lines was higher than line x tester interaction (Table 4.12)

Table 4.11: Overall specific combining ability status of hybrids in maize

Testers	HKI-164-4-1-3(H)	HKI-193-2(L)	CML-411(H)	Hybrids with high OSCA status
Lines				
1232 (H)	L(245)	L(185)	H(293)	1
1005(H)	L(131)	L(211)	H(331)	1
1201(L)	L(229)	H(298)	L(193)	1
1396(H)	L(234)	H(260)	H(292)	2
772-2(L)	H(294)	H(264)	L(165)	2
1410-1(L)	L(240)	L(166)	H(282)	1
2422(L)	H(272)	L(231)	L(189)	1
2-62-55(H)	L(226)	L(202)	H(291)	1
634-2(H)	L(168)	H(340)	L(206)	1
NAI-137-2(L)	H(249)	L(205)	H(570)	2
MAI-105(H)	H(352)	H(249)	L(131)	2
SKV-50(L)	L(234)	H(288)	L(223)	1
Hybrids with high OSCA status	4	6	6	16

FINAL NORM : 248.4

(H): Overall high combiner

(L): Overall low combiner

H: Over all high specific combiner

L: Over all low specific combiner

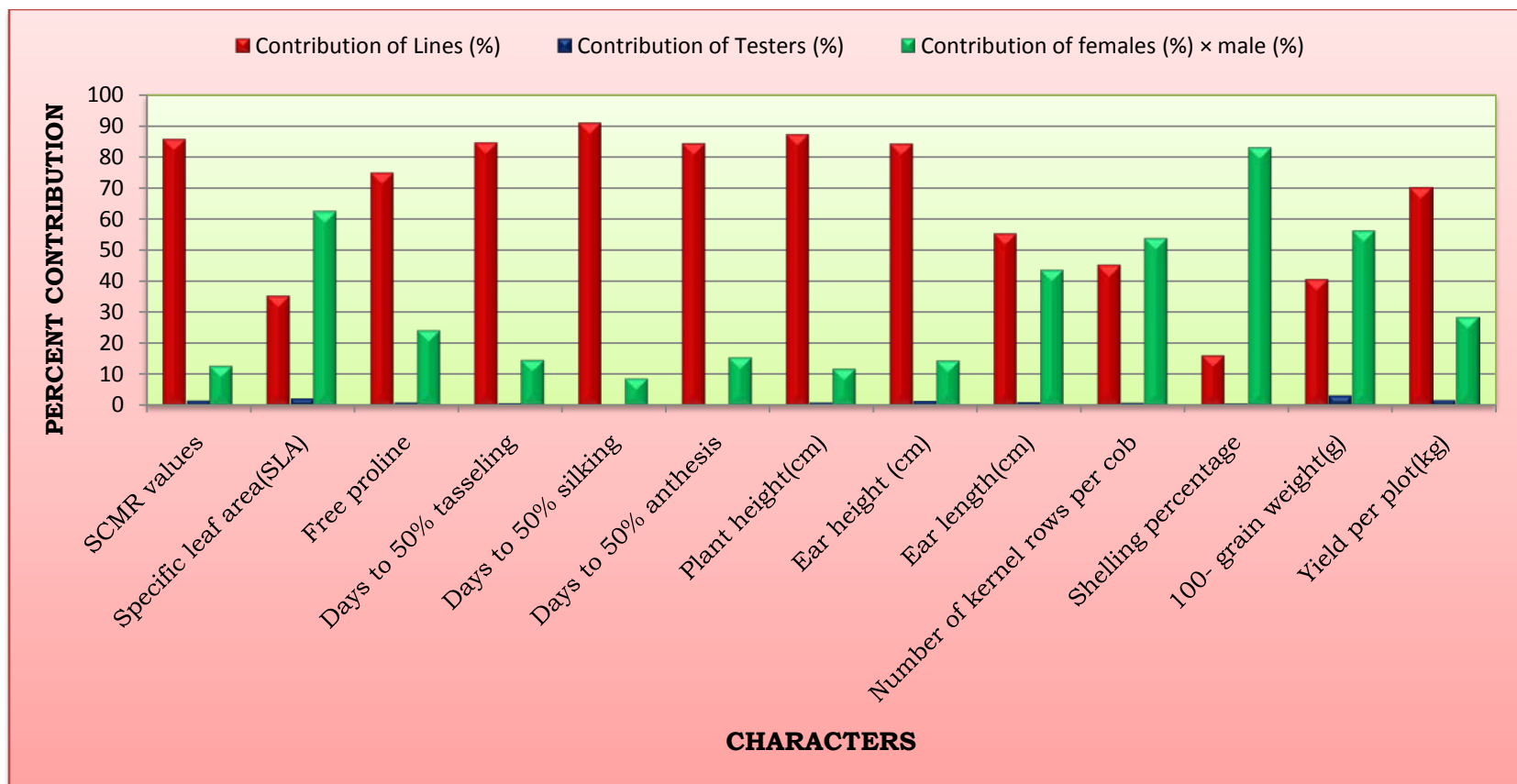


Fig 1: Proportional contribution of lines, testers and their interaction towards variance in hybrids of Maize

Table 4.12: Proportional contribution of lines, testers and interaction of line × tester for various droughts tolerant, yield and yield contributing characters in maize

Sl. no	Characters	Contribution of Lines (%)	Contribution of Testers (%)	Contribution of females (%) × male (%)
1	SCMR values	85.52	1.47	13.01
2	Specific leaf area(SLA)	35.41	2.01	62.58
3	Free proline	74.78	0.91	24.30
4	Days to 50% tasseling	84.42	0.73	14.85
5	Days to 50% silking	90.75	0.33	8.92
6	Days to 50% anthesis	84.11	0.19	15.70
7	Plant height(cm)	87.05	0.90	12.05
8	Ear height (cm)	83.98	1.32	14.69
9	Ear length(cm)	55.27	0.97	43.75
10	Number of kernel rows per cob	45.21	0.80	53.99
11	Shelling percentage	16.32	0.59	83.10
12	100- grain weight(g)	40.70	2.86	56.44
13	Yield per plot(kg)	70.0	1.49	28.52

4.6 Heterosis

The percentage heterosis of thirty six single cross hybrids over mid parent (mid parent heterosis) and over the best checks (standard heterosis) in respect of thirteen traits is presented in Table 4.13. Two commercial hybrids NAH-2049 and NAH-1137 have been used as check 1 and check 2, respectively.

4.6.1 Drought tolerant traits

4.6.1.1 SPAD chlorophyll meter reading (SCMR)

The percentage heterosis over mid parent, commercial check 1 (NAH-2049) and commercial check 2 (NAH-1137) ranged from – 63.44 to 33.54 %, -62.44 to 15.03 % and -63.77 to 10.95 % respectively.

Among thirty six crosses, five crosses exhibited significant standard heterosis over NAH-2049 and two over NAH-1137 in the desirable direction (positive). The crosses exhibited significant standard heterosis over NAH-2049 were 2422 x HKI-164-4-1-3 (15.03 %), SKV-50 x HKI-164-4-1-3 (13.19 %) and over NAH-1137 were 2422 x HKI-164-4-1-3 (10.95 %) and SKV-50 x HKI-164-4-1-3 (9.18 %).

4.6.1.2 Specific leaf area (cm²/g)

Among thirty six crosses almost all single cross exhibited significant positive heterosis over standard check 1 (NAH-2049) but was significant and standard check 2 (NAH-1137). The magnitude of mid parent heterosis ranged from -31.27 to 19.21.

4.6.1.3 Proline content (µg g dry weight⁻¹)

Among thirty six crosses, sixteen and six crosses exhibited significant positive heterosis over commercial check1 and commercial check 2 ranged from -15.60 % to 30.33 % and -14.84 to 38.31 %, respectively.

Table 4.13: Percent heterosis over mid parent (MP) and standard checks (SH) for drought tolerant, yield and yield attributing traits in maize

Single cross hybrids	SCMR values			Specific leaf area(SLA)			Free proline			Days to 50% tasseling		
	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂
1232xHKI-164-4-1-3	-46.40**	-45.91	-47.83	-7.54	-44.67	-48.43	-33.14**	7.62*	14.21	17.0**	4.46**	19.39**
1232xHKI-193-2	-55.09**	-60.60	-62.00	-4.34	-49.28	-52.73	-40.44**	9.66*	16.38	15.90**	0.89**	15.31
1232xCML411	-28.01**	-36.06	-38.33	2.15	-53.22	-56.40	-42.64**	7.72*	14.33	13.73**	3.57**	18.37**
1005x HKI-164-4-1-3	-35.17**	-37.23	-39.45	-11.09	-33.33	-37.87	17.13**	10.33**	17.09	8.74**	0.00**	14.29
1005x HKI-193-2	-34.93**	-45.58	-47.50	-26.34**	-51.87	-55.15	-18.87**	-9.90	-4.38	23.38**	10.71**	26.53**
1005x CML411	-41.28**	-50.25	-52.01	-5.75	-57.73	-60.61	-24.14**	6.64*	13.17	7.62**	0.89**	15.31
1201x HKI-164-4-1-3	-38.73**	-44.41	-46.38	2.04	-55.52	-58.55	-40.68**	30.33**	38.31**	14.29**	0.00	14.29
1201x HKI-193-2	-20.78**	-38.56	-40.74	-21.32**	-75.12	-76.81	-67.85**	-0.89	5.19	21.47**	3.57**	18.37**
1201x CML411	-43.52**	-55.59	-57.17	-1.33	-70.03	-72.07	-59.38**	15.22**	22.28**	12.0**	0.00	14.29
1396x HKI-164-4-1-3	-45.47**	-50.25	-52.01	-19.31*	-76.18	-77.80	-69.61**	0.20	6.34	11.33**	0.89**	15.31
1396x HKI-193-2	-31.34**	-46.41	-48.31	-17.59*	-70.12	-72.16	-63.02**	0.89	7.07	14.14**	0.89**	15.31
1396x CML411	-51.69**	-61.77	-63.12	11.68	-68.40	-70.55	-59.05**	26.46**	34.21**	9.18**	0.89**	15.31
772-2x HKI-164-4-1-3	-63.44**	-62.44	-63.77	6.52	-74.45	-76.19	-70.79**	20.02**	27.38**	5.94**	-4.46**	9.18
772-2x HKI-193-2	-32.71**	-39.73	-41.87	-9.77	-59.75	-62.49	-55.21**	0.09	6.23	12.69**	-0.89**	13.27
772-2x CML411	-42.36**	-47.75	-49.60	-8.81	-26.22	-31.24	-14.48**	-7.23	-1.54	13.59**	4.46**	19.39**
1410-1x HKI-164-4-1-3	5.94	7.18	3.38	-31.27**	-13.45	-19.34	4.16	-7.53	-1.87	4.04*	-8.04**	5.10
1410-1x HKI-193-2	22.01**	7.35	3.54	-27.03**	-5.57	-12.00	10.45**	-3.11	2.83	5.70**	-8.93**	4.08
1410-1x CML411	17.71**	4.84	1.13	-14.88	-60.04	-62.76	-51.20**	5.20*	11.65	-2.97	-12.50	0.00
2422x HKI-164-4-1-3	22.60**	15.03**	10.95**	19.23*	-28.72	-33.57	-18.19**	27.05**	34.84**	-3.03	-14.29	-2.04

Single cross hybrids	SCMR values			Specific leaf area(SLA)			Free proline			Days to 50% tasseling		
	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂
2422x HKI-193-2	21.74**	-1.84	-5.31	-2.52	-18.06	-23.63	-8.48**	2.16	8.43	5.70**	-8.93**	4.08
2422x CML411	3.17	-15.69	-18.68	-4.37	-17.20	-22.83	-3.63	-8.56	-2.95	-0.99	-10.71	2.04
262-55x HKI-164-4-1-3	-4.08	-1.84	-5.31	4.57	-10.47	-16.56	10.49**	10.51**	17.28	-6.28**	-13.39	-1.02
262-55x HKI-193-2	-12.17**	-21.70	-24.48	9.39	-1.25	-7.97	18.36**	13.68**	20.65	0.0	-9.82**	3.06
262-55x CML411	-13.60**	-22.04	-24.80	0.52	-16.62	-22.29	4.45	-4.77	1.06	-3.32*	-8.93**	4.08
634-2x HKI-164-4-1-3	-14.73**	-13.52	-16.59	-28.72**	2.21	-4.74	33.67**	-14.98	-9.76	3.92*	-5.36**	8.16
634-2x HKI-193-2	-5.58	-16.69	-19.65	-1.46	-29.49	-34.29	-10.60**	15.81**	22.91**	6.53**	-5.36**	8.16
634-2x CML411	1.87	-9.02	-12.24	0.08	-11.53	-17.55	17.55**	8.42**	15.06	1.92	-5.36**	8.16
NAI-137-2x HKI-164-4-1-3	18.33**	11.02**	7.09	-28.53**	0.58	-6.27	9.58**	-15.60	-10.43	-1.96	-10.71	2.04
NAI-137-2x HKI-193-2	9.73*	-11.52	-14.65	-23.98**	0.00	-6.80	6.17**	-11.56	-6.14	1.51	-9.82**	3.06
NAI-137-2x CML411	3.58	-15.36	-18.36	-25.11**	-1.54	-8.24	8.70**	-19.76	-14.84	-0.96	-8.04**	5.10
MAI-105x HKI-164-4-1-3	-16.19**	-21.37	-24.15	-3.63	-28.05	-32.95	-13.51**	7.32**	13.90	5.05**	-7.14**	6.12
MAI-105x HKI-193-2	33.54**	7.68*	3.86	-10.12	-56.39	-59.36	-49.05**	-1.48	4.55	6.74**	-8.04**	5.10
MAI-105x CML411	19.51**	-2.34	-5.80	-6.64	3.07	-3.94	25.72**	-6.24	-0.50	-1.98	-11.61	1.02
SKV-50x HKI-164-4-1-3	1.12	13.19**	9.18**	-22.59**	-2.11	-8.77	14.30**	-8.14	-2.51	4.35*	-3.57**	10.20
SKV-50x HKI-193-2	-1378**	-14.86	-17.87	-3.17	-20.56	-25.96	-9.77**	13.19**	20.13	-0.99	-10.71	2.04
SKV-50x CML411	-3.51	-3.67	-7.09	-10.39	-17.10	-22.74	-1.82	-3.48	2.44	-0.47	-6.25**	7.14

Single cross hybrids	Days to 50% silking			Days to 50% anthesis			Plant height (cm)			Ear height (cm)		
	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂
1232xHKI-164-4-1-3	19.25**	6.72**	22.12**	18.27**	5.13**	20.59**	-9.42	-19.68	-21.99	-26.19**	-22.98	-37.06
1232xHKI-193-2	16.98**	4.20**	19.23**	17.24**	1.71**	16.67	-11.77	-20.22	-22.51	-33.33**	-27.95	-41.12
1232xCML411	17.05**	6.72**	22.12**	16.04**	5.13**	20.59**	-24.41**	-30.73	-32.72	-35.34**	-26.71	-40.10
1005x HKI-164-4-1-3	11.42**	2.52**	17.31	6.91**	-0.85**	13.73	-4.62	-2.70	-5.50	-3.47	3.73	-15.23
1005x HKI-193-2	21.10**	10.92**	26.92**	20.75**	9.40**	25.49**	-12.47	-9.16	-11.78	-14.53	-4.97	-22.34
1005x CML411	12.11**	5.04**	20.19**	8.60**	2.56**	17.65*	-26.06**	-22.37	-24.61	-30.67**	-19.25	-34.01
1201x HKI-164-4-1-3	19.81**	6.72**	22.12**	18.63**	3.42**	18.63**	-15.26*	-13.21	-15.71	-16.52*	-13.66	-29.44
1201x HKI-193-2	21.33**	7.56**	23.08**	23.62**	5.13**	20.59**	-32.47**	-29.65	-31.68	-38.55**	-34.16	-46.19
1201x CML411	14.81**	4.20**	19.23**	15.38**	2.56**	17.65*	-25.83**	-21.83	-24.08	-35.91**	-27.95	-41.12
1396x HKI-164-4-1-3	17.21**	5.88**	21.15**	14.69**	3.42**	18.63**	-14.25*	-12.40	-14.92	-16.32*	-12.42	-28.43
1396x HKI-193-2	18.69**	6.72**	22.12**	16.50**	2.56**	17.65*	-32.04**	-29.38	-31.41	-46.70**	-42.24	-52.79
1396x CML411	14.16**	5.04**	20.19**	10.70**	1.71**	16.67	-24.62**	-20.75	-23.04	-42.08**	-34.16	-46.19
772-2x HKI-164-4-1-3	13.89**	3.36**	18.27*	10.48**	-0.85**	13.73	-30.14**	-25.34	-27.49	-45.30**	-38.51	-49.75
772-2x HKI-193-2	18.14**	6.72**	22.12**	16.10**	1.71**	16.67	-30.02**	-23.99	-26.18	-43.32**	-34.16	-46.19
772-2x CML411	21.82**	12.61**	28.85**	19.63**	9.40**	25.49**	-26.13**	-18.87	-21.20	-28.90**	-13.66	-29.44
1410-1x HKI-164-4-1-3	9.43**	-2.52**	11.54	8.74**	-4.27**	9.80	-1.76	-2.43	-5.24	10.43	11.80	-8.63*
1410-1x HKI-193-2	7.11**	-5.04**	8.65	9.45**	-5.98**	7.84	4.27	5.12	2.09	9.47	14.91	-6.09**
1410-1x CML411	0.0	-9.24*	3.85	-0.95	-11.11	1.96	-3.29	-1.08	-3.93	1.97	12.42	-8.12**
2422x HKI-164-4-1-3	1.89	-9.24*	3.85	0.0	-11.97	0.98	-7.31	-4.31	-7.07	-19.78**	-9.32	-25.89

Single cross hybrids	Days to 50% silking			Days to 50% anthesis			Plant height (cm)			Ear height (cm)		
	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂
2422x HKI-193-2	7.11**	-5.04**	8.65	7.46**	-7.69**	5.88	-6.80	-2.16	-4.97	-0.53	16.15	-5.08**
2422x CML411	1.85	-7.56**	5.77	0.0	-10.26**	2.94	-8.12	-2.43	-5.24	-8.91	11.18	-9.14*
262-55x HKI-164-4-1-3	1.37	-6.72**	6.73	-3.26**	-11.11	1.96	0.52	4.31	1.31	-1.08	13.66	-7.11**
262-55x HKI-193-2	0.92	-7.56**	5.77	1.90	-8.55**	4.90	-0.38	5.12	2.09	-3.14	14.91	-6.09**
262-55x CML411	1.35	-5.04**	8.65	-0.46	-6.84**	6.86	-4.29	1.89	-1.05	-15.79*	4.35	-14.72
634-2x HKI-164-4-1-3	5.56**	-4.20**	9.62	5.66**	-4.27**	9.80	7.10	7.82	4.71*	9.52	14.29	-6.60**
634-2x HKI-193-2	6.98**	-3.36**	10.58	8.21**	-4.27**	9.80	-7.37	-5.12	-7.85	-10.34	-3.11	-20.81
634-2x CML411	3.64*	-4.20**	9.62	3.70**	-4.27**	9.80	7.93	11.86*	8.64**	2.47	16.15	-5.08**
NAI-137-2x HKI-164-4-1-3	0.0	-9.24	3.85	2.86*	-7.69**	5.88	5.35	8.89	5.76**	-5.06	4.97	-14.21
NAI-137-2x HKI-193-2	3.26*	-6.72**	6.73	4.39**	-8.55**	4.90	3.59	8.89	5.76**	-2.72	11.18	-9.14*
NAI-137-2x CML411	1.82	-5.88**	7.69	2.80*	-5.98**	7.84	7.48	14.29*	10.99**	10.65	32.30	8.12**
MAI-105x HKI-164-4-1-3	6.10**	-5.04**	8.65	7.77**	-5.13**	8.82	-0.95	-1.62	-4.45	10.70	12.42	-8.12**
MAI-105x HKI-193-2	5.66**	-5.88**	7.69	9.45**	-5.98**	7.84	4.53	5.66	2.62	2.65	8.07	-11.68
MAI-105x CML411	4.15*	-5.04**	8.65	-0.95	-11.11	1.96	6.98	9.43*	6.28**	15.17*	27.33	4.06**
SKV-50x HKI-164-4-1-3	2.73	-5.04**	8.65	2.78*	-5.13**	8.82	4.05	10.78*	7.59**	9.73	26.09	3.05**
SKV-50x HKI-193-2	-0.46	-8.40**	4.81	-1.42	-11.11	1.96	-1.87	6.20	3.14	2.62	21.74	-0.51**
SKV-50x CML411	-0.89	-6.72**	6.73	-0.91	-6.84**	6.86	3.69	13.48**	10.21**	3.76	28.57	5.08**

Single cross hybrids	Ear length (cm)			Number of kernel rows per cob			Shelling percentage		
	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂
1232xHKI-164-4-1-3	-8.40**	-18.92	-2.60	-0.34	5.76	-11.71**	-1.22	6.55	3.88**
1232xHKI-193-2	13.40**	-1.62**	18.18	-7.94**	-8.27	-23.42	-3.68	4.46	1.84**
1232xCML411	-9.55**	-18.11	-1.62	-19.33**	-21.94	-34.83	1.95	6.89*	4.21**
1005x HKI-164-4-1-3	-12.75**	-23.24	-7.79	-8.47**	-2.88	-18.92	-0.76	5.65	3.00*
1005x HKI-193-2	7.21**	-7.57**	11.04	30.32**	29.86**	8.41**	-2.62	4.78	2.15*
1005x CML411	-23.42**	-31.08	-17.21	8.55**	5.04	-12.31**	-1.54	1.84	-0.72
1201x HKI-164-4-1-3	-33.23**	-42.70	-31.17	-8.09**	-10.07	-24.92	-15.51**	1.42	-1.12
1201x HKI-193-2	-14.47**	-28.11	-13.64	20.87**	10.43	-7.81**	-17.79**	-0.85	-3.34
1201x CML411	-4.31*	-15.95	0.97	33.74**	18.35	-1.20**	-13.56**	1.13	-1.41
1396x HKI-164-4-1-3	-2.01	-14.32	2.92	-11.07**	-1.80	-18.02	-4.17	-0.55	-3.05
1396x HKI-193-2	-11.04**	-23.78	-8.44	-2.08	1.80	-15.02	-2.44	1.82	-0.74
1396x CML411	-24.17**	-32.16	-18.51	-28.47**	-27.70	-39.64	13.57**	14.45**	11.58**
772-2x HKI-164-4-1-3	-16.44**	-23.78	-8.44	-9.19**	-5.76	-21.32	-6.09	2.02	-0.54
772-2x HKI-193-2	-12.08**	-21.35	-5.52	-7.95**	-10.43	-25.23	-5.85	2.83	0.25
772-2x CML411	-1.16	-7.84**	10.71	9.33**	3.24	-13.81	-1.68	3.84	1.23
1410-1x HKI-164-4-1-3	1.94	-7.57**	11.04	8.05**	15.83	-3.30**	-2.12	8.62**	5.89**
1410-1x HKI-193-2	-3.95	-14.59	2.60	2.14	2.88	-14.11	-3.19	7.97**	5.26**
1410-1x CML411	-13.41**	-19.73	-3.57	4.78*	2.52	-14.41	-31.23**	-25.76	-27.62
2422x HKI-164-4-1-3	2.35	-11.89**	5.84	4.79*	10.07	-8.11**	-13.44**	-7.33	-9.66

Single cross hybrids	Ear length (cm)			Number of kernel rows per cob			Shelling percentage		
	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂
2422x HKI-193-2	8.97**	-8.11**	10.39	11.68**	10.07	-8.11**	-1.81	5.70	3.05**
2422x CML411	13.19**	-0.27**	19.81	22.56**	17.27	-2.10**	-2.71	1.24	-1.30
262-55x HKI-164-4-1-3	1.74	-12.97*	4.55	-4.79*	3.60	-13.51	-4.94*	1.61	-0.94
262-55x HKI-193-2	5.81**	-11.35**	6.49	6.15**	8.63	-9.31**	-5.84**	1.19	-1.34
262-55x CML411	2.47	-10.27**	7.79	3.44	2.88	-14.11	0.85	4.73	2.11**
634-2x HKI-164-4-1-3	20.43**	5.95**	27.27	13.67**	13.67	-5.11**	-1.31	3.63	1.03
634-2x HKI-193-2	7.21**	-7.57**	11.04	7.69**	0.72	-15.92	-2.03	3.45	0.85
634-2x CML411	10.51**	-0.54**	19.48	14.29**	3.60	-13.51	0.73	2.71	0.13
NAI-137-2x HKI-164-4-1-3	4.33*	-5.68**	13.31	4.80*	6.12	-11.41**	-5.32*	1.54	-1.01
NAI-137-2x HKI-193-2	1.52	-10.00**	8.12	35.86**	28.78	7.51**	-4.43*	3.06	0.47
NAI-137-2x CML411	-14.62**	-21.08	-5.19	34.64**	23.74	3.30**	-1.01	3.17	0.58
MAI-105x HKI-164-4-1-3	7.08**	-5.95**	12.99	3.75	9.35	-8.71**	-3.96	1.88	-0.67
MAI-105x HKI-193-2	17.43**	1.08**	21.43	1.82	0.72	-15.92	-3.91	2.48	-0.09
MAI-105x CML411	-0.75	-10.81**	7.14	6.37**	2.16	-14.71	6.45**	9.70**	6.94**
SKV-50x HKI-164-4-1-3	-3.41	-15.68	1.30	-1.22	2.16	-14.71	-5.33*	3.22	0.63
SKV-50x HKI-193-2	-2.05	-16.22	0.65	0.93	-2.16	-18.32	-6.38**	2.60	0.02
SKV-50x CML411	7.11**	-4.32**	14.94	23.90**	16.55	-2.70**	-3.09	2.71	0.13

Single cross hybrids	100-grain weight (g)			Yield per plot (kg)		
	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂
1232xHKI-164-4-1-3	3.39	-17.57	-6.15	-39.57**	-20.65	-15.12
1232xHKI-193-2	23.21**	-6.76	6.15	-52.38**	-17.39	-11.63
1232xCML411	-8.33**	-25.68	-15.38	-31.71**	-67.39**	-65.12
1005x HKI-164-4-1-3	5.08*	-16.22	-4.62	22.50	-51.09*	-47.67
1005x HKI-193-2	1.79	-22.97	-12.31	-18.18	-19.57	-13.95
1005x CML411	-21.67**	-36.49	-27.69	-18.75	-16.30	-10.47
1201x HKI-164-4-1-3	-7.81**	-20.27	-9.23	-34.55**	-22.83	-17.44
1201x HKI-193-2	-31.15**	-43.24	-35.38	-74.58**	9.78*	17.44
1201x CML411	-9.23**	-20.27	-9.23	-36.17	-28.26	-23.26
1396x HKI-164-4-1-3	-30.51**	-44.59	-36.92	-72.58**	-7.61	-1.16
1396x HKI-193-2	-23.21**	-41.89	-33.85	-71.21**	-51.09	-47.67
1396x CML411	15.0**	-6.76	6.15	-59.26**	-17.39	-11.63
772-2x HKI-164-4-1-3	-18.33**	-33.78	-24.62	-73.15**	22.52*	28.34**
772-2x HKI-193-2	-24.56**	-41.89	-33.85	-65.61**	16.30*	24.42**
772-2x CML411	16.39**	-4.05**	9.23	-8.27	-8.70	-2.33
1410-1x HKI-164-4-1-3	-10.94**	-22.97	-12.31	2.10	-41.30	-37.21
1410-1x HKI-193-2	14.75**	-5.41**	7.69	0.66	-64.13	-61.63
1410-1x CML411	-3.08	-14.86	-3.08	-52.76**	-6.52	0.00
2422x HKI-164-4-1-3	13.11**	-6.76**	6.15	-38.36**	-14.13	-8.14

Single cross hybrids	100-grain weight (g)			Yield per plot (kg)		
	MP	SH ₁	SH ₂	MP	SH ₁	SH ₂
2422x HKI-193-2	15.52**	-9.46*	3.08	-3.90	-33.70	-29.07
2422x CML411	4.84*	-12.16	0.00	18.46*	-27.17	-22.09
262-55x HKI-164-4-1-3	10.53**	-14.86	-3.08	0.0	-18.48	-12.79
262-55x HKI-193-2	24.07**	-9.46*	3.08	8.0	-82.61	-81.40
262-55x CML411	22.41**	-4.05**	9.23	4.76	-50.00	-46.51
634-2x HKI-164-4-1-3	10.61**	-1.35**	12.31	33.86**	-34.78	-30.23
634-2x HKI-193-2	0.0	-14.86	-3.08	-33.33**	-7.61	-1.16
634-2x CML411	-2.99	-12.16	0.00	36.94**	-14.13	-8.14
NAI-137-2x HKI-164-4-1-3	-7.58**	-17.57	-6.15	2.99	21.74**	30.23**
NAI-137-2x HKI-193-2	3.17	-12.16	0.00	-0.57	29.30**	37.22**
NAI-137-2x CML411	-8.96**	-17.57	-6.15	11.26	-31.52	-26.74
MAI-105x HKI-164-4-1-3	-20.31**	-31.08	-21.54	-18.80**	11.96*	19.77
MAI-105x HKI-193-2	13.11**	-6.76**	6.15	-53.19**	-25.00	-19.77
MAI-105x CML411	3.08	-9.46*	3.08	47.01**	24.57**	36.12**
SKV-50x HKI-164-4-1-3	26.23**	4.05**	18.46	8.22	-30.43	-25.58
SKV-50x HKI-193-2	8.62**	-14.86	-3.08	-20.78**	-21.74	-16.28
SKV-50x CML411	8.06**	-9.46	3.08	3.08	-47.83	-44.19

The top three crosses which exhibited significant positive standard heterosis over NAH-2049 were 1201 x HKI-164-4-1-3 (30.33 %), 2422 x HKI-164-4-1-3 (27.05 %) and 1396 x HKI-193-2 (26.46 %) and over NAH-1137 were 1201 x HKI-164-4-1-3 (38.31 %), 2422 x HKI-164-4-1-3 (34.84 %) and 1396 x CML-411 (34.21 %).

4.6.2 Yield and yield attributing traits

4.6.2.1 Days to 50 per cent tasseling

The percentage heterosis over mid parent, commercial check 1 (NAH-2049) and commercial check 2 (NAH-1137) ranged from -6.28 to 23.38%, -14.29 to 10.71 %, and -2.04 to 26.53 %, respectively.

Top three crosses which exhibited significant standard heterosis over NAH-2049 in the desirable direction (negative) are 2-62-55 x HKI-193-2 (-9.82 %), NAI-137-2 x HKI-193-2 (-9.82 %) and 2422 x HKI-193-2 (-8.93 %) and no single cross exhibited significant standard heterosis over NAH-1137 in desirable direction (negative).

4.6.2.2 Days to 50 per cent silking

Among 36 crosses, no crosses exhibited significant negative heterosis over the mid parent and the magnitude of which ranged from - 0.89 to 21.82 %. The magnitude of heterosis over commercial check 1 and commercial check 2 ranged from -9.24 to 12.61 % and 3.85 to 28.85 % respectively.

Twenty crosses exhibited significant negative standard heterosis over NAH-2049 of which 1410-1 x CML-411 (-9.24 %), 2422 x HKI-164-4-1-3 (-9.24 %) and SKV-50 x HKI-193-2 (-8.40%) are early to silk. Contrary to this none showed significant negative heterosis over NAH-1137.

4.6.2.3 Days to 50 per cent anthesis

The magnitude of heterosis over mid parent, standard check1 (NAH-2049) and standard check 2 (NAH-1137) ranged from -3.26 to 23.62%, -11.11 to 9.4 % and – 0.98% to 25.49 %, respectively.

Among 36 crosses, 18 crosses exhibited significant standard heterosis in the desired direction of which crosses *viz.*, 2422 x CML-411 (-10.26 %), 2-62-55 x HKI-193-2 (-8.55 %) and NAI-137-2 x HKI-193-2 (-8.55 %) recorded highest negative standard heterosis over NAH-2049 and no single cross recorded significant negative standard heterosis over NAH-1137.

4.6.2.4 Plant height (cm)

No single cross exhibited significant positive standard heterosis over mid parent. The crosses *viz.*, NAI-137-2 x CML-411 (14.29 %), SKV-50 x CML-411(13.48 %) and 634-2 x CML-411(11.86 %) recorded highest positive standard heterosis over NAH-2049 and the crosses, NAI-137-2 x CML-411 (10.99 %), SKV-50 x CML-411 (10.21 %) and 634-2 x CML-411 (8.64 %) recorded highest standard heterosis over NAH-2049.

4.6.2.5 Ear height (cm)

The magnitude of mid parent heterosis varied from -46.70% to 15.17%. None of the hybrids showed positive heterosis over mid parent significantly. The magnitude of heterosis over commercial check 1 and commercial check 2 ranged from -42.24 to 32.30% and -49.75 to 8.12 %, respectively.

Among 36 crosses, no single cross exhibited significant standard heterosis, significant heterosis in positive direction over NAH-2049. While 4 crosses exhibited significant heterosis in positive direction over NAH-

1137. Out of which which crosses NAI-137-2 x CML-411 (8.12 %) and SKV-50 x CML-411(5.08 %) showed higher heterosis.

4.6.2.6 Ear length (cm)

Among 36 crosses, twelve crosses recorded significant positive heterosis over the mid parent and the magnitude of which ranged from -33.23 to 20.43 per cent.

Among 36 crosses, two crosses, 634-2 x HKI-164-4-1-3 (5.95 %) and MAI -105 x HKI-193-2 (1.08 %) exhibited significant standard heterosis over NAH-2049 which ranged from -42.70 to 5.95 per cent. And a single cross 634-2 x HKI-164-4-1-3 (27.27 %) recorded significant standard heterosis in the positive (desired) direction. and the magnitude ranged from -31.17 to 27.2723.13 per cent.

4.6.2.7 Kernel rows per cob

Mid parent heterosis ranged between -28.47 to 35.86 %. The cross 1005 x HKI-193-2 (29.86 %) recorded significant positive standard heterosis over NAH-2049 and it ranged between -27.70 to 29.86 %. And three crosses, 1005 x HKI-193-2 (8.41 %), NAI-137-2 x HKI-193-2 (7.51 %) and NAI-137-2 x CML-411 (3.30 %) recorded significant heterosis in the positive direction over NAH-1137 and it ranged from -27.70 to 29.86 per cent.

4.6.2.8 Shelling percentage

The mid parent heterosis ranged from -31.23 to 13.57 per cent. On the other hand the standard heterosis over NAH-2049 and NAH-1137 ranged from -25.76 to 14.45 per cent and -27.62 to 11.58 per cent, respectively.

Among 36 crosses, 5 recorded significant standard heterosis over NAH-2049 in desired direction (positive) of which 1396 x CML-411 (14.45 %) and MAI-105 x CML-411 (9.70 %) recorded highest standard heterosis. And eleven crosses exhibited significant standard heterosis over NAH-1137 in positive direction. Of which, 1396 x CML-411 (11.58 %) and MAI-105 x CML-411 (6.94 %) had maximum standard heterosis.

4.6.2.9 Test weight (g)

Mid parent heterosis for this trait ranged between -31.15 to 26.23 per cent. The standard heterosis ranged from -44.59 to 4.05 per cent over NAH-2049 and only one cross, SKV-50 x HKI-164-4-1-3 (4.05 %) recorded significant heterosis in desired direction (positive). No cross showed significant heterosis over NAH-1137 and the magnitude ranged from -36.92 to 18.46 %.

4.6.2.10 Grain yield per plot (kg)

The mid parent heterosis for grain yield per plot ranged between -74.58 to 47.01 per cent. On the other hand, standard heterosis ranged from -83.33 to -3.33 % and -86.61 to -22.32 per cent over NAH-2049 and NAH-1137, respectively. NAI-137-2XHKI193-2 (37.22% and 29.30% over SH1 AND SH2 respectively) and 772-2XHKI-164-4-1-3 (28.34% and 22.52% over SH1 AND SH2 respectively) crosses recorded significant standard heterosis over both the standard checks.

4.6.3 Overall heterotic status of hybrids

In addition to determining the overall general combining ability status of parents and overall specific combining ability status of crosses, it is important to determine overall heterotic status of crosses across the traits. Overall heterotic status of each cross was determined. From the results (Table 4.14), it was evident that 14 out of 36 hybrids had overall high heterotic (H) status and the remaining had overall low (L) heterotic status across the traits.

Table 4.14: Overall heterotic status of single cross maize hybrids

Testers	HKI-164-4-1-3(H)	HKI-193-2(L)	CML-411(H)	Hybrids with high overall heterotic status
Lines				
1232 (H)	(H) 324	(H) 337	(H) 337	3
1005(H)	(L) 228	(H) 269	(H) 304	2
1201(L)	(H) 383	(H) 384	(H) 344	3
1396(H)	(H) 353	(H) 366	(H) 347	3
772-2(L)	(H) 403	(H) 378	(H) 288	3
1410-1(L)	(L) 181	(L) 173	(L) 223	0
2422(L)	(L) 223	(L) 186	(L) 152	0
2-62-55(H)	(L) 177	(L) 201	(L) 159	0
634-2(H)	(L) 122	(L) 241	(L) 146	0
NAI-137-2(L)	(L) 150	(L) 165	(L) 132	0
MAI-105(H)	(L) 231	(L) 200	(L) 112	0
SKV-50(L)	(L) 170	(L) 203	(L) 127	0
Hybrids with high overall heterotic status	4	5	5	14

FINAL NORM : 242.19

(H): Overall high combiner

(L): Overall low combiner

H: Over all high specific combiner

L: Over all low specific combiner

4.7 Reaction to Sorghum downy mildew

4.7.1 Phenotypic screening of parental lines for downy mildew disease

Screening of 12 lines and 3 testers for sorghum downy mildew disease has been done and the results revealed that no parental lines were found resistant to the disease instead two parental lines were susceptible and 13 were highly susceptible (Table 4.15).

4.7.2 Phenotypic screening of hybrids for downy mildew disease

Screening of 36 hybrids for sorghum downy mildew disease has been done and the results revealed that no hybrids were found resistant to the disease instead three hybrids were susceptible and remaining were highly susceptible (Table 4.15).

4.7.3 Validation of SSR markers for downy mildew disease incidence

Twelve lines and three testers were surveyed by using three SSR DNA primers for sorghum downy mildew resistance for validation of markers (Fig 4.15). Following SSR markers bnlgl198 (located on chromosome no. 2), bnlgl1702 and nc013 (present on chromosome no. 6) which were reported to be linked to sorghum downy mildew resistance (Nair, S. K., *et al.*, 2005). The results revealed that all the parental lines were shown susceptible banding pattern and hence, these available results depicted parental lines were found to be susceptible. This Molecular DNA marker assay was in accordance with the phenotypic results.

Table 4.15: PDI of parental lines and hybrids for reaction to sorghum downy mildew disease in maize

Per cent disease	Reaction category	No. of inbreed lines	No. of hybrids
0.0	Immune	0	0
1-10	Resistant	0	0
11-15	Moderately resistant	0	0
16-30	Moderately susceptible	0	0
31-50	Susceptible	3	3
Above 51	Highly susceptible	13	33

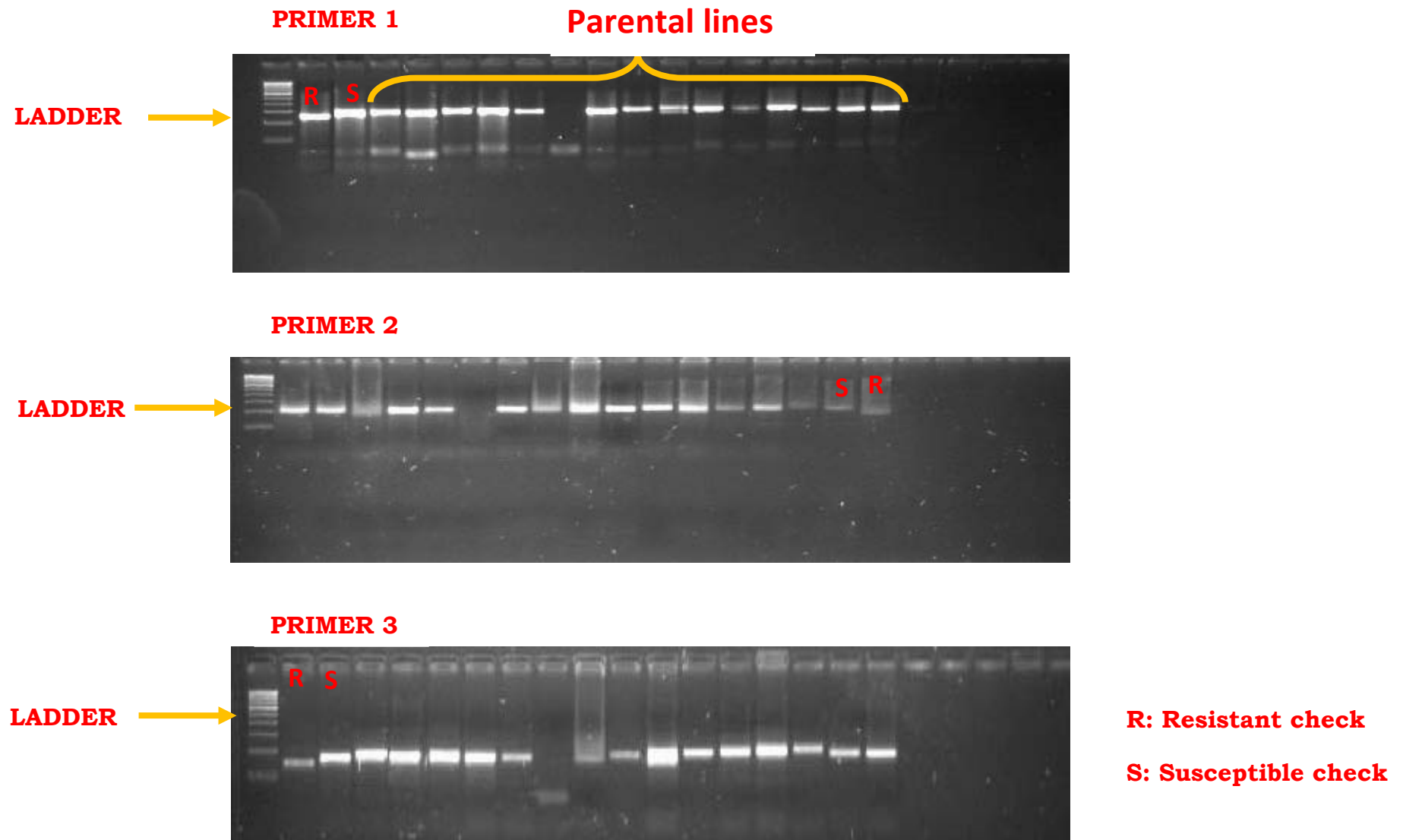


Fig 2: Screening of parental lines for downy mildew disease using SSR markers

V. DISCUSSION

The main objective of plant breeding programme is to develop superior hybrids or high yielding varieties with resistance to important biotic and abiotic stresses. To accomplish this, breeding programme are efficiently planned with prior knowledge of the genetic makeup of economic traits. It is, therefore, necessary to examine the genetic architecture of various traits in relation to breeding worth of the genetic material available.

Nowadays, considerable emphasis is being laid on the development of hybrids and high yielding varieties. The phenomenon of heterosis has attracted the attention of plant breeders due to its conspicuous effect on economic characters, especially grain yield. Heterosis has been successfully exploited in many cross pollinated crops among which maize is the major one. The knowledge of combining ability provides a useful clue for selection of desirable parents to be involved in hybrid development.

In this direction, the present investigation entitled “Heterosis and Combining ability study for drought, seed yield and yield attributes in Maize” was undertaken to identify the best drought and disease tolerant inbreds and hybrids coupled with increased yield and its attributing characters. The results of the present study are discussed in the light of available literature under the following headings.

5.1 Analysis of variance

5.2 Mean performance of parents and crosses

5.3 Combining ability variances and gene action

5.4 General combining ability of parents and overall gca status of parents.

- 5.5 Specific combining ability of hybrids and overall sca status of hybrids.
- 5.6 Proportional contribution of lines, testers and line x tester interaction for the performance of hybrids
- 5.7 Heterosis and Overall heterotic status of hybrids
- 5.8 Inter-relationship of overall gca status, sca status and heterotic status
- 5.9 Reaction to sorghum downy mildew
- 5.10 Selection of desirable lines and hybrids for future use.

5.1 Analysis of variance

The analysis of variance in respect of three drought tolerant parameters and nine yields and yield attributing parameters (Table 4.5) indicated highly significant differences among the parents (lines and testers) for all the characters there by justifying the appropriateness of the material being utilized in the study.

The mean sum of squares for parents was highly significant for all the characters indicating the presence of sufficient variability among parents. Highly significant mean square variances for all the characters were also observed in case of females and also for males except some characters, which indicate the significance of additive variance and significance of mean sum of squares for line x tester indicate the significance of dominance variance.

The mean sum of squares for hybrids was highly significant, indicating the diverse performance of different cross combinations for all traits. The parents versus hybrids mean sum of squares were highly significant for all traits except number of kernel rows per cob, revealing the presence of heterosis due to the significant difference in the mean performance of hybrids and parents.

5.2 Mean performance of parents and crosses

The results on mean performance of parent's revealed substantial variability for all the characters studied. In general, no single line or tester was found to exhibited better mean performance for all the drought tolerant and yield and yield attributing characters under study. The lines, SKV-50, 772-2 and 1410-1 were exhibited better performance for the drought tolerant characters like SCMR value, proline content and specific leaf area, respectively. The line SKV-50 showed higher mean performance for days to 50 % tasselling, days to 50 % silking and ear height. The line 772-2 showed higher mean performance for plant height and ear length. And the lines 1005, 1396 and 1201 have exhibited higher mean performance for the characters like days to 50 % anthesis, number of kernel rows per cob and shelling percentage, respectively. The line 1201 showed lower mean performance for SCMR values, days to 50 per cent tasselling, days to 50 % silking, days to 50 per cent anthesis and number of kernel rows per cob and line NAI-137-2 showed higher mean performance for 100-grain weight and grain yield per plant.

Among the testers, HKI-164-4-1-3 exhibited better mean performance for drought tolerant traits like SPAD chlorophyll meter reading (SCMR) and specific leaf area (SLA) and the tester, HKI-193-2 exhibited better mean performance for proline content. No single tester had exhibited better mean performance for all yield and yield attributing traits like cob length, cob width, number of kernels rows per cob, number of kernels per row, shelling percentage and grain yield per plant. The tester CML-411 exhibited better mean performance for days to 50 % tasselling, days to 50 % silking, days to 50 % anthesis, plant height, ear height, ear length and 100- grain weight. The lines HKI-164-4-1-3 and HKI-193-2 exhibited higher mean performance for number of kernel rows per cob and grain yield per plot, respectively.

In general, mean performance of hybrids was lower than that of parents. Among the hybrids, 2422 x HKI-164-4-1-3, MAI-105 x CML-411 and 1201 x HKI-164-4-1-3 showed higher mean performance for drought tolerant traits like SPAD chlorophyll meter reading (SCMR), proline content and specific leaf area (cm²/g), respectively. Tawat (1992) noticed that the maize cultivars, which were in high proline accumulation group, gave higher grain yield in contrast to maize cultivars that were in the low proline accumulation group.

No single cross was found significant for all yield and yield attributing traits under study. Among the hybrids 2422 x HKI-164-4-1-3 exhibited lower mean performance for days to 50 per cent tasselling, days to 50 per cent anthesis. The cross NAI-137-2 x CML-411 exhibited higher mean performance for plant height and ear height. For ear length, number of kernel rows per cob and shelling percentage, the crosses 634-2 x HKI-164-4-1-3, 1005 x HKI-193-2 and 1396 x CML-411 exhibited better mean performance, respectively. SKV-50 x HKI-164-4-1-3 and NAI-137-2 x HKI-193-2 exhibited better mean performance for 100-grain weight and grain yield per plant, respectively.

5.3 Combining ability variance and gene action

5.3.1 Drought tolerant traits

Among the three drought tolerant characters studied, *viz.*, SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA) and proline content. SCMR values manifested higher degree of SCA variance as compared to GCA variance. Similar results were also reported by Milla and Reich (2007) and Schepers *et al.* (1992). Specific leaf area (SLA) also manifested higher degree of SCA variance as compared to GCA variance. Same trend was observed by Zebarth *et al.* (2002), Tumbo *et al.* (2000) and Costa *et al.* (2001).

5.3.2 Yield and yield attributing traits

Among ten yield and yield attributing traits studied all manifested higher degree of SCA variance as compared to GCA variance, the higher SCA variance indicated the predominance of non additive genetic variance. Similar trend was observed by Mathur and Bhatnagar (1995), Paul and Debanath (1999) for days to 50 per cent tasselling and days to 50 percent silking. Pal *et al.* (1986), Dehghanapour *et al.* (1997) and Petrovic (1998) for plant height, ear height and kernels per cob. Ananth (2004) and Abhishek (2006) also reported similar results for all the yield and yield related characters.

5.4 General combining ability effects of parents and overall gca status of parents

Most often *per se* performance of a parent is not always a true indicator of its potentiality in hybrid combination. Therefore, general combining ability, which is also the breeding value of parent, has proved to be a very useful tool for choosing the parents for hybridization. Among the parents with significant gca effects, the ones with higher magnitude of gca effects were considered as superior to those with lower magnitude.

5.4.1 General combining ability effects for drought tolerant traits

5.4.1.1 SPAD chlorophyll meter reading (SCMR)

The lines, 1410-1 and SKV-50 were found to be good general combiners for higher SCMR values. Thus, they tend to produce hybrids with higher water use efficiency. Therefore, these lines could be used in synthesis of better water use efficient hybrids. On the contrary, the line 1396 and 772-2 were good general combiners for lower water use efficiency.

Among the testers, HKI-164-4-1-3 was found to possess high breeding value for higher water use efficiency (WUE), suggesting its use

as one of the parent to synthesize drought tolerant hybrids. However, the testers CML-411 and HKI-193-2 were found to transmit increasing alleles for delayed water use efficiency (WUE).

5.4.1.2 Specific leaf area (cm²/g)

The gca effects for this important trait varied both in magnitude and direction among both lines and testers. The line NAI-137-2 appeared to transmit increasing alleles for lower SLA with additive effects to their progeny as evident from its significant negative gca effect. Among testers CML-411 appeared as good combiner. Tumbo *et al.* (2000), Costa *et al.* (2001), Zebarth *et al.* (2002) also reported good general combiners for the SLA.

5.4.1.3 Free proline (µg /g dry weight)

Although, seven lines are exhibited significant gca effects. In which only three lines *viz.*, NAI-137-2, 2-62-55 and 634-2 was found to be desirable general combiners. Among testers HKI-164-4-1-3 exhibited significant good gca effects for higher proline content.

5.4.2 General combining ability effects for yield and yield attributing traits

5.4.2.1 Days to 50 per cent tasseling

Among the lines 2422, 2-62-55 and 1410-1 with significant negative gca effects were identified as good general combiner. Whereas, none of the tester was found to be good general combiners for days to 50 per cent tasseling. Hassaballa *et al.* (1980), Sanghi (1982), Desai and Singh (2001) and Rather *et al.* (2009) also identified good general combiners for this trait.

5.4.2.2 Days to 50 per cent silking

The lines 2422 and 2-62-55 among the twelve lines manifested significant gca effect in negative direction. Among testers no single individual exhibited significant gca effect in negative direction. Najera *et al.* (1998), Kumar *et al.* (1999), Desai and Singh (2001) have also showed similar results.

5.4.2.3 .Days to 50 per cent anthesis

The lines 2-62-55 and 2422 exhibited significant negative gca effects. While no testers exhibited desirable gca effects in positive direction. Present findings are in agreement with Singh and Mishra (1996), Amer *et al.* (2002), Reddy *et al.* (2009), Bello *et al.* (2009).

5.4.2.4 Plant height (cm)

The lines NAI-137-2, SKV-50 and 634-2 manifested significant positive gca effects suggesting that they are the good general combiners for plant height. But none of the testers exhibited significant positive gca effect. Kumar *et al.* (1999), Desai and Singh (2001), Amer *et al.* (2002), Singh and Jha (2004) reported predominant role of gca effects for this trait.

5.4.2.5 Ear height (cm)

Among the lines SKV-50 and NAI-137-2 exhibited positive gca effects for the ear height and no tester has recorded significant positive gca effect. Yield is positively correlated with ear height as reported by Ananth (2004), Singh and Jha (2004) and Rather *et al.* (2009).

5.4.2.6 Ear length (cm)

Genotype 634-2, MAI-105 and 2422 among the lines and a tester HKI-193-2 manifested significant positive gca effects suggesting that they are the good general combiners for ear length. Vasal *et al.* (1992), Desai

and Singh (2001), Singh and Jha (2004), Reddy *et al.* (2009), Rather *et al.* (2009) also reported good general combiners for this trait.

5.4.2.7 Number of kernels rows per cob

Among the lines NAI-137-2 and 2422 exhibited positive gca effects for kernel rows per cob. While, the tester HKI-193-2 indicated high utility in the breeding programme as suggested from their significant positive gca effects. Pal and Prodhan (1994), Dehghanapour *et al.* (1997), Kumar *et al.* (1998) Ananth (2004), Singh and Jha (2004) and Abhishek (2006) also reported good general combiners for this trait.

5.4.2.8 Shelling percentage

Among the lines 1232 and 1396 exhibited positive gca effects for the test weight indicated high utility in the breeding programme. While none of the tester exhibited significant positive gca effect for this trait. Mathur *et al.* (1998), Mohamed *et al.* (1993), Desai and Singh (2001), Amer *et al.* (2002), reported significant gca effect for shelling percentage.

5.4.2.11 Test weight (g)

SKV-50, 2422, 2-62-55 and 634-2 among the lines, with significant positive gca effect were identified as good general combiners. Whereas, the tester CML-411 was found to be good general combiners for test weight among tester. Hence, these lines and testers need to be used in breeding programme to synthesize hybrids with higher test weight. Petrovic (1998), Ananth (2004) and Abhishek (2006) also reported good general combiners for this trait.

5.4.2.12 Yield per plot (kg)

The lines NAI-137-2, 2-62-55 and SKV-50 and a tester, CML-411 were good general combiners for yield per plot as evident from their high

gca effects. Mohamed (1993), Kumar *et al.* (1999), Amer *et al.* (2002), Mohammad Akber *et al.* (2008), also reported good general combiners for this trait.

5.4.3 Overall gca status of parents

Six out of twelve lines and two out of three testers had overall high general combining ability status (H), while the remaining parents had overall general low combining ability status (L) implying that 50 per cent of the lines and testers were high overall general combiners suggesting their ability to transmit additive genes in desirable direction for the traits under study. Therefore, these lines and testers are to be evaluated further to confirm their superiority with respect to their gca effects.

5.5 Specific combining ability of hybrids and overall sca status of hybrids

5.5.1 Specific combining ability effects for drought tolerant traits

Among the hybrids with significant sca effects, the ones with high magnitudes were considered as superior. The hybrids from different combinations of the parents with high/low gca effects are referred as H x H (High x High), H x L (High x Low) and L x L (Low x Low) combinations.

5.5.1.1 SPAD chlorophyll meter reading (SCMR)

The estimates of sca effects varied both in magnitude and direction. 10 crosses exhibited significant positive sca effects. The cross 1232 x CML-411 (H x H) had highest significant sca effects followed by Mai-105 x HKI-193-2 (H x L) and NAI-137-2 x HKI-164-4-1-3 (L x H). The involvement of high combiners in first cross revealed the importance of additive gene action. and high and low combiners in second and third crosses revealed significance of over dominance, epistasis genetic variance and non additive gene action respectively. Zebrath *et al.* (2002) also reported good specific combiner for this trait.

5.5.1.2 The Specific leaf area (cm²/g)

Only a single cross, 634-2 x HKI-164-4-1-3 (H x H) exhibited significant sca effects in desirable direction (negative). The involvement of both high general combiners indicating importance of additive gene action. Milla and Reich (2007) reported good specific combiners for this trait.

5.5.1.3 Free proline (µg /g dry weight)

Among 36 crosses twelve crosses recorded significant sca effects in positive direction. The cross MAI-105 x CML-411 (H x H) registered the highest significant positive sca effects for proline content followed by 772-2 x CML-411 (L x H) and 1410-1 x HKI-193-2 (L x L). Involvement of high combiner revealed the importance of additive gene action in the first cross. In the second and third cross involvement low and low combiners revealed the significance of over dominance, epistasis and additive genetic variance respectively.

5.5.2 Specific combining ability effects for yield and yield attributing traits

5.5.2.1 Days to 50 per cent tasseling

Seven crosses exhibited significant sca effects of which four were in the desirable direction. The promising among them were SKV-50 x HKI-193-2 (L x L), 772-2 x HKI-164-4-1-3 (L x H) and 1005 x HKI-164-4-1-3 (H x H). In the first cross involvement of parents both with low general combining ability indicating the importance of additive genetic variance for this trait. In third cross involvement of both high combiners indicating the importance of additive gene action. Mathur and Bhatnagar (1995), Ananth (2004) and Abhishek (2006) reported important of this trait.

Table 5.1: Top ranking maize hybrids with desirable sca effects for drought tolerant characters

Characters	Cross	sca effects	Type of combination
SCMR values	1232xCML411	4.40**	H X H
	MAI-105x HKI-193-2	4.06**	H X L
	NAI-137-2x HKI-164-4-1-3	3.745**	L X H
	2422x HKI-164-4-1-3	3.62**	L X H
	SKV-50x HKI-164-4-1-3	3.35**	L X H
Specific leaf area(SLA)	634-2 x HKI-164-4-1-3	-26.74**	H X H
	1201 x HKI-193-2	-19.55	L X L
	2422 x CML 411	-18.15	L X H
	1005 x HKI-193-2	-14.94	H X L
	1396 x HKI-164-4-1-3	-14.87	H X H
Free proline	MAI-105x CML411	15.59**	H X H
	772-2x CML411	14.06**	L X H
	1410-1x HKI-193-2	12.47**	L X L
	634-2x HKI-164-4-1-3	6.36**	H X H
	1005x HKI-164-4-1-3	5.92**	H X H

* Significant at P = 0.05 **Significant at P = 0.01

Table 5.2: Top ranking maize hybrids with desirable sca effects for yield and yield attributing Characters

Characters	Cross	sca effects	Type of combination
Days to 50% tasseling	SKV-50 x HKI-193-2	-2.51**	L X L
	772-2 x HKI-164-4-1-3	-1.97*	L X H
	1005 x HKI-164-4-1-3	-1.81*	H X H
	1005 x CML 411	-1.68*	H X H
	1232 x HKI-193-2	-1.51	H X L
Days to 50% silking	772-2 x HKI-164-4-1-3	-2.21**	L X H
	1410-1 x CML 411	-2.21**	L X H
	1005 x HKI-164-4-1-3	-1.88**	H X H
	1232 x HKI- 193-2	-1.25	H X L
	SKV-50 x HKI-193-2	-1.25	L X L
Days to 50% anthesis	1005 x HKI-164-4-1-3	-2.47**	H X H
	1410-1 x CML 411	-2.35**	L X H
	772-2x HKI-164-4-1-3	-2.31**	L X H
	MAI-105 x CML411	-2.18**	H X L
	SKV-50 x HKI-193-2	-1.25	L X L
Plant height (cm)	1005 x HKI-164-4-1-3	13.31	H X H
	1396 x HKI-164-4-1-3	12.81	H X H
	634-2 x CML 411	12.76	H X H
	1201 x HKI-164-4-1-3	12.64	L X H
	1410-1 x HKI-193-2	11.93	L X L
Ear height (cm)	1396 x HKI-164-4-1-3	13.18*	H X H
	NAI-137-2 x CML 411	10.97	L X H
	2422 x HKI-193-2	10.85	L X L
	772-2 x CML 411	10.14	L X H
	1201 x HKI-164-4-1-3	8.68	L X H
Ear length (cm)	1201 x CML 411	2.49**	L X H
	1005 x HKI-193-2	2.16**	H X L
	772-2 x CML 411	1.91**	L X H
	1396 x HKI-164-4-1-3	1.85**	H X H
	1232 x HKI-193-2	1.82**	H X L

Characters	Cross	sca effects	Type of combination
Number of kernel rows per cob	1005 x HKI-193-2	2.46	H X L
	1232 x HKI-164-4-1-3	2.04**	H X H
	1201 x CML 411	1.79**	L X H
	SKV-50 x CML 411	1.64**	L X H
	1396 x HKI-193-2	1.32**	H X L
Shelling percentage	1410-1 x HKI-164-4-1-3	5.19**	L X H
	1410-1 x HKI-193-2	4.53**	L X L
	1396 x CML 411	4.17**	H X H
	2422 x HKI-164-4-1-3	3.02**	L X H
	MAI 105 x CML 411	2.35**	H X H
100- grain weight (g)	772-2 x CML 411	7.24**	L X H
	SKV-50 x HKI-164-4-1-3	4.44**	L X H
	1232 x HKI-193-2	4.32**	H X L
	1410-1 x HKI-193-2	3.99**	L X L
	MAI-105 x HKI-193-2	3.99**	H X L
Yield per plot (kg)	MAI-105 x CML 411	1.29*	H X H
	772-2 x CML 411	1.13**	L X H
	1410-1 x HKI-193-2	1.02**	L X L
	634-2 x HKI-164-4-1-3	0.74**	H X H
	262-55 x HKI-193-2	0.62**	H X L

5.5.2.2 Days to 50 per cent silking

Among 36 crosses six crosses recorded significant sca effects of which three crosses registered significant effects in negative direction. The cross 772-2 x HKI-164-4-1-3 (L x H) registered the highest significant negative sca for 50 per cent silking followed by 1410-1 x CML-411 (L x H) and 1005 x HKI-164-4-1-3 (H x H). Paul and Debanath (1999), Tallei *et al.* (1999), Ananth (2004) and Abhishek (2006) also reported good specific combiners for this important trait.

5.5.2.3 Days to 50 per cent anthesis

Out of thirty six crosses, seven crosses exhibited significant effect in negative direction. This includes 1005 x HKI-164-4-1-3 (H x H), 1410-1 x CML-411 (L x H) and 772-2 x HKI-164-4-1-3 (L x H). In the second and third cross involvement of non additive gene action and in first cross additive gene action were observed. Nass *et al.* (2000), Vacaro *et al.* (2002), Rather *et al.* (2009) reported good specific combiners for days to 50 per cent anthesis.

5.5.2.4 Plant height (cm)

No single cross has recorded significant sca effect in desirable direction. However, the cross, 1005 x HKI-164-4-1-3 (H x H) shown higher sca effect in positive direction.

5.5.2.5 Ear height (cm)

Among thirty six crosses only one cross, 1396 x HKI-164-4-1-3 (H x H) has showed significant sca effect in desirable direction. The cross exhibited additive gene action in inheritance of ear height because this involved high general combiners. The results are in line with Kayalvizhi (2002), Amer. *et al.* (2002), Barakat and Moula *et al.* (2003).

5.5.2.6 Ear length (cm)

Out of seventy crosses, eleven were in the positive direction. Three best specific combiners among those with positive sca effects were 1201 x CML-411 (L x H), 1005 x HKI-193-2 (H x L) and 772-2 x CML-411 (L x H). In all the crosses involved parents with high and low general combining ability for ear length, therefore nonadditive gene action may be imperative in these crosses for the inheritance of ear length. Mathur and Bhatnagar (1995), Ananth (2004) and Abhishek (2006) reported good specific combiners for this important trait.

5.5.2.7 Number of kernels rows per cob

Crosses *viz.*, 1005 x HKI-193-2 (H x L), 1232 x HKI-164-4-1-3 (H x H) and 1201 x CML-411 (L x H) exhibited significant sca effects in positive direction. It was note that very high proportion genetic variance indicating the importance of non-additive gene action in the inheritance of this character which is in agreement with the reports of Pal and Prodhan (1994), Dehghanapour *et al.* (1997), Kumar *et al.* (1998) Ananth (2004) and Abhishek (2006) because these crosses (first and third) involved one parent having good general combining ability and other was low general combiner.

5.5.2.8 Shelling percentage

The crosses, *viz.*, 1410-1 x HKI-164-4-1-3 (L x H), 1410-1 x HKI-193-2 (L x L) and 1396 x CML-411 (H x H) were identified as top three specific combiners for shelling percentage among six crosses showing positive sca effects. The first cross involved one parent with good general combining ability and other with low general combining ability, therefore non additive gene action may be imperative in these crosses in making it good specific combiner and in the second cross it was showing the involvement of over dominance and epistasis and in third cross there is a additive gene action in the inheritance of shelling percentage. Ananth

(2004) and Abhishek (2006) reported the importance of non additive variance for inheritance of this trait.

5.5.2.9 100- grain weight (g)

Among thirteen crosses *viz.*, 772-2 x CML-411 (L x H), SKV-50 x HKI-164-4-1-3 (L x H) and 1232 HKI-193-2 (H x L) were identified as top specific combiners for this trait among crosses showing positive sca effects. It was interesting to note that all the crosses indicating the involvement of non additive gene action because these crosses involved one parent having good general combining ability and other was low general combiner. Kumar *et al.* (1999), Nass *et al.* (2000), Srdic *et al.* (2007), Muhammad Akbar *et al.* (2008) also identified good specific combiners for test weight.

5.5.2.12 Grain yield per plot (kg)

Among thirty crosses, eleven crosses were in the positive direction. The crosses *viz.*, MAI-105 x CML-411 (H x H), 772-2 x CML-411 (L x H) and 1410-1 x HKI-193-2 (L x L) were top three specific combiners in the desirable direction. The first cross showing the additive gene action for this trait. In second cross non-additive gene action may be imperative and In the third cross involvement of parents both with low general combining ability indicated the importance of over dominance and epistasis for this trait. Murthy (1997), Ananth (2004) and Abhishek (2006) reported that grain yield per plot was predominantly governed by non-additive gene action.

5.5.3 Overall specific combining ability status

As observed for gca effects, none of the crosses were found to be good specific combinations for all the traits studied. Hence, to determine the sca status of crosses across all the characters it becomes important to determine the crosses possessing good sca values across the traits.

Table 5.3: Distribution of heterotic crosses in relation to overall gca, sca of parent and crosses in maize

Parental gca	No. of crosses under category	No of crosses with high overall sca effect	No. of crosses with high heterotic
H × H	12	6	5
H × L	6	4	3
L × H	12	4	4
L × L	6	3	2

Table 5.4: Best single cross maize hybrids for grain yield

Sl. no	Cross name	Grain yield (kg/plot)	Per cent increase over check (SH₁)	Per cent increase over check (SH₂)
1	NAI- 137-2 X HKI-164-4-1-3	4.35	-22.32	-3.33
2	NAI- 137-2 X HKI-193-2	4.30	-23.21	-4.44
3	MAI-105 X CML 411	4.30	-23.21	-4.44
4	634-2 X HKI-164-4-1-3	4.25	-24.11	-5.56
5	NAI-137-2 X CML-411	4.2	-25.00	-6.67
6	262-55 X HKI-193-2	4.05	-27.68	-10.00
7	SKV-50 X HKI-193-2	3.95	-29.46	-12.22
8	2422 X CML-411	3.85	-31.25	-14.44
9	634-2 X CML-411	3.80	-32.14	-15.56
10	1410-1 X HKI-193-2	3.80	-32.14	-15.56
11	NAH-2049 (Nithyashree)	5.6	-	-
12	NAH-NAH-1137(Hema)	4.5	-	-

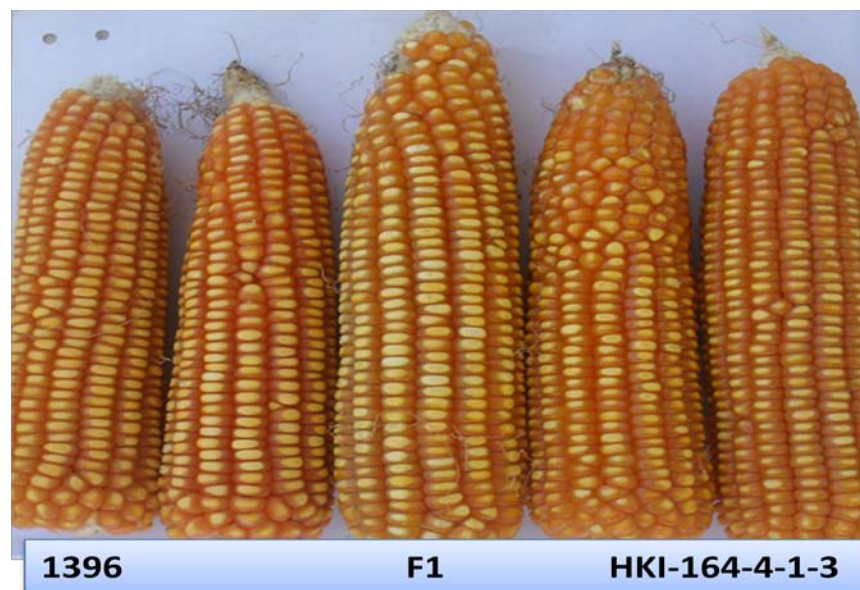
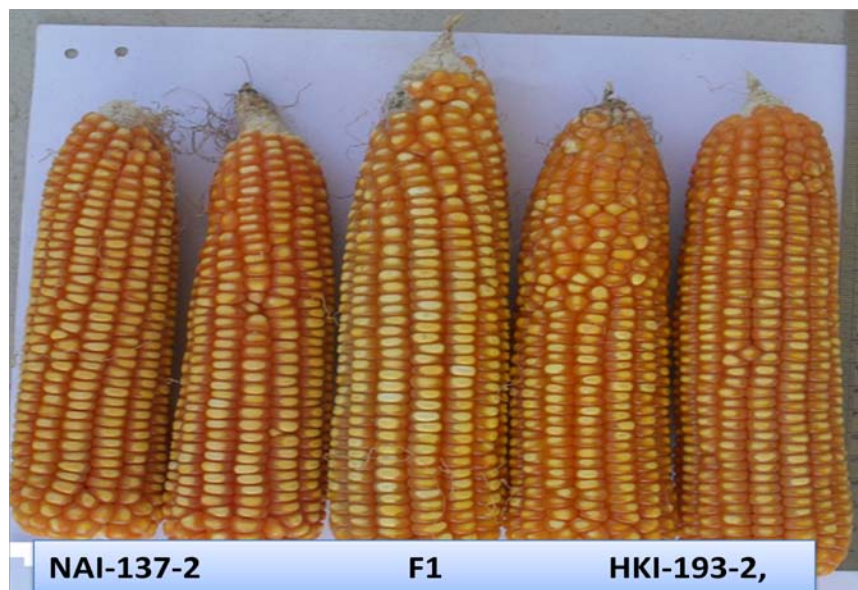


Plate 2: Best single cross Maize hybrids for grain yield

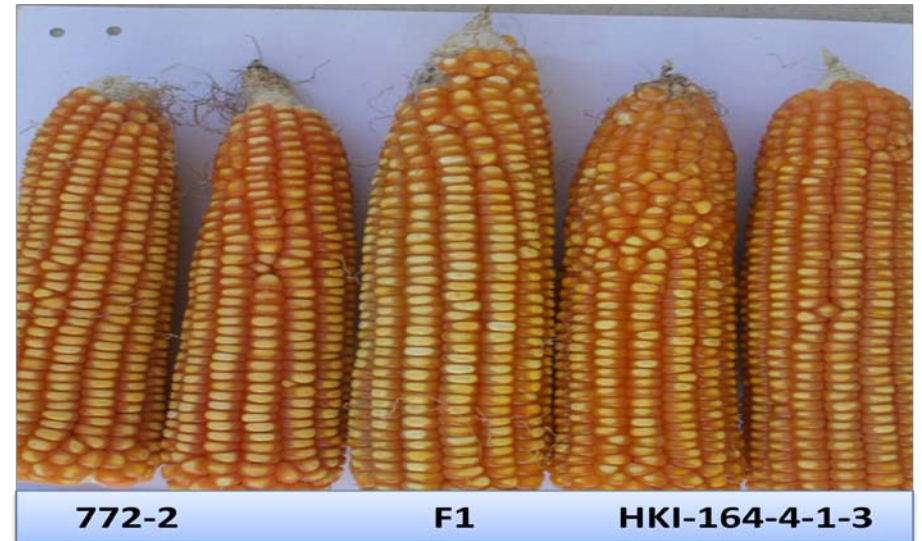


Plate 2: Best single cross Maize hybrids for grain yield

Hence, the method explained by Arunachalam and Bandopadyaya (1979) and modified by Mohan Rao *et al.* (2004) was used to determine the sca status of crosses across all the traits.

Sixteen out of 36 hybrids had high overall specific combining ability status, implying that 44 per cent of the hybrids were high overall specific combiners. Based on overall sca effects, the crosses were classified into H × H (both the parents in a cross with high overall gca status), H × L (one parent with high overall gca status and other parent with low overall gca status) and L × L (both the parents in a cross with low overall gca status). Those hybrids with H × H showed the involvement of additive gene action and H × L showed the involvement of non additive gene action and L × L showed the involvement of over dominance and epistasis.

5.6 Proportional contribution of lines, testers and line x tester interaction for the performance of hybrids

From the results it was evident that per cent contribution of lines depicting to contribute to the bulk of the variation observed in hybrids which was higher for two drought tolerant characters and eight yield and yield attributing traits and percent contribution of line x tester interaction was higher for specific leaf area and yield attributes like number of kernel rows per cob, shelling percentage and 100-garin weight. Per cent contribution of testers appeared to contribute lesser of the variation observed in the hybrids. (Fig 5.1)

Lines have an important role in the variation among the hybrids, while selecting the inbred lines, emphasis needs to be given to the lines which are to be used as female parent. However, the same thing cannot be done with respect to lines and tester interaction as it is not under the breeder's control, but it depends on the particular way in which the lines

and testers interact. It also depends on the environment in which the hybrids are grown. Therefore utmost care needs to be taken while selecting the inbred lines to be used as females for hybridization.

5.7 Heterosis

5.7.1 Heterosis for drought tolerant traits

5.7.1.1 SPAD chlorophyll meter reading (SCMR)

Seven crosses showed significant mid parent heterosis in the desired direction (positive). Five crosses showed positive heterosis for SCMR than standard check (NAH-2049), while only two crosses which showed positive heterosis for SCMR than standard check (NAH-1137). Earlier workers including Schepers *et al.* (1992), Zebarth *et al.* (2002) also reported highly significant heterotic effects for SCMR.

The crosses, which exhibited significant heterosis, were obtained from parents with good general combining ability for drought tolerance. Hence, it is suggested that these hybrids will serve as useful genetic material for development of high water use efficient (WUE) parents by selection in advanced generations.

5.7.1.2 Specific leaf area (cm²/g)

Among thirty six crosses no single cross exhibited significant negative heterosis over standard check 1 (NAH-2049) and standard check 2 (NAH-1137). But the importance of expression of negative heterosis for this trait was reported by Milla and Reich (2007).

5.7.1.3 Free proline (µg /g dry weight)

Among thirty six crosses, seventeen and six crosses exhibited significant positive heterosis over commercial check 1 (NAH-2049) and commercial check 2 (NAH-1137).

Table 5.5: Top ranking maize hybrids with desirable standard heterosis status for drought tolerant traits with their respective yield.

Characters	Crosses	Grain yield (kg/plot)	% standard heterosis over NAH-2049	% standard heterosis over NAH - 1137	Type of cross
SPAD Chlorophyll meter reading	772-2 x HKI-164-4-1-3	1.0	-62.44	-63.77	L X H
	1396 x CML 411	1.10	-61.77	-63.12	H X H
	1232 x HKI-193-2	2.10	-60.60	-62.0	H X L
	1201 x CML 411	1.50	-55.59	-57.17	L X H
Specific leaf area (cm²/g)	1396 x HKI-164-4-1-3	0.85	-76.18	-77.80	H X H
	1201 X HKI-193-2	0.75	-75.12	-76.81	L X L
	772-2 x HKI-164-4-1-3	1.0	-74.45	-76.19	L X H
	1396 x HKI-193-2	0.95	-70.12	-72.16	H X L
Free proline	1201 x HKI-164-4-1-3	1.80	30.33	38.31	L X H
	2422 x HKI-164-4-1-3	2.25	27.05	34.84	L X H
	1396 x CML 411	1.10	26.46	34.21	H X H
	772-2 x HKI-164-4-1-3	1.0	20.02	27.38	L X H

5.7.2 Heterosis for yield and yield attributing traits

5.7.2.1 Days to 50 per cent tasselling

One cross showed significant mid parent heterosis in the desired direction (negative). Sixteen crosses took less number of days for tasseling than standard check (NAH-2049) while no single cross which took less number of days for tasseling than standard check NAH-1137. Earlier workers including Hassaballa *et al.* (1980), Ananth (2004), Abhishek (2006) also reported highly significant heterotic effects for early anthesis.

The crosses, which exhibited significant heterosis, were obtained from parents with good general combining ability for earliness. Hence, it is suggested that these hybrids will serve as useful genetic material for development of early parents by selection in advanced generations.

5.7.2.2 Days to 50 per cent silking

No single cross expressed significant mid parent heterosis in respect of this trait was expressed in the desired direction (negative). Twenty single individuals were earlier than the check NAH-2049 and no cross were earlier than the checks NAH-1137 in respect of silk development. Bhatnagar *et al.* (1993), Vasal *et al.* (1993), Ganguli *et al.* (1995), Saidaiah *et al.* (2008) also reported highly significant heterotic effects for early silking.

5.7.2.3 Days to 50 per cent anthesis

Eighteen crosses exhibited significant negative heterosis over the standard check NAH-2049 and none exceeded NAH-1137 in desired direction. One cross was significant over the mid parent. The expression of negative heterosis in this trait was also reported by Kalsy and Sharma (1970), Murthy *et al.*, (1981), Ananth (2004) and Abhishek (2006).

Table 5.6: Top ranking maize hybrids with desirable standard heterosis status for yield and yield attributing traits.

characters	Crosses	% standard heterosis over NAH-2049	% standard heterosis over NAH-1137	Type of cross
days to 50 % tasseling	2422 x HKI-164-4-1-3	-14.29	-2.04	L X H
	262-55 x HKI-164-4-1-3	-13.39	-1.02	H X H
	1410-1 x CML 411	-12.50	0.0	L X H
	MAI 105 x CML 411	-11.61	1.02	H X H
days to 50 % silking	1410-1 x CML 411	-9.24	3.85	L X H
	2422 x HKI-164-4-1-3	-9.24	3.85	L X H
	NAI 137-2 x HKI-164-4-1-3	-9.24	3.85	L X H
	SKV 50 x HKI-193-2	-8.40	4.81	L X L
days to 50% anthesis	2422 x HKI-164-4-1-3	-11.97	0.98	L X H
	262-55 x HKI-164-4-1-3	-11.11	1.96	H X H
	MAI-105 x CML 411	-11.11	1.96	H X H
	SKV-50 x HKI-193-2	-11.11	1.96	L X L
Plant height(cm)	NAI-137-2 x CML 411	14.29	10.99	L X H
	SKV 50 x CML 411	13.48	10.21	L X H
	634-2 x CML 411	11.86	8.64	H X H
	SKV-50 x HKI-164-4-1-3	10.78	7.59	L X H
Ear height(cm)	NAI-137-2 x CML 411	32.30	8.12	L X H
	SKV-50 x CML 411	28.57	5.08	L X H
	MAI 105 x CML 411	27.33	4.08	H X H
	SKV-50 x HKI-164-4-1-3	26.09	3.05	L X H
Ear length(cm)	634-2 x HKI-164-4-1-3	5.95	27.27	H X H
	MAI 105 x HKI-193-2	1.08	21.43	H X L
	2422 x CML 411	-0.27	19.81	L X H
	634-2 x CML 411	-0.54	19.48	H X H
Number of kernel rows	1005 x HKI 193-2	29.86	8.41	H X L
	NAI-137-2 x HKI-193-2	28.78	7.51	H X L
	NAI-137-2 x CML 411	23.74	3.30	H X H
	1201 x CML 411	18.35	-1.20	L X H
Shelling per cent age	1396 x CML411	14.45	11.58	H X H
	MAI-105 x CML 411	9.70	6.94	H X H
	1410 x HKI-164-4-1-3	8.62	5.89	L X H
	1410-1 x HKI-193-2	7.97	5.26	L X L
Test weight(g)	SKV 50 x HKI-164-4-1-3	4.05	18.46	L X H
	634-2 x HKI-164-4-1-3	-1.35	12.31	H X H
	262-55 x HKI-164-4-1-3	-4.05	9.23	H X H
	772-2 x CML 411	-4.05	9.23	L X H
Yield per plot(kg)	1201 x HKI-193-2	-83.3	-86.61	L X L
	1396 x HKI-164-4-1-3	-81.11	-84.82	H X H
	1396 x HKI-193-2	-78.89	-83.04	H X L
	772-2 x HKI-164-4-1-3	-77.78	-82.14	L X H

5.7.2.4 Plant height (cm)

None of the crosses exhibited significant positive heterosis over mid parent and five crosses showed positive heterosis over the check NAH-2049 and eight crosses over NAH-1137. Gupta *et al.* (1994), Ganguli *et al.* (1995), Verma and Singh (1996), Saha and Mukherjee (1996), Sidaiah *et al.* (2008) reported good heterosis in desirable direction.

5.7.2.5 Ear height

The study of heterosis indicated that one, none and four among the crosses showed positive mid parent heterosis and standard heterosis over NAH-2049 and NAH-1137, respectively. Heterosis expression for this trait was also reported by many workers like Verma and Singh (1996), Petrovic (1998), Ananth (2004) and Abhishek (2006), Saidaiah *et al.* (2008).

5.7.2.6 Ear length

Out of 36 crosses, twelve crosses showed significant mid parent heterosis in the desired direction (positive). These results were in accordance with those of Verma and Singh (1980), Debnath and Sarkar (1987), Kayalvizhi (2002), Saidaiah *et al.* (2008).

Positive standard heterosis was expressed in two crosses, 634-2 x HKI-164-4-1-3 (5.95 %) and MAI -105 x HKI-193-2 (1.08 %) over NAH-2049 and 634-2 x HKI-164-4-1-3 (27.27 %) showed standard heterosis over NAH-1137. They also showed significant relative heterosis and heterobeltiosis. From this study, the importance of non-additive gene action in the inheritance of ear length was evident as reported earlier by Ananth (2004) and Abhishek (2006).

5.7.2.7 Number of kernel rows per cob

Out of the 36 crosses, 19, 1 and 3 crosses showed significant positive mid parent heterosis, standard heterosis over NAH-2049 and NAH-1137, respectively and this was in line with the findings of Ananth (2004) and Abhishek (2006), who reported the expression of heterosis in this trait.

5.7.2.18 Shelling percentage

Among 36 crosses, 5 crosses showed significant positive standard heterosis over NAH-2049 and eleven crosses exhibited positive standard heterosis over NAH-1137. The relatively less number of crosses with significant sca effects indicates the lower contribution of additive gene action. Verma and Singh (1996), Ling *et al.* (1996), Singh and Jha (2006), Saidaiah *et al.* (2008) also reported highly significant heterotic effects for shelling percentage.

5.7.2.8 Test weight

Significant positive mid parent heterosis was exhibited by 15 crosses and one and none crosses exhibited positive standard heterosis over NAH-2049 and NAH-1137, respectively. Similar expression of heterosis in this character was reported by Petrovic (1998), Ananth (2004) and Abhishek (2006).

5.7.2.10 Grain yield per plot (kg)

Four crosses showed significant positive relative heterosis over mid parent. However, none of the crosses showed positive standard heterosis over NAH-2049 and NAH-1137.

5.7.3 Overall heterotic status of hybrids

As in the case of gca and sca, the magnitude and direction of heterosis varied considerably among the characters and therefore, it was difficult to decide the superiority of a hybrid over standard parent. Hence, to decide whether a hybrid could be considered overall heterotic or not, the method proposed by Arunachalam and Bandyopadhyay (1979), which was modified by Mohan Rao *et al.*, (2004) was used. The results obtained are discussed below.

From the results (Table 4.14) it is clearly evident that, 14 hybrids had high (H) overall heterotic status. Whereas, the remaining 22 hybrids had low (L) heterotic status. The hybrids, 1201 x HKI-193-2, 1201 x HKI-164-4-1-3, 1396 x HKI-193-2, 772-2 x HKI-193-2, 1232 x HKI-164-4-1-3, 1232 x HKI-193-2 and 1232 x CML-411 had highest total score over the final norm.

To summarise, the hybrids involving both parents (male and female parents) having high gca status (H x H) and hybrids involving high gca female and low gca male produced hybrids with overall high heterotic status. Whereas, hybrids involving low gca status female and high gca status male (L x H) and low gca status female and low gca status male (L x L) produced hybrids with overall low heterotic status. This clearly indicates in heterosis breeding, it is always better to have high gca status female as parent or at least one of the parent should be having high gca status. In total, the crosses involving parents with high overall gca status produced hybrids with high overall heterotic status in most of the cases. Similarly crosses involving parents with low overall gca status produced hybrids with low overall heterotic status in most of the time. On the other hand, the combinations involving parents with high and low gca status (H x L or L x H) produces hybrids with high or low overall heterotic status.

5.8 Inter-relationship of overall gca status, sca status and heterotic status

Based on the overall gca effects, the crosses were classified as HH (both the parents of the cross with high overall gca status), HL (one parent with high and the other parent with low overall gca status) and LL (both the parents in a hybrid with low overall gca status). The relationship between overall gca and sca status (Table 4.9 & 4.14) clearly indicated that both the parents with low overall gca status (L x L) expressed low (L) overall sca status and the hybrids with H x H combination expressed high (H) overall sca status. Contrary to this, the hybrids involving high (H) x low (L) gca status expressed high (H) overall sca status in higher frequency of crosses indicating major role of non-additive gene action.

When overall gca status and overall heterotic status was considered, it clearly indicated that the hybrids involving H x H parental combination produced high (H) overall heterotic status, while, L x L parental combination produced low (L) overall heterotic status in the hybrids. This suggested major role of additive gene action or additive x additive interaction in such hybrids. However, the hybrids with H x L or L x H type of parental combination always produced hybrids with high (H) over all heterotic status in most of the cases, which indicated clearly the importance of non-additive gene action in the genetic control of this trait. So these types of hybrid combinations are suitable for heterosis breeding. Whereas, the other combinations of H x H or L x L can be utilized to get useful transgressive segregants in the subsequent generation.

In total, the overall heterotic status depends on the gca status of parents, the best combiners always produced best hybrids.

5.9 Reaction to sorghum downy mildew

Phenotypic screening of parental lines and hybrids has been done and the results revealed that no parental lines and no hybrids found resistant. And validation of SSR markers for downy mildew disease resistance using three reported SSR markers showed that all the parental lines were susceptible which is in conformation with the phenotypic results and these results are reflected in the hybrids that all the hybrids were showed susceptibility for the disease in phenotypic screening.

5.10 Selection of desirable lines and hybrids for future use

Based on the general combining ability effects, among the lines SKV-50 and NAI-137-2 and among the testers HKI-164-4-1-3 were exhibiting better mean performance in desirable direction for drought tolerant traits. Among the lines and testers CML-411 and NAI-137-2 manifested better mean performance for grain yield.

From the present study, ten crosses *viz.*, NAI-137-2 x HKI-193-2, NAI-137-2 x HKI-164-4-1-3, MAI-105 x CML-411 , 634-2 x HKI-164-4-1-3, 2-62-55 x HKI-193-2, NAI-137-2 x CML-411, SKV-50 x HKI-193-2, 2422 x CML-411, 634-2 x CML-411 and 1410-1 x HKI-193-2 were identified as promising single cross hybrids on the basis of yield (Table 19. On the other hand crosses *viz.*, 772-2 x HKI-164-4-1-3, 1396 x CML-411, 1232 x HKI-193-2 and 1201 x CML-411 were identified as the best combinations for drought tolerant traits.

Future line of work

1. Promising cross combinations identified in this study could be further evaluated across locations under drought condition and over seasons to select best promising drought tolerant and high

yielding hybrids for commercial utilization by the farming community.

2. Further the promising single cross hybrids having parental combination of high $\times$ high and high $\times$ low gca effects could be used for the improvement of parental lines for drought tolerant and grain yield characters by selection in advanced generations.

VI. SUMMARY

The present investigation was taken up to identify drought, disease tolerant and high yielding maize inbreds, hybrids and to assess the combining ability, gene action and heterosis in thirty six hybrids generated by crossing twelve drought tolerant lines and three drought susceptible testers in a line $\times$ tester mating design at ZARS, Mandya during kharif 2011. Three drought tolerant traits *viz.*, SPAD Chlorophyll Meter reading (SCMR), Specific leaf area (SLA) and free proline content and Ten yield and yield attributing traits *viz.*, days to 50 per cent tasselling, days to 50 per cent silking, days to 50 per cent anthesis, plant height, ear height, ear length, number of kernel rows per cob, test weight, shelling percentage and yield per plot were recorded. Here under the salient findings of the investigation are summarized below.

- Among the lines SKV-50 and NAI-137-2 and among the testers HKI-164-4-1-3 exhibited better mean performance in desirable direction for drought tolerant traits.
- Among the lines and testers NAI-137-2, HKI-193-2 manifested better mean performance for grain yield, while among hybrids 772-2 $\times$ HKI-164-4-1-3, 1396 $\times$ HKI-164-4-1-3 and 1396 $\times$ CML-411 exhibited better mean for drought tolerant traits.
- The hybrid NAI-137-2 $\times$ HKI-193-2 was found to be better for the grain yield.
- Analysis of variance clearly indicated the presence of significant differences among parents and hybrids for most of the characters.
- Significance of mean sum of squares due to parents v/s crosses indicated the presence of average heterosis.
- Highly significant variance due to line $\times$ tester interaction component indicated the presence of dominance and/or epistatic

gene interaction in the inheritance of all the characters under study.

- The analysis of variance for combining ability revealed higher magnitude of SCA than GCA variance for all the characters.
- The study on the general combining ability effects of parents showed that, six out of twelve lines and two out of three testers had high (H) overall general combining ability status.
- Among the twelve lines NAI-137-2 and 1410-1 were the best general combiners which exhibited high gca effects in desirable direction for drought tolerant traits and the line 2422 and NAI-137-2 were the best general combiner which exhibited high gca effects in desirable direction for yield traits.
- Among the testers (male parents), HKI-193-2 and HKI-164-4-1-3 were the best combiners for most of the drought tolerant and yield traits.
- The hybrids *viz.*, 1232 x CML-411, 634-2 x HKI-164-4-1-3 and MAI-105 x CML-411 were promising with respect to sca effects for drought tolerant traits and the crosses *viz.*, MAI-105 x CML-411, 772-2 x CML-411 and 1410-1 x HKI-193-2 were promising with respect to sca effects for grain yield.
- Two hybrids, 2422 x HKI-164-4-1-3 and 1396 x CML-411 showed positive standard heterosis for all the drought tolerant traits. These crosses are from parents with low x high and high x high overall gca effects.
- Top ranking hybrids with high (H) overall sca/heterosis status for several traits.
- The study clearly established superiority of H x L and H x H combination of crosses and hence when a breeder has to attempt successful hybridization economically it is worthwhile to start with

H × H and H × L combinations for realizing hybrids with high heterotic and sca effects

- The hybrids such as NAI-137-2 x HKI-193-2, NAI-137-2 x HKI-164-4-1-3, MAI-105 x CML-411 , 634-2 x HKI-164-4-1-3, 2-62-55 x HKI-193-2, NAI-137-2 x CML-411, SKV-50 x HKI-193-2, 2422 x CML-411, 634-2 x CML-411 and 1410-1 x HKI-193-2.
- On the other hand crosses *viz.*, 772-2 x HKI-164-4-1-3, 1396 x CML-411, 1232 x HKI-193-2 and 1201 x CML-411 were identified as the best combinations for drought tolerant traits.



Plate 1: General view of experimental plot

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