

Genetic enhancement of maize (*Zea mays* L.) for drought using phenotyping, genotyping and conventional breeding approaches

THESIS



Submitted to the

Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya

In partial fulfilment of the requirement for the degree of

DOCTOR OF PHILOSOPHY

In

GENETICS AND PLANT BREEDING

By

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2023

CERTIFICATE – I

This is to certify that the thesis entitled “**Genetic enhancement of maize (*Zea mays* L.) for drought using phenotyping, genotyping and conventional breeding approaches**” submitted in partial fulfilment of the requirement for the degree of **DOCTOR OF PHILOSOPHY** in **GENETICS AND PLANT BREEDING** of **Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior** is a record of the bona-fide research work carried out by Mr. **PRAMOD KUMAR YADAV** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and Director of Instruction.

No part of the thesis has been submitted for any other degree or diploma or has been published. All the assistance and help received during the course of this investigation has been acknowledged by the scholar.

Place: Gwalior

(Dr. A. K. Singh)

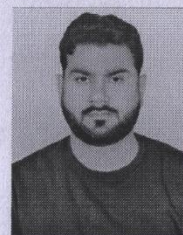
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ACKNOWLEDGEMENT

It is by the lavish and boundless blessing of the almighty that I have been able to complete my studies successfully hitherto and present this humble piece of work, for which I am eternally indebted.

I would like to express my special appreciation and thanks to my advisor Prof. (Dr.) A. K. Singh Director Instruction of R.V.S.K.V.V., Gwalior, you have been a tremendous mentor for me. I would like to thank you for encouraging my research. Your advice on both research as well as on my career have been priceless.

I would like to express my sincere thanks and deep sense honor to my Co-Advisor Prof. (Dr.) M. K. Tripathi, Professor and HOD Department of Genetics and Plant breeding, whose able guidance Endeavour for perfection, keen interest and noble advice become an impetus behind my effort from the very conception to the end of this work.

I would also like to thanks my committee members, Scientist Dr. Sushma Tiwari, Department of Genetics and Plant Breeding, professor Dr. N. S. Bhaduarua, Department of Entomology, professor and HOD Dr. V. B. Singh, Department of Statistics for serving as my committee members even at hardship.

I also wish to extend my thanks to Dr. R. S. Sikarwar, Assistant Professor, Department of Genetics and Plant Breeding for their utmost cooperation and immense help & Guidance during course of study.

I am in dearth of words to express my respect, love and gratitude towards Prof. (Dr.) Arvind Kumar Shukla, Hon'ble Vice-Chancellor, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya, Gwalior, for providing necessary facilities and all possible helps rendered to carry out the present study, encouragement help me to reach this stage. To complete this beautiful journey in the most wonderful way one could have ever done. I won't let this chance go without saying thanks to him.

I would like to thanks Professor Dr. Shailesh Marker. Director Research Services, Sam Higgonbottom Agriculture Science & Technology University, Prayagraj, U.P., India for providing maize inbreed lines to conduct my research work.

I would like to express my special thanks to Dr. Neha Gupta, guest faculty, Department of Plant Molecular Biology and Biotechnology, Dr. R. S. Solanki, Dr. Shailja Chauhan & Dr. Munesh Kushwah Guest Faculty Department of Genetics and Plant Breeding to help me for doing my biochemical work.

I am also thankful to, Shri R.S. Parmar, Mr. Saurabh Thengahe, Mr. Rajesh Pal and Mr. Balkishan Kushwah for their cooperation.

I would like to thank all the non-teaching staff of the Department of Genetics and Plant Breeding for their affectionate encouragement and constant help.

I wish to pay highly indebted thanks from the core of my heart to my respected father Shri. Mukhram Yadav and mother Smt. Sukhwanti Devi and other members of my family my elder brother Mr. Krishna Kumar Yadav, sister-in-law Babita Yadav younger brother Mr. Om Prakash Yadav, Abhishek Yadav, Vivek Yadav, Younger sister Suman Yadav, Neelam Yadav, Niece Kritika Yadav and Nephew Rudransh & Shivansh for their regular encouragement and moral support throughout my study. I am deeply indebted for their invaluable contribution in sustaining my studies with great difficulties.

My sincere thanks are lesser to express my gratitude to my seniors Dr. Dinesh awasthi, Dr. Sanjeev kumar Yadav, Dr. pooja Yadav, Dr. Prashant Singh, Dr. Vivek Kashyap, Dr. Jagdish Patidar, Dr. Pramod Fatehpuri and Dr. Suhel Mehendi. who helped every stage during my Ph.D. course.

It is time to surface out my genuflect love, affectionate gratitude bestowed upon me by my friends Ashish singh, Dr. Sunil Rawat, Dr. Jaya Rathore, for his sincere help to complete my dissertation work.

I would like to extend my sincere thanks to my junior namely Vijay Kashyap, Sunil Yadav, Madhurjit Rathor, Nagmi, Om Prakash Varma, Dhhaleshwar, Vipul

Rajput, Shashank Bhargava, Kiran, Vinod Patel, Rakesh Yadav, Ruchi, Pawan Chokshey, Yashi Singh Tomar, Deepak, Poonam Rajput and Ayushi Soni for their help and support during my dissertation work.

Everyone is not mentioned, but no one is forgotten.

Finally, I want to submit all the best earnings of my life to my parents.

Place: Gwalior

Date: / /2023

(Pramod Kumar Yadav)

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Abbreviations and Acronyms

Abbreviations	Meaning
%	Percentage
&	And
/	Per
⁰ C	Degree Centigrade
ANOVA	Analysis of Variance
C.D.	Critical Difference
cm	Centimeter
d.f.	Degree of freedom
e.g.	For example
<i>et al.</i>	And others
F.(cal)	F calculated
F.(tab)	F table
gm	Gram
<i>i.e.</i>	That is
kg	Kilogram
M.S	Mean of Squares
M.S.S.	Mean Sum of Square
mg	Milligram
S.D.	Standard Deviation
S.Ed.	Standard Error of difference
ml	Milliliter
mm	Millimeter
N.S.	Non-significant
R.B.D.	Randomized Block Design
R.H.	Relative Humidity
S	Significant

S.S.	Sum of squares
No.	Number
Fig.	Figure
Ha	Hectare
bs	Broad sense
Ag.	Agriculture
@	At the rate of
dSm ⁻¹	Deci Siemens per meter
Dist.	District
EC	Electrical conductivity
Gms	Gram
kg ha ⁻¹	Kilogram per hectare
Max.	Maximum
M	Meter
mg kg ⁻¹	Milligram per kilogram
Min	Minimum
Mm	Milli meter
M.P.	Madhya Pradesh
Mt	Metric tones
Viz	Namely
RDF	Recommended dose of fertilizer
RGR	Relative growth rate
RH	Relative humidity
R.V.S.K.V.V.	Rajmata Vijayaraje Scindia Krishi Vishwa Vidhyalaya
Sy.	Symbol
Temp.	Temperature
t ha ⁻¹	Tonnes per hectare
Wt.	Weight

CHAPTER - 1

INTRODUCTION

Maize (*Zea mays* L.) $2n=20$ is one of the most important cereal crops of the world and contributes to food security in the most of the developing countries. Maize is third imperative crop after rice and wheat in the world. It has assumed a place of prominence in Indian agriculture owing to its varied uses *viz.*, human consumption, poultry feed, green fodder, value added products and industrial usage. Globally 67 percent of maize is used for livestock feed, 25 percent for human consumption and rest for industrial purposes. In addition to staple food for human being and quality feed for animals, maize serves as a basic raw material as an ingredient to thousands of industrial products that includes starch, oil, protein, alcoholic beverages, food sweeteners, pharmaceutical, cosmetic, film, textile, gum, package and paper industries *etc.* Corn starch (Approximately 70 percent starch) is a major ingredient in home cooking and in many industrialized food products. Oil content of maize grain is about 4.5 percent, which has a high nutritional quality *i.e.*, it is being considered as the highest Poly Unsaturated Fatty Acid (PUFA), linoleic acid (61.99%). Furthermore, maize contains 9% protein (Zein). Zein has a variety of industrial and food uses. There is a strong possibility to develop hybrids having higher yielding ability and nutritionally superior and industrially important with respect to high starch, protein and oil content. There is no other cereal crop which has immense potential as maize and therefore, maize occupies the unique place as “Queen of cereals” or “Miracle Crop”.

By origin, maize is native to South America. In India maize crop produced in the two seasons, *Rabi* and *Kharif*, the vast majority of the Indian Maize is developed in the *Kharif* season analogize to the *Rabi* season. Seasons of Maize *Kharif* are in June to July and August and harvested in December. These are the maize cropping season in India. The major states for *Kharif* corn farming in India are Andhra Pradesh, Uttar Pradesh, Karnataka, Madhya

Pradesh and Maharashtra. In Madhya Pradesh, It is predominantly cultivated as *Kharif* season crop in Chhindwara, Seoni, Betul, Barwani and Dhar districts of Madhya Pradesh. These districts contributed more than 60 percent and 70 percent of area and production respectively of maize for the state.

In India, it is cultivated on an area of 98 lakh ha with production of 261.4 lakh tones and productivity 2679 kg ha^{-1} (Anonymous, 2016-17), among Indian states Madhya Pradesh and Karnataka has highest area under maize (15% each) followed by Maharashtra (10%), Rajasthan (9%), Uttar Pradesh (8%) and others. In Madhya Pradesh it occupied an area of 8 lakh ha with the production of 9.62 lakh tones and the productivity of less than 2 tones ha^{-1} (Anonymous, 2017). Maize is highly allogamous crop and it has been successfully exploited in the production of hybrids (Venkatesh *et al.*, 2003). Paul and Duara (1991) pointed out that the combining ability gave useful information on the choice of parents in terms of expected performance of the hybrids and their progenies. In India, development of maize hybrids was aimed mainly to capitalize on the expression of heterosis for grain yield. Very less emphasis was given for exploitation of heterosis for quality traits like oil, protein and starch. There is strong possibility to develop maize hybrids which are nutritionally superior and industrially important with respect to high oil, protein and starch content.

Drought is the most pervasive limitation to the realization of yield potential in maize (Edmeades *et al.*, 2001). Average annual global losses due to drought in maize range from 15% in temperate zone to 17% in tropical zone as estimated by empirical methods (Edmeades *et al.*, 2000). During recent years, India has witnessed an erratic pattern of rainfall which resulted into frequent occurrence of drought. Maize crop is vulnerable to monsoon vagaries which suffer severely due to stress at flowering/grain filling stage. Maize is very sensitive to water stress in the period one week before flowering to two weeks after flowering (Grant *et al.*, 1989). Drought during this period results in an easily measured increase in the anthesis silking interval (ASI) as the silk emergence is delayed (Edmeades *et al.*, 2000) and in grain abortion (Boyle *et al.*, 1991). When the drought occurs at 75

percent silking, a yield loss to the extent of 53 percent is noticed (Classon and Shaw, 1970). The extreme susceptibility of maize to drought stress has been attributed to the spatial separation of male and female flowers on the same plant, differential partitioning of assimilates in favour of the tassel *versus* the ear when the plants are stressed at flowering (Edmeades *et al.*, 1993). Limited water availability to the cells of plants can be due to the physical and climatic characteristics of the environment, the soil precipitation, the soil plant relationship, the atmospheric-plant relationship, excessive demand by the plant or any combination of these, obviously, low precipitation is a cause of water limitation (Leith, 1973).

Breeding maize for drought tolerance is important to close the gap between rainfed and well-watered yields. Water-conserving growing practices with limited or complete irrigation play a critical part, but are limited in many parts of the country because of water availability or economic reasons for non-adoption. Escaping drought by manipulating planting date and using early maturing varieties is an effective strategy for the early and latter parts of the growing cycle. While, breeding for drought tolerance it is expected that genetic gain would be more rapid and predictable if desired secondary traits could be identified and selected. It is imperative that while breeding for drought tolerance, morphological and physiological characters which are less sensitive to genotype x environment should be utilized. Besides this, the requirements for selection criteria of physiological traits include high genetic variability, heritability, and easy, accurate and rapid measurement, high correlation with yield and not associated with yield loss under ideal growing condition (Hegeman and Lambert, 1988; Edmeades *et al.* 1999). It is very difficult to separate the physiological and structural responses of plants to environmental condition as the environment with limited water have co-occurring high heat, light or salinity therefore, we need experimental series. Maize with high level of tolerance is characterized by short anthesis-silking interval, prolificacy, small tassel size, erect leaves and high yield under stress condition.

A thorough knowledge of association of characters in a crop species is a pre-requisite for a successful breeding programme. Information on direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection process. The variability for selection and expected genetic advance is largest among single crosses, least in double crosses and intermediate in three-way crosses. The whole of additive, dominance and epistatic components of genetic variation is available for exploitation in single crosses. Single cross hybrids exhibit 40 to 53 percent superiority over open pollinated varieties, while three-way crosses and double crosses exhibit 26 to 33 percent and 20 to 26 percent superiority over open pollinated varieties (OPV's), respectively (Vasal *et al.*, 1995).

Heterosis is the genetic expression of the superiority of a hybrid in relation to its parents. The term heterobeltiosis has been suggested to describe the increased performance of the hybrid over the better parent. It is also modified by the interaction between genotypes and environment. It is a complex genetical phenomenon depending upon the balance of additive, dominance and interaction components as well as the distribution of genes in the parental lines. Heterosis and combining ability is prerequisite for developing good economically viable hybrids of maize. Information on the heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development. Combining ability is one of the most effective tools in deciding the appropriate parents for hybridization especially when a large number of parental lines are available and most promising ones are to be identified on the basis of their ability to give superior hybrids. In order to identify potential cross combinations, it is very important to screen out the parent materials for their genetic diversity and combining ability. Hybrid cultivars have played a vital role in increasing acreage and productivity of maize. Combining ability is the relative ability of a genotype to transmit its desirable performance to its crosses. Combining ability analysis is the rapidest method to understand the genetic architecture of various characters that enable to breeder to design effective breeding plan for other improvement of the existing breeding material.

The gca effects which included additive and additive x additive interactions (Griffing, 1956b; Sprague, 1966) represent fixable genetic variance (Gilbert, 1967). The additive parental effects measured by gca effects are of practical use. On the other hand, sca effects representing dominance and epistatic components would not contribute much to the improvement of often cross-pollinated crops except in cases where commercial exploitation of heterosis is feasible. The crosses involving good general combiners having high sca effects may be utilized for further breeding purpose. Desirable transgressive segregants are also expected to be produced by making a large number of crosses. Jinks and Jones (1958) further suggested that the superiority of many hybrids may not indicate their ability to produce transgressive segregants due to non-fixable genetic effects. Therefore, study of sca effects in segregating generations would be important.

Development of varieties with high yielding potential should be the first step in the direction of up-grading the Maize yield. In order to develop a sound breeding programme to identify such varieties, the knowledge of combining ability together with *per se* performance of parents and hybrids over environments is essential to selection of suitable parents and crosses. Combining ability studies in varietal crosses, thus become very essential to either develop new elite populations for use *per se* or in further breeding programme or to have new varietal hybrids.

Among different abiotic stresses, moisture stress is one of the major constraints in maize productivity. Moisture stress is very common in the areas where maize is pre-dominantly grown under rainfed condition. Most of the world maize area is grown under rainfed conditions and maize is more susceptible to drought than all other cereals (Hall *et al.*, 1981).

The unpredictability of drought, geographically and across seasons, has emphasized the importance of drought tolerance as a maize breeding objective. Breeding for drought tolerance in maize is a complex task, because drought affects the different developmental stages of crop growth.

Drought is the major problem for corn plants and has become a source of dietary threat to food security and human health. Drought stress is directly proportional to climate change. Because of the catastrophic loss of arable land due to drought stress, meeting the need of an overpopulated globe for food, shelter and clothing will be a worrisome concern in the future. The water deficiencies lead to reducing the overall plant growth by lowering photosynthetic activity, hormone production and membrane stability. Lack of water causes the production of reactive oxygen species (ROS) in plants and induces irreversible damage to a metabolic system that ultimately triggers the cell damage.

Many breeders have focused on alleviating the effects of drought at flowering and during grain filling, because maize is most vulnerable to drought at these stages.

The characteristic of maize under drought stress is a delay in silking, resulting in an increase in the anthesis to silking interval (ASI), incomplete or nil fertilization and decrease or nil kernel development (Hall *et al.*, 1981), by evaluating maize under moisture stress during flowering, it is possible to identify maize genotype capable of maintaining a shorter ASI and achieving the high grain yield.

The rapid advancement in molecular marker technology has provided new classes of genetic markers at the DNA level. The advent of DNA based markers has opened up new avenues and uncommon opportunities for biological science in the area of evolutionary studies, plant systematic and more recently in the tagging of genes coding for traits of agronomic importance.

Among the DNA based markers microsatellite or SSR markers are PCR based, genetically co-dominant, robust, reproducible, hyper variable, informative and reasonably easy-to-use. Along with the Single Nucleotide Polymorphisms (SNPs), the SSR markers, which are abundant in maize genome offer significant advantages in DNA fingerprinting, genetic diversity analysis, gene/ QTL mapping and molecular marker-assisted breeding.

Identifying parental material with strong heterosis for yield and obtain genetic parameters are the important steps in the development of new cultivars. It is important to have information about the desirable parental combinations which can represent a high degree of heterotic response. By exploiting heterosis in the F_1 hybrids, production cost could be reduced by increasing yield level and enhancing input use efficiency by Pingali (1997).

Selection of parents is an important step for planning an appropriate hybridization programme. The combining ability analysis furnishes useful information of this aspect. Knowledge of the relative importance of additive and non-additive gene action is essential to a plant breeder. The *per se* performance, gca and sca effects determine the potentiality of parents/crosses for mobilizing them in an efficient breeding programme.

The present investigation is planned on twelve inbred lines of maize. The objectives of the study are:

1. Screening of maize inbred lines and crosses for drought tolerance using physiological and yield responsive traits.
2. To study the GCA and SCA for morpho-physiological, yield and yield attributing traits.
3. To estimate the magnitude of heterosis for various quantitative traits.
4. To asses morphological, biochemical and physiological changes under drought stress.
5. Molecular characterization of inbred lines along with their crosses against drought using gene based molecular markers.

CHAPTER - 2

REVIEW OF LITERATURE

Maize is one of the most important cereals of the world. Exploitation of hybrid has gained much significance in view of its tremendous yield increase and considered as outstanding accomplishment of plant breeding. There is continuous need to evolve new hybrids exceeded the existing hybrids in yield and quality (Dass *et al.*, 2010). Heterosis and combining ability were exploited in maize by many maize breeders. Brief accounts of research carried out and published by previous workers on the studies related to the selected topics are reviewed as under:

2.1 Drought situation

2.2 Morpho-physiological and yield related traits under drought situation

2.3. Heterosis

2.4. Combining Ability

2.5. Biochemical nature of drought tolerance

2.6. Molecular assisted breeding for drought situation

2.1 Drought situation

In India, arid regions are very prone to drought because of which their share in total food production is less. Arid region like eastern Rajasthan drought occurs once in three years and in states like Karnataka and Madhya Pradesh drought occurs once in 5-6 years. Tropical semi-arid regions are characterized by high evapo-transpiration demand and low water holding capacity of soils rendering them more drought susceptible than semi-arid areas of temperate regions. The type drought situation in which crop grown, greatly influence the type of breeding methods should be followed and kind of genotype will be developed to overcome the existing drought situation. There are mainly three drought situations under which crop experience the drought stress during their life cycle.

2.1.1 Agricultural drought

Agricultural drought refers to the shortage of the sufficient water available for a crop at any given stage of its development resulting in impaired growth, wilting and ultimately reduced crop yields (Banziger *et al.*, 2006). This definition looks at the link between meteorological and/or hydrological droughts and agricultural impacts, and focuses more on the vulnerability of the crops at their different growth stages *vis-à-vis* plant-water needs. Drought affecting agriculture is the most prevalent abiotic stress which limits plant growth and productivity worldwide, with devastating socio-economic impacts. It is a major cause of food insecurity for many households as it has been estimated to cause annual maize yield loss of 24 million tonnes in the developing world (FAOSTAT 2010; Edmeades, 2008). Breeding for drought tolerance mainly focuses on this type of drought.

2.1.2 Hydrological drought

Hydrological drought refers to the reduction in precipitation on surface and sub-surface water resources which affects water-reliant activities like irrigation, hydro-electricity generation, fishing and recreational activities such as water rafting (Mutasa, 2010). This also affects the availability of groundwater inducing water stress on communities relying on groundwater for their household needs. River basins often face the brunt of hydrological droughts, though such droughts rarely coincide with meteorological and agricultural droughts. Although climate is the primary contributor to hydrological drought, other factors such as land use, land degradation and dam construction also affect hydrological characteristics of the river basin (Moneo and Iglesias, 2004).

2.1.3 Meteorological drought

Meteorological drought occurs when there is a reduction in expected rainfall supply over a particular period. Meteorological drought is based on the degree of dryness and the length of the dry period. The meteorological definitions are site or region-specific, and measure dryness and rainfall received comparing this

against a given baseline (Moneo and Iglesias, 2004). This type of drought is often based on an internationally accepted 30-year precipitation period.

2.2 Morpho-physiological and yield related traits under drought situation

Drought resistance is a complex trait, expression of which depends on action and interaction of different morpho-physiological and biochemical reactions. When the maize plant is under drought stress, it shows the symptoms like, stunted growth, tip firing, tassel blast, leaf firing in lower leaves, both mild and extreme rolling and wilting of the leaves, silk delay, poor seed set, barrenness, reduced root system and dead plants and ultimately poor yield (Sain *et al.*, 2001).

2.2.1 Plant height

Plant height is influenced by the interaction of environmental conditions and genetic constitution of the plant. Though plant height is genetically controlled, but water stress also plays an important role in its regulation. Severe drought stress in early growing stage affects the length of internodes (Jurgens *et al.*, 1978). Plant height reduction had been reported when crop was subjected to drought stress (Subba Rao, 1992). Reduction in ear height was also reported in maize when subjected to drought (Babu, 1992).

Sain *et al.* (2001) evaluated 160 maize inbred lines and hybrids for drought tolerance and they opined that the morphological traits associated with drought tolerance in maize included plant height, leaf number, leaf area and its senescence. Further they found that plant height was severely affected when irrigation was limited during the knee height stage in majority of the genotypes. Similarly, Dass *et al.* (2001) evaluated 166 genetically diverse lines of maize under different artificially given stress conditions; *viz.*, control, mild, intermediate and severe stresses and among the majority of the genotypes screened they confirmed that plant height was affected severely when irrigation was restricted at knee height stage.

Selmani and Wasson (2003) showed that genotypic differences occur in growth response of maize to drought stress. Characteristic differences in response to

drought stress have also been identified for a range of morphological and physiological characteristics, including leaf number, leaf area and its senescence. They confirmed that plant height was affected severely when irrigation was restricted at knee height stage and leads to a stunted growth.

Liu *et al.* (2004) reported that increase in drought intensity resulted in reduced plant height. This is due to the adaptation of the maize plants to cope with drought stress with the initial effects of drought stress, the maize plants started to divert the assimilates from stem and utilized them for shoot growth in order to increase the absorption of light. Hence, the plant height was affected significantly.

In the experiment of Ahsan *et al.* (2011) highest performance was shown by Q67 tracked by WF-9 and lowest performance was shown by W64SP for fresh shoot length and this in turn total plant height and from this finally they opined overall shoot length was reduced during water stress.

2.2.2 Delay in silking and increase in anthesis silking interval (ASI)

In maize floral development and flowering is greatly affected by drought stress if drought occurs at the stage of flowering. Silk delay has been found to be a primary cause of yield reduction in field condition (Jensen, 1971). Short period of water shortage at flowering stage reduces the fertilization, seed set and grain yield and ear size (Hall *et al.*, 1981).

Edmeades *et al.* (1989) revealed that reduced anthesis-silking interval in maize is caused by increased partitioning of assimilate to the development of ear rather than by changes in phenology of development rate. Drought stress delayed silking and anthesis-dates and reduced grain filling period but little effect on physiological maturity. Delay in silking and anthesis dates and widening of anthesis silking interval was also reported by Ribaut *et al.* (1996) in maize crop.

Ribaut *et al.* (1996) reported that delay in anthesis and silking dates and extending anthesis silking interval (ASI) if drought is imposed at flowering period.

Sain *et al.* (2001) evaluated one hundred and sixty maize inbred lines and hybrids for drought tolerance. Results showed ASI increased during water stress.

Magorokosho *et al.* (2003) noticed that value of ASI may be considered as an indirect selection criterion for improving grain yield under drought stressed conditions.

Meena Kumari *et al.* (2004) reported that under severe stress, the anthesis-silking interval ranged from 3-5 days in drought tolerant inbred lines and 9-17 days in drought sensitive inbred lines.

Saidaiah *et al.* (2008) investigated correlation and path analysis for 11 characters on 40 F₁s of maize, their 14 parents along with two standard checks. Results showed that correlation coefficient of grain yield with anthesis silking interval (ASI) was negative and significant.

Kahiu *et al.* (2013) evaluated KVD2 x CML442 F₂ population and identified 74-80 % of the early flowering genotypes ranging between 49 and 57 days and had an ASI segregation in range of 2 to 10 days. The results showed that ASI and earliness can be combined and selected in the same maize genetic background.

2.2.3 Dry matter production

Dry matter accumulation and distribution is an important factor indicating partitioning efficiency of photosynthetic assimilated. In general, soil moisture determines the distribution and accumulation of dry matter in different plant parts. Further, the moisture stress occurring at various stages ultimately influence the economic yield.

Classen and Shaw (1970) reported maximum reduction in dry matter was due to stress three weeks before 75 percent silking.

Kabra and Rao (1985) noticed that stress during tasseling reduced dry matter and the reduction was more when stress was at knee-high stage and grain formation stage.

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 and observed that the early maturing cultivar was the most drought tolerant with large biomass accumulation in both stress and non-stress environments.

Saeed *et al.* (1998) studied the genotypic response to drought stress in three maize genotypes. Drought during reproductive development caused the maximum reduction (50%) in grain yield of all the three cultivars followed by drought during vegetative development (37 %). Drought during the reproductive development had greater suppressive effect on the physiological determinants like Crop Growth Rate (CGR), average Net Assimilation Rate (NAR) and harvest index (HI) of the three cultivars than that during vegetative development.

Pan *et al.* (2002) reported the stress factors especially drought, negatively affect plant growth and development and causes a sharp decrease of dry matter production.

Shoukofar *et al.* (2011) reported that moisture stress imposed at vegetative growth stage decreases production drop up to 32-28 percent dry matter.

Ahsan *et al.* (2011) evaluated 500 S₁ maize families at seedling stage and they reported that the higher coefficients of variation for fresh shoot and root weight. Among the genotypes maximum performance was shown by B34-2B tracked by WF-9 for fresh shoot weight while, higher performance was shown by Q67 followed by WF-9 for fresh shoot length and from this finally they opined overall shoot length and weight was reduced during water stress.

2.2.4 Grain yield under stress

In different studies conducted by various workers in maize reported that the dry matter production was positively related to grain yield (Donatelli *et al.*, 1992; Krishnan and Natarajan, 1995) reported high positive correlation of grain yield with dry matter production and harvest index. Path analysis revealed that selection on any trait in maize may influence the grain yield only through dry matter production. Further, Petcu and Terbea (1996) reported that the dry matter

accumulation was lower in water stressed roots and leaves than in the control and shoot length was shorter in the water stressed plants than in the control.

Reyes *et al.* (2000) showed that grain yield was negatively and significantly associated with anthesis-silking interval. This relationship suggests that a combination of early lines with a reduced anthesis-silking interval could be used as a good selection criterion for improving the grain yield of maize in drought prone areas.

Khan *et al.* (2001) investigated the effects of water stress on growth and grain yield of maize cultivar YHS-202. The study was comprised of six treatments one control (six irrigations), five, four, three, two and one irrigation only. The data revealed that leaf area, leaf dry weight, stem dry weight and stem diameter decreased significantly with increased water stress.

Campos *et al.* (2006) noticed largest genetic gains for grain yield under conditions of full irrigation and severe flowering stress. ASI and barrenness, especially under stress at flowering, were significantly reduced by selection. Though flowering remains the most susceptible stage to drought in maize, selection has reduced its negative effects and susceptibility during early grain filling.

Hossien *et al.* (2013) reported that plant height and grain yield per ha were decreased under water limitation at grain filling stage. As water stress occurred in reproductive stage leaf number per plant, stem diameter and cob diameter were found non-significant. As, stem diameter during water stress was not declined, this indicates that remobilization of assimilate was not occurred in this condition.

2.2.5 Physiological characters

Crop plants which are subjected to a range of abiotic and biotic stress that affects their growth, development and physiology. It is predicted that water stress will continue to be a major limiting factor affecting global agriculture production and productivity of crop plants. To cope up with drought stress plant use various mechanism and modifies its physiology. These mechanisms can be classified in

to three groups *namely*, drought escape, drought avoidance and drought tolerance (Turner, 1979). In case of drought escape mechanism crop complete its life cycle before onset of the drought, generally the life cycle of the crop is shorter and plants set some seeds instead of complete crop loss. The second mechanism, drought avoidance involves various morpho-physiological strategies which helps the plants to maintain higher water status during period of drought stress. These strategies are either by efficient water absorption from the roots or by reducing evapo-transpiration from the aerial plant parts. The third mechanism of drought tolerance allows the plant to maintain turgor and continue metabolism even at low water potential characteristic differences in response to drought stress have also been identified for a range of morphological and physiological characteristics, including leaf area, root development, stomatal activity, osmotic adjustment, abscisic acid and proline levels in the whole plant. But mean while many scientists reported that excess abscisic acid accumulation has negative effect on the yield. The some of the review related to physiological response of crop plants under stress are represented below.

With increasing stress, the RWC decreased, while free proline content increased (Patil *et al.*, 1984). Popovic *et al.* (1989) reported the correlation between relative water content and water potential indicating an osmotic adjustment under mild stress conditions. Further, Chen *et al.* (1990a) interpreted that water potential and relative water content decreased under water stress condition. Chen *et al.*, (1990b) also concluded that relative water content in leaves decreased significantly in drought susceptible variety than resistant variety. Similarly, higher relative water content was observed throughout the period of water stress in drought resistant cultivar than in the drought sensitive cultivar (O'Regan *et al.*, 1993; 1994; Pelleschi *et al.*, 1995).

In a simulation study on responses of maize to various soil water levels, Li-Ping *et al.* (2006) compared to well-watered conditions during the silking and blister stages moderate stress did not significantly change the relative water content (RWC) but it did change significantly the relative conductivity ($P < 0.05$) of the

leaves. However, severe stress did significantly decrease ($P < 0.01$) the leaf RWC.

Li-Ping *et al.* (2006) compared to well-watered conditions during the silking and blister stages and found that moderate stress did not significantly change the relative water content (RWC) but it did change significantly the relative conductivity ($P < 0.05$) of the leaves. However, severe stress did significantly decrease ($P < 0.01$) the leaf RWC.

Guang-hua Yin *et al.* (2012) reported that RWC differed significantly with soil water content and maize variety but not with the interactions. Leaf RWC declined significantly in response to water stress and the RWC ranged between 85.6% to 92.2% for the varieties Zhengdan 958 and Beiyu 288, respectively. When exposed to water stress conditions, Beiyu 288 showed the greatest RWC, reaching 76.6%. RWC in leaves is already established as an important characteristic that influences plant water relations with the maintaining high RWC under drought conditions can maintain metabolic activity in tissues and enhance drought tolerance. So, they reviewed that RWC can be said to be a good parameter suitable to screening drought-tolerant maize varieties.

2.3. Heterosis

The phenomenon of heterosis is most important genetic tool in increasing the yield of self as well as cross pollinated crops. Hybrid development has provided the most important genetic tools for substantial improvement in yield of crop plants. This was also recognized by Mendel, Darwin, Knight, Burbank, but it was only the work on hybrid corn that brought recognition to the concept of heterosis.

Geeta (2001) carried out 10 X 10 diallel cross for yield and its components traits in maize and reported higher magnitude of heterosis over better parents in 90 hybrids. The hybrids showed highest heterosis for grain yield plant⁻¹ followed by cob weight and number of grain cob⁻¹.

Srivastava and Singh (2003) studied 80 single crosses for heterosis in maize and reported highest mean for the grain yield and 1000-kernel weight in the cross L17

X T4 along with higher positive relatives heterosis. Similarly, the hybrid L15 X T1 exhibited the highest relative heterosis for grain yield and 1000-kernel weight and negative heterosis for days to 50% silking.

Chattopadhyay and Dhiman (2006) evaluated three lines and two testers along with their F_1 and reported significant heterosis for all the characters except ear length and seeds cob^{-1} . Negative heterosis showed by all crosses for crop duration. Positive significant standard heterosis reported by all crosses for plant height and ear girth, whereas negative significant heterosis observed in all crosses for ear length, seeds cob^{-1} and 100- grain weight

Ali *et al.* (2007) assessed thirteen parents, three testers and their hybrids and reported presence of high economic heterosis for grain yield plant⁻¹.

Saidaiah *et al.* (2008) evaluated 40 F_1 along with 14 parents and two standard checks for yield and its attributing traits. Twenty-three crosses showed highly significant heterosis over better parent whereas 11 crosses exhibited highly significant standard heterosis for grain yield plant⁻¹. The crosses viz., DMR 156 X EI 34, DMR 201 X EI 34 and DMR 274 X HOL 34 exhibited heterosis over better parent and standard check (DMR 103) for grain yield plant⁻¹, 100-seed weight, ear length and plant height.

Alam *et al.* (2008) crossed 5 lines in diallel fashion and evaluated hybrids for yield and its contributing traits in maize. The highest percentage of heterobeltiosis was showed by cross P2 X P3 whereas crosses P1×P3 and P1×P5 showed significant negative heterosis for days to maturity.

Uddin *et al.* (2008) crossed 12 lines with 3 testers in maize to study heterosis for yield and component traits. Standard heterosis ranged from - 28.29 to 28.41% for grain yield plant⁻¹; 12.29 to 24.38% for number of grains row⁻¹; -1.11 to 24.44% for number of rows ear⁻¹; -14.75 to 6.67% for ear length; -17.24 to 11.26% for ear diameter and -10.94 to 20.83% for 00-kernel weight.

Singh *et al.* (2009) developed 15 single crosses to study heterosis for grain yield and its associated traits. For grain yield, high percentage of positive significant

heterosis (193.2 to 154.82%) was reported over better parent among the hybrids LM11 X CM135, LM12 X CM135, CML228 X CM13 and LM11 X Y-500. High percentage of positive significant standard heterosis for grain yield plant⁻¹ was recorded in hybrids LM11 x CM135, LM11 x Y-500, LM9 x Y-500 and LM9 x CM139.

Dubey *et al.* (2009) crossed twelve lines with three testers to estimate heterosis over mid parent (MP), better parent (BP) and standard check (SC) for seed oil content, starch content and grain yield plant⁻¹. The highest positive significant heterosis for mid parent, better parent and standard check was exhibited by the non-conventional hybrid L10 x T1 - VC for oil content and grain yield plant⁻¹. This hybrid also exhibited highest *per se* performance for grain yield per plant.

Ron *et al.* (2010) evaluated nine narrow genetic base populations along with thirty-six crosses and reported the positive significant heterosis for all characters viz., grain yield, plant height, ear height, root lodging and stalk lodging. V424 and S132 observed highest yielding population (19 % heterosis) for yield and concluded that these two parents could be the best female parents in seed production.

Avinashe *et al.* (2013) evaluated 45 crosses obtained by crossing 15 lines with 3 testers for yield and its contributing characters in maize and observed mean performance coupled with positive significant heterosis for grain yield plant⁻¹ in the crosses 1-07-10-1 x HKI-163, I-7-8-6 x CLQ-30 and I-07-7-4 x CLQ-30. The cross I-07-10-1 X CLQ-30 recorded highest significant positive standard heterosis for grain yield plant⁻¹ and 1000- kernel weight.

Devi *et al.* (2013) developed 15 crosses in diallel fashion and evaluated along with parents and reported significant variation due to variety for all characters except for ear length. The variance due to average heterosis was found significant for girth of cob, kernels row⁻¹, ear length, 100-kernel weight and grain yield. The cross UP 2596 X DBW 17 was recognized as the best heterotic cross for grain yield. The cross HW 2019 x UP 2338 exhibited highest and significant

positive heterosis over better parent, mid parent and standard checks for numbers of grains per spike.

Tajwar *et al.* (2013) crossed twelve inbred lines with five tester and evaluated hybrids to estimate heterosis maize for yield and its components. The cross (L9 × T2) recorded highest magnitude of economic heterosis of 84.60% over the best standard check (Vivek hybrid-9).

Moneam *et al.* (2014) performed a diallel cross among 6 inbred lines of maize and estimated heterosis for ear length, ear diameter, number of rows ear⁻¹, number of kernels row⁻¹, weight of 100-kernels and grain yield. P₁ × P₄ showed maximum positive heterosis over better-parent and mid-parent for ear length.

Habtamu (2015) crossed 8 lines in diallel fashion for yield and yield component traits in maize and reported highly significant variation between the genotypes for all the traits. The highest standard heterosis for grain yield was observed in the cross L₁ × L₄ followed by crosses L₁ × L₅, L₃ × L₅ and L₁ × L₇.

Mir *et al.* (2015) evaluated 10 inbred lines and 45 F₁'s along with check for 13 characters *viz.*, days to 50% tasseling, days to 50% silking, days to 75% husk browning, plant height, ear height, cob length, cobs plant⁻¹, kernel rows cob⁻¹, kernels row⁻¹, cob diameter, 100-seed weight, protein content and grain yield plant⁻¹. The most desirable cross combination *viz.*, NAI-113 × NAI-123 for seed yield plant⁻¹ also showed desirable heterosis for cob length, kernel rows cob⁻¹, kernels row⁻¹, cob diameter and 100-seed weight over check. The cross W₅ × NAI-116 was most desirable cross combination for early maturity. These cross combinations also revealed high *per se* performance.

Reddy *et al.* (2015) evaluated 45 maize hybrids for 11 characters to estimate standard heterosis and heterobeltiosis. Three hybrids, BML- 2782 × BML-5233-5, CM-211 × BML-5233-5 and BML-2486 × BML-2 showed negative standard heterosis for days to 50 % tasseling, days to 50 % silking and days to maturity. Five crosses *viz.*, BML-15 × BML-2910, BML-7 × BML-3044, CM-211 × BML-7, BML-6 × BML-2 and BML-2782 × BML-6 showed heterobeltiosis for grain yield.

Talukder *et al.* (2016) estimated heterosis in corn for yield and yield contributing traits in hybrid developed by 7×7 half diallel cross. The standard heterosis for kernel yield differs from -51.39 to 12.53%. Among the 21 F₁s, 3 crosses showed significant positive heterosis for kernel yield. The highest heterosis was showed by the cross P₄×P₆ followed P₆×P₇ and P₂×P₃.

Naggar *et al.* (2016) studied heterosis in 15 F₁ crosses for different plant densities (D) and observed significant heterosis for all traits under study. Significant positive heterobeltiosis was observed for grain yield plant⁻¹ for all crosses studied.

Ojo *et al.* (2017) crossed seven tropical and temperate inbred lines to estimate heterosis for yield and yield components. Crosses involving tropical x temperate lines produced hybrids with the highest heterosis for all the traits. Positive heterotic values observed for ear length, ear diameter and grain yield.

2.4. Combining Ability

Sprague and Tatum (1942) introduced the concepts of general combining ability (GCA) and specific combining ability (SCA) to distinguishing between the average performance of parents in cross combinations (GCA) and the division of individual crosses from the average performance of parents involved (SCA). Combining ability analysis is one of the powerful tools in identifying the best combiners that may be used in crosses either to exploit heterosis or to accumulate contributing for an understanding of many questions of productive genes. In 1988, IR-28-8, VIR-44 and HG-5 lines had high combining ability for grain yield observed by Ivakhneko and Antsferov in maize.

Kabdal *et al.* (2003) evaluated 7 inbred lines and 21 direct crosses developed through half diallel fashion. Five single crosses identified as potential cross combinations for days to 50% tasseling, 100-kernel weight, numbers of kernels rows ear⁻¹ and grain yield and five parents were identified good combiner for grain yield.

Malik *et al.* (2004) studied nine inbred lines of maize through diallel mating design excluding reciprocals and reported high significant values for GCA and SCA for all the traits. Inbred QPM-1 and QPM-5 identified as the best general combiner for ear height. The best specific cross combinations found for pollen shading NCML-1061 × NCML-1082 followed by NCML-1061s × NCML-1083. High GCA effects were observed by QPM-1 followed by QPM-5 and NCML-1083 for plant height and grain yield.

Alam *et al.* (2008) crossed maize inbred lines in 5×5 diallel fashion study the combining ability for yield and its contributing traits and reported the significant general and specific combining ability variances for all the characters except ear height. Additive and non-additive gene actions were observed for days to maturity. The inbred lines P₂ and P₅ were observed to be best general combiner for 1000-grain weight.

Singh *et al.* (2009) evaluated 15 crosses for twelve yields and yield related traits and reported the significant differences among lines. Inbred lines L₂, L₃, L₄, L₁₉, L₂₂ and L₂₁ were good general combiners for most of the traits. Twenty-one crosses revealed significant positive SCA effects for grain yield plant⁻¹. Three types of cross combinations were resulted due to high × high, high × low and low × low GCA effects, when one or both the parents were poor general combiners, they resulted into a hybrid having highly significant SCA effects.

Zivanovic *et al.* (2010) evaluated five inbred lines and their hybrid combinations developed by full diallel mating design crosses for grain yield, ear length, ear diameter, number of kernels row⁻¹, number of kernels row⁻¹. Significant GCA and SCA values were observed for all traits. The inbred line NS-1445 showed best GCA effect for grain yield.

Mohammad *et al.* (2011) carried out diallel cross of 7 maize inbred lines to assess combining ability and reported highly significant variance due to GCA and SCA for all characters concluded that presence of both additive and non-additive type of gene action. Parent Q7 identified as best general combiner for higher grain yield and Q1 was also good general combiner for grain yield and lateness in

maturity. Four crosses showed significant SCA effects and may be used for developing high yielding hybrids.

Amiruzzaman *et al.* (2012) studied combining ability in 7×7 diallel cross in maize for yield and yield contributing characters and reported the significant estimates of GCA and SCA variances suggested the importance of both additive and non-additive gene actions. The parent Q7 was identified the best general combiner for grain yield and all the yield components. Parents Q₁, Q₄ and Q₅ were found suitable for higher number of kernels and Q₁ and Q₇ were desirable for bold kernels. Significant negative GCA effects for days to tasseling and silking showed by parents Q₂, Q₃, Q₄ whereas Q₄, Q₅ and Q₇ for both plant and ear height.

Gowda *et al.* (2013) crossed 34 lines with five testers and evaluated developed hybrids along with parents to assess the GCA effects of parents and SCA effects of crosses for yield and its contributing traits. The inbred lines *viz.*, MAI708, MAI109, MAI111, MAI121, Cynt 3 and Cynt 30 were identified as good general combiners. Highest significant SCA effects were exhibited by crosses *viz.*, MAI109 X MAI105, MAI109 X CM202, Cynt30 X NAI137, Cynt 3 X SKV50 and Cynt 3 X CM 202 among all hybrids.

Tajwar *et al.* (2013) crossed twelve inbred lines with five testers in L X T design to estimated combining ability for yield attributing characters. L₉ among the parental lines and T₂ among the testers were identified as the best general combiner for grain yield. Whereas among the hybrids, (L₆ × T₅) was identified as a potentials cross combination for grain yield.

Lahane *et al.* (2015) evaluated 8 lines, 22 crosses along with two checks to study the combining ability for yield and its components. Parents P₁, P₄, P₅ and P₇ showed GCA effect in desirable direction for days to tasseling and days to maturity. Positive significant general combining ability effects exhibited by the parents P₂, P₄, P₅ and P₇ for most of the traits. None of the hybrid found as good specific combiner for all the traits.

Mohammad *et al.* (2015) crossed five inbred lines in full diallel fashion and evaluated F_1 hybrids with parents to estimate combining ability in respect of quantitative and qualitative traits. Higher significant mean square values of both general (GCA) and specific (SCA) combining ability were reported for days to 50% tasseling and silking, plant and ear height, leaf area, 300-kernels weight, number of rows ear⁻¹ and kernel yield plant⁻¹. The crosses (A105×DK), (A₁₁₉×A₁₃₂) and (DK×A₁₃₂) showed significant SCA effect and considered as a good combination for improving the trait.

Nartam *et al.* (2015) evaluated thirty-two F_1 crosses along with four females and eight males' crosses in line x tester fashion for studying the general and specific combining ability effects of parents and crosses respectively. High significant SCA effect in the desirable direction reported for all the characters. High significant variation observed by GCA and SCA effects for different characters. The parents NM-32-1-1, NM-62-4-1 and NM-60-4 were identified as good general combiner for yield and yield contributing characters. Among the crosses, NM-32-1-1 x NM-62-4-1 and NM-32-1-1 x NM-60-4 were identified as best crosses on the basis of higher se performance and high significant SCA effect in the desirable direction.

Niyonzima *et al.* (2015) studied 15 inbred lines and 4 testers along their F_1 's of maize to assess the combining ability for 13 characters. High significant GCA effect in desirable direction was observed for maturity traits *viz.*, days to 50 percent tasseling, days to 50 percent silking. The lines *viz.*, MAI31, MAI32, MAI33, MAI35, MAI40, MAI43 MAI48 and testers MAI105, NAI137 were the best general combiners for plant height and ear height. Lines MAI31, MAI32, MAI33, MAI35 and MAI38 showed high general combining ability effects for traits like kernel rows per cob and kernels per row.

Shah *et al.* (2015) evaluated 6 inbred lines along with 30 F_1 hybrids developed by diallel fashion and reported highly significant variation among genotypes for grain yield and its component traits. Mean square values due to general combining ability were found highly significant for all characters except kernels ear⁻¹ and

grain yield. Highly significant variations for specific combining ability of direct and reciprocal effects were observed for all traits. Islamabad White $\times$ Sadaf was the best combiner for grain yield. For reciprocal cross effects, BS-I $\times$ Sahiwal 2002 proved good combiner for kernels row⁻¹ and kernels ear⁻¹ while BS-I $\times$ Islamabad White for grain yield.

Shamarka *et al.* (2015) evaluated eight inbred lines, 28 crosses along with checks and reported highly significant mean square due to GCA and SCA for all the traits. The parental lines P₁, P₆ and P₇ exhibited positive significant GCA effects for grain yield and parent P₅ and P₇ for earliness. The crosses P₂ $\times$ P₄ and P₃ $\times$ P₆ identified as best cross combination for earliness and the crosses P₁ $\times$ P₆, P₂ $\times$ P₄, P₃ $\times$ P₆ and P₇ $\times$ P₈ had the best SCA effects for grain yield.

Hoque *et al.* (2016) evaluated 6 parents along with 30 crosses to study combining ability for grain yield, maturity and growth parameters in maize. High significant GCA and SCA effect observed for all characters except SCA in days tasseling and days to maturity. Variances due to GCA were higher in magnitude than SCA indicated additive gene effects for all characters except cob length, 1000 grain weight and ear height. The Parent P₅ was the best general combiner and the Parent P₁ and P₂ was best general combiner for dwarf and earliness.

Suthamathi *et al.* (2016) studied 91 cross combinations along with 14 selected inbred lines to assessed the combining ability and reported the predominance of non-additive gene action for yield contributing traits. The cross combination P₄ $\times$ P₆ and P₄ $\times$ P₅ possessed desirable *per se* performance and SCA effects for grain yieldplant⁻¹, kernel rows cob⁻¹, number of kernelsrow⁻¹ and 100- grain weight. The parents P₁, P₂, P₃ and P₄ were identified as good general combiners.

Patel and Kathiria (2016) evaluated 10 inbred lines of maize along with their hybrids and observed that mean square due SCA was higher than that of GCA it indicated predominance of non-additive gene action for all the characters. Analysis of variance exhibited high significant difference among genotypes for all the traits.

Sali *et al.* (2016) crossed ten inbred lines in a full diallel fashion and evaluated parents along with their hybrids to estimate combining ability for yield and its contributing traits. High magnitude of SCA than GCA was observed in all crosses for all traits except for number of kernels row ear⁻¹. Significant positive GCA effect showed by parents viz., L₂, L₅, L₆, L₇ and L₉ for grain yield whereas 35 crosses showed significant positive SCA effects for grain yield.

Kuselan *et al.* (2017) evaluated 42 lines and 3 testers along with their hybrids in maize and assessed combining ability for yield and its associated traits. Among the lines, the line RML12 was identified as the best general combiner for most of the yield contributing traits followed by RML1, RML 26, RML 27 and RML 34. The parent RML48 was found as the best general combiner tester for most of the yield contributing traits followed by RML47. Positive significant SCA effect observed in cross combination RML12 x RML48 for grain yield, cob girth and numbers of grains rowscob⁻¹ and numbers of grainscob⁻¹. Similar positive significant SCA effects with better mean performance observed in RML26 x RML48 for number of grainscob⁻¹, grain yieldplant⁻¹ and grain yieldplot⁻¹, RML27 x RML48 for grain yieldplant⁻¹, grain rowscob⁻¹, grainscob⁻¹ and RML37 x RML48 for (cob girth, 100-grain weight, grain yieldplant⁻¹ and grain yieldplot⁻¹).

Aslam *et al.* (2017) studied 30 F₁ crosses along with 6 parents to estimate general combining ability and specific combining ability. Non-additive gene action exhibited for ear diameter, ear length, grain row ear⁻¹ and grain ear⁻¹ whereas seeding emergence and 100- grain weight exhibited additive type of gene action.

Avinash *et al.* (2017) evaluated 45 hybrids, 10 parents along with 4 checks to determine GCA and SCA effects of parents and crosses respectively for yield and its contributing traits. Positive significant SCA effects for grain yield plant⁻¹ were observed in 20 and 17 hybrids in E₁ and E₂ environments respectively. EIQ-112, EIQ-109 and EIQ-106 in E₁ environment while, EIQ-109 and EIQ-112 in E₂ environment were the good general combiner for grain yield plant⁻¹.

Mohammad *et al.* (2017) crossed seven inbred lines in diallel fashion in maize to determine the GCA and SCA of parents and the crosses respectively. Significant

general and specific combining ability variances were observed for some of the characters. The overall study of GCA effects suggested that parent WL3 was significant for general combiner for yield, WL2 and WL3 for earliness and WL1 for short stature. These parents could be used in future breeding programme to increase maize yield with desirable traits.

Arsode *et al.* (2017) evaluated 8 lines, 3 testers, their F_1 's along with 2 checks to study combining ability for yield and its contributing traits. The lines DQL685 (Orange) -18-2, DQL596 (U)-2-1-1 and DQL 639 -1-7 and the tester, DMRQPM -03-124 had recorded significant GCA for yield and its component traits. The hybrid, DQL599(U)-4-2 x DMRQPM 03-124 reported negative significant SCA values for earliness while considering days to 50% flowering and days to maturity.

Karad *et al.* (2017) evaluated 30 crosses developed by diallel mating design along with 6 parents and 2 checks to estimate combining ability for yield and its components. High significant variability exhibited among genotypes for all characters. The three parents *viz.*, NAUM-21, NAUM-8 and DC-7 were identified as best general combiner for yield.

2.5. Biochemical nature of drought tolerance

In general, water stress triggers many biochemical changes such as accumulation of various stress metabolites in plants. Changes in leaf angle reduce water loss by providing more shading of lower leaves and by reducing canopy temperature. Reduced tassel size, narrow leaves and leaf enlargement following drought stress were considered to be good and easy to evaluate (Jurgens *et al.*, 1978). Free proline accumulates under water stress (Singh *et al.*, 1972 and Waldren *et al.*, 1974). During moisture stress, the enzymatic action is extremely altered and variation of its activity plays a vital role in plant growth (Jurgens *et al.*, 1978). Under wilting conditions, the activities of invertase and proteases increase in both seedling and full-grown plants. The level of growth inhibitors in plants increase when plants are subjected to moisture stress. The major inhibitor is abscisic acid (ABA) which mainly controls stomatal closure

(Aspinall, 1980) and indirectly the rate of transpiration (Milborrow, 1981). The high concentration of ABA reduces transpiration by promoting stomatal closure and therefore, may promote tolerance to drought.

Jurgens *et al.* (1978) during moisture stress, the enzymatic action is extremely altered and variation of its activity plays a vital role in plant growth. Under wilting conditions, the activities of invertase and proteases increase in both seedling and full-grown plants.

Bennet and Hammond (1983) reported that drought reduced leaf area by 19 percent and plant height by 17 percent due to stress during vegetative growth. However, there was no difference between the stress and non-stressed plants with respect to total number of leaves. Water stress caused a fall in leaf chlorophyll. It is well established that drought stress impairs numerous metabolic and physiological processes in plants.

Quiang *et al.* (1996) observed 12.6 percent higher chlorophyll content in drought tolerant variety than the susceptible one under drought conditions.

Tumbo *et al.* (2000) reported that chlorophyll levels, which are strong indicators of nitrogen status and photosynthetic status in plants are measured using SPAD chlorophyll meter. Under drought conditions, the decrease in chlorophyll content was reported by Chaves *et al.* (2003).

Kumari *et al.* (2004) reported that chlorophyll content and stability index decreased under drought stress and observed up to 60 percent decrease in chlorophyll content when the drought stress was applied at flowering. But when the stress was applied at grain filling period the reduction in chlorophyll content was noticed up to 50 percent. The susceptible inbred lines showed large reduction in the chlorophyll content under drought. The drought tolerant inbred lines either resisted the decrease in chlorophyll content or showed very little reduction and also observed that under stress, drought tolerant inbred lines showed less leaf temperature but transpiration rate was comparatively high.

Swee Yin *et al.* (2012) reported that yellow super sweet corn variety and Thai super sweet corn varieties showed decreasing value in chlorophyll content due to low photosynthesis rate resulting from water stress. The observed reduction of chlorophyll in water stressed plants may be due to a reduction in the lamellar content of the light harvesting chlorophyll a/b protein (Randall *et al.*, 1977). Under more prolonged water deficit, dehydration of plant tissue can result in an increase in oxidative stress, which causes deterioration in chloroplast structure and an associated loss of chlorophyll. This leads to a decrease in the photosynthetic activity. Reduction in chlorophyll concentration in water stressed plants could indirectly lead to a decrease in photosynthetic activity. Increase in chlorophyll concentration in well-watered plants, could have in turn led to increased protein synthesis and this has a direct consequence on the plant growth and photosynthesis, hence increase in shoot dry weight (Muthomi and Musyimi, 2009).

Yadav *et al.* (2003) reported that accumulation of total soluble sugars and free amino acids under stress at all the growth stages of sorghum indicated the possibility of their involvement in osmotic adjustment.

Mohamed and Naglaa (2010) stated that soluble sugars are major constituents of osmoregulation in the expanded leaves of many species. The accumulation of sugars in response to drought stress is also well documented. Soluble sugar may also function as a typical osmo-protectant, stabilizing cellular membranes and maintaining turgor pressure.

Guang-hua Yin *et al.* (2012) reported that soluble sugar content was significantly affected by soil water content and variety. The effect of soil water content, maize variety, and interactions between the two on soluble sugar was found significant. Under normal water conditions, the content of soluble sugar varied from 24.6 mg g⁻¹ FW in Ningyu 309 to 36.4 mg g⁻¹ FW in Beiyu 288. When subjected to drought stress conditions, Beiyu 288 showed the greatest soluble sugar content, reaching 72.8 mg g⁻¹ FW. Soluble sugars are the main osmolytes in maize plants. They are used for osmotic adjustment. Increases in soluble sugar content in plant cells

have been observed during drought conditions. This shows significant differences in soluble sugar content across varieties indicating that soluble sugar is a very sensitive factor for drought tolerance and it was concluded that soluble sugar is a parameter suitable to screening for drought tolerance in maize varieties.

McCue and Hanson (1990) proposed proline accumulation as a mechanism conferring adaptive value to plant under water deficits. In a simulation study on responses of maize to various soil water levels, Li-Ping *et al.* (2006) observed decreased activity of antioxidant enzymes in the later stages, superoxide dismutase during anthesis and blister stages, peroxidase during milk stage and catalase during the anthesis, blister and milk stages. But membrane lipid peroxidation significantly increased in all stages.

In a simulation study on responses of maize to various soil water levels Li-Ping *et al.* (2006) were observed decreased activity of antioxidant enzymes in the later stages; superoxide dismutase (SOD) during tasseling and blister stages, peroxidase (POD) during milk stage and catalase (CAT) during the tasseling, blister, and milk stages. But membrane lipid peroxidation (measured as malondialdehyde content) significantly increased ($P < 0.01$) in all stages.

Harrigan *et al.* (2007) reported significant accumulation of free glutamine and free proline, with induction of drought in grains of at least four maize hybrids out of seven hybrids.

Kolarovic *et al.* (2009) reported significant activation of antioxidative defense mechanisms correlated with drought-induced oxidative stress tolerance, and this phenomenon was shown to be characteristic of the drought-tolerant cv. Nova. Activities of some ROS-scavenging enzymes, superoxide dismutase (SOD), guaiacol peroxidase (POX), catalase (CAT) and ascorbate peroxidase (APX) were enhanced significantly 4 h after the start of drought exposure in the drought-tolerant cv. Nova. Furthermore, a significant increase in the ascorbate pool was observed in this cultivar. On the other hand, in the drought-sensitive cv. Ankora only SOD and POD activities and the thiol pool were increased. No

changes in APX activity or the level of ascorbate were recorded in cv. Ankora. Studies of root cell viability indicated that marked oxidative damage appeared only in cv. Ankora. Mohammadkhani *et al.* (2008) reported that the drought stress induced changes in protein synthesis in maize. The accumulation of proteins was detected in the leaves of stressed plants and they opined that these proteins were released during severe stress condition leads tolerance to stress.

Swee Yin *et al.* (2012) reported that free proline accumulates in response to a wide range of stresses, such as drought and salinity. In his experiment, proline concentration was shown to be generally higher in stressed maize where in yellow super sweet corn variety which irrigated with 9 days interval and Thai super sweet corn variety irrigated with 6 days interval are relatively higher as compared to the control (watering everyday) treatment 65 DAS. They also stated that proline accumulation in maize might be enough for osmotic adjustment under stress conditions, increasing proline content of leaves with decreasing available water means an efficient mechanism for osmotic regulation, stabilizing sub-cellular structures and cellular adaptation to water stress was provided. They confined that the increase in proline contents may be an adaptive mechanism and increases drought tolerance.

Chugh *et al.* (2011) reported that seedlings of selected six genotypes of maize (*Zea mays* L.) differing in their drought sensitivity (LM₅ and Parkash drought-tolerant and PMH2, JH3459, Paras and LM14 as drought-sensitive) were exposed to 72 h drought stress at two leaf stage. Alterations in their antioxidant pools combined with activities of enzymes involved in defense against oxidative stress were also investigated in leaves. Activities of some reactive oxygen species (ROS)-scavenging enzymes, catalase (CAT) and ascorbate peroxidase (APX) were enhanced in tolerant genotypes in response to drought stress. Superoxide dismutase (SOD) activity was significantly decreased in sensitive genotypes but remained unchanged in tolerant genotypes under stress. Peroxidase (POX) activity was significantly induced in tolerant, as well as sensitive genotypes. Imposition of stress led to increase in H₂O₂ and malondialdehyde (MDA, a marker for lipid peroxidation) content in sensitive

genotypes, while in tolerant genotypes no change was observed. Significant increase in glutathione content was observed in sensitive genotypes. Significant activation of antioxidative defense mechanisms correlated with drought-induced oxidative stress tolerance was the characteristic of the drought tolerant genotypes. These studies provide a mechanism for drought tolerance in maize seedlings.

Chugh *et al.* (2013) defined the role of oxidative stress management in two maize (*Zea mays* L.) genotypes - Parkash (drought-resistant) and Paras (drought-sensitive), subjected to drought stress during reproductive stage. Alterations in their antioxidant pools - glutathione (GSH) and ascorbic acid (AsA) combined with activities of enzymes glutathione reductase (GR), ascorbate peroxidase (APX), peroxidase (POX) and catalase (CAT) involved in defense against oxidative stress. Stress parameters, *namely* chlorophyll (Chl), hydrogen peroxide (H_2O_2) and malondialdehyde (MDA) were investigated in flag leaves from silk emergence till maturity. The drought caused transient increase in GR, APX, POX and CAT activities in drought-tolerant genotype (Parkash) which decreased at later stages with the extended period of drought stress. However, in Paras, drought stress caused decrease in activities of GR and CAT from initial period of stress till the end of experiment, except for POX which showed slight increase in activity. A significant increase in GSH content was observed in Parkash till 35 days after silking (DAS), whereas in Paras, GSH content remained lower than irrigated till maturity. Parkash which had higher AsA and Chl contents, also showed lower H_2O_2 and MDA levels than Paras under drought stress conditions. However, at the later stages, decline in antioxidant enzyme activities in Parkash due to severe drought stress led to enhanced membrane damage, as revealed by the accumulation of MDA. These data indicated that significant activation of antioxidant system in Parkash might be responsible for its drought-tolerant behavior under drought stress and helped it to cope with the stress up to a definite period. Thus, the results indicated that antioxidant status and lipid peroxidation in flag leaves can be used as indices of drought tolerance in maize

plants and also as potential biochemical targets for the crop improvement programmes to develop drought-tolerant cultivars.

2.6. Molecular assisted breeding for drought situation

Integrating molecular approaches in breeding for drought tolerance could increase significantly the potential for genetic gain under water-limited conditions (Ribuat *et al.*, 2009). The rapid advancement in molecular marker technology has provided new classes of genetic markers at the DNA level. The advent of DNA based markers has opened up new avenues and uncommon opportunities for biological science in the area of evolutionary studies, plant systematic and more recently in the tagging of genes coding for traits of agronomic importance. Among the DNA based markers microsatellite or SSR markers are PCR based, genetically co-dominant, robust, reproducible, hyper variable, informative and reasonably easy-to-use. Along with the Single Nucleotide Polymorphisms (SNPs), the SSR markers, which are abundant in maize genome offer significant advantages in DNA fingerprinting, genetic diversity analysis, gene/ QTL mapping and molecular marker-assisted breeding.

Dubey *et al.* (2009) analyzed a set of 24 tropical maize lines with differential responses to drought stress, including 16 lines from CIMMYT (Mexico) and eight lines from India, were characterized using 37 polymorphic microsatellite/SSR markers, including 29 SSRs tagging specific candidate genes involved in drought stress tolerance in maize. A total of 119 SSR alleles with a mean of 3.22 alleles per locus were identified. Polymorphism Information Content (PIC) of the 37 SSR loci ranged from 0.09 (umc1627) to 0.78 (umc1056 and bnlg1866), with a mean PIC of 0.56. The study resulted in identification of eleven highly informative markers with PIC values ≥ 0.65 , as well as five unique SSR alleles in DTPW-C9-F55-2-3, DTPW-C9-F115-1-4, DTPY-C9-F142-1-2, K64R and CML537. Pair-wise genetic similarity (GS) values, estimated using Jaccard's coefficient, ranged between 0.14 (HKI1025- K64R; HKI1025-CML247) and 0.74 (HKI-335-HKI-209), with an average GS of 0.31, indicating high level of genetic divergence among the genotypes selected for the study. These SSR markers could be further

validated and potentially deployed in molecular marker-assisted breeding for drought tolerance in maize.

Shiri (2011) used 38 maize hybrids in the evaluation and breeding for drought tolerance and to determine informative markers for drought tolerance, 12 microsatellite primers were employed. Genomic DNA was extracted with the CTAB method and PCR was performed based on the common method for microsatellite markers. PCR products were separated using 6% polyacrylamide denaturing gel. Stepwise multiple regression analysis was used to determine the chromosomal regions related to drought tolerance. A total of 40 SSR alleles (bands) with a mean of 3.33 alleles per locus were identified. Polymorphism information content (PIC) of the 12 SSR loci ranged from 0.23 (Phi080) to 0.79 (UMC2359), with a mean PIC of 0.53. The analysis also led to identification of informative SSR markers, *namely*, UMC1862 (bin 1.11), UMC1719 (bin 4.10-4.11), UMC1447 (bin 5.03), UMC2359 (bin 9.07) and UMC1432 (bin 10.02), which significantly contributed to the differentiation of the drought tolerant and susceptible genotypes.

Tharwat El Ameen (2013) characterized drought tolerance in six wheat genotypes with developed marker assisted drought tolerance. Four of them were tolerant and two were drought sensitive genotypes. The results indicated that tolerant genotypes harbored seven positive RAPD markers, while sensitive genotypes had only one negative RAPD markers. In tolerant genotypes, seven positive PCR-RAPD markers with molecular sizes of 1050, 390, 200, 230, 850, 430 and 800 bp was exhibited by A-12, B-05, C-12, E-10 and B-02 primers. This study indicates that the seven positive markers can be employed indicators to discard drought tolerance in wheat marker -assisted breeding programmes.

Ahmed (2013) evaluated two maize inbred lines for their drought stress tolerance in the field. These two inbred lines were chosen as drought tolerant (Sd-63) and drought sensitive (Gm-18) for hybridization to obtain the F_1 generation and then selfed to obtain the F_2 generation. These two maize inbred lines and their F_1 and bulks of the two extreme F_2 plant groups (the most

tolerant F₂ group and the most sensitive F₂ group) were tested against six RAPD primers to determine some molecular markers for drought tolerance in maize. This analysis revealed that, four RAPD primers (A₀₁, A₀₅, A₀₆ and B₀₈) out of the six developed molecular markers against drought tolerance in maize. These RAPD markers could be considered as reliable molecular markers associated with drought tolerance in maize that can be utilized during breeding programmes *via* marker-assisted selection.

Arshad *et al.* (2021) characterized 113 maize lines using two molecular markers *viz.*, dhnC397 and rspC1090, the polymorphic SNP sites of dhnl and rsp41 were determined. As a result of this, using dhnC397, a 164-bp segment was found at the dhnl site. For a genotype, carrying (CCAAGG) variants, PCR products were digested by using StyI restriction enzyme resulting in 02 bands, 131-bp and 33-bp. A similar approach was used for the identification of rsp41 gene polymorphism. Passing through the HpaII restriction enzyme, resulted in 02 bands, 225-bp and 61-bp. The alleles produced by using PCR and restriction enzymes are associated with drought resistance in maize. In this study, the alleles associated with drought resistance were identified in about 68 lines out of 113 by using these molecular markers.

Saad-Allah (2022) investigated drought-responsive gene expression patterns in five maize (*Zea mays* L.) genotypes *viz.*, G314, G2, G10, G123 and G326. On the expression of drought-responsive genes *i.e.*, LOS5, Rad17, NCED1, CAT1 and ZmP5CS1 with G10 and G123 genotypes being the most drought-resistant.

In Genome-wide association studies were carried out by Khan *et al.* (2022) using phenotypic values under WS, WW and drought-tolerance index (WS-WW or WS/WW) and applying a mixed linear model that controls both population structure and relative kinship. In total, 71, 159 and 21 SNPs, located in 32, 59 and 12 genes, were significantly ($P < 10^{-5}$) associated with ASI, EBM, and PH, respectively. Only a few overlapped candidate genes were found to be associated with the same drought-related traits under different environments, for example, ARABIDILLO 1, glycoprotein, Tic22-like and zinc-finger family protein

for ASI; 26S proteasome non-ATPase and pyridoxal phosphate transferase for EBM; 11- β -hydroxysteroid dehydrogenase, uncharacterized, Leu-rich repeat protein kinase and SF16 protein for PH. Furthermore, most candidate genes were revealed to be drought-responsive in an association panel. Meanwhile, the favorable alleles/key variations were identified with a haplotype analysis. These candidate genes and their key variations provide insight into the genetic basis of drought tolerance, especially for the female inflorescence, and will facilitate drought-tolerant maize breeding.

Kyu Jin *et al.* (2022) assessed the genetic and phenotypic variation of 12 flint maize inbred lines and performed association analysis of 11 drought-related traits using 360 simple sequence repeats (SSRs), detecting 1,604 alleles, with an average of 4.4 alleles per locus. The average values of gene diversity (GD) and polymorphism information content (PIC) were 0.648 and 0.598, respectively. In principal component analysis (PCA), shoot fresh weight (SFW), shoot dry weight (SDW), stem weight (SW), leaf weight (LW), root fresh weight (RFW), root dry weight (RDW) and leaf area (LA) traits contributed greatly to the PIC. Association analysis was performed using a general linear model with a Q-matrix (Q GLM) and a mixed linear model with Q and K-matrices (Q + K MLM). Twelve SSR markers for drought tolerance trait were detected by QGLM and all maize inbred lines were clearly divided into two groups in accordance with their drought tolerance. Duplicated significant marker-trait associations (SMTAs) between Q GLM and Q + K MLM identified eight marker-trait associations involving four SSR markers that were associated with the traits of SW, SFW, RFW and RDW with a significant level of $P < 0.05$. The *umc1175* and *umc2092* were associated with SW and SFW; *umc1503* was associated with RFW, SFW and SW; and *umc2341* was associated with RDW. The detection of loci associated with drought-related traits may provide better opportunities to improve maize drought tolerance by marker-assisted selection (MAS). These results will be useful for breeders in producing tolerant varieties as well as markers for using MAS in maize breeding programs.

CHAPTER - 3

MATERIAL AND METHODS

The present investigation entitled “Genetic enhancement of maize (*Zea mays* L.) for drought using phenotyping, genotyping and conventional breeding approaches” was carried out to elicit the information on magnitude of heterosis, general and specific combining ability effects of parents and their hybrids for seed yield and its attributing traits. The detail of experimental site, materials used and technology adopted during use of present investigation are described in this chapter.

3.1 Experimentation Site

3.2 Location and climate

3.3 Experimental Materials

3.4 Experimental Design

3.5. Experimental details

3.6 Development of breeding material and Year wise plan of work

3.7 Observations recorded

3.8 Statistical Analysis

3.9 Drought tolerance parameters

3.10 Molecular Analysis

3.1 Experimentation Site:

The present investigation entitled “Genetic enhancement of maize (*Zea mays* L.) for drought using phenotyping, genotyping and conventional breeding approaches ” was carried out to elicit the information on magnitude of heterosis, general and specific combining ability effects of parents and their hybrids for seed yield and its component traits. The breeding material developments and field experiments was carried out in the Experimental field of Department of

Genetics & Plant Breeding, College of Agriculture, R.V.S.K.V.V., Gwalior (M.P.) during *Rabi* 2019-20 and *kharif* 2020.

Table 1. Weekly weather data *rabi* seasons 2019-20 recorded at Department of Agriculture Meteorology, College of Agriculture, Gwalior (M.P).

Met. Week	Date	Temperature (°C)		Humidity (%)		Rainfall (mm)	Evapo-ration (mm)
		Max.	Min.	Morning	Evening		
1	Nov.5-11	30.8	14.0	88.9	37.3	000.0	2.5
2	Nov.12-18	29.7	14.7	84.4	43.1	000.0	2.6
3	Nov. 19-25	28.5	11.0	93.3	41.7	000.0	2.6
4	Nov.26 –Dec.2	27.1	12.4	92	52	000.0	1.7
5	Dec.3-9	24.0	6.7	94.7	43.3	000.0	1.7
6	Dec.10-16	21.3	9.5	95.9	62.3	002.1	1.2
7	Dec.17-23	19.2	4.9	94.4	54.7	000.0	1.4
8	Dec.24-31	13.5	2.3	96.6	75.9	000.0	1.2
9	January 1-7	21.7	6.6	96.3	59.0	000.0	1.2
10	January 8-14	20.4	5.6	91.3	72.6	011.2	2.1
11	January 15-21	18.3	7.6	96.1	70.7	040.4	0.5
12	January 22-28	22.8	5.2	88.4	45.6	000.0	2.9
13	Jan.29-Feb.4	22.2	6.0	94.0	56.9	000.0	2.9
14	Feb. 5-11	22.4	4.9	93.7	44.9	000.0	2.7
15	Feb. 12-18	26.8	6.4	79.7	36.4	000.0	4.6
16	Feb. 19-25	26.5	9.6	93.6	46.9	000.0	3.1
17	Feb.26-March4	29.4	13.2	89.1	53.1	002.4	3.9
18	March 5-11	26.3	11.1	90.3	53.1	009.2	2.1
17	March 12-18	28.9	11.5	80.0	39.4	000.0	4.1
20	March 19-25	33.9	14.5	82.0	37.1	003.2	3.6
21	March26-April1	32.7	15.3	80.0	54.5	008.7	3.4
22	April 2-8	36.1	14.7	60.3	44.6	000.0	6.4
23	April 9-15	38.2	17.8	61.4	28.4	000.0	7.4
24	April 16-22	38.8	18.7	55.3	29.0	000.8	7.6
25	April 23-29	37.6	20.2	64.3	35.7	000.2	7.1

Table 2. Weekly weather data *Kharif* seasons 2020 recorded at Department of Agriculture Meteorology, College of Agriculture, Gwalior (M.P).

Met. Week	Date	Temperature (°C)		Humidity (%)		Rainfall (mm)	Evapo-ration (mm)
		Max.	Min.	Morning	Evening		
1	June 4-10	37.6	23.9	70.9	37.6	015.7	7.7
2	June 11-17	41.8	27.0	67.9	32.3	004.0	11.3
3	June 18-24	41.1	27.0	71.4	44.9	025.5	10.9
4	June25-July1	39.2	27.1	71.3	48.6	003.4	6.6
5	July 2-8	39.4	27.4	74.6	57.1	005.3	8.2
6	July 9-15	37.0	26.1	75.3	59.1	031.6	5.7
7	July 16-22	36.5	25.5	84.3	63.3	062.5	5.6
8	July 23-29	35.9	25.6	82.7	62.7	001.8	6.4
9	July30- Aug.5	35.6	24.5	88.1	61.3	070.8	4.2
10	Aug. 6-12	33.5	24.9	90.3	74.6	057.6	3.6
11	Aug. 13-19	33.3	24.9	94.9	73.6	063.7	3.5
12	Aug. 20-26	32.8	23.9	91.4	75.3	058.9	4.6
13	Aug.27-Sept.2	32.3	23.9	88.4	78.1	028.1	4.2
14	Sept. 3-9	34.5	24.3	88.9	64.3	040.3	4.8
15	Sept. 10-16	36.6	24.8	85.7	50.3	000.0	5.3
16	Sept. 17-23	36.2	24.9	81.7	54.6	005.1	5.7
17	Sept. 24-30	36.9	22.3	80.6	43.3	000.0	5.9
18	Oct. 1-7	37.0	16.4	84.3	31.0	000.0	6.0
17	Oct. 8-14	36.6	17.6	85.9	34.6	000.0	5.7
20	Oct. 15-21	35.6	18.4	76.1	33.6	000.0	4.7
21	Oct. 22-28	34.8	14.9	83.4	29.1	000.0	4.9
22	Oct. 29 –Nov.4	31.8	9.9	78.4	35.3	000.0	4.5
23	Nov.5-11	31.1	9.3	90.1	34.9	000.0	3.6
24	Nov.12-18	28.0	12.5	94.0	58.7	050.0	1.9
25	Nov. 19-25	24.9	8.6	89.8	50.1	000.0	3.4

3.2 Location and climate:

Geographically, Gwalior is situated at 27°12' North latitude and 77°00' East longitude with an altitude of 498.77 meters above the mean sea level. The weather conditions during cropping period were normal and favorable for the crop growth and development.

3.3 Experimental Materials

The seeds of 12 inbred lines of maize obtained from SHUATS (Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, U.P. India and their 66 F₁'s were made at experimental field, Department of Genetics & Plant Breeding, College of Agriculture, R.V.S.K.V.V., Gwalior, M.P., India and biochemical and molecular work was carried out at Biochemical Analysis and Molecular Biology Laboratories, Department of Plant Molecular Biology & Biotechnology, College of Agriculture, R.V.S.K.V.V. Gwalior, M. P., India.

Details of Experimental breeding material

The 12 inbred lines of maize obtained from SHUATS (Sam Higginbottom University of Agriculture Technology and Sciences), Prayagraj, U.P. India listed below.

Table 3. List of inbred lines, checks and its source of maize

Inbred Lines (Parent) / Checks	Pedigree	Source of Material
IL-1	CM-13	SHUATS, Prayagraj, U.P.
IL-2	CML-193	Do
IL-3	CML-439	Do
IL-4	NBPGR-36417	Do
IL-5	NBPGR-36417 × NBPGR-33000	Do
IL-6	(103) NBPGR-36548 × (97) NBPGR-36407	Do
IL-7	DMR-N 21 × NBPGR-32809	Do
IL-8	LM- 13 × NBPGR-31899	Do
IL-9	CML-224-1 × NBPGR-32809	Do
IL-10	NBPGR-36550 × NBPGR-36407	Do
IL-11	KL- 153237 × VL- 1016536	Do
IL-12	CML- 161 × VL- 1056	Do
HKI 1105	Cargill 633	IARI, New Delhi
HKI 1128	Unknown source	Do

3.4 Experimental Design

A set of 12 parents and their 66 F₁ hybrids along with two national checks (drought tolerant HKI1105 and drought susceptible HKI1128), total 80 entries were sown in a Randomized Block Design with two replications during *rabi* 2019-20 and in *kharif* 2020. Each genotype was sown in single row of 5-meter length. The distance between rows and plants was 60 cm x 20 cm, respectively. Other recommended agronomic practices and plant protection measures were adopted throughout the crop period and growth.

3.5. Experimental details

Environments	:	4
a) Seasons	:	<i>Kharif</i> and <i>Rabi</i> (2019-20)
b) Water stress	:	Irrigated and partial irrigated (at reproductive stages)
Design	:	Randomized Block Design
Replication	:	2
Plot size	:	3.6 m ² (1.2m x 3 m)
Spacing	:	60 cm x 20 cm (R to R and P to P)
Breeding material	:	80
a) Number of inbred lines	:	12
b) Number of crosses	:	66
c) No of checks	:	2

3.6. Development of breeding material and Year wise plane of work

3.6.1. *Kharif* 2018

Evaluation and multiplication of 12 maize inbred lines was carried out in the research field, Department of Genetics & Plant Breeding, College of Agriculture, Gwalior.

3.6.2. *Kharif* 2019

A crossing programme was initiated with 12 maize inbred lines following half diallel patterns (Jinks and Hayman, 1954) to raise 66 F₁ hybrids among them by hand pollination.

3.6.3. *Rabi* 2019-20

A study was carried out by undertaking trials of 12 inbred lines and their 66 F₁ hybrids along with two national checks (a total of 80 entries) was evaluated in Randomized Block Design with two replications in the research field of Genetics and Plant Breeding; College of Agriculture, R.V.S.K.V.V., Gwalior (M.P.) and molecular work was done in the Department of Plant Molecular Biology and Biotechnology, Biotechnology Centre, R.V.S.K.V.V. Gwalior (M.P.).

3.6.4. *Kharif* 2020

A study was carried out by undertaking trails of 12 inbred lines and their 66 F₂ populations along with two national checks (a total of 80 entries) was evaluated in Randomized Block Design with two replications in the research field.

3.7 Observations recorded

The observations were recorded on five randomly selective competitive plants from each replication for studies on heterosis, combining ability and inbreeding depression in the entry for each replication for all the characters except days to flowering and days to maturity, which were recorded on plot basis. The replication wise mean values were finally subjected to statistical analysis.

Observation was taken on the following characters:

3.7.1 Morphological

(i) Days to 50 % tasseling

Number of days from planting to when 50% of the plants in a plot started to shed pollen.

(ii) Days to 50 % silking

Number of days from planting to when 50% of plants in a plot produced 2-3 cm long silk.

(iii) Days to maturity

The number of days from planting to the stage when 75% of the plants in a plot reached to the physiological maturity *i.e.*, when the kernels formed black layers on the tip.



Plate1. Seed multiplication of 12 maize inbred lines



Plate 2. crossing programme carried out with 12 maize inbred lines

(iv) Plant height (cm)

Height of the plant was measured from the base of the plant to the tip of the main shoot of individual plant at the time of harvest and mean value for the plot recorded.

(v) Cob length (cm)

The ear length was measured in cm from the base of the ear to its tip. The average values of five randomly selected ears were considered.

(vi) Number of kernel rows per cob

The total number of kernel rows was counted from five randomly selected ears and the average value was used as kernel rows per-ear.

(vii) Numbers of kernel per rows

The total number of kernels present in a row was counted from five randomly selected ears and the average value was used as KPR for a given plot.

(viii) 100-grain weight (g)

Seeds from the bulk of the plot were randomly taken and counted using seed counter and weighed. One hundred seeds were counted from the total seeds obtained and weighed in gram and averaged.

(ix) Grain yield per plant (g)

The cobs from randomly selected five plants were dried, shelled, cleaned and weight of grains was recorded and expressed as grams per plant.

(x) Number of cobs per plant

Cobs per plant were computed as the ratio of number cobs per plot to number of plants per plot.

(xi) Anthesis silking interval (ASI)

The difference between days to 50 per cent tasseling (anthesis) and days to 50 per cent silking was recorded as anthesis-silking interval.



Plate 5. Showing canopy temperature and membrane stability test

(xii) Cob girth (cm)

The diameters of five randomly selected ears measured in cm at mid-length and the average value was computed. The same ears used for measuring ear length were also used to measure ear diameter.

(xiii) Shelling %

The shelling percentage was computed as the ratio of kernel weight to weight of cob (grain wt. + pith wt.), then the value was expressed in per cent.

$$\text{Shelling percentage (\%)} = \frac{\text{Grain weight per plant}}{\text{Cob weight per plant}} \times 100$$

(xiv) Canopy temperature (at reproductive stages)

Canopy temperature is the indirectly measures the plant transpiration and plant water status. Canopy temperature was measured on expanded second leaf from the tip of the main stem between 11.00 am to 12.00 noon using infrared thermometer at reproductive stage. A mean of the five-reading plot⁻¹ was taken from two tagged plants. During measurement, the same position (distance, angle) was maintained. Cloudy or windy conditions were avoided. Additionally, the readings were made with the sun at the back of the operator around noon.

(xv) Turgid weight (g)

Turgid weight (TW) was determined after floating of plants on water for overnight at room temperature.

(xvi) Relative water content

The plants were sampled and third fully expanded leaf from the top was detached from the shoots at mid-day (between 9.0 AM to 11.0 AM), quickly sealed in humified polythene bags, and transported to the laboratory on ice. Weighed immediately to take their fresh weight. Then the leaf was kept in Petri dishes filled with distilled water for 3 h. After that the leaf (fully turgid) was weighed again and then kept in oven at 65 °C for 72 h till a constant dry weight.

These three weights were used to calculate RWC (%) of leaves according to the formula given by Weatherley (1950).

$$\text{RWC (\%)} = (\text{Fresh weight} - \text{dry weight}) / (\text{Turgid weight} - \text{dry weight}) \times 100$$

(xvii) Saturation water deficit

It was calculated after subtracting the value of RWC from 100.

$$\text{SWD} = 100 - \text{RWC}$$

(xviii) Membrane stability index

Membrane stability index (MSI) was estimated taking two sets of 200 mgs of leaf samples in test tube containing 10 ml of double distilled water. One set was heated at 40°C for 30 min in a water bath to record the electrical conductivity (C_1) of the solution by an electrical conductivity meter. Second set was subjected to 100°C on a boiling water bath for 10 min to measure its conductivity (C_2) as explained above. Membrane stability index was calculated as following formulae given by Razzaq *et al.* (2013).

$$\text{MSI} = [1 - \{C_1/C_2\}] \times 100$$

C_1 = electrical conductivity of water containing the leaf sample in set one.

C_2 = electrical conductivity of water containing the leaf sample in set two.

3.7.2 Biochemical Observations

(i) Chlorophyll content (mg cm^{-2})

Total chlorophyll was calculated as per method suggested by Arnon *et al.* (1949).

- Total chlorophyll content was estimated on 60 days of sowing procedure was followed.
- Take 100mg fresh random leaf sample (each row) from field after 60 days sowing, respectively.
- Then leaf sample was crushed in 10 ml (80% Acetone) finely and transferred into falcon tube.

- Then Centrifuged for 15 minutes at 10000 rpm and the green supernatant was transferred into fresh 15ml falcon tube.
- Readings were taken in a spectrophotometer at 645 nm, 663 nm and 470nm.

(ii) Estimation of Proline content

Proline was determined spectrophotometrically using the ninhydrin method as described by Bates *et al.* (1973).

- A 0.25 mg fresh random leaf sample from each row was taken from field after 70 days of sowing.
- Sample was crushed very fine in 3 ml (3% homogenize sulpho salicylic acid) solution in mortar pestle.
- Sample was centrifuged at 1000 rpm for 15 minutes and the supernatant was taken (used as proline content) in 15 ml falcon tube.
- Then 2 ml supernatant from falcon tube was taken and 2.0 ml Ninhydrin acid (ninhydrin + Glacial acetic acid) was added.
- Sample was heated at 100 °C for 60 minutes in water bath and mixture was cooled (Ice bath) until temperature comes at room temperature 25°C.
- Then 4.0 ml toluene was added and a pink layer should come after adding, then the upper layer was taken for absorbance at 520 nm in spectrophotometer reading.

(iii) Estimation of sugar content (mgg⁻¹ fresh weight)

Estimation of sugar content by using the anthrone reagent method as described by Dubois *et al.* (1956).

- Fresh random leaf sample (100 mg) from each row from field after 60 days of sowing was taken.
- Leaf sample was crushed in 5.0ml (80% ethanol) in mortar pestle until the leaf completely disappear and makes fine liquid solution.

- The solution (Leaf & ethanol) was poured in the 15.0 ml falcon tube and centrifuged at 1000 rpm for 10 minutes.
- Then the supernatant was transferred in fresh 15.0 ml falcon tube and more 5 ml (80% ethanol) was added into the old tube which has leaf extract and again centrifuged at 1000 rpm for 10 minutes.
- The supernatant was transferred in the falcon tube. Total 10.0 ml (5.0 ml+5.0 ml), supernatant was dried in glass bottle in Oven at 65°C until it gets dried.
- After drying 1.0 ml distil water was added and it was left until it gets dissolved.
- Then 100 micro liters was taken with the help of pipette and add anthrone reagent was added in falcon tube.
- The falcon tube was heated at 100°C for 30 minutes and cooled until it comes at room temperature and then taken the reading at absorption at 630 nm in the spectrophotometer.

(iv) Malondialdehyde (MDA) test (Lipid peroxidation Assay)

The method suggested by Heath and Packer (1968) was employed for measuring the lipid peroxidation in terms of MDA content.

- Leaf sample (25 mg) was taken and was crushed in liquid nitrogen.
- Then 500 microliters of 0.1% trichloro-acetic acid were added and vortexed and centrifuged at 10,000 rpm for 10 min.
- 100 microliters of supernatant were taken in an Eppendorf tube and 200 microliters 0.5% TBA was added.
- Then reaction mixture was heated for 95°C for 30 minutes and quickly kept at -80°C for 2 minutes to stop the reaction.
- After 2 minutes let it come at room temperature and centrifuged at 10000 rpm for 10 min and supernatant was taken to take absorption at 532 nm.

(v) Determination of antioxidant enzyme activity

v.i. Catalase activity

Catalase activity was measured according to the protocol given by Aebi (1983).

- Leaf sample (100 mg) sample was collected from normal and water-logged plants were taken and homogenized in 5.0 ml of 0.1M phosphate buffer (pH 6.4) in a chilled pestle and mortar.
- The crude extract was centrifuged at 10,000 rpm for 20 minutes at 4°C. The enzyme extract was stored at low temperature until completion of enzyme assay.
- The activity of enzyme was assayed by taking 2.6 ml, 0.1M phosphate buffer (pH 6.4), 0.1 ml enzyme extract and 0.1 ml and 1.0 percent H₂O₂. The reaction mixture was mixed rapidly at room temperature.
- A blank was prepared similarly in which 0.1M phosphate buffer (pH 6.4) was added in reaction mixture instead of enzyme extract. Changes in absorbance at 230 nm at an interval of 15 second were noted for 2 minutes.

vii. Peroxidase activity

Peroxidase activity assay was performed as per the protocol given by Kar and Mishra (1976).

- Enzyme extraction was done by homogenizing 100 mg plant sample (leaf sample) of normal and water-logged plants in 5.0 ml, 0.1M phosphate buffer (pH 6.4) in a chilled pestle and mortar.
- The crude extract was centrifuged at 10,000 rpm for 20 minutes at 4°C.
- Supernatant was stored at 4°C till the enzyme assay was performed.
- Reaction mixture was prepared by adding 4.6 ml 0.1M phosphate buffer (pH 6.4), 0.2 ml pyragallol (50 µM) and 0.1 ml 50 µM H₂O₂ and 0.1 ml enzyme extract. Mixture was incubated at 25°C for 5 minutes.
- Then 0.5 ml 5.0 per cent H₂SO₄ was added to terminate the reaction. Absorbance was measured at 420 nm with the help of spectrophotometer.

v.iii. Glutathione reductase activity (GR)

GR activity was estimated by the method of Smith *et al.* (1989).

- The reagents used were 50 mM potassium phosphate buffer (pH 7.6) containing 1 mM EDTA, 5 mM NADPH, 6 mM 5,5'-dithio-bis (2-nitrobenzoic acid) [DTNB] and 0.2 mM oxidized glutathione (GSSG).

- To prepare the reaction mixture to determine GR activity, diluted enzyme extract (25 μ l), DTNB (250 μ l), 1mM EDTA (20 μ l) and 0.2 mM GSSG (100 μ l) were added in 175 μ l of 50 mM potassium phosphate buffer (pH 7.6).
- To initiate GR activity 50 μ l of 5 mM NADPH added to the reaction mixture.
- Absorbance at 412 nm was followed at 15 s interval up to 2 min.

(vi) Estimation of hydrogen peroxide (H_2O_2 , mmol g^{-1} FW)

Estimation of hydrogen peroxide was performed as per protocol proposed by Alexieva *et al.* (2001).

- Leaf sample (25.0 mg) was taken and crushed in liquid nitrogen.
- 500 microliters of 0.1% trichloro-acetic acid was added and vortexed and centrifuged at 10000 rpm for 10 min.
- 100 microliters of supernatant were taken in an Eppendorf tube and 200 microliters of 0.5% TBA was added.
- The reaction mixture was heated at 95°C for 30 minutes and quickly kept at - 80°C for 2 minutes to stop the reaction.
- After 2 minutes let it come at room temperature and centrifuged it at 10000 rpm for 10 min and supernatant was taken to take reading at 532 nm absorption.



Plate 6. Biochemical parameter analysis at biochemical analysis lab

3.8 Statistical Analysis

The replication wise mean values of each genotype for various characters were subjected to statistical analysis as per the procedure of Randomized Block Design as suggested by Panse and Sukhatme (1978).

3.8.1 Analysis of variance

3.8.2 Combining ability analyses

3.7.2.1 Analyses of variance for combining ability (diallel)

3.7.2.2 Estimates of general and specific combining ability effects

3.8.1 Analysis of variance for experiment design

The data pertaining to various characters were analyzed as per the procedure of Randomized Block Design given by Panse and Sukhatme (1978). The following linear additive statistical model was used.

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = Mean Performance of the i th genotype in j th replication,

μ = General mean,

g_i = Effect of i th genotype,

r_j = Effect of j th replication,

e_{ij} = Random experimental error associated with i^{th} genotype and j^{th} replication.

$i = 1, 2, \dots, g$

$j = 1, 2, \dots, r$

The usual form of analysis of variance is given in (Table 4) To provide comparison, genotypic sum of square was partitioned in to parents, hybrids and parents vs. hybrids.

Table 4. Analysis of variance (ANOVA)

Source of Variation	df	MSS	Expected MS	Cal. F
Replication	(r-1)	Mr	$\sigma^2_e + g \sigma^2_r$	
Genotypes	(g-1)	Mg	$\sigma^2_e + r \sigma^2_g$	
Parents	(p-1)	Mp	$\sigma^2_e + r \sigma^2_p$	
F1 hybrids	(h-1)	Mh	$\sigma^2_e + r \sigma^2_h$	
Parents Vs Hybrids	1	Mph	$\sigma^2_e + r \sigma^2_{ph}$	
Error	(p-1) (h-1)	Me	σ^2_e	
Total	(rg-1)	-	-	

Where,

r = Number of replications,

g = Number of genotypes (Parents + Hybrids),

p = Number of parents,

h = Number of F₁'s hybrids,

σ^2_r = Variance due to replications,

σ^2_g = Variance due to genotypes,

σ^2_p = Variance due to parents,

σ^2_h = Variance due to hybrids,

σ^2_{ph} = Variance due to parents vs. hybrids,

σ^2_e = Error variance.

The significance of each source was tested against the error mean square by applying the usual 'F' test.

The standard error of mean (S.Em.), Critical Difference (C.D.) and percent coefficient of variance (C.V. %) were estimated as under.

$$\text{S.Em.} = (2M_e/r)^{1/2}$$

$$\text{C.D. at 5 \%} = \text{S.Em.} \times (2)^{0.5} \times \text{table } t^{0.05} \text{ at error d.f.}$$

$$\text{C.V. (\%)} = [(\text{Me})^{1/2} / \text{general mean}] 100$$

Where,

S.Em. = Standard error of mean

r = Number of replications

3.8.2 Combining ability analysis

3.8.2.1 Analysis of variance for combining ability (diallel)

Mean value of 36 entries (parents and hybrids) were entered in computer and combining ability analysis was carried out according to the procedure given by Griffing (1956a) as per Method II (in which parents and a set of F1s without reciprocals are included) and Model I [which assumes that the genotypes and block effects are constant (fixed) but environmental effect is variable]. The combining ability analysis was carried out as per the method suggested by Griffing (1956a) Method- II, Model-I which assumes that variety and block effects are constant (fixed).

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + [1/r] \sum e_{ijk}$$

Where,

Y_{ijk} = Performance of hybrid of ij th cross in k th replication,

$i, j = 1, 2, 3, \dots, P$ (Number of parents)

$k = 1, 2, 3, \dots, b$ (Number of replications)

μ = General mean,

g_i = General combining ability effect of i th parent,

g_j = General combining ability effect of j th parent,

s_{ij} = Specific combining ability effect of the cross between i th and j th parents,

e_{ijk} = Environmental effect pertaining to ijk th observation.

Table 5. Analysis of variance for combining ability

Source	Df	S.S.	M.S.S.	E.M.S.
GCA	(p-1)	Sg	Mg	$\sigma^2_e + (p+2) \sum (p-1) / 1g2i$
SCA	P (p -1)/ 2	Ss	Ms	$\sigma^2_e + \sum \sum p (p -1) i \leq j 2S2ij$
Error	(g-1) (r-1)	Se	Me	σ^2_e

The sum of squares due to various sources was calculated as follows:

$$S_g = \frac{1}{p+2} \sum_i \sum_j (Y_i + Y_{ii}) - \frac{4}{p} Y^2 \dots$$

Sum of square due to sca (Ss) was estimated as:

$$S_s = \sum_i \sum_j Y^2_{ij} - \frac{1}{p+2} \sum_i (Y_{i.} + Y_{ii})^2 + \frac{2}{(p+1)(p+2)} Y^2_{..}$$

Where,

p = Number of parents,

g = Number of progenies,

S_g = Sum of squares due to general combining ability,

S_s = Sum of squares due to specific combining ability,

Y_i = Array totals of ith parent,

Y_{ii} = Mean value of ith parent,

Y... = Grand total, parents and half diallel matrix,

Y_{ij} = Mean value of ijth cross,

Me = Error mean square in the analysis of the experimental design (R.B.D.) Me/r

R = Number of replications,

Me was used for calculation of variance ratio (F) as a test of gca and sca mean squares.

Genetic component of variance was estimated as under:

$$\text{Variance due to gca (g i}^2) = (Mg - Me') \times (p/p+2)$$

Variance due to sca (s_{ij}^2) = (Ms – Me')

3.8.2.2 Estimates of general and specific combining ability effects

The gca and sca effects were calculated by applying the following formulae.

$$\text{gca effect } g_i = 1/(p+2) [\sum (Y_{i.} + Y_{ii}) - 2/p \sum Y_{...}]$$

$$\text{sca effect } s_{ij} = Y_{ij} - 1/(p+2) [Y_{i.} + Y_{ii} + Y_{.j} + Y_{jj}] + 2/(p+1)(p+2) Y_{..}$$

Where,

$Y_{i.} + Y_{ii}$ = Total of i^{th} array + mean value of parent i

$Y_{.j} + Y_{jj}$ = Total of j^{th} array + mean value of parent j

The estimation of standard errors of general combining ability and specific combining ability effects were obtained as under:

$$\text{S.E. } (g_i) = [(p-1) \sigma^2_e / p(p+2)]^{1/2}$$

(to test individual gca effect)

$$\text{S.E. } (s_{ij}) = [p(p-1) \sigma^2_e / (p+1) (p+2)]^{1/2}$$

(to test individual sca effect)

$$\text{S.E. } (g_i - g_j) = [2 \sigma^2_e / (p+2)]^{1/2}$$

(to test the difference between two gca effects)

$$\text{S.E. } (s_{ij} - s_{ik}) = [2 \sigma^2_e / (p+2)]^{1/2}$$

(to test the difference between sca of the same array or column)

$$\text{S.E. } (s_{ij} - s_{kl}) = [2 p \sigma^2_e / (p+2)]^{1/2}$$

(to test the sca of any two crosses)

Where,

p = Number of parents

σ^2_e = Error mean square (Me)

Each gca and sca effects were subjected to 't' test for testing of significance.

't' test for gca = $(g_i - 0) / \text{S.E. } (g_i)$

't' test for sca = $(s_{ij} - 0) / \text{S.E. } (s_{ij})$

Since error degree of freedom are greater than 30, the value of calculated 't' is regarded as significant if it exceeds 1.96 and 2.58 at 5 per cent and 1 per cent levels of significance, respectively.

Alternatively, gca and sca effects were compared with critical difference calculated by following formula:

$$\text{C. D.}_{(g_i)} = \text{S.E. } (g_i) \times \text{table } t_{0.05} \text{ and } t_{0.01}$$

$$\text{C. D.}_{(s_{ij})} = \text{S.E. } (s_{ij}) \times \text{table } t_{0.05} \text{ and } t_{0.01}$$

3.8.3 Estimation of Heterosis

Heterosis is expressed as per cent increase or decrease of F_1 over the mid-parent (MP), better parent (BP) and standard check (SC) referred as relative heterosis, heterobeltiosis and standard heterosis respectively. Heterosis, heterobeltiosis and economic heterosis were calculated according to the method suggested by Shull (1908), Fonseca and Patterson (1968) and Meredith and Bridge (1972), respectively for individual as well as over the environments.

$$\text{Heterosis (\%)} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

Its significance was tested by using student "t" test.

$$t_{EDF} = \frac{\overline{F_1} - \overline{MP}}{SE(\overline{F_1} - \overline{MP})}$$

$$SE(\overline{F_1} - \overline{MP}) = \sqrt{\frac{3MSE}{2n}}$$

Heterobeltiosis:

$$\text{Heterobeltiosis (\%)} = \frac{(\overline{F_1} - \overline{BP})}{\overline{BP}} \times 100$$

Its significance was tested by using student "t" test.

$$t_{EDF} = \frac{\overline{F_1} - \overline{BP}}{SE(\overline{F_1} - \overline{BP})}$$

$$SE(\overline{F_1} - \overline{BP}) = \sqrt{\frac{2MSE}{n}}$$

Economic heterosis:

$$\text{Economic heterosis (\%)} = \frac{(\overline{F_1} - \overline{BC})}{\overline{BC}} \times 100$$

Its significance was tested by using student “t” test.

$$t_{EDF} = \frac{\overline{F_1} - \overline{BC}}{SE(\overline{F_1} - \overline{BC})}$$

$$SE(\overline{F_1} - \overline{BC}) = \sqrt{\frac{2MSE}{n}}$$

Where,

F_1	=	Mean value of hybrid
MP	=	Mean of two parents of corresponding F_1 i.e. $(P_1 + P_2)/2$
BP	=	Mean value of better parent
BC	=	Mean value of best checks
n	=	Divisor in respective conditions i.e. r in case of individual environment and rs in over the environments.
r, s	=	Number of replications and environments respectively.
MSE	=	Error mean square for individual and over the environments, respectively.
t_{EDF}	=	Student’s ‘t’ at error degree of freedom

To calculate heterobeltiosis and economic heterosis parents and checks had higher mean values were considered desirable for all the characters except traits like days to 50 percent tasselling, days to 50 per cent silking, ASI, days to

maturity, plant height and ear height, where lower mean value was considered desirable and both were calculated in desirable directions only.

The significance of heterosis was tested using the t-test against the critical difference (CD). The CD for testing the significance of mid parent (MP), better parent (BP), and standard heterosis (SH) were calculated as suggested by Cochran and Cox (1960) and Singh *et. al.* (1985) as follows:

1. Critical difference (CD) for heterosis over mid parent (MP)

$$CD \text{ for MP} = \pm \left(\frac{\sqrt{3eMs}}{2r} \right) * t$$

$$SE(d) \text{ for MP} = \pm \left(\frac{\sqrt{3eMs}}{2r} \right)$$

$$t \text{ (Mid-parent)} = \frac{F1-MP}{SE(d)}$$

2. Critical difference for heterosis over better parent or standard heterosis (SH)

$$CD \text{ for BP/SH} = \pm \left(\frac{\sqrt{2eMs}}{r} \right) * t$$

$$SE(d) \text{ for BP/SH} = \pm \left(\frac{\sqrt{2eMs}}{r} \right)$$

$$t \text{ (Better-parent)} = \frac{F1-BP}{SE(d)}$$

$$t \text{ (Standard hybrid)} = \frac{F1-SV}{SE(d)}$$

Where,

SE (d) = standard error of the difference

EMS = error mean square

r = number of replications

F₁, MP, BP, and SV are mean values of the hybrids, mid parent, a better parent, and standard variety, respectively.

The computed t values were tested against the t value at the error degrees of freedom for table value at 5% and 1% probability levels.

3.8.4 Estimation of genetic parameters

To prove the adequacy of genetic model, the genetic parameters were estimated as described by Hayman (1954a) as shown in the Table 6. Where, E is measured as the average shifting of all genotypes from the origin due to environmental causes.

h^2 is estimated as the algebraic sum of heterozygous loci in all the crosses $(H1/D)^{1/2}$ value is between zero to unity in case of partial dominance and it exceeds unity in case of over dominance. $H_2/4H_1$ has maximum value 0.25 when there is an equal distribution of alleles over the loci. KD/KR ratio shows an excess of dominant alleles in the parents, if it is greater than unity. h^2/H^2 is based on the assumptions that positive and negative effects bearing alleles are equally frequent at all the loci with unidirectional dominance.

Table 6. Genetic parameters

Genetic Parameters	Symbols	Formulae
Environmental variance	E	$\{(ESS+RSS)/Edf+Rdf\}/nR$
Additive variance	D	$VOLO1 - E$
Variation due to dominant effect of genes	$H1$	$VOLO1 - 4WOLO1 + 4V1L1 - E(3n-2/n)$
Variation due to dominant effect of gene correlated with gene distribution	$H2$	$4V1L1 - 4VOL1 - 2E$
Over all dominant effect of heterozygous loci	$h2$	$4(ML1-MLO)2 - 4(n-1) E/n2$
Relative frequency of dominant to recessive alleles	F	$2VOLO1 - 4WOLO1 - 2(n-2) E/n$
Mean degree of dominance	$(H1 / D)^{1/2}$	
Proportion of genes with positive and negative effect in the parents	$H2 / 4H1$	
Proportion of dominant and recessive genes in the parents	KD/KR	$(4DH1)^{1/2} + F/(4DH1)^{1/2} - F$
The number of groups of genes which control the character and exhibit dominance	$h2/H2$	
Narrow sense heritability	$h2\ ns$	$\frac{1}{2} D + \frac{1}{2} H1 - \frac{1}{2} H2 - \frac{1}{2} F / \frac{1}{2} D + \frac{1}{2} H1 - \frac{1}{4} H3 - \frac{1}{2} F + E1$

This can be presented as:

Variance of family means with an array

$$\text{Var (Vr)} = [\Sigma x^2 - (\Sigma x)^2/n] / (n-1)$$

Covariance of these means with non-recurrent parent

$$\text{Var (Wr)} = [\Sigma x y - (\Sigma x \cdot \Sigma y)/n] / n - 1$$

3.9 Genetic components of variance

The genetic components of variance viz., phenotypic and genotypic coefficients of variation percent were computed by the following formulae given by Burton (1952).

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\text{phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

heritability

Heritability percent in broad sense was estimated by the following formula as given by Singh and Choudhary (1977).

$$\text{Heritability (h}^2\text{)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Genetic advance

The estimates of expected genetic advance from selection, G (s), was obtained by the formula suggested by Comstock *et al.* (1949).

$$G(s) = k \times h^2 \times \sigma_p$$

Where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h² = Heritability in broad sense

σ_p = Phenotypic standard deviation

3.10 Molecular Analysis

A. Plant Material:

Total eighty genotypes including 12 inbred lines/parents, 66 crosses and two check varieties were used in this study.

B. Genomic DNA extraction:

Total genomic DNA of eighty genotypes was isolated from young leaves following the procedure of Doyle and Doyle (1990).

- i. Young leaves from four-week-old plants were collected and were placed in glassine bags and stored in ice.
- ii. The leaves were ground to paste using pre-chilled pestle and mortar after adding pre-warmed (60°C) 500µl CTAB buffer and 3-mercaptoethanol to make leaves brittle as well as to stop DNase activity. The composition of extraction buffer is given in (Table 7).
- iii. The powder was transferred immediately to a 2.0 ml Eppendorf tube.
- iv. The tubes were incubated at 60°C for half hour in a water bath. The samples were mixed occasionally while maintaining at 60°C.
- v. After incubation, tubes were allowed to come to room temperature and 50 µl of chloroform: isoamyl alcohol (24:1) was added and tubes were swirled, till it made a dark green emulsion. The tubes were centrifuged at 6,000 rpm for 10 minutes at 24°C. After centrifugation three layers were obtained: Top (Aqueous phase), Middle (Debris and Proteins) and Bottom (Chloroform). The tubes were handled very carefully to prevent disturbance of layers.
- vi. The supernatant was transferred to another 2.0 ml Eppendorf tube. Then double volume of chilled isopropanol was added and kept for overnight at 0 °C.

- vii. Next day sample was centrifuged at 6000 rpm for 10 minutes at 4°C.
- viii. Following centrifugation, supernatant was discarded and the pellet was air dried by opening the lid of tube and kept at room temperature.

Table 7. Composition of CTAB extraction buffer (for 300 ml)

Components	Working Concentration (Final volume)
CTAB	3% (9g)
Tris HCL (pH 8.0)	100mM (30 ml)
NaCl	1.4 M (105 ml)
EDTA (pH 8.0)	20 mM (12 ml)
Polyvinylpyrrolidone (PVP)	2% (6g)

C. Purification of genomic DNA

Freshly isolated DNA contained certain impurities like, polyphenolics, proteins, polypeptides *etc.*, it was necessary to purify the DNA before PCR analysis was performed.

- I. First of all, 100 µl TE buffer was added to dissolve the pellet.
- II. Then to avoid RNA impurities 3µ RNase (10mg/ml of RNase in buffer, 10mM Tris HCL, 15mM NaCl pH 7.5) was added to each tube and incubated at 37°C in water bath for 1 hour.
- III. Then equal volume of PCI Phenol: Chloroform: Isoamyl alcohol (25:24:1) was added to each tube and inverted gently and centrifuged at 6000 rpm for 10 minutes at 24°C.
- IV. The upper phase was again pipette out in 2.0 ml Eppendorf tube. Then Chloroform: Isoamyl alcohol (24:1) were added and centrifuged at 5000 rpm at room temperature, after centrifugation supernatant was transferred in 1.5 ml Eppendorf tubes. Then double volume chilled isopropanol was added to each tube and mixed it with inverting the tubes for few times to aggregate DNA fibers and then kept it for overnight at 0°C in refrigerator.

- V. Next day samples were centrifuged at 5000 rpm for 10 minutes at 4°C and after centrifugation supernatant was discarded.
- VI. The DNA pellets were dried into air for 2 to 4 hrs.
- VII. The dry pellet was dissolved in appropriate volume of TE buffer (Tris EDTA buffer-10 mM, TrisHCl, 1 mM EDTA, pH 8.0) or nuclease free water. The DNA samples were dissolved at room temperature and stored at -20°C until used.

Composition of 50X TAE buffer (for 1 lt.)

Component	Quantity
Tris base	242g
0.5M EDTA (pH 8.0)	100 ml
Glacial acetic acid	57.1 ml
ddH ₂ O	To make up to the volume to 1 lt.

Note: After making the solution pH was kept at 8-8.5

Preparation of 6X Gel loading Dye

Components	Working Concentration
TrisHCl (pH 7.6)	10 mM
Bromophenol blue	0.03% w/v
Xylene cyanol	0.03% w/v
Glycerol	60%
EDTA	60 mM

Composition of TE Buffer (for 100 ml)

Components	Quantity
1M Tris	1000μl
0.5M EDTA (pH-8.0)	200 μl
ddH ₂ O	To make up the volume to 100ml

D. Assessment of quality and quantity of DNA

Quality and quantity of DNA were checked on 0.8% agarose gel electrophoresis. This technique is very simple and rapid to perform and capable of resolving fragments of DNA.

Preparation of 1X TAE Buffer

100 ml of 1XTAE buffer was prepared by adding 2.0 ml 50 X TAE Buffer in 98 ml sterilized water.

Preparation of Agarose Gel

Agarose gel (0.8 %) was prepared by dissolving 1.6 g agarose in 200 ml of 1X TAE buffer (147.0 ml water + 3.0 ml 50X TAE). The mixture was boiled until it become transparent, then it was allowed to cool.

Casting Agarose Gel

Ethidium Bromide (2.0 µl) was added in solution. Comb was placed in a casting tray and agarose was poured into the tray and allowed to solidify. The combs were removed to open off wells. Two µl of extracted DNA from sample was loaded into each individual well with 2µl 6X loading dye. Then gel was allowed to run at 60V for 40 minutes. After that gel was transferred into Gel documentation System to see the presence or absence of DNA.

D. Selection of primers

In the present study, 20 SSR primers (Table 9) were selected from the reported work (Maheswari *et al.*, 2016).

Determination of annealing temperature of the primers

The temperature at which primer binds to the template DNA is called annealing temperature. The formula provided by Mazers *et al.* (1990) was employed to calculate melting Temperature (T_m), whereas annealing temperature of primer ranged 2°C below melting temperature.

$$T_m (^{\circ}\text{C}) = 2 (A+T) + 4(G+C)$$

E. PCR amplification

PCR was developed by Kary Mullis 1983. This method is based on periodic heating and cooling of the reaction mixture. Heating causes denaturation of DNA whereas lower temperatures permit binding of the primers and enzymatic replication of the DNA. Primers (short DNA fragments) complementary to the target region along with a DNA polymerase are key components to enable selective and repeated amplification. The reaction was performed into a 96 well micro litter plate in a G-STORM Master Cyclor gradient using 25-30ng of genomic DNA of each genotype to make final volume of 20µl per reaction. The stock and final concentration of different components used in PCR are given in Table 8.

Table 8 Stock and final concentration of different components used in PCR reaction

Components	Stock Conc.	Volume (µl)	Final Conc.
Water	--	6.6	---
PCR buffer+MgCl ₂	10X*	2.0	1X
dNTPs	10mM	4.0	200µM
Primer Forward	5pM	1.0	0.5 µM
Primer Reverse	5pM	1.0	0.5 µM
Taq Polymerase	3U/µl	0.2	1 Unit
DNA template	25ng/ µl	2	50 ng
Total		20	

*10X PCR buffer: 10mM Tris HCl, pH 8.3, 50mM KCl, 1.5mM MgCl₂, 0.01 % Gelatin

Table 9 Details of twenty SSR primers employed for study of genetic diversity among different maize genotypes

Sr. No.	Marker	Forward primer (5'–3')	Reverse primer (5'–3')	No. of Repeats
1	bnlg1028	AGGAAACGAACACAGCAGCT	TGCATAGACAAAACCGACGT	AG (12)
2	bnlg1035	TGCTTGCACTGTCAGGAATC	CAGCTCTGACACACCACACA	AG (13)
3	bnlg1063	GGAGACAACCCCGACGAC	GGTACCAGAGCCACAGATCC	AG (42)
4	bnlg1083	ACAGTCTGTTGGGGAACAGG	CAACGCTGGTTTGTCGTTTA	AG (29)
5	bnlg1136	CATCAGCTTCAACGAGTTTCG	TAACCGGATGAGCATCTTCC	AG (14)
6	bnlg1225	GCAGTAGAAGAGCGAGCGAG	CATACGCTGTCACTGCCACT	AG (14)
7	bnlg1297	TCTCGATCGCTCCGATCTAT	GACTCAACTCCAAAAGGCGA	AG (32)
8	bnlg1327	CTCTCTCGCGTGTGTGC	TGGGTCTCCTTCTCCGTCTA	CT (25)
9	bnlg1346	CATCATGAAGCAATGAAGCC	CCGCGCCATTATCTAGTTGT	AG (24)
10	bnlg1614	CCAACCCACCCAGAGGAGA	AGCGGGCGAGATCTTCAT	AG (15)
11	bnlg1812	CGAGAAGACTTGCGTGAACA	TTACGTGCGTCGTCAGAATC	AG (22)
12	bnlg1866	CCCAGCGCATGTCAACTCT	CCCCGGTAATTCAGTGGATA	AG (11)
13	bnlg2190	TCCTCCTTCATCCCCTTCTT	CCCAGTATCATTGCCCAATC	AG (31)
14	bnlg2248	CCACCACATCCGTTACATCA	ACTTTGACACCGGCGAATAC	AG (30)
15	bnlg2252	GTCTTTGACCCCTTCCTCTTCTTG	CACTGCACTGCAAGGTACATACG	TCC (4)
16	bnlg2328	AGCAGTGAGGAAGAAGCAGG	TTACCCTCCCTTGTCGTGAC	AG (33)
17	bnlg439	TTGACATCGCCATCTTGGTGACCA	TCTTAATGCGATCGTACGAAGTTGTGGAA	NA
18	dupssr13	CAAATATCTCTCATCTTTGCTGAC	TCGTTCCGGTCCATGAAAT	–
19	nc012	TAATTTAAACACCACACCACCG	ACACACGCCAAAGAAAAACC	CT
20	phi053	CTGCCTCTCAGATTCAGAGATTGAC	AACCCAACGTA CTCCGGCAG	ATAC



Plate 7. Molecular work performed at Molecular Biology lab

PCR amplification was performed using temperature profile mentioned in Table 9. The standard PCR profile was used with 35 polymerization cycles to

get sufficient yield of targeted amplicon to be visualized. The annealing temperature of the primers employed ranged between 45-55°C.

Table 10. Temperature profile used in PCR

Step	Temperature (°C)	Time (minutes)	No. of cycles
Initial denaturation	94	3	1
Denaturation	94	1	35
Annealing	45-55	1	35
Elongation	72	2	35
Final Extension	72	7	1
Hold	4	-	-

F. Resolution and visualization of PCR products

After PCR amplification, electrophoresis of the amplified product was done by loading it into 3% agarose gel, prepared in 1X TAE buffer. The process of gel running was same as described before contrasting the agarose concentration.

G. Scoring of SSR alleles and data analysis

The SSR allele sizes were determined by the position of bands relative to the DNA ladder. Total number of alleles was recorded for each SSR primers across all the genotypes under study by giving the number to amplified alleles as 1, 2, 3 and so on. The amplified bands were recorded as 1 (band present) and 0 (band absent) in a binary matrix. The amplicon size was made out from the 50 or 100 by ladder run along with the PCR products on the gel.

The allelic data of 20 polymorphic SSRs primers collected in the form of binary data [*i.e.*, presence (1) or absence (0) of bands] were subjected to statistical analysis using Power Marker ver. 4.0 (Liu and Muse, 2005) to calculate the total number of alleles, allele frequency, major allele frequency (MAF), gene diversity (GD) and expected heterozygosity (He). Polymorphic information content (PIC) was calculated following Botstein *et al.* (1980) for the estimation of marker informativeness. The major allelic frequency, polymorphism information content and genetic distance-based clustering was performed with Unweighted Pair Group Method for Arithmetic Average (UPGMA) tree using power Marker v3.25 software.

CHAPTER – 4

RESULTS

The experimental results of the present investigation entitled “Genetic enhancement of maize (*Zea mays* L.) for drought using phenotyping, genotyping and conventional breeding approaches” are presented under following heads:

4.1 Analysis of variance for different quantitative traits

4.2 *Per se* performance of parents and their hybrids in individual and over the environments.

4.3 Combining ability analysis

4.3.1 Analysis of variance for combining ability

4.3.2: Estimation of combining ability (*gca* and *sca*) effects

4.4 Components of genetic variance

4.5 Magnitude of heterosis

4.6 Genetic variability, heritability, genetic advance and genetic advance as percent of mean

4.7 Biochemical test

4.8 Molecular characterization

4.1 Analysis of variance for different quantitative traits

Analysis of variance was performed to test the difference amongst parents and hybrids for all the eighteen traits and the result are presented in Table 11 & 12. The results revealed that the MSS (Mean Sum of Squares) due to genotypes were highly significant for all the characters studied. The MSS due to genotypes were further partitioned into parents, hybrids and parents vs. hybrids. The analysis of variance for experimental design in individual environment revealed significant differences among genotypes for all the characters in both the environments

Further partitioning of genotypic variance into parents, hybrids and parent's v/s hybrids revealed that for all the characters under study there were significant difference in all environments.

The Mean Sum of Squares of hybrids were also significant for all the characters in all the environments. This indicated the existence of appreciable amount of genetic variability in the experimental material of present study. (Table 11 & 12).

Table 11 Pooled ANOVA for different quantitative traits over (two) environments studied in maize (*Zea mays* L.) under irrigated condition

Source of Variations	df	Days to 50 % tasseling	Days to 50 % silking	Anthesis silking interval	Plant height (cm)	Cob length (cm)	Number of kernel rows per cob	Numbers of kernel per rows	100 grain weight (g)	Seed Yield per plant (g)
Env.	1	7262051.28**	77143.70**	7020.51**	185644.12**	0.2	802.24**	307.4**	4160.27**	275.83**
Blk. Within Env.	2	10339.1**	105.4**	4402.56**	472.5**	10.92**	329.62**	182.25**	988.91**	62.40**
Treat.	77	16432.45**	159.87**	323.36**	1289.42**	6.88**	694.14**	65.03**	3590.61**	1652.03**
Prnt.	11	24445.45**	245.59**	258.33**	2744.3**	3.4**	833.60**	91.91**	4588.9**	801.30**
Hyb.	65	13365.43**	122.76**	304.55**	866.82**	6.5**	652.25**	40.64**	3444.5**	1550.33**
Prnt. vs. Hyb.	1	127645.69**	1629.13**	2261.6**	12754.91**	71.25**	1883.08**	1355.01**	2107.05**	17620.77**
Treat. * Env.	77	13149.98**	122.08	238.05**	673.42**	0.79	45.63	3.99**	335.06**	22.61**
Prnt * Env.	11	14044.7**	140.56**	297.72**	1215.13**	0.85	48.65	3.76	1281.56**	26.28**
Hyb. * Env.	65	12004.87**	107.83**	229.67**	485.5**	0.78	43.12	4.05**	141.37**	21.08**
Prnt vs. Hyb. * Env.	1	77740.38**	844.77**	128.73*	6929.11**	0.66	175.51	3.01	2513.70**	81.38**
Error	154	48.19	0.59	14.90	1.68	0.59	41.08	2.07	40.87	1.18
Total	311	30765.27	318.82	197.26	1086.78	2.26	208.2	20.28	1011.93	416.49

* and ** significant at 5% and 1% level of significance, respectively,

Env. = Environment, Blk.= Blocks, Treat. = Treatments, Prnt. = Parent, Hyb. = Hybrid

Contd.....

Table 11 contd.....

Source of Variations	df	Number of cobs per plant	Days to maturity	Cob girth (cm)	Shelling %	Canopy temp.	Turgid weight (g)	Relative water content	Saturation water deficit	Membrane stability index
Env.	1	6.20*	17239601.28**	1453.85**	21.78	19.80**	29.54**	3.10*	3.20*	34318.24**
Blk. Within Env.	2	14.68**	10339.10**	988.91**	81.00**	32.57**	90.78**	16.05**	16.19**	12.22
Treat.	77	41.78**	2475.04**	719.98**	148.86**	7.57**	2180.38**	168.43**	168.49**	65578.13
Prnt.	11	39.17**	3396.97**	209.10**	74.66**	4.55**	2395.11**	272.68**	272.68**	53173.32**
Hyb.	65	42.7**	2304.62**	756.17**	163.70**	7.76**	2001.40**	152.95**	153.01**	68576.49**
Prnt. vs. Hyb.	1	11.14*	3412.82**	3987.11**	0.46	28.94**	11451.92**	28.21**	28.08**	7137.67**
Treat. * Env.	77	5.85**	2048.03**	67.71**	11.92**	0.21	27.56**	3.54**	3.53**	10529.90**
Prnt * Env.	11	2.53*	984.09**	82.15**	23.25**	0.42	25.79**	5.03**	5.03**	11944.42**
Hyb. * Env.	65	6.5**	2224.80**	64.87**	9.58*	0.17	27.83**	3.31**	3.30**	10194.76**
Prnt vs. Hyb. * Env.	1	0.04	2261.6**	93.38	39.69*	0.80	29.76**	1.26	1.28	16754.37**
Error	154	1.11	48.19	40.87	6.50	1.19	0.81	0.77	0.77	32.93
Total	311	12.46	56643.02	226.3	43.62	2.79	547.74	43.07	43.08	18970.2

* and ** significant at 5% and 1% level of significance, respectively,

Env. = Environment, Blk.= Blocks, Treat. = Treatments, Prnt. = Parent, Hyb. = Hybrid

Table 12 Pooled ANOVA for different quantitative traits over (two) environments studied in maize (*Zea mays* L.) under partially irrigated condition

Source of Variations	df	Days to 50 % tasseling	Days to 50 % silking	Anthesis silking interval	Plant height (cm)	Cob length (cm)	Number of kernel rows per cob	Numbers of kernel per rows	100 grain weight (g)	Seed Yield per plant (g)
Env.	1	5713232.1**	6829312.82**	23538.8**	57152.35**	1.58	974.14**	29.51**	5006753.37**	300.90**
Blk. Within Env.	2	10339.10**	13805.13**	4119.55**	472.49**	10.92**	345.41**	219.91**	988.91**	62.41**
Treat.	77	17336.8**	16555.58**	266.12**	1111.46**	5.67**	818.30**	54.18**	5192886.78**	1148.2**
Prnt.	11	23662.88**	22817.42**	483.90**	1930.29**	3.02**	1872.53**	106.07**	5029.63**	884.47**
Hyb.	65	14862.49**	14035.78**	231.59**	705.42**	5.53**	563.98**	38.31**	6136227.05**	1009.92**
Prnt. vs. Hyb.	1	108579.55**	111462.06**	115.4**	18497.25**	43.72**	5753.02**	514.27**	942198.10**	13037.54**
Treat. * Env.	77	13616.47**	12758.28**	230.99**	859.17**	4.12**	314.81**	16.02**	5196501	365.67**
Prnt * Env.	11	16224.24**	15690.15**	247.54**	604.64**	3.90**	543.01**	14.39**	3838.02**	169.47**
Hyb. * Env.	65	12231.72**	11391.26**	230.90**	871.49**	4.17**	256.02**	16.31**	6141254.47**	404.31**
Prnt vs. Hyb. * Env.	1	74939.16**	69363.70**	54.21*	2857.81**	3.50*	1626.40	15.34**	906789.06**	11.75*
Error	154	48.19	34.35	11.76	1.68	0.59	40.87	0.88	40.87	1.19
Total	311	26124.54	29322.76	231.08	675.55	2.79	306.14	19.32	2588.42	376.77

* and ** significant at 5% and 1% level of significance, respectively,

Env. = Environment, Blk.= Blocks, Treat. = Treatments, Prnt. = Parent, Hyb. = Hybrid

Contd.....

Table 12 contd....

Source of Variations	df	Number of cobs per plant	Days to maturity	Cob girth (cm),	Shelling %	Canopy temp.	Turgid weight (g)	Relative water content	Saturation water deficit	Membrane stability index
Env.	1	0.42	15490482.05**	3429.43**	84.4	49.28**	262.17**	5570.24**	5629.55**	556.51**
Blk. Within Env.	2	16.32**	10339.10**	964.91**	40.51	32.57**	90.78**	2007.82**	2033.25**	0.32
Treat.	77	31.12**	2903.45**	378.68**	124.13**	7.01**	2169.87**	16130.61**	16120.29**	1287.49**
Prnt.	11	37.63**	4187.88**	700.93**	108.75**	2.82*	2448.06**	27299.36**	27299.36**	858.27**
Hyb.	65	30.28**	2669.21**	272.50**	126.7**	7.75**	1989.64**	14474.15**	14462.08**	1354.80**
Prnt. vs. Hyb.	1	14.27**	4000.23**	3735.73**	126.32	3.88	10825.23**	944.51**	934.16**	1633.58**
Treat. * Env.	77	7.1**	2154.78**	266.31**	92.23**	4.6**	25.88**	576.91**	577.28**	98.37**
Prnt * Env.	11	5.48**	3208.33**	309.81**	107.38**	3.89**	30.75**	606.82**	606.82**	85.65**
Hyb. * Env.	65	7.47**	1950.42**	262.7**	90.6**	4.25**	24.01**	556.36**	556.59**	99.20**
Prnt vs. Hyb. * Env.	1	0.82	3849.01**	22.36	32.06	35.04**	94.64**	1583.66**	1597.13**	184.38**
Error	154	1.10	48.19	41.03	34.83	1.19	0.81	31.83	31.69	0.68
Total	311	10.12	51151.34	197.24	71.35	3.83	545.47	4183.17	4180.99	345.25

* and ** significant at 5% and 1% level of significance, respectively,

Env. = Environment, Blk.= Blocks, Treat. = Treatments, Prnt. = Parent, Hyb. = Hybrid

4.2 Per se performance of parents their hybrids and checks under irrigated and partially irrigated condition

The observation recorded for the *per se* performance of 12 Inbred lines, 66 hybrids and two checks are presented in Table 13 (a, b) & 14 (a, b).

The characters days to 50% flowering, days to maturity, plant height, the low scoring parent was considered as better parent. On the hand, the parents yielded higher are also considered as better parents. The salient findings are described character wise in this section.

4.2.1 Under Irrigated condition

4.2.1.1 Days to 50% tasseling

Mean data revealed that days to 50% tasseling ranged from 59.50 days (IL11) to 107.50 days (IL1) and 55.00 days (IL7 × IL8) to 112.00 days (IL2 × IL12) for parents and hybrids respectively, while the grand mean was of 72.06, 77.91 and 90.63 days were observed for parents, hybrids and checks respectively (Table 13 a).

4.2.1.2 Days to 50 % silking

Mean data revealed that days to 50% silking ranged from 63.25 days (IL11) to 112.75 days (IL1) for parents, 58.50 days (IL7 × IL8) to 114.75 days (IL3 × IL12) for hybrids respectively, while the grand mean was of 80.89, 75.94, 81.79 and 95.75 mean was observed for parents, hybrids and checks respectively (Table 13 a).

4.2.1.3 Anthesis silking interval (ASI)

Mean data revealed that anthesis silking interval ranged from 2.25 days (IL7) to 5.25 days (IL1) and 1.75 days (IL1 × IL11) to 6.50 days (IL4 × IL5) for parents and hybrids respectively, while the grand mean was of 3.91 days while 3.92, 3.91 and 5.25 mean was observed for parents, hybrids and checks correspondingly. (Table 13 a).

4.2.1.4 Plant height (cm)

Mean data revealed that plant height ranged from 108.30 cm (IL3) to 186.13 cm (IL7) and 80.40 cm (IL4 × IL5) to 199.28 (IL9 × IL10) for parents and hybrids individually, while the grand mean was of 138.30 cm while the 148.81, 136.39 and 88.74 cm mean was documented for parents, hybrids and checks respectively (Table 13 a).

4.2.1.5 Cob length (cm)

Mean data revealed that cob length ranged from 12.56 cm (IL11) to 15.18 cm (IL3) and 11.53 cm (IL1 × IL12) to 16.05 cm (IL1 × IL10) for parents and hybrids respectively, while the grand mean was of 13.62 cm, 13.22 cm, 13.69 cm and 13.77 cm mean was observed for parents, hybrids and checks respectively. Table 13 (a).

4.2.1.6 Number of kernel rows per cob (NKRC)

Mean data revealed that number of kernel rows per cob ranged from 11.68 (IL2) to 15.68 (IL10) and 10.09 (IL6 × IL11) to 15.12 (IL5 × IL8) for parents and hybrids respectively, while the grand mean was of 13.29 while the 13.76, 13.20 and 13.43 mean was observed for parents, hybrids and checks respectively. Table 13 (a).

4.2.1.7 Numbers of kernel per rows (NKR)

Mean data revealed that numbers of kernel per rows ranged from 18.86 (IL3) to 26.39 (IL8) and 14.85 (IL2 × IL12) to 29.40 (IL5 × IL10) for parents and hybrids respectively, while the grand mean was of 21.18, 22.26, 20.98 and 19.63 mean were observed for parents, hybrids and checks respectively (Table 13a).

4.2.1.8 100 grain weight (g)

Mean data revealed that 100 grain weight ranged from 17.81g (IL2) to 24.37g (IL12) and 16.51g (IL5 × IL12) to 25.31g (IL8 × IL9) for parents and hybrids correspondingly, while the grand mean was of 21.15g, 21.92g, 21.02g and 19.97g mean were documented for parents, hybrids and checks respectively (Table 13a).

4.2.1.9 Yield per plant (g)

Mean data revealed that yield per plant ranged from 50.14g (IL6) to 97.14g (IL9) and 38.63g (IL5 × IL9) to 108.95g (IL6 × IL10) for parents and hybrids respectively, while the grand mean was of 72.02g, 73.13g, 71.82g and 74.12g mean were observed for parents, hybrids and checks respectively (Table 13 a).

4.2.1.10 Number of cobs per plant (NCP)

Mean data revealed that numbers of cobs per plant ranged from 1.30 (IL8) to 2.45 (IL7) and 1.38 (IL7 × IL11) to 2.45 (IL2 × IL8) for parents and hybrids correspondingly, while the grand mean was of 1.85, 1.86, 1.84 and 1.90 mean were observed for parents, hybrids and checks respectively (Table 13 b).

4.2.1.11 Days to maturity

Mean data revealed that days to maturity ranged from 95.75 days (IL9) to 114.50 days (IL2) and 92.00 days (IL9 × IL12) to 150.25 days (IL1 × IL4) for parents and hybrids correspondingly, while the grand mean was of 120.14, 112.81, 121.47- and 143.38-days mean was documented for parents, hybrids and checks respectively (Table 13 b).

4.2.1.12 Cob girth (cm)

Mean data revealed that cob girth ranged from 9.93 cm (IL2) to 14.42 cm (IL3) and 9.85 cm (IL6 × IL7) to 15.90 cm (IL8 × IL10) for parents and hybrids respectively, while the grand mean was of 12.01, 12.53, 11.92 and 11.84 cm mean were observed for parents, hybrids and checks respectively (Table 13 b).

4.2.1.13 Shelling (%)

Mean data revealed that shelling (%) ranged from 73.31 (IL2) to 84.44 (IL9) and 63.60 (IL2 × IL12) to 85.09 (IL2 × IL4) for parents and hybrids respectively, while the grand mean was of 77.81, 78.92, 77.61 and 78.14 mean were documented for parents, hybrids and checks respectively (Table 13 b).

4.2.1.14 Canopy temperature (at reproductive stages)

Mean data revealed that canopy temperature ranged from 25.64 (IL3) to 28.84 (IL11) and 24.05 (IL2 × IL12) to 29.63 (IL1 × IL10) for parents and hybrids

respectively, whilst the grand mean was 26.90, 26.89, 26.91 and 28.26 mean values were detected for parents, hybrids and checks correspondingly (Table 13 b).

4.2.1.15 Turgid weight (g)

Mean data signified that turgid weight (g) arrayed between 0.17g (IL1) to 0.24g (IL5) and 0.17g (IL1 × IL2, IL1 × IL3, IL4 × IL11, IL4 × IL12) to 0.25g (IL10 × IL11) for parents and hybrids respectively, while the grand mean was of 0.21g, 0.21g, 0.21g and 0.23g mean were observed for parents, hybrids and checks respectively (Table 13 b).

4.2.1.16 Relative water content

Mean data revealed that relative water content ranged from 64.86 (IL9) to 82.20 (IL6) and 64.31 (IL11 × IL12) to 84.96 (IL1 × IL12) for parents and hybrids correspondingly, while the grand mean was of 72.58, 72.88, 72.52 and 78.05 mean were detected for parents, hybrids and checks respectively (Table 13 b).

4.2.1.17 Saturation water deficit

Mean data exposed that saturation water deficit arrayed from 17.81 (IL6) to 35.14 (IL9) and 15.05 (IL1 × IL12) to 35.69 (IL11 × IL12) for parents and hybrids correspondingly, while the grand mean was of 27.42, 27.12, 27.48 and 21.95 average worth were documented for parents, hybrids and checks respectively (Table 13 b).

4.2.1.18 Membrane stability index

Mean data revealed that membrane stability index ranged from 15.65 (IL12) to 34.95 (IL2) and 9.37 (IL3 × IL4) to 52.25 (IL2 × IL5) for parents and hybrids respectively, whereas the grand mean was of 25.38, 22.93, 25.82 and 14.29 were documented for parents, hybrids and checks correspondingly (Table 13 b).

4.2.2 Under Partial irrigated condition

4.2.2.1 Days to 50% tasseling

Mean data revealed those days to 50% tasseling ranged from 64.50 days (IL11) to 107.00 days (IL1) and 61.00 days (IL7 × IL8) to 114.00 days (IL2 × IL12) for parents and hybrids respectively, whilst the grand mean was of 80.17, 76.10, 80.91 and 64.63 days were noted for parents, hybrids and checks respectively (Table 14 a).

4.2.2.2 Days to 50 % silking

Mean data revealed that days to 50 % silking varied from 69.50 days (IL11) to 113.75 days (IL1) and 65.50 days (IL7 × IL8) to 119.75 days (IL2 × IL12) for parents and hybrids correspondingly, whilst the grand mean was of 85.86, 81.29, 86.69 and 69.00 days were documented for parents, hybrids and checks correspondingly (Table 14 a).

4.2.2.3 Anthesis silking interval (ASI)

Mean data revealed that anthesis silking interval ranged from 4.00 days (IL8) to 7.50 days (IL4) and 3.25 days (IL8 × IL11) to 8.75 days (IL2 × IL8) for parents and hybrids respectively, while the grand mean was observed 6.09, 5.79, 6.14 and 5.13 days for parents, hybrids and checks respectively (Table 14 a).

4.2.2.4 Plant height (cm)

Mean data revealed that plant height ranged from 105.10 cm (IL2) to 164.48 cm (IL6) and 85.55 cm (IL1 × IL10) to 170.89 (IL5 × IL8) for parents and hybrids respectively, while the grand mean was of 132.58 cm, 134.96, 132.14 and 139.16 cm mean were observed for parents, hybrids and checks respectively (Table 14 a).

4.2.2.5 Cob length (cm)

Mean data exposed that cob length ranged from 11.44 cm (IL12) to 14.48 cm (IL3) and 10.27 cm (IL6 × IL10) to 15.49 cm (IL6 × IL12) for parents and hybrids correspondingly, while the grand mean was of 12.50 cm, 12.69, 12.46 and 12.95 cm mean were documented for parents, hybrids and checks respectively (Table 14 a).

4.2.2.6 Number of kernel rows per cob (NKRC)

Mean data discovered that Numbers of kernel rows per cob ranged from 10.33 (IL12) to 14.68 (IL10) and 7.72 (IL6 × IL11) to 14.79 (IL5 × IL8) for parents and hybrids correspondingly, whilst the grand mean was of 12.07, 12.39, 12.01 and 12.00 were documented for parents, hybrids and checks respectively (Table 14 a).

4.2.2.7 Numbers of kernel per rows (NKR)

Mean data exposed that numbers of kernel per rows ranged from 13.49 (IL7) to 22.32 (IL1) and 10.08 (IL5 × IL9) to 26.63 (IL5 × IL10) for parents and hybrids respectively, while the grand mean was of 18.54, 17.83, 18.67 and 24.14 were experimented for parents, hybrids and checks correspondingly (Table 14 a).

4.2.2.8 100 grain weight (g)

Mean data revealed that 100-grain weight arrayed from 16.95g (IL6) to 24.74g (IL9) and 15.54g (IL7 × IL11) to 27.67g (IL7 × IL10) for parents and hybrids respectively, whilst the grand mean was evidenced 33.29g and the 20.47g, 35.62g and 18.87g were documented for parents, hybrids and checks respectively (Table 14 a).

4.2.2.9 Yield per plant (g)

Mean data revealed that yield per plant arrayed between 41.70g (IL7) to 78.20g (IL3) and 35.13g (IL5 × IL9) to 103.92g (IL6 × IL10) for parents and hybrids respectively, whereas the grand mean was documented 67.20g, 64.57g, 67.68g and 80.05g for parents, hybrids and checks respectively (Table 14 a).

4.2.2.10 Numbers of cobs per plant (NCP)

Mean data revealed that numbers of cobs per plant ranged from 1.28 (IL1) to 2.06 (IL7) and 1.19 (IL6 × IL7) to 2.38 (IL2 × IL8) for parents and hybrids respectively, whilst the grand mean was documented 1.61 and the 1.59, 1.62 and 1.56 mean was observed for parents, hybrids and checks respectively (Table 14 b).

4.2.2.11 Days to maturity

Mean data revealed that days to maturity varied between 92.75 days (IL7) to 146.50 days (IL1) and 87.75 days (IL6 × IL10) to 143.00 days (IL2 × IL12 and IL3 × IL8) for parents and hybrids correspondingly, whereas the grand mean was detected 116.33 days whilst 110.33, 117.44 and 93.38 mean was documented for parents, hybrids and checks correspondingly (Table 14 b).

4.2.2.12 Cob girth (cm)

Mean data exposed that cob girth varied between 10.55 cm (IL2) to 12.63 cm (IL5) and 7.87 cm (IL6 × IL11) to 14.68 cm (IL9 × IL12) for parents and hybrids respectively, whilst the grand mean was documented 11.57 cm and the 11.78, 11.53 and 11.73 cm values was observed for parents, hybrids and checks respectively (Table 14 b).

4.2.2.13 Shelling (%)

Mean data signified that shelling (%) ranged from 70.86 (IL2) to 83.36 (IL3) and 62.30 (IL2 × IL12) to 89.75 (IL3 × IL4) for parents and hybrids respectively, while the grand mean was of 78.48 while the 78.33, 78.51 and 80.14 mean was observed for parents, hybrids and checks respectively (Table 14 b).

4.2.2.14 Canopy temperature (at reproductive stages)

Mean data exposed that canopy temperature arrayed between 24.30 (IL2) to 30.20 (IL4) and 23.20 (IL2 × IL3) to 30.08 (IL4 × IL6) for parents and hybrids correspondingly, whereas the grand mean was documented 26.66 and the 27.33, 26.54 and 26.58 values was detected for parents, hybrids and checks respectively (Table 14 b).

4.2.2.15 Turgid weight (g)

Mean data revealed that turgid weight (g) ranged from 0.18 (g) (IL1) to 0.24 (g) (IL7 and IL8) and 0.17 (g) (IL1 × IL2, IL1 × IL3, IL4 × IL11, IL4 × IL12) to 0.25 (g) (IL4 × IL5, IL10 × IL11 and IL11 × IL12) for parents and hybrids correspondingly, whereas the grand mean was found 0.21 (g) and the 0.21, 0.21 and 0.19 (g) worth was documented for parents, hybrids and checks respectively (Table 14 b).

4.2.2.16 Relative water content

Mean data revealed that relative water content varied between 64.84 (IL9) to 80.20 (IL6) and 62.08 (IL11 × IL12) to 83.60 (IL1 × IL12) for parents and hybrids correspondingly, whereas the grand mean was documented 71.75 and the 71.76, 71.74 and 69.41 values were documented for parents, hybrids and checks respectively (Table 14 b).

4.2.2.17 Saturation water deficit

Mean data revealed that saturation water deficit ranged between 19.81 (IL6) to 37.16 (IL9) and 16.40 (IL1 × IL12) to 37.97 (IL11 × IL12) for parents and hybrids correspondingly, whilst the grand mean was documented 28.26 and the 28.24, 28.26 and 30.59 mean was documented for parents, hybrids and checks correspondingly (Table 14 b).

4.2.2.18 Membrane stability index

Mean data exposed that membrane stability index varied from 4.99 (IL8) to 53.70 (IL2) and 7.63 (IL7 × IL12) to 68.40 (IL1 × IL9) for parents and hybrids correspondingly, whereas the grand mean was documented 29.97 and the 25.97, 30.70 and 32.67 values was documented for parents, hybrids and checks respectively (Table 14b).

Table: 13 (a) *Per se* performances of parents, their crosses and checks for various characters under irrigated condition

Genotypes	Days to 50 % tasseling	Days to 50 % silking	Anthesis silking interval	Plant height (cm)	Cob length (cm)	Number of kernel rows per cob	Numbers of kernel rows per	100 grain weight (g)	Seed Yield per plant (g)
IL1	107.5	112.75	5.25	108.59	12.85	12.03	22.62	19.23	63.33
IL2	84	88.25	4.25	124.55	13.15	11.68	18.91	17.81	55.29
IL3	95.25	100	4.75	108.3	15.18	13.75	18.86	23.52	83.78
IL4	83.5	87.75	4.25	122.8	12.66	15	22.69	22.25	72.84
IL5	62.75	65.75	3	177.61	12.65	14.68	23.92	22.85	86.77
IL6	64	67.25	3.25	170.23	12.64	13.32	21.06	21.87	50.14
IL7	62.25	64	2.25	186.13	12.95	12.28	22.42	22.77	53.6
IL8	61.5	65.5	4	168.45	13.79	14.54	26.39	21.4	86.16
IL9	61.75	66	4.25	160.1	13.86	14.72	24.59	22.89	97.14
IL10	61	65.25	4.25	172.8	13.26	15.68	25.98	24.19	74.69
IL11	59.5	63.25	3.75	133.73	12.56	13.82	19.87	19.89	66.02
IL12	61.75	65.5	3.75	152.44	13.09	13.61	19.78	24.37	87.83
IL1 × IL2	84	87.75	3.75	116.61	14.73	12.87	21.22	20.8	75.76
IL1 × IL3	92.25	95.75	3.5	110.6	13.55	12.63	20.59	19.5	53.71
IL1 × IL4	91.25	95.25	4	109.18	13.5	14.3	23.15	22.07	83.73
IL1 × IL5	84.75	89.75	5.25	112.35	13.05	13.3	21.8	19.15	76.3
IL1 × IL6	90.5	94.25	4	126.84	12.88	12.7	16.99	17.8	63.8
IL1 × IL7	96.5	100	3.5	115.44	11.78	13.68	20.06	21.88	72.23
IL1 × IL8	90	94.5	4.5	107.1	13.1	12.6	17.83	19.5	44.62
IL1 × IL9	83.75	88.75	5	131.83	14.8	13.67	26.11	19.22	93.17
IL1 × IL10	86.5	91.5	5	106	16.05	12.65	21.48	22.43	83.46
IL1 × IL11	86	87.5	1.75	138.82	13.92	13.53	19.09	16.88	62.62
IL1 × IL12	91.5	96.25	4.75	140.11	11.53	12.53	16.86	20.43	49.33
IL2 × IL3	96	99	3	98.75	13.65	12.46	21.52	24.64	77.54
IL2 × IL4	83.25	88.5	5.25	121.76	12.04	13.58	19.9	21.39	72.5 7
IL2 × IL5	91.25	95.75	4.5	107.93	14.3	13.46	20.27	20.03	99.95
IL2 × IL6	98	103	5	106.12	14.22	10.3	16.6	21.45	47.6

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Genotypes	Days to 50 % tasseling	Days to 50 % silking	Anthesis silking interval	Plant height (cm)	Cob length (cm)	Number of kernel rows per cob	Numbers of kernel per rows	100 grain weight (g)	Seed Yield per plant (g)
IL2 × IL7	106	109.5	3.5	100.84	13.88	13.37	21.82	19.85	81.21
IL2 × IL8	81.75	87.25	5.5	145.74	12.98	12.38	19.46	20.93	53.74
IL2 × IL9	82.5	87.25	4.75	99.9	14.75	13.5	26.26	20.45	69.13
IL2 × IL10	84.5	89	4.5	109.61	15.03	13.22	23.36	19.48	85.62
IL2 × IL11	96.5	99.5	3	96.48	11.6	11.15	16.93	21.94	54.63
IL2 × IL12	112	114.75	2.75	95.8	14.35	11.47	14.85	18.93	43.49
IL3 × IL4	96	101	5	123.21	13.94	14.34	23.77	21.44	85.99
IL3 × IL5	86	89	3	119.76	13.23	12.37	21.02	22.68	79.82
IL3 × IL6	83	88.75	5.75	113.54	12.88	14.09	16.86	23.1	65.77
IL3 × IL7	84.25	89.25	5	115.08	15.6	12.05	23.26	21.03	76.41
IL3 × IL8	96	100.25	4.5	148.59	14.38	14.47	18.47	20.74	72.03
IL3 × IL9	100.75	104.75	4	111.84	13.87	14.37	22.16	22.35	91.85
IL3 × IL10	84.25	88.25	4	144.28	14.3	14.08	21.95	21.4	83.54
IL3 × IL11	99.75	103.75	4	95.14	13.58	14.3	18.58	20.48	77.92
IL3 × IL12	110.5	114.75	4.25	104.99	13.48	14.07	22.22	24.2	71.76
IL4 × IL5	85	91.5	6.5	80.4	14.65	13.25	15.94	19	81.8
IL4 × IL6	96.25	100	4	97.08	12.9	13.6	23.33	20.94	66.45
IL4 × IL7	97.5	103.5	6	108.94	12.37	12.89	17.25	19.55	68.07
IL4 × IL8	98.25	103	4.75	115.08	12.3	13.45	15.51	19.28	52.62
IL4 × IL9	101.75	106.75	5	102.48	13.3	12.95	17.85	23.09	78.86
IL4 × IL10	66	69.5	3.75	114.6	13.64	12.38	22.39	19.02	64.82
IL4 × IL11	64.5	68.25	3.75	156.13	14.53	13.23	23.61	21.03	81.82
IL4 × IL12	64.75	68.75	4	164.33	13.25	12.9	23.07	19.6	52.9
IL5 × IL6	65.75	69.5	3.75	160.69	12.48	14.15	24.15	20.17	78.09
IL5 × IL7	67	69	2	158.14	12.29	13.73	17.82	17.79	62.49
IL5 × IL8	59.5	64	4.5	180.29	13.04	15.12	23.12	24.04	77.34
IL5 × IL9	64	67.25	3.25	149.36	12.75	12.96	20.71	20.25	38.63
IL5 × IL10	58.75	61.25	2.5	187.23	15.08	13.48	29.4	19.3	100.07
IL5 × IL11	59.5	63.5	4	143.48	15.92	12.74	23.72	23.08	83.67
IL5 × IL12	63.5	65.75	2.25	155.55	13.4	14.21	20.74	16.51	62.16
IL6 × IL7	64.5	66.5	2	170.58	14.14	11.85	19.42	17.18	51.33

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Genotypes	Days to 50 % tasseling	Days to 50 % silking	Anthesis silking interval	Plant height (cm)	Cob length (cm)	Number of kernel rows per cob	Numbers of kernel per rows	100 grain weight (g)	Seed Yield per plant (g)
IL6 × IL8	60	63.75	3.75	167.61	14.33	12.26	22.95	24.98	85.12
IL6 × IL9	57.75	61.25	3.5	161.97	13	13.99	21.65	22.79	68.92
IL6 × IL10	58.75	62.25	3.5	168.32	14.35	13.61	23.88	19.24	108.95
IL6 × IL11	60.5	64	3.5	163.49	14.06	10.09	15.8	22.14	48.83
IL6 × IL12	61.5	65.25	3.75	181.6	14.07	13.4	27.48	19.76	82.8
IL7 × IL8	55	58.5	3.5	167.18	14.75	13.13	24.04	19.73	71.18
IL7 × IL9	63	66.75	3.75	181.35	14.54	13.1	25.48	21.52	90.62
IL7 × IL10	61	63.75	2.75	176.26	12.33	12.21	18.28	22.58	53.81
IL7 × IL11	64.5	67.5	3	164.71	14.21	11.5	15.33	17.84	47.98
IL7 × IL12	61.75	66.5	4.75	158.13	13.76	13.67	20.15	23.34	84.7
IL8 × IL9	63.5	67.25	3.75	173.99	14.39	13.29	23.78	25.31	81.54
IL8 × IL10	61.5	66.5	5	140.41	14.15	14.89	19.67	23.38	68.14
IL8 × IL11	60.75	62.75	2	182.03	14.86	11.51	24.13	21.72	79.74
IL8 × IL12	62.5	66.25	3.75	163.09	13.54	14.14	19.99	21.99	72.54
IL9 × IL10	63.25	65.75	2.5	199.28	13.52	14.11	23.78	22.57	84.84
IL9 × IL11	61.25	65.75	4.5	167.92	13.28	14.1	21.54	20.55	80.29
IL9 × IL12	55.5	59	3.5	151.18	13.6	14.52	25.02	24.7	75.44
IL10 × IL11	63	65.25	2.25	112.16	14.23	13.05	17.52	25.31	86.86
IL10 × IL12	60.25	63.75	3.5	154.75	13.47	14.29	25.36	22.72	66.13
IL11 × IL12	60.75	64	3.25	147.76	12.52	14.36	16.86	18.97	51.55
HKI 1105	85	91.5	6.5	80.4	14.65	13.25	15.94	19	81.8
HKI 1128	96.25	100	4	97.08	12.9	13.6	23.33	20.94	66.45
Grand Mean	77.01	80.89	3.91	138.3	13.62	13.29	21.18	21.15	72.02
Patent Mean	72.06	75.94	3.92	148.81	13.22	13.76	22.26	21.92	73.13
F1 Mean	77.91	81.79	3.91	136.39	13.69	13.2	20.98	21.02	71.82
Check Mean	90.63	95.75	5.25	88.74	13.77	13.43	19.63	19.97	74.12
C.V.	9.06	8.42	29.11	12.33	9.46	8.37	16.28	13.15	21.83
C.D. 5%	9.72	9.49	1.59	23.75	1.79	1.55	4.8	3.87	21.91
S.E.	3.49	3.4	0.57	8.52	0.64	0.56	1.72	1.39	7.86

Table: 13 (b) *Per se* performances of parents, their crosses and checks for various characters under irrigated condition

Genotypes	Number of cobs per plant	Days to maturity	Cob girth (cm)	Shelling %	Canopy temp.	Turgid weight (g)	Relative water content	Saturation water deficit	Membrane stability index
IL1	1.65	141	11.62	73.48	25.99	0.17	71.64	28.37	28.03
IL2	2.23	144.5	9.93	73.31	26.1	0.2	69.66	30.34	34.95
IL3	1.58	143.25	14.42	76.74	25.64	0.2	69.39	30.61	15.88
IL4	2.09	143.5	12.8	81.31	26.55	0.2	78.47	21.53	23.61
IL5	1.88	98.75	12.34	75.67	27.08	0.24	66.29	33.71	29.45
P6	1.95	97	12	77.77	27.16	0.21	82.2	17.81	33.84
IL7	2.45	99.25	12.94	76.33	27.79	0.24	68.71	31.29	20.47
IL8	1.3	96	13.06	83.02	27.11	0.23	71.86	28.14	16.16
IL9	1.88	95.75	13.54	84.44	25.89	0.23	64.86	35.14	15.87
IL10	1.95	96.5	13.84	82.35	26.95	0.2	77.61	22.39	25.2
IL11	1.88	99	11.39	81.53	28.84	0.2	75.42	24.58	16.13
IL12	1.55	99.25	12.52	81.09	27.58	0.19	78.43	21.58	15.65
IL1 × IL2	1.94	138.5	11.78	73.59	25.61	0.17	75.17	24.83	33.84
IL1 × IL3	2.15	147.25	11.5	76.56	26.65	0.17	70.11	29.9	33.34
IL1 × IL4	1.94	150.25	11.37	75.33	26.38	0.22	68.92	31.08	33.23
IL1 × IL5	2.3	149.25	13.75	82.56	26.05	0.2	71.54	28.46	35.43
IL1 × IL6	1.95	147.5	12	81.52	26.79	0.18	72.65	27.36	24.2
IL1 × IL7	2.1	148	12.1	80.82	27.69	0.19	83.36	16.64	33.98
IL1 × IL8	2	146.5	10.72	77.2	27.08	0.19	68.18	31.82	34.1
IL1 × IL9	1.71	150.75	11.02	77.02	25.23	0.2	68.75	31.26	28.83
IL1 × IL10	2	143	12	76.79	24.05	0.2	72.34	27.67	34.86
IL1 × IL11	2.15	143	11.18	78.36	26.32	0.2	75.61	24.39	47.77
IL1 × IL12	1.73	142	10.57	76.9	26.71	0.2	84.96	15.05	26.29
IL2 × IL3	1.84	140	10.67	78.18	28.15	0.23	70.46	29.55	39.4
IL2 × IL4	2.15	139.75	11.65	85.09	29.31	0.18	69.36	30.64	42.55
IL2 × IL5	2.08	137.25	12.19	77.44	27.08	0.19	68.17	31.83	52.25
IL2 × IL6	1.75	142	10.32	72.05	26.12	0.22	69.86	30.15	23.55
IL2 × IL7	1.86	141	11.69	76.72	27.19	0.21	72.17	27.83	23.98
IL2 × IL8	2.45	135.75	12.21	77.2	27.24	0.24	68.97	31.03	29.44

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Genotypes	Number of cobs per plant	Days to maturity	Cob girth (cm)	Shelling %,	Canopy temp.	Turgid weight (g)	Relative water content	Saturation water deficit	Membrane stability index
IL2 × IL9	1.8	136	12.26	72.01	27.75	0.22	69.25	30.75	26.17
IL2 × IL10	1.93	143	11.23	75.7	25.21	0.2	64.34	35.66	26.42
IL2 × IL11	1.93	142.5	11	79.61	27.43	0.21	76.43	23.58	27.15
IL2 × IL12	1.45	145	10.25	63.6	26.9	0.21	70.39	29.61	27.58
IL3 × IL4	1.45	146.5	13.1	82.93	27.06	0.23	73.67	26.33	9.37
IL3 × IL5	1.8	144.5	11.82	77.91	26.16	0.21	73.98	26.02	11.61
IL3 × IL6	1.69	142.5	14.23	78.22	27.14	0.21	77.2	22.8	32.74
IL3 × IL7	1.55	140.25	12.65	73.37	25.48	0.19	69.45	30.55	13.42
IL3 × IL8	1.69	149	11.42	76.93	26.79	0.23	71.24	28.76	19.76
IL3 × IL9	1.88	145.25	12.75	81.89	24.84	0.23	64.64	35.36	6.01
IL3 × IL10	1.63	143.75	11.78	77.27	25.18	0.21	75.85	24.15	22.89
IL3 × IL11	2	143.75	12.2	81.08	26.64	0.21	77.84	22.16	22.39
IL3 × IL12	1.5	144	11.9	79.74	26.74	0.2	76.1	23.9	21.81
IL4 × IL5	2	142	11.45	75.36	27.25	0.25	76.71	23.29	24.19
IL4 × IL6	1.8	144.75	12.23	80.93	29.28	0.21	79.4	20.61	4.38
IL4 × IL7	1.88	142	10.53	83.35	27.94	0.2	77.19	22.81	18.07
IL4 × IL8	1.48	145.25	11.6	78.97	26.68	0.24	64.88	35.12	18.47
IL4 × IL9	1.55	148.25	12.32	77.23	27.13	0.2	76.15	23.85	18.77
IL4 × IL10	1.5	94.5	12.1	74.56	26.94	0.18	70.38	29.62	13.3
IL4 × IL11	2	95	12.4	77.12	25.91	0.17	73.83	26.17	38.93
IL4 × IL12	1.94	94.25	11.9	74.81	27.05	0.17	70.62	29.38	26.9
IL5 × IL6	2.15	95.25	14.94	83.7	26.6	0.19	71.71	28.29	45.39
IL5 × IL7	2.15	99.5	12.7	80.32	26.84	0.18	73.92	26.09	18.04
IL5 × IL8	2.03	97.5	13.12	83.95	27.79	0.19	82.15	17.85	32.66
IL5 × IL9	2	94.5	11.21	69.79	27.78	0.19	69.41	30.59	34.52
IL5 × IL10	1.9	93.25	10.74	80.35	25.58	0.2	69.82	30.19	31.52
IL5 × IL11	1.94	95	12.62	76.85	24.5	0.2	70.82	29.18	31.96
IL5 × IL12	2.15	94.5	10.99	77.55	26.97	0.2	78.25	21.76	30.11
IL6 × IL7	1.65	98.5	9.85	69.84	26.6	0.2	69.94	30.07	41.5
IL6 × IL8	1.94	96	11.35	82.49	28.25	0.23	70.2	29.8	34.94
IL6 × IL9	2.05	95.25	12.76	82.49	29.26	0.18	68.07	32.06	28.31

Contd.....

Genotypes	Number of cobs per plant	Days maturity to	Cob (cm) girth	Shelling %,	Canopy temp.	Turgid weight (g)	Relative water content	Saturation water deficit	Membrane stability index
IL6 × IL10	2.15	95.75	12.36	81.35	28.13	0.19	67.91	32.09	48.9
IL6 × IL11	1.75	96.5	10.48	73.23	26.52	0.22	70.09	29.91	14.56
IL6 × IL12	1.63	94.5	11.32	77.4	27.64	0.21	71.1	28.91	26.4
IL7 × IL8	1.8	97.5	11.47	71.81	28.15	0.22	69.51	30.5	22.46
IL7 × IL9	1.88	98.5	11.28	78.29	25.66	0.2	64.55	35.45	24.01
IL7 × IL10	1.96	97.5	11.94	77.97	28.23	0.2	77.5	22.5	18.71
IL7 × IL11	1.38	96.5	9.92	67.74	27.4	0.21	70.39	29.61	26.36
IL7 × IL12	1.53	98.25	14.64	77.24	26.64	0.2	69.33	30.67	12.57
IL8 × IL9	1.8	98	12.97	77.76	26.86	0.21	72.31	27.7	3.55
IL8 × IL10	1.56	98.5	15.9	79.78	27.39	0.21	76.51	23.49	26.15
IL8 × IL11	1.63	96.75	12.28	75.28	26.28	0.19	69.54	30.46	11.47
IL8 × IL12	2	98	11.62	74.82	27.19	0.23	71.48	28.52	21.69
IL9 × IL10	1.5	96.75	11.86	77.69	25.43	0.21	74.49	25.51	17.37
IL9 × IL11	1.88	95.25	12.6	81.47	26.79	0.21	78.07	21.94	24.35
IL9 × IL12	1.5	92	12.43	82.08	27.24	0.2	76.2	23.8	19.15
IL10 × IL11	1.94	97.5	11.02	78.11	28.05	0.25	76.73	23.27	31.6
IL10 × IL12	1.8	97.25	12.99	80.37	29.63	0.2	82.16	17.84	5.66
IL11 × IL12	1.63	99.25	11.66	76.46	27.48	0.24	64.31	35.69	13.07
HKI 1105	2	142	11.45	75.36	27.25	0.25	76.71	23.29	24.19
HKI 1128	1.8	144.75	12.23	80.93	29.28	0.21	79.4	20.61	4.38
Grand Mean	1.85	120.14	12.01	77.81	26.9	0.21	72.58	27.42	25.38
Patent Mean	1.86	112.81	12.53	78.92	26.89	0.21	72.88	27.12	22.93
F1 Mean	1.84	121.47	11.92	77.61	26.91	0.21	72.52	27.48	25.82
Check Mean	1.9	143.38	11.84	78.14	28.26	0.23	78.05	21.95	14.29
C.V.	15.93	1.74	9.16	7.6	5.22	8.07	7.31	19.36	41.72
C.D. 5%	0.41	2.92	1.53	8.24	1.96	0.02	7.4	7.4	14.75
S.E.	0.15	1.05	0.55	2.96	0.7	0.01	2.65	2.65	5.29

Table: 14 (a) *Per se* performances of parents, their crosses and checks for various characters under partial irrigated condition

Genotypes	Days to 50 % tasseling	Days to 50 % silking	Anthesis silking interval	Plant height (cm)	Cob length (cm)	Number of kernel rows per cob	Numbers of kernel rows per	100 grain weight (g)	Seed Yield per plant (g)
IL1	107	113.75	6.75	115.89	12.93	11.3	22.32	17.51	63.45
IL2	86	92.5	6.5	105.1	11.88	10.46	17.05	18.7	52.68
IL3	98.75	104	5.25	108.64	14.48	11.77	17.73	22.91	78.2
IL4	86	93.5	7.5	129.55	11.87	12.8	20.65	21.75	70.89
IL5	66.25	71.25	6.25	152.91	12.59	12.01	17.13	19.69	71.34
P6	69	74	5.5	164.48	13.85	13.56	18.28	16.95	52.12
IL7	67.25	71	4.5	141.43	11.73	12.04	13.49	19.17	41.7
IL8	68.5	72	4	143.35	12.04	13.21	22.16	19.58	71.51
IL9	65.25	70.25	6	140.4	11.66	13.41	15.29	24.74	76.81
IL10	66	71	6	163.55	13.73	14.68	18.09	21.48	74.91
IL11	64.5	69.5	6	120.43	14.09	13.16	16.89	19.79	67.74
IL12	68.75	72.75	5.25	133.74	11.44	10.33	14.88	23.42	53.54
IL1 × IL2	90	97	7	111.21	13.48	12.09	19.97	20.64	70.94
IL1 × IL3	86.25	93.75	7.5	121.95	12.62	11.64	19.27	19.02	53.92
IL1 × IL4	92.25	99.75	7.5	116.53	12.65	12.27	22.78	21.31	78.48
IL1 × IL5	84.25	90.75	6.25	133.45	12.58	11.95	20.73	20.56	73.12
IL1 × IL6	93	100	7	104.54	11.88	10.75	15.38	16.65	65.17
IL1 × IL7	98.5	103.25	4.75	126.29	11.23	12.97	18.5	20.13	70.12
IL1 × IL8	92	98.75	6.75	113.83	11.85	11.98	17.33	19.57	46.83
IL1 × IL9	85.25	91.75	6.5	109.18	14.3	12.37	24.56	19.54	88.44
IL1 × IL10	87.5	95.5	8	85.55	14.73	11.93	19.68	21.93	80.09
IL1 × IL11	87	92.75	5.75	126.82	12.38	11.95	17.92	16.02	62.07
IL1 × IL12	93.5	100.5	7	134.11	10.87	12.23	17.5	20.56	49.62
IL2 × IL3	98.5	104.75	6.25	88.5	12.45	10.95	19.87	23.66	72.51
IL2 × IL4	83.75	90.5	6.75	105.46	11.58	11.9	19.59	19.78	67.76
IL2 × IL5	92.75	100.75	7.75	114.18	13.93	11.93	18.8	19.63	94.24
IL2 × IL6	98.5	105.5	7	111.32	13.36	9.1	16.23	21.08	48.23

Contd.....

Genotypes	Days to 50 % tasseling	Days to 50 % silking	Anthesis silking interval	Plant height (cm)	Cob length (cm)	Number of kernel rows per cob	Numbers of kernel per rows	100 grain weight (g)	Seed Yield per plant (g)
IL2 × IL7	106.5	112.5	6	123.69	12.03	12.03	20.6	26.7	76.79
IL2 × IL8	82.25	91	8.75	145.54	12.68	10.88	17.19	20.22	52.49
IL2 × IL9	83	90.5	7.5	122.9	13.53	12	20.18	18.86	64.94
IL2 × IL10	85	93	8	123.91	13.23	11.93	20.97	17.81	78.38
IL2 × IL11	97.5	105	7.5	120.98	10.55	10.45	15.79	21.51	50.94
IL2 × IL12	114	119.75	5.75	116.25	13.48	11.03	15.23	17.77	40.51
IL3 × IL4	99.5	106	6.5	118.31	12.93	12.85	22.62	21.32	82.87
IL3 × IL5	86.5	93	6.5	121.56	11.97	11.38	20.32	21.39	73.35
IL3 × IL6	83.5	91.75	8.25	127.44	10.42	12.98	15.23	20.59	61.19
IL3 × IL7	84.75	91.75	7	129.38	14.49	10.95	23.68	20.35	76.69
IL3 × IL8	97.5	104.5	7	148.39	13.45	13.48	16.8	20.32	70.88
IL3 × IL9	102.75	108.5	5.75	140.34	12.82	13.3	21.21	22.18	87.82
IL3 × IL10	85.75	92.75	7	161.28	12.88	12.85	20.25	19.23	77.35
IL3 × IL11	101.75	109	7.5	95.84	12.94	13.05	17.33	21.62	73.31
IL3 × IL12	113	119	6	124.29	12.15	13	20.02	22.89	66.32
IL4 × IL5	87	94.5	7.75	90.55	13.22	12.6	14.2	20.23	78.38
IL4 × IL6	97.75	105.5	7.5	113.93	11.65	12.48	21.84	19.41	64.63
IL4 × IL7	99	106.75	7.75	119.99	12.02	11.75	15.71	19.83	65.92
IL4 × IL8	101.25	108.75	7.5	117.78	10.73	11.85	13.31	18.17	53.52
IL4 × IL9	105.25	113	8	118.23	12.08	10.76	16.7	21.17	76.18
IL4 × IL10	65.5	69.75	4.5	114.1	12.79	11.38	21.66	19.04	66.41
IL4 × IL11	68.5	73.75	5.75	102.23	11.69	11.73	16.65	20.94	72.87
IL4 × IL12	67.75	74	7	129.23	11.53	9.02	14.07	19.06	47.53
IL5 × IL6	69.75	74	5	114.39	13.19	13.6	22.25	23.15	84.92
IL5 × IL7	71.5	74.5	4	154.84	10.4	11.94	13.04	24.51	48.74
IL5 × IL8	64.5	70.5	6.5	170.89	12.09	14.79	22.84	24.22	79.4
IL5 × IL9	71	76.5	5.5	158.36	12.03	10.93	10.08	16.75	35.13
IL5 × IL10	63.75	68.25	5.75	164.23	13.11	12.63	26.63	18.7	93.7
IL5 × IL11	63.5	68	5	139.53	14.88	11.98	22.24	22	78.76
IL5 × IL12	64	68.25	5.25	165.95	12.38	13.22	17.87	15.86	56.28
IL6 × IL7	70.5	74.5	5	162.28	13.1	11.85	20.07	18.68	67.26

Contd.....

Genotypes	Days to 50 % tasseling	Days to 50 % silking	Anthesis silking interval	Plant height (cm)	Cob length (cm)	Number of kernel rows per cob	Numbers of kernel per rows	100 grain weight (g)	Seed Yield per plant (g)
IL6 × IL8	67.5	72	5	167.86	13.15	12.83	21.6	22.97	64.15
IL6 × IL9	63.75	66.75	4.25	167.62	12.46	13.68	23.26	18.19	72.91
IL6 × IL10	62.75	67.5	5	168.37	10.27	13.18	23.86	18.08	103.92
IL6 × IL11	67.5	71.5	5	147.29	11.07	7.72	11.66	18.63	35.39
IL6 × IL12	66.5	70.5	5	157.1	15.49	10.69	21.89	17.61	66.91
IL7 × IL8	61	65.5	5	130.43	14.05	12.3	21.46	23.54	75.34
IL7 × IL9	67.5	72	5.5	160.55	13.16	12.26	25.34	21.67	67.39
IL7 × IL10	66.5	70.25	4.75	129.56	10.66	11.21	17.33	27.67	56.04
IL7 × IL11	69.5	74.5	5	170.81	12.58	12.5	16.25	15.54	61.13
IL7 × IL12	66.25	71	5.5	154.03	11.58	13.67	16.86	21.49	74.63
IL8 × IL9	68	72.75	5.75	137.79	11.34	11.06	15.1	22.56	53.22
IL8 × IL10	66.5	71	5.5	129.51	10.51	10.57	13.73	21.92	49.71
IL8 × IL11	66.75	69.25	3.25	146.28	12.58	11.38	17.55	20.9	59.29
IL8 × IL12	67.5	71.5	5	140.74	12.02	11.99	16.07	23.52	47.19
IL9 × IL10	68.75	73.5	5.5	156.58	11.46	13.52	18.19	18.59	79.44
IL9 × IL11	66.25	71.5	6	154.27	10.76	12.19	13.8	19.2	62.4
IL9 × IL12	61	66.5	5.5	149.03	13.79	14.6	21.16	22.49	91.85
IL10 × IL11	68	71.25	4.25	107.56	14.03	11.92	18.62	26.16	74.12
IL10 × IL12	64.75	68.25	4.75	153.25	12.72	14.21	17.88	20.17	80.27
IL11 × IL12	66.75	70.75	5.25	133.36	12.74	10.83	15.83	15.76	66.67
HKI 1105	65.5	69.75	4.5	114.1	12.79	11.38	21.66	19.04	66.41
HKI 1128	63.75	68.25	5.75	164.23	13.11	12.63	26.63	18.7	93.7
Grand Mean	80.17	85.86	6.09	132.58	12.5	12.07	18.54	33.29	67.2
Patent Mean	76.1	81.29	5.79	134.96	12.69	12.39	17.83	20.47	64.57
F1 Mean	80.91	86.69	6.14	132.14	12.46	12.01	18.67	35.62	67.68
Check Mean	64.63	69	5.13	139.16	12.95	12	24.14	18.87	80.05
C.V.	8.8	8.13	18.09	12.52	10.99	11.66	16.53	5.18	22.53
C.D. 5%	9.83	9.72	1.53	23.13	1.91	1.96	4.27	3.29	21.1
S.E.	3.53	3.49	0.55	8.3	0.69	0.7	1.53	5.78	7.57

Table: 14 (b) *Per se* performances of parents, their crosses and checks for various characters under partial irrigated condition

Genotypes	Number of cobs per plant	Days to maturity	Cob girth (cm)	Shelling %,	Canopy temp.	Turgid weight (g)	Relative water content	Saturation water deficit	Membrane stability index
IL2	1.38	136.5	10.55	70.86	24.3	0.2	68.12	31.89	53.7
IL3	1.4	137.75	12.19	83.36	26.99	0.2	68.28	31.73	14.76
IL4	1.63	141	12.43	78.93	30.2	0.2	78.52	21.48	51.12
IL5	2	96.25	12.63	79.16	27.58	0.22	67.35	32.65	18.45
P6	1.75	96.5	11.81	76.42	27.21	0.21	80.2	19.81	11.44
IL7	2.06	92.75	10.64	73.3	27.84	0.24	67.99	32.01	20.55
IL8	1.28	94	12.04	81.82	26.81	0.24	71.1	28.9	4.99
IL9	1.63	97.75	11.99	83.18	25.19	0.23	62.84	37.16	32.01
IL10	1.75	93.5	12.59	81.57	26.6	0.21	76.01	23.99	51.45
IL11	1.63	93.5	11.44	76.52	29.59	0.21	73.78	26.22	26.07
IL12	1.29	96.75	11.75	76.82	28.08	0.2	76.25	23.75	8.82
IL1 × IL2	1.3	136.5	10.98	80.3	26.91	0.17	73.79	26.21	15.01
IL1 × IL3	1.71	138.25	11.22	82.52	27.3	0.17	71.4	28.6	11.33
IL1 × IL4	1.88	138.75	10.99	84.26	26.93	0.22	68.14	31.86	15.31
IL1 × IL5	1.8	138.25	12.18	78.14	27.3	0.2	70.37	29.63	49.4
IL1 × IL6	1.53	140.5	10.57	83.02	28.04	0.19	72.03	27.97	28.85
IL1 × IL7	1.55	140.5	11.65	79.69	27.44	0.19	82.28	17.72	27.36
IL1 × IL8	1.7	138	11.08	84.45	26.58	0.2	67.25	32.75	47.39
IL1 × IL9	1.68	140.25	11.46	77.38	25.43	0.2	68.63	31.37	68.4
IL1 × IL10	1.58	135	11.81	76.69	24.3	0.2	71.52	28.48	38.08
IL1 × IL11	1.63	141	12.37	79.11	25.22	0.21	75.15	24.85	34.62
IL1 × IL12	1.56	139	10.54	75.77	25.76	0.2	83.6	16.4	13
IL2 × IL3	1.33	136	10.93	79.58	23.2	0.23	69.83	30.17	31.53
IL2 × IL4	2	137.25	10.5	80.86	26.06	0.18	69.95	30.05	29.81
IL2 × IL5	1.9	134.75	10.4	80.02	24.58	0.19	68.73	31.27	53.49
IL2 × IL6	1.39	138.5	10.07	84.47	24.57	0.22	68.49	31.52	48.97
IL2 × IL7	1.8	137	12.63	74.71	24.74	0.21	71.96	28.05	39.98
IL2 × IL8	2.38	132.25	11.92	80.75	25.24	0.24	68.77	31.23	35.81

Contd.....

Genotypes	Number of cobs per plant	Days to maturity	Cob girth (cm)	Shelling %,	Canopy temp.	Turgid weight (g)	Relative water content	Saturation water deficit	Membrane stability index
IL2 × IL9	1.75	133	11.57	69.51	25	0.22	69.22	30.78	25.55
IL2 × IL10	1.81	136	11.82	74.46	24.36	0.2	64.17	35.83	20.15
IL2 × IL11	1.63	136.5	10.28	76.96	26.23	0.21	76.14	23.87	36.61
IL2 × IL12	1.31	143	9.83	62.3	27.55	0.21	70.18	29.83	37.79
IL3 × IL4	1.44	141	11.15	89.75	25.21	0.23	74.06	25.94	11.97
IL3 × IL5	1.63	134.5	11.18	80.05	25.26	0.21	72.26	27.74	28.62
IL3 × IL6	1.38	138.5	12.28	88.77	25.79	0.21	77.92	22.09	48.27
IL3 × IL7	1.38	136.75	12.2	83.69	25.23	0.19	69.54	30.46	33.39
IL3 × IL8	1.75	143	11.51	81.85	25.59	0.22	72.97	27.03	30.8
IL3 × IL9	1.81	142.25	11.69	84.52	27.34	0.23	64.08	35.92	33.74
IL3 × IL10	1.69	137.75	10.6	82.26	24.63	0.21	74.2	25.8	10.51
IL3 × IL11	1.63	139.25	12.22	81.45	26.39	0.21	77.27	22.73	39.72
IL3 × IL12	1.5	141	10.47	66.58	28.34	0.2	74.3	25.7	42.91
IL4 × IL5	1.81	141	10.73	83.42	26.45	0.25	76.62	23.38	13.3
IL4 × IL6	1.63	142.75	12.07	73.61	30.08	0.21	79.67	20.33	25.94
IL4 × IL7	1.63	134.5	9.58	77.31	27.59	0.2	75.37	24.63	25.95
IL4 × IL8	1.69	141.75	10.2	69.22	27.03	0.24	63.72	36.28	11.05
IL4 × IL9	1.23	139.75	11.22	82.53	27.58	0.2	75.45	24.56	18.61
IL4 × IL10	1.45	94.5	12.04	80.17	27.64	0.18	70.22	29.78	18.91
IL4 × IL11	1.23	92.5	12.14	81.87	26.26	0.17	74.88	25.12	12.06
IL4 × IL12	1.68	88.75	10.55	75.37	27.2	0.17	70.22	29.78	17.65
IL5 × IL6	1.71	98.75	13.18	78.76	26.6	0.19	73.71	26.29	55.13
IL5 × IL7	1.8	100.5	12.04	78.81	27.09	0.18	74.74	25.26	15.57
IL5 × IL8	1.69	93.5	12.69	85.48	27.59	0.2	80.27	19.73	22.2
IL5 × IL9	1.6	90.5	9.93	69.72	27.43	0.19	67.76	32.24	46.26
IL5 × IL10	1.68	92.25	11.43	80.11	25.53	0.2	68.6	31.41	46.43
IL5 × IL11	1.73	92.5	12.38	75.86	24.45	0.21	69.85	30.15	35.09
IL5 × IL12	1.63	93	10.72	76.84	26.37	0.21	76.08	23.92	36.44
IL6 × IL7	1.19	98	10.75	80.51	26.55	0.2	68.85	31.28	56.45
IL6 × IL8	1.39	94.5	11.4	78.5	28.2	0.23	69.83	30.17	26
IL6 × IL9	1.63	91.75	12.46	83.44	28.91	0.19	66.2	33.8	20.68

Contd.....

Genotypes	Number of cobs per plant	Days maturity to	Cob (cm) girth	Shelling %,	Canopy temp.	Turgid weight (g)	Relative water content	Saturation water deficit	Membrane stability index
IL6 × IL10	2	87.75	12.13	85.4	27.63	0.19	65.64	34.36	52.78
IL6 × IL11	1.58	93.5	7.87	68.23	26.72	0.22	70.71	29.29	46.42
IL6 × IL12	1.58	90	10.59	67.83	27.59	0.22	69.23	30.77	37.99
IL7 × IL8	1.75	94.5	12.05	75.64	27.9	0.22	68.74	31.26	22.59
IL7 × IL9	1.63	94	11.59	74.43	25.41	0.2	63.13	36.87	23.39
IL7 × IL10	1.75	93	12.68	81.84	27.83	0.2	77.9	22.1	35.5
IL7 × IL11	1.35	92	11.58	73.22	26.7	0.21	67.91	32.1	22.01
IL7 × IL12	1.34	93.75	14.25	80.85	26.49	0.21	66.8	33.2	7.63
IL8 × IL9	1.6	97.5	12.73	77.62	26.51	0.21	70.86	29.14	25.22
IL8 × IL10	1.5	95	11.74	77.49	26.89	0.21	74.78	25.22	49.08
IL8 × IL11	1.63	95.25	11.71	76.06	25.73	0.2	66.99	33.01	35.94
IL8 × IL12	1.94	95	12.24	71.23	26.99	0.23	69.22	30.79	36.07
IL9 × IL10	1.63	94.25	12.11	83.47	24.83	0.22	72.55	27.51	12.34
IL9 × IL11	1.7	92.75	12.29	76.01	26.54	0.21	76.86	23.15	38.84
IL9 × IL12	1.25	89.5	14.68	79.05	26.54	0.2	75.96	24.04	26.8
IL10 × IL11	1.88	95	12.25	80.58	28.7	0.25	75.87	24.13	21.33
IL10 × IL12	1.51	95.25	13.48	83.36	29.43	0.21	79.68	20.32	26.57
IL11 × IL12	1.4	97.75	11.68	74.11	28.23	0.25	62.08	37.92	13.79
HKI 1105	1.45	94.5	12.04	80.17	27.64	0.18	70.22	29.78	18.91
HKI 1128	1.68	92.25	11.43	80.11	25.53	0.2	68.6	31.41	46.43
Grand Mean	1.61	116.33	11.57	78.48	26.66	0.21	71.75	28.26	29.97
Patent Mean	1.59	110.23	11.78	78.33	27.33	0.21	71.76	28.24	25.97
F1 Mean	1.62	117.44	11.53	78.51	26.54	0.21	71.74	28.26	30.7
Check Mean	1.56	93.38	11.73	80.14	26.58	0.19	69.41	30.59	32.67
C.V.	16.3	2.13	9.27	9.93	5.64	7.75	7.17	18.18	45.92
C.D. 5%	0.37	3.46	1.49	10.85	2.1	0.02	7.16	7.16	19.18
S.E.	0.13	1.24	0.54	3.89	0.75	0.01	2.57	2.57	6.88

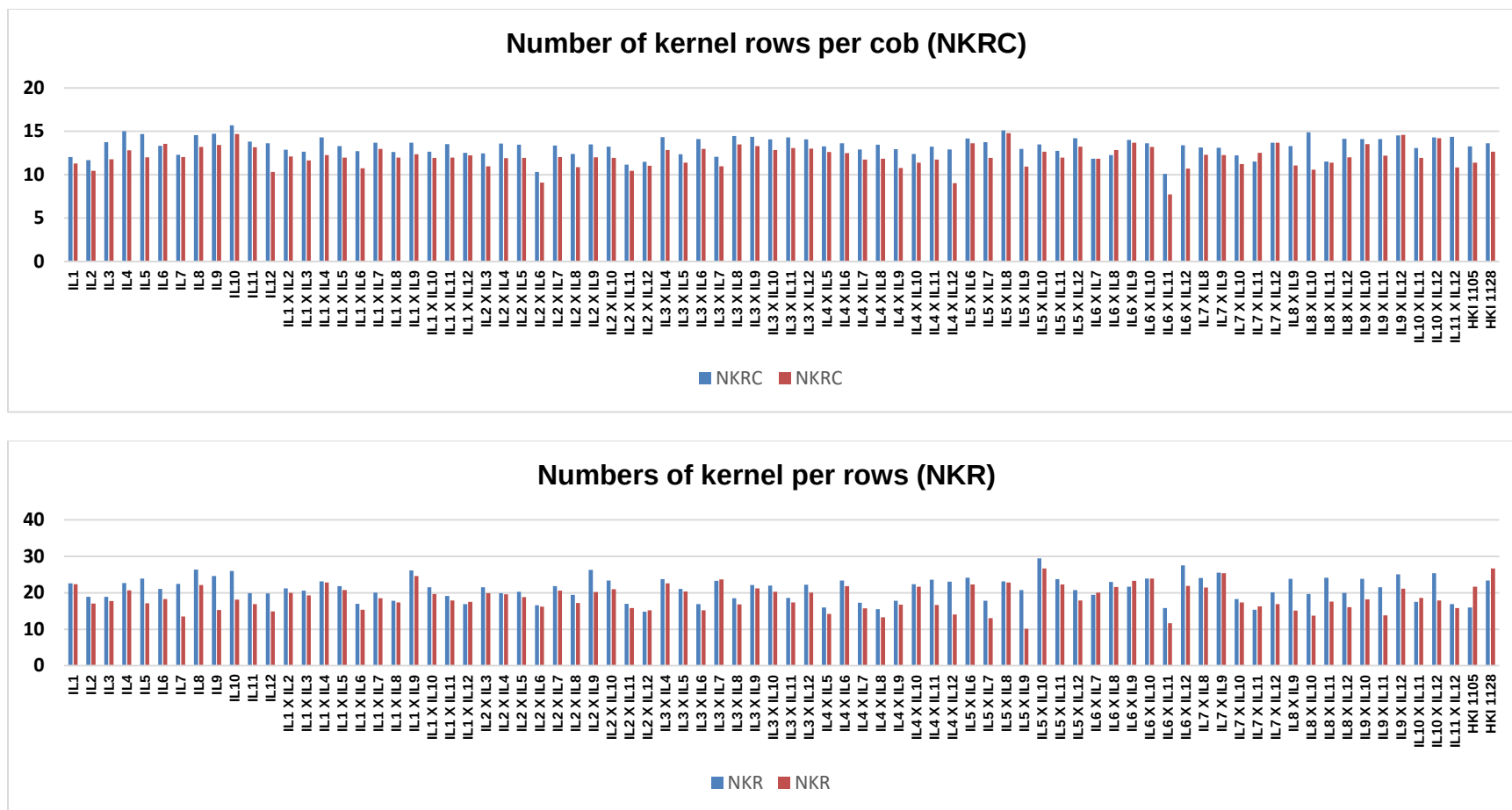


Fig 1. Clustered column of NKRC and NKR morphological traits recorded for 80 maize genotypes under irrigated (I) and partial irrigated conditions (PI).

4.3 Combining ability analysis

The success of any breeding programme largely depends upon the choice of parents and the breeding procedure adopted. Combining ability is an efficient tool to discriminate good as well as poor combiners and for choosing suitable parental lines in hybridization programme. It also provides information of specific promising combinations to exploit heterosis.

The analysis of variance for combining ability and estimation of variance components for various characters in different environments were carried out as per the procedure suggested by Kempthorne (1957).

4.3.1 Analysis of variance for combining ability

The Analysis of variance of combining ability for partitioning the total genetic variance into general combining ability, (gca representing additive type of gene action) and specific combining ability (sca, a measure of non-additive gene action) was carried out by the procedure suggested by Griffing (1956b) Method-2 and Model-I. Variance due to gca as well as sca was found significant for all the characters studied. Magnitudes of gca variance component was higher than sca for all the characters. Table 15 & 16.

ANOVA for combining ability of 12 x 12 half diallel set of hybrids evaluated over two seasons under irrigated and partial irrigated environments is presented in Table 15 & 16.

Table 15 ANOVA for combining ability for different characters studied in maize (*Zea mays* L.) under irrigated condition

SOV	GCA	SCA	Environments	GCA/ SCA	GCA Vs Env.	SCA Vs Env.	Error
df	11	65	1	1	11	65	154
DFT	24445.45**	13365.43**	7262051.28**	127645.68**	14044.69**	12004.87**	48.19
DFS	245.59**	122.75**	77143.70**	1629.12**	140.56**	107.82**	0.59
ASI	258.33**	304.54**	7020.51**	2261.59**	297.72**	229.62**	14.90
PH	2744.29**	866.82**	185643.99**	12754.91**	1215.13**	485.49**	1.68
CL	3.39**	6.48**	0.19	71.25**	0.85	0.78	0.59
NKRC	833.60**	652.24**	802.24**	1883.08**	48.65	43.11	41.07
NKR	91.91**	40.63**	307.39**	1355.01**	3.76	4.04**	2.07
HGW	4588.89**	3444.49**	4160.27**	2107.05**	1281.56**	141.36**	40.87
SYP	801.30**	1550.33**	275.83**	17620.77**	26.28**	21.08**	1.18
NCP	39.17**	42.69**	6.20*	11.13*	2.52*	6.49**	1.11
DM	3396.96**	2304.61**	17239601.28**	3412.82**	984.09**	2224.80**	48.19
CG	209.10**	756.17**	1453.85**	3987.11**	82.14**	64.87**	40.87
SP	74.66**	163.70**	21.77	0.46	23.24**	9.57*	6.49
CT	4.54**	7.75**	19.80**	28.94**	0.42	0.16	1.187
TW	2395.11**	2001.40**	29.53**	11451.91**	25.78**	27.83**	0.808
RWC	272.68**	152.95**	3.10*	28.208**	5.03**	3.31**	0.77
SWD	272.68**	153.01**	3.20*	28.08**	5.03**	3.30**	0.77
MSI	53173.32**	68576.49**	34318.24**	7137.67**	11944.42**	10194.76**	32.9

* and ** significant at 5% and 1% level of significance, respectively,

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, DM= Days to maturity, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob, NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, ASI = Anthesis silking interval, CG = Cob girth (cm), SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

Table 16 ANOVA for combining ability for different characters studied in maize (*Zea mays* L.) under partially irrigated condition

SOV	GCA	SCA	Environments	GCA/ SCA	GCA Vs Env.	SCA Vs Env.	Error
df	11	65	1	1	11	65	154
DFT	23662.87**	14862.49**	5713232.05**	108579.54**	16224.24**	12231.72**	48.19
DFS	22817.42**	14035.78**	6829312.82**	111462.06**	15690.15**	11391.25**	34.34
ASI	483.90**	231.58**	23538.78**	115.39**	247.53**	230.90**	11.75
PH	1930.28**	705.42**	57152.34**	18497.24**	604.64**	871.49**	1.68
CL	3.01**	5.53**	1.57	43.72**	3.89**	4.17**	0.59
NKRC	1872.53**	563.97**	974.14**	5753.00**	543.00**	256.02**	40.87
NKR	106.07**	38.31**	29.50**	514.27**	14.38**	16.30**	0.88
HGW	5029.63**	6136227.05**	5006753.37**	942198.09**	3838.01**	6141254.47**	40.87
SYP	884.46**	1009.91**	300.90**	13037.54**	169.46**	404.32**	1.18
NCP	37.62**	30.27**	0.42	14.27**	5.48**	7.46**	1.10
DM	4187.87**	2669.20**	15490482.05**	4000.23**	3208.33**	1950.41**	48.19
CG	700.92**	272.50**	3429.43**	3735.73**	309.80**	262.69**	41.02
SP	108.74**	126.67**	84.39	126.32	107.37**	90.59**	34.82
CT	2.81*	7.75**	49.28**	3.87	3.89**	4.24**	1.18
TW	2448.06**	1989.63**	262.16**	10825.23**	30.75**	23.99**	0.80
RWC	27299.36**	14474.15**	5570.24**	944.51**	606.81**	556.35**	31.82
SWD	27299.36**	14462.07**	5629.55**	934.15**	606.81**	556.59**	31.69
MSI	858.26**	1354.80**	556.50**	1633.58**	85.64**	99.19**	0.68

* and ** significant at 5% and 1% level of significance, respectively,

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, DM= Days to maturity, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob, NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, ASI = Anthesis silking interval, CG = Cob girth (cm), SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

4.3.2 Estimation of combining ability (*gca* and *sca*) effects

The combining ability analysis was carried out to find information on parents and hybrids about GCA and SCA variance with respect to eighteen traits studied. The estimates of general combining ability effects of parents and specific combining ability effects of the crosses for all the eighteen traits are presented under irrigated condition in Table 17 & Table 18 (a & b) and partial irrigated condition Table 19 & Table 20 (a & b).

The salient features of the results on combining ability effects for different characters are presented as under irrigated condition and partial irrigated condition.

4.3.2.1 Irrigated condition

4.3.2.1.1 Days to 50% tasseling

The estimates of *gca* effects for days to 50 percent tasseling ranged from -30.77 (IL4) to 40.30 (IL12) under irrigated condition. The parental inbred lines -30.77 (IL4), IL3 (-30.77), IL11 (-20.06), IL6 (-19.35) and IL10 (-11.13) showed negative significant *gca* effects under irrigated condition. Which indicate its superiority in transmitting desirable genes for early tasseling. On the other hand, the parents IL12 (40.30), IL5 (36.73), IL1 (22.44) and IL7 (14.23) showed positive significant *gca* effects under irrigated condition (Table 17).

The estimates of *sca* effects for days to 50 percent tasseling ranged between -94.23 (IL10 × IL12) to 106.84 (IL7 × IL9) under irrigated condition. The hybrid IL10 × IL12 (-94.23) showed high negative significant *sca* effect followed by IL1 × IL7 (-86.73), IL5 × IL10 (-85.65), IL8 × IL12 (-84.23), IL5 × IL11 (-81.73), IL11 × IL12 (-80.30). The hybrid IL7 × IL9 (106.84) exhibited high positive significant *sca* effect tracked by IL4 × IL6 (100.05), IL5 × IL8 (89.34), IL8 × IL9 (82.19) and IL4 × IL5 (78.98) (Table 18 a).

4.3.2.1.2 Days to 50 % silking

The estimates of gca effects for days to 50 % silking ranged from -2.85 (IL4) to 4.01 (IL12) under irrigated condition. The parental inbred lines IL2 (-0.27), IL3 (-2.52), IL4 (-2.85), IL6 (-2.08) and IL11 (-2.06) showed negative significant gca effects under irrigated condition. Which indicate its superiority in transmitting desirable genes for early tasseling. On the other hand, the parents viz., IL1 (2.28), IL5 (3.41), IL7 (1.14), IL9 (0.17), IL12 (4.01) showed positive significant gca effects under irrigated condition (Table 17).

The estimates of sca effects for days to days to 50 % silking ranged between -9.95 (IL10 × IL12) to 10.55 (IL7 × IL9) under irrigated condition. The hybrid IL10 × IL12 (-9.95) demonstrated high negative significant sca effect tracked by IL8 × IL12 (-8.38), IL1 × IL7 (-8.31), IL11 × IL12 (-7.84), IL1 × IL5 (-7.58). The hybrid IL7 × IL9 (10.55) showed high positive significant sca effect tracked by IL8 × IL9 (6.71), IL4 × IL5 (8.30), IL5 × IL8 (8.48), IL4 × IL6 (9.03) (Table 18 a).

4.3.2.1.3 Anthesis silking interval (ASI)

The estimates of gca effects for anthesis silking interval was found between -3.10 (IL2) to 3.51 (IL8) under irrigated condition. While the parental inbred lines IL2 (-3.10), IL5 (-2.92), IL9 (-2.80) and IL7 (-2.74) demonstrated negative significant gca effects under irrigated condition. Which indicate its superiority for transmitting desirable genes for early tasseling. On the other hand, the parents viz., IL8 (3.51), IL4 (2.44), IL10 (1.73) and IL1 (0.83) showed positive significant gca effects under irrigated condition (Table 17).

The estimates of sca effects for anthesis silking interval ranged from -20.51 (IL2 × IL11) to 19.231 (IL5 × IL11) under irrigated condition. The hybrid IL2 × IL11 (-20.59) showed high negative significant sca effect tracked by IL8 × IL9 (-15.41), IL1 × IL8 (-13.45), IL7 × IL10 (-13.09) and IL2 × IL10 (-12.73). The hybrid IL6 × IL9 (12.26) demonstrated high positive significant sca effect tracked by IL6 × IL8 (14.05), IL5 × IL10 (14.59), IL2 × IL4 (16.55), IL5 × IL11 (19.23) (Table 18 a).

4.3.2.1.4 Plant height (cm)

The estimates of gca effects for plant height ranges from -19.55 (IL9) to 14.89 (IL7) under irrigated condition. The parental inbred lines IL9 (-19.55), IL1 (-7.15) and IL10 (-3.48) showed negative significant gca effects under irrigated condition. Which indicate its superiority in transmitting desirable genes for short plant height. On the other hand, the parents viz., IL7 (14.89), IL11 (4.75), IL3 (4.33) showed positive significant gca effects under irrigated condition (Table 17).

The estimates of sca effects for plant height (cm) ranged from -37.04 (IL1 $\times$ IL4) to 23.53 (IL6 $\times$ IL10) under irrigated condition. The hybrid IL1 $\times$ IL4 (-37.04) showed high negative significant sca effect tracked by IL9 $\times$ IL10 (-30.49), IL8 $\times$ IL9 (-25.24), IL2 $\times$ IL7 (-24.13), IL6 $\times$ IL9 (-23.04). The hybrid IL6 $\times$ IL10 (23.53) showed high positive significant sca effect tracked by IL1 $\times$ IL12 (16.10), IL5 $\times$ IL12 (16.45), IL3 $\times$ IL7 (18.73), IL3 $\times$ IL8 (20.82) (Table 18 a).

4.3.2.1.5 Cob length (cm)

The estimates of gca effects for cob length (cm) ranged from -0.43 (IL1) to 0.61 (IL4) under irrigated condition. The parental inbred line IL4 (0.61) showed highest significant gca effects tracked by parental inbred lines IL9 (0.51), IL 6 (0.34) and IL7 (0.19) under irrigated condition. On the other hand, the parental inbred line IL1 (-0.43) demonstrated lowest significant gca effects tracked by parental inbred lines IL8 (-0.40), IL5 (-0.38) and IL11 (-0.37) under irrigated condition (Table 17).

The estimates of sca effects for cob length (cm) ranged from -2.07 (IL1 $\times$ IL7) to 3.78 (IL2 $\times$ IL9) under irrigated condition. The hybrid IL1 $\times$ IL7 (-2.07) showed higher negative significant sca effect tracked by IL4 $\times$ IL7 (-1.72), IL5 $\times$ IL6 (-1.59), IL3 $\times$ IL8 (-1.42) and IL2 $\times$ IL12 (-1.29). The hybrid IL2 $\times$ IL9 (3.78) showed high positive significant sca effect tracked by IL5 $\times$ IL7 (2.70), IL6 $\times$ IL11 (2.43), IL2 $\times$ IL7 (2.31) and IL1 $\times$ IL4 (2.24) (Table 18 a).

4.3.2.1.6 Number of kernel rows per cob (NKRC)

The estimates of gca effects for number of kernel rows per cob ranged from -7.88 (IL3) to 5.11 (IL11) under irrigated condition. The parental inbred line IL11 (5.11) showed highest gca effects for tracked by parental inbred lines IL12 (4.65), IL8 (4.63) and IL9 (3.89) under irrigated condition. On the other hand, the parental inbred line IL3 (-7.88) showed lowest gca effects tracked by parental inbred lines IL4 (-7.82), IL5 (-4.08) and IL6 (-3.53) under irrigated condition (Table 17).

The estimates of sca effects for Number of kernel rows per cob ranged from -27.66 (IL3 × IL12) to 25.31 (IL5 × IL10) under irrigated condition. The hybrid IL3 × IL12 (-27.64) showed high negative significant sca effect followed by IL2 × IL8 (-25.97), IL5 × IL8 (-19.54), IL6 × IL11 (-17.92) and IL5 × IL7 (-17.00). The hybrid IL5 × IL10 (25.31) showed high positive significant sca effect followed IL6 × IL12 (19.09), IL7 × IL8 (18.89), IL8 × IL12 (18.69) and IL4 × IL5 (16.76) (Table 18 a).

4.3.2.1.7 Numbers of kernel per rows (NKR)

The estimates of gca effects for Numbers of kernel per rows ranged from -1.27 (IL5) to 1.50 (IL16) under irrigated condition. The parental inbred line IL6 (1.50) showed highest gca effects for tracked by parental inbred lines IL2 (0.92), IL4 (0.72) and IL1 (0.11) under irrigated condition. On the other hand, the parental inbred line IL5 (-1.27) demonstrated lowest gca effects tracked by parental inbred lines IL3 (-1.08), IL8 (-0.68) and IL11 (-0.15) under irrigated condition (Table 17).

The estimates of sca effects for numbers of kernel per rows ranged from -5.65 (IL5 × IL8) to 6.71 (IL2 × IL6) under irrigated condition. The hybrid IL5 × IL8 (-5.65) demonstrated high negative significant sca effect tracked by IL6 × IL9 (5.60), IL1 × IL12 (-4.99), IL4 × IL7 (-4.10) and IL2 × IL11 (-3.90). The hybrid IL2 × IL6 (6.71) showed high positive significant sca effect tracked by IL9 × IL11 (6.37), IL5 × IL12 (5.44), IL8 × IL11 (5.39) and IL7 × IL8 (5.33) (Table 18 a).

4.3.2.1.8 100- grain weight (g)

The estimates of gca effects for 100-grain weight ranged from -12.52 (IL1) to 21.02 (IL9) under irrigated condition. The parental inbred line IL9 (21.02) showed highest gca effects for tracked by parental inbred lines IL6 (13.74), IL7 (13.67) and IL3 (2.65) under irrigated condition. On the other hand, the parental inbred line IL1 (-12.52) showed lowest gca effects followed by parental inbred lines IL5 (-10.14), IL10 (-9.84) and IL2 (-8.45) under irrigated condition (Table 17).

The estimates of sca effects for 100 grain weight ranged from -49.51 (IL3 $\times$ IL7) to 65.32 (IL8 $\times$ IL10) under irrigated condition. The hybrid IL2 $\times$ IL7 (-49.51), showed high negative significant sca effect followed by IL5 $\times$ IL8 (-49.45), IL1 $\times$ IL12 (-46.06), IL3 $\times$ IL4 (-44.30) and IL2 $\times$ IL10 (-35.09). The hybrid IL8 $\times$ IL10 (65.32) showed high positive significant sca effect followed IL3 $\times$ IL7 (60.49) IL5 $\times$ IL6 (56.31), IL8 $\times$ IL11 (54.36), IL5 $\times$ IL9 (42.81) (Table 18a).

4.3.2.1.9 Yield per plant (g)

The estimates of gca effects for yield per plant (g) ranged from -9.16 (IL5) to 9.47 (IL7) under irrigated condition. The parental inbred line IL7 (9.47) showed highest gca effects for tracked by parental inbred lines IL10 (4.64), IL9 (3.44) and IL6 (2.21) under irrigated condition. On the other hand, the parental inbred line IL5 (-9.16) showed lowest gca effects followed by parental inbred lines IL4 (-5.00), IL8 (-3.06) and IL3 (-2.96) under irrigated condition (Table 17).

The estimates of sca effects for yield per plant (g) ranged from -32.34 (IL4 $\times$ IL7) to 45.65 (IL11 $\times$ IL12) under irrigated condition. The hybrid IL11 $\times$ IL12 (45.65) showed high positive significant sca effect followed by IL1 $\times$ IL7 (39.63), IL3 $\times$ IL10 (38.89), IL4 $\times$ IL6 (31.67) and IL7 $\times$ IL8 (28.67). The hybrid IL4 $\times$ IL7 (-32.34) showed high negative significant sca effect tracked by IL1 $\times$ IL6 (-32.18), IL5 $\times$ IL7 (-27.52), IL2 $\times$ IL4 (-24.26) and IL3 $\times$ IL12 (-20.58) (Table 18 a).

4.3.2.1.10 Number of cobs per plant (NCP)

The estimates of gca effects for number of cobs per plant ranged from -1.22 (IL12) to 2.12 (IL3) under irrigated condition. The parental inbred line IL3 (2.12)

demonstrated highest gca effects tracked by parental inbred lines IL2 (0.72), IL1 (0.48) and IL4 (0.35) under irrigated condition. On the other hand, the parental inbred line IL12 (-1.22) showed lowest gca effects tracked by parental inbred lines IL6 (-1.00), IL5 (-0.67) and IL11 (-0.32) under irrigated condition (Table 17).

The estimates of sca effects for number of cobs per plant ranged from -6.28 (IL7 × IL10) to 7.02 (IL4 × IL8) under irrigated condition. The hybrid IL7 × IL8 (6.46) showed higher positive significant sca effect tracked by IL11 × IL12, (1.93), IL1 × IL7 (1.13) and IL4 × IL6 (3.82). The hybrid IL4 × IL7 (-4.25) showed high negative significant sca effect tracked by IL1 × IL6 (-2.04), IL5 × IL7 (-1.71) and IL3 × IL12 (-0.62) (Table 18 b).

4.3.2.1.11 Days to maturity

The estimates of gca effects for days to maturity ranged from -17.74 (IL3) to 15.83 (IL12) under irrigated condition. The parental inbred line IL12 (15.83) showed highest gca effects tracked by parental inbred lines IL5 (8.69), IL7 (7.62) and IL2 (5.48) under irrigated condition. Conversely, the parental inbred line IL3 (-17.74) demonstrated lowest gca effects tracked by parental inbred lines IL4 (-15.24), IL9 (-5.95) and IL10 (-4.17) under irrigated condition (Table 17).

The estimates of sca effects for days to maturity arrayed between -54.86 (IL7 × IL12) to 56.57 (IL1 × IL7) under irrigated condition. The hybrid IL1 × IL7 (56.57) demonstrated high positive significant sca effect tracked by IL3 × IL5 (47.63), IL2 × IL3 (45.85), IL1 × IL10 (28.35) and IL6 × IL7 (27.10). The hybrid IL7 × IL12 (-54.86) demonstrated high negative significant sca effect tracked by IL8 × IL9 (-35.22), IL6 × IL11 (-32.72), IL4 × IL10 (-32.00) and IL1 × IL3 (-28.07) (Table 18 b).

4.3.2.1.12 Cob girth (cm)

The estimates of gca effects for cob girth (cm) ranged between -5.61 (IL3) to 5.38 (IL8) under irrigated condition. The parental inbred line IL8 (5.38) demonstrated highest gca effects tracked by parental inbred lines IL9 (5.08), IL1

(3.27) and IL6 (1.66) under irrigated condition. On the other hand, the parental inbred line IL3 (-5.61) demonstrated lowest gca effects followed by parental inbred lines IL4 (-4.66), IL2 (-4.05) and IL5 (-3.12) under irrigated condition (Table 17).

The estimates of sca effects for cob girth (cm) ranged from -21.01 (IL5 × IL7) to 49.12 (IL6 × IL8) under irrigated condition. The hybrid IL6 × IL8 (49.12) showed high positive significant sca effect tracked by IL5 × IL10 (34.19), IL1 × IL9 (30.16), IL2 × IL3 (21.17) and IL5 × IL9 (18.03). The hybrid IL5 × IL7 (-21.01) showed high negative significant sca effect tracked by IL5 × IL8 (-17.25), IL2 × IL6 (-17.20), IL2 × IL5 (-16.72) and IL1 × IL7 (-15.95) (Table 18 b).

4.3.2.1.13 Shelling (%)

The estimates of gca effects for shelling (%) ranged from -4.06 (IL4) to 2.10 (IL10) under irrigated condition. The parental inbred line IL10 (2.10) showed highest gca effects for followed by parental inbred lines IL11 (1.50), IL8 (1.29) and IL12 (0.51) under irrigated condition. Alternatively, the parental inbred line IL4 (-4.06) displayed lowest gca effects followed by parental inbred lines IL5 (-0.86), IL6 (-0.62) and IL9 (-0.19) under irrigated condition (Table 17).

The estimates of sca effects for shelling (%) arrayed between -20.32 (IL5 × IL7) to 10.80 (IL1 × IL7) under irrigated condition. The hybrid IL5 × IL7 (-20.32) displayed high negative significant sca effect tracked by IL1 × IL8 (-16.82), IL6 × IL11 (-12.86), IL7 × IL10 (-10.24) and IL3 × IL4 (-10.16). The hybrid IL11 × IL12 (6.74) displayed high positive significant sca effect tracked by IL1 × IL7 (10.80) IL4 × IL11 (8.72), IL3 × IL8 (6.93) and IL5 × IL12 (6.93) (Table 18 b).

4.3.2.1.14 Canopy temperature (at reproductive stages)

The estimates of gca effects for canopy temperature ranged from -0.51 (IL2) to 0.50 (IL9) under irrigated condition. The parental inbred line IL9 (0.50) demonstrated highest gca effects followed by parental inbred lines IL3 (0.40), IL10 (0.19) and IL5 (0.13) under irrigated condition. Alternatively, the parental

inbred line IL2 (-0.51) displayed lowest gca effects trailed by parental inbred lines IL1 (-0.34), IL11 (-0.25) and IL7 (-0.24) under irrigated condition (Table 17).

The estimates of sca effects for canopy temperature arrayed from -3.74 (IL2 × IL9) to 2.75 (IL3 × IL8) under irrigated condition. The hybrid IL3 × IL8 (2.75) exhibited high positive significant sca effect tracked IL5 × IL6 (2.44), IL9 × IL11 (2.14), IL9 × IL12 (2.11), IL2 × IL3 (1.81). The hybrid IL2 × IL9 (-3.74), showed high negative significant sca effect tracked by IL3 × IL12 (-2.54), IL3 × IL4 (-2.45), IL8 × IL10 (-2.14) and IL7 × IL11 (-1.87) (Table 18 b).

4.3.2.1.15 Turgid weight (g)

The estimates of gca effects for Turgid weight (g) ranged from -17.62 (IL1) to 15.52 (IL7) under irrigated condition. The parental inbred line IL7 (15.52) showed highest gca effects for followed by parental inbred lines IL9 (10.81), IL5 (6.74) and IL12 (6.53) under irrigated condition. On the other hand, the parental inbred line IL1 (-17.62) showed lowest gca effects followed by parental inbred lines IL3 (-10.33), IL2 (-5.87) and IL6 (-5.69) under irrigated condition (Table 17).

The estimates of sca effects for Turgid weight (g) varied between -34.04 (IL3 × IL4) to 50.64 (IL4 × IL8) under irrigated condition. The hybrid IL4 × IL8 (50.64) exhibited high positive significant sca effect tracked by IL1 × IL7 (45.93), IL5 × IL12 (33.07), IL3 × IL6 (31.36) and IL3 × IL12 (30.14). The hybrid IL3 × IL4 (-34.04) showed high negative significant sca effect tracked by IL11 × IL12 (-33.25), IL8 × IL11 (-30.21), IL7 × IL12 (-28.71) and IL5 × IL9 (-27.21) (Table 18 b).

4.3.2.1.16 Relative water content

The estimates of gca effects for Relative water content ranged between -4.07 (IL4) to 3.52 (IL10) under irrigated condition. The parental inbred line IL10 (3.52) showed highest gca effects tracked by parental inbred lines IL12 (2.36), IL2 (2.16) and IL5 (1.45) under irrigated condition. Conversely, the parental inbred

line IL4 (-4.07) showed lowest gca effects tracked by parental inbred lines IL11 (-2.28), IL1 (-1.37) and IL8 (-0.89) under irrigated condition (Table 17).

The estimates of sca effects for Relative water content ranged between -9.66 (IL6 × IL10) to 13.37 (IL2 × IL3) under irrigated condition. The hybrid IL2 × IL3 (13.37) showed high positive significant sca effect tracked by IL1 × IL4 (9.63), IL6 × IL8 (9.48), IL8 × IL11 (9.41) and IL7 × IL12 (9.02). The hybrid IL6 × IL10 (-9.66), demonstrated high negative significant sca effect tracked by IL3 × IL10 (-9.58), IL3 × IL4 (-8.87), IL7 × IL9 (-8.19) and IL2 × IL4 (-7.85) (Table 18 b).

4.3.2.1.17 Saturation water deficit

The estimates of gca effects for Saturation water deficit ranged from -3.52 (IL12) to 4.07 (IL4) under irrigated condition. The parental inbred line IL4 (4.07) showed highest gca effects tracked by parental inbred lines IL11 (2.45), IL1 (1.16) and IL8 (0.90) under irrigated condition. In contrast, the parental inbred line IL12 (-3.52) exhibited lowest gca effects followed by parental inbred lines IL10 (-2.36), IL2 (-2.16) and IL5 (-1.45) under irrigated condition (Table 17).

The estimates of sca effects for Saturation water deficit ranged between -13.38 (IL2 × IL3) to 9.66 (IL6 × IL10) under irrigated condition. The hybrid IL6 × IL10 (9.66) displayed high positive significant sca effect tracked by IL3 × IL10 (9.57), IL3 × IL4 (8.86), IL7 × IL9 (8.19) and IL2 × IL4 (7.86). The hybrid IL2 × IL3 (-13.38) disclosed high negative significant sca effect tracked by IL1 × IL4 (-9.62), IL6 × IL8 (-9.48), IL8 × IL11 (-9.42) and IL7 × IL12 (-9.02) (Table 18 b).

4.3.2.1.18 Membrane stability index

The estimates of gca effects for Membrane stability index varied from -78.75 (IL12) to 121.26 (IL3) under irrigated condition. The parental inbred line IL3 (121.26) disclosed highest gca effects followed by parental inbred lines IL2 (55.29), IL1 (32.01) and IL8 (15.96) under irrigated condition. On the other hand, the parental inbred line IL12 (-78.75) exhibited lowest gca effects tracked by

parental inbred lines IL6 (-46.41), IL7 (-36.64) and IL10 (-27.31) under irrigated condition (Table 17).

The estimates of sca effects for membrane stability index varied from -173.90 (IL9 × IL11) to 238.40 (IL1 × IL9) under irrigated condition. The hybrid IL1 × IL9 (238.39) displayed high positive significant sca effect tracked by IL3 × IL11 (230.88), IL3 × IL6 (219.62), IL1 × IL4 (188.14) and IL2 × IL6 (166.73). The hybrid IL9 × IL11 (-173.90) displayed high negative significant sca effect followed by IL1 × IL3 (-160.01), IL3 × IL7 (-143.20), IL5 × IL11 (-134.05) and IL7 × IL8 (-131.08) (Table 18 b).

4.3.2.2 Partially irrigated condition

4.3.2.2.1 Days to 50% tasseling

The estimates of gca effects for days to 50% tasseling ranged between -30.48 (IL4) to 50.95 (IL12) under partially irrigated condition. The parental inbred line IL4 (-30.48) displayed lowest gca effects followed by parental inbred lines IL6 (-26.91), IL11 (-19.76) and IL3 (-18.33) under partially irrigated condition. Alternatively, the parental inbred line IL12 (50.95) displayed highest gca effects followed by parental inbred lines IL5 (40.02), IL7 (16.67) and IL1 (4.88) under partially irrigated condition (Table 19).

The estimates of sca effects for days to 50% tasseling ranged from -97.14 (IL10 × IL12) to 103.57 (IL7 × IL9) under partially irrigated condition. The hybrid IL10 × IL12 (-97.14) showed high negative significant sca effects tracked by IL5 × IL10 (-88.21), IL1 × IL5 (-83.57) and IL1 × IL7 (-83.21). The hybrid IL7 × IL9 (103.5) disclosed high positive significant sca effects tracked by IL4 × IL6 (100.71), IL8 × IL9 (96.42) and IL5 × IL8 (87.50) (Table 20 a).

4.3.2.2.2 Days to 50 % silking

The estimates of gca effects for days to 50 % silking varied from -28.16 (IL6) to 50.24 (IL12) under partially irrigated condition. The parental inbred line IL6 (-28.16) disclosed lowest gca effects tracked by parental inbred lines IL4 (-27.08),

IL11 (-19.94) and IL3 (-16.23) under partially irrigated condition. Conversely, the parental inbred line IL12 (50.24) displayed highest gca effects tracked by parental inbred lines IL5 (38.63), IL7 (17.38) and IL1 (4.70) under partially irrigated condition (Table 19).

The estimates of sca effects for days to 50 % silking ranged between -97.10 (IL10 $\times$ IL12) to 98.26 (IL7 $\times$ IL9) under partially irrigated condition. The hybrid IL10 $\times$ IL12 (-97.10) showed high negative significant sca effects followed by IL5 $\times$ IL10 (-87.99), IL5 $\times$ IL11 (-79.78) and IL1 $\times$ IL5 (-74.42). The hybrid IL9 $\times$ IL9 (98.26) showed high positive significant sca effects tracked by IL4 $\times$ IL6 (89.14), IL5 $\times$ IL8 (88.97) and IL8 $\times$ IL9 (84.32) (Table 20 a).

4.3.2.2.3 Anthesis silking interval (ASI)

The estimates of gca effects for Anthesis silking interval ranged from -3.66 (IL5) to 2.95 (IL4) under partially irrigated condition. The parental inbred line IL5 (-3.66) showed lowest gca effects for followed by parental inbred lines IL9 (-1.52), IL3 (-0.98) and IL1 (-0.80) under partially irrigated condition. On the other hand, the parental inbred line IL4 (2.95) showed highest gca effects for followed by parental inbred lines IL8 (2.77), IL10 (1.16) and IL12 (0.98) under partially irrigated condition (Table 19).

The estimates of sca effects for Anthesis silking interval ranged between -19.2 (IL5 $\times$ IL11) to 17.89 (IL1 $\times$ IL2) under partially irrigated condition. The hybrid IL5 $\times$ IL11 (-19.2) displayed high negative significant sca effects tracked by IL8 $\times$ IL9 (-17.12), IL6 $\times$ IL10 (-13.9) and IL1 $\times$ IL8 (-13.5). The hybrid IL1 $\times$ IL2 (17.88) showed high positive significant sca effects tracked by IL1 $\times$ IL7 (16.81), IL2 $\times$ IL4 (16.55) and IL1 $\times$ IL6 (15.56) (Table 20 a).

4.3.2.2.4 Plant height (cm)

The estimates of gca effects for plant height (cm) ranged from -13.24 (IL9) to 11.67 (IL7) under partially irrigated condition. The parental inbred line IL9 (-13.24) showed lowest gca effects tracked by parental inbred lines IL1 (-10.58),

IL6 (-1.98) and IL4 (-1.74) under partially irrigated condition. Conversely, the parental inbred line IL7 (11.67) displayed highest gca effects followed by parental inbred lines IL11 (5.90), IL2 (4.68) and IL12 (3.40) under partially irrigated condition (Table 19).

The estimates of sca effects for plant height (cm) ranged from -31.69 (IL1 $\times$ IL3) to 26.76 (IL8 $\times$ IL11) under partially irrigated condition. The hybrid IL1 $\times$ IL3 (-31.69) displayed high negative significant sca effects tracked by IL3 $\times$ IL7 (-26.34), IL2 $\times$ IL8 (-18.52) and IL11 $\times$ IL12 (-17.46). The hybrid IL8 $\times$ IL11 (26.76) exposed high positive significant sca effects tracked by IL1 $\times$ IL9 (22.58) IL4 $\times$ IL5 (21.78) and IL7 $\times$ IL10 (20.01) (Table 20 a).

4.3.2.2.5 Cob length (cm)

The estimates of gca effects for cob length (cm) varied between -0.37 (IL7) to 0.68 (IL9) under partially irrigated condition. The parental inbred line IL7 (-0.37) exposed lowest gca effects followed by parental inbred lines IL11 (-0.35), IL5 (-0.31) and IL8 (-0.27) under partially irrigated condition. Alternatively, the parental inbred line IL9 (0.68) displayed highest gca effects tracked by parental inbred lines IL4 (0.37), IL10 (0.28) and IL2 (0.27) under partially irrigated condition (Table 19).

The estimates of sca effects for cob length (cm) ranged from -2.73 (IL6 $\times$ IL8) to 2.85 (IL2 $\times$ IL9) under partially irrigated condition. The hybrid IL6 $\times$ IL8 (-2.37) showed higher negative significant sca effect tracked by IL1 $\times$ IL12 (-1.87), IL5 $\times$ IL6 (-1.82) and IL6 $\times$ IL9 (-1.62). The hybrid IL2 $\times$ IL9 (2.85) showed high positive significant sca effect tracked by IL6 $\times$ IL12 (2.82), IL5 $\times$ IL7 (2.52) and IL10 $\times$ IL11 (2.06) (Table 20 a).

4.3.2.2.6 Number of kernel rows per cob (NKRC)

The estimates of gca effects for number of kernel rows per cob varied from -11.15 (IL4) to 4.86 (IL10) under partially irrigated condition. The parental inbred line IL4 (-11.15) exhibited lowest gca effects followed by parental inbred lines IL6

(-4.50), IL5 (-3.38) and IL1 (-3.35) under partially irrigated condition. Alternatively, the parental inbred line IL10 (4.86) disclosed highest gca effects followed by parental inbred lines IL9 (4.85), IL7 (4.70) and IL2 (4.65) under partially irrigated condition (Table 19).

The estimates of sca effects for Number of kernel rows per cob ranged from -23.03 (IL2 × IL8) to 23.67 (IL4 × IL12) under partially irrigated condition. The hybrid IL2 × IL8 (-23.03) showed high negative significant sca effect followed by IL1 × IL2 (-20.85), IL1 × IL5 (-19.72) and IL3 × IL12 (-18.23). The hybrid IL4 × IL12 (23.67) showed high positive significant sca effect followed IL1 × IL4 (23.34), IL7 × IL12 (22.66) and IL5 × IL10 (21.31) (Table 20 a).

4.3.2.2.7 Numbers of kernel per rows (NKR)

The estimates of gca effects for numbers of kernel per rows ranged between -1.14 (IL8) to 1.09 (IL2) under partially irrigated condition. The parental inbred line IL8 (-1.14) disclosed lowest gca effects tracked by parental inbred lines IL4 (-0.70), IL12 (-0.68) and IL5 (-0.59) under partially irrigated condition. Conversely, the parental inbred line IL2 (1.09) disclosed highest gca effects tracked by parental inbred lines IL3 (0.82), IL1 (0.75) and IL10 (0.50) under partially irrigated condition (Table 19).

The estimates of sca effects for numbers of kernel per rows ranged from -5.77 (IL6 × IL9) to 7.73 (IL2 × IL6) under partially irrigated condition. The hybrid IL6 × IL9 (-5.77) demonstrated high negative significant sca effect tracked by IL2 × IL4 (-5.30), IL2 × IL5 (-5.25) and IL1 × IL12 (-4.51). The hybrid IL2 × IL6 (7.73) showed high positive significant sca effect tracked by IL4 × IL11 (6.41), IL5 × IL12 (6.23) and IL4 × IL5 (6.15) (Table 20 a).

4.3.2.2.8 100-grain weight (g)

The estimates of gca effects for 100-grain weight (g) varied from -133.35 (IL11) to 107.01 (IL6) under partially irrigated condition. The parental inbred line IL11 (-133.35) exhibited lowest gca effects tracked by parental inbred lines IL2 (-

128.40), IL8 (-123.80) and IL1 (-123.40) under partially irrigated condition. Alternatively, the parental inbred line IL6 (107.01) displayed highest gca effects tracked by parental inbred lines IL4 (102.68), IL9 (98.14) and IL7 (90.12) under partially irrigated condition (Table 19).

The estimates of sca effects for 100-grain weight (g) ranged from -94.84 (IL2 $\times$ IL4) to 171.07 (IL3 $\times$ IL7) under partially irrigated condition. The hybrid IL2 $\times$ IL4 (-94.84) exhibited high positive significant sca effects trailed by IL4 $\times$ IL8 (-90.91), IL5 $\times$ IL10 (-88.79) and IL4 $\times$ IL11 (-83.89). The hybrid IL3 $\times$ IL7 (171.07) exhibited high negative significant sca effects tracked by IL8 $\times$ IL11 (164.77), IL8 $\times$ IL10 (156.89) and IL2 $\times$ IL9 (146.63) (Table 20 a).

4.3.2.2.9 Yield per plant (g)

The estimates of gca effects for yield per plant (g) varied from -6.42 (IL4) to 9.02 (IL10) under partially irrigated condition. The parental inbred line IL4 (-6.42) exhibited lowest gca effects followed by parental inbred lines IL5 (-6.40), IL8 (-4.16) and IL6 (-3.47) under partially irrigated condition. On the other hand, the parental inbred line IL10 (9.20) showed highest gca effects followed by parental inbred lines IL9 (6.11), IL7 (6.10) and IL12 (1.30) under partially irrigated condition (Table 19).

The estimates of sca effects for Yield per plant (g) ranged from -25.91 (IL4 $\times$ IL7) to 49.71 (IL3 $\times$ IL10) under partially irrigated condition. The hybrid IL4 $\times$ IL7 (-25.91) showed high negative significant sca effects tracked by IL1 $\times$ IL6 (-23.18), IL2 $\times$ IL5 (-21.62) and IL2 $\times$ IL12 (-20.57). The hybrid IL3 $\times$ IL10 (49.71) exhibited high positive significant sca effects tracked by IL1 $\times$ IL7 (28.35), IL1 $\times$ IL4 (23.13) and IL7 $\times$ IL12 (22.87) (Table 20 a).

4.3.2.2.10 Number of cobs per plant (NCP)

The estimates of gca effects for number of cobs per plant ranged from -1.44 (IL12) to 1.31 (IL8) under partially irrigated condition. The parental inbred line IL12 (-1.44) showed lowest gca effects for followed by parental inbred lines IL6 (-

0.77), IL5 (-0.51) and IL1 (-0.33) under partially irrigated condition. Alternatively, the parental inbred line IL8 (1.31) exhibited highest gca effects tracked by parental inbred lines IL7 (0.83), IL3 (0.40) and IL11 (0.35) under partially irrigated condition (Table 19).

The estimates of sca effects for number of cobs per plant ranged from -4.25 (IL3 × IL4) to 7.35 (IL4 × IL8) under partially irrigated condition. The hybrid IL3 × IL4 (-4.25) exhibited high negative significant sca effects tracked by IL6 × IL8 (-4.16), IL3 × IL7 (-4.11) and IL5 × IL8 (-4.05). The hybrid IL4 × IL8 (7.35) exposed high positive significant sca effects trailed by IL4 × IL5 (5.66), IL3 × IL11 (4.62) and IL1 × IL10 (4.30) (Table 20 b).

4.3.2.2.11 Days to maturity

The estimates of gca effects for days to maturity ranged from -20.18 (IL4) to 18.04 (IL12) under partially irrigated condition. The parental inbred line IL4 (-20.18) exhibited lowest gca effects tracked by parental inbred lines IL3 (-15.54), IL10 (-9.82) and IL6 (-5.18) under partially irrigated condition. Conversely, the parental inbred line IL12 (18.04) exhibited highest gca effects trailed by parental inbred lines IL1 (15.54), IL11 (9.46) and IL7 (6.25) under partially irrigated condition (Table 19).

The estimates of sca effects for days to maturity ranged from -63.62 (IL1 × IL6) to 42.44 (IL3 × IL4) under partially irrigated condition. The hybrid IL1 × IL6 (-63.62) exhibited high positive significant sca effects tracked by IL2 × IL9 (-42.2), IL3 × IL11 (-42.2) and IL2 × IL4 (-38.26). The hybrid IL3 × IL4 (42.44) exposed high negative significant sca effects tracked by IL2 × IL12 (38.52), IL9 × IL10 (32.80) and IL3 × IL6 (32.44) (Table 20 b).

4.3.2.2.12 Cob girth (cm)

The estimates of gca effects for Cob girth (cm) ranged from -6.80 (IL4) to 4.22 (IL9) under partially irrigated condition. The parental inbred line IL4 (-6.80) showed lowest gca effects for followed by parental inbred lines IL3 (-3.93), IL5 (-

1.76) and IL11 (-1.17) under partially irrigated condition. On the other hand, the parental inbred line IL9 (4.22) showed highest gca effects for followed by parental inbred lines IL7 (3.32), IL12 (1.95) and IL8 (1.53) under partially irrigated condition (Table 19).

The estimates of sca effects for Cob girth (cm) ranged from -14.57 (IL3 × IL6) to 19.34 (IL5 × IL10) under partially irrigated condition. The hybrid IL3 × IL6 (-14.57) showed high positive significant sca effects followed by IL7 × IL10 (-11.44), IL2 × IL5 (-10.66) and IL5 × IL8 (-10.66). The hybrid IL5 × IL10 (19.34) showed high positive significant sca effects followed by IL7 × IL12 (19.14), IL5 × IL6 (17.34) and IL4 × IL5 (14.37) (Table 20 b).

4.3.2.2.13 Shelling (%)

The estimates of gca effects for shelling (%) ranged from -3.59 (IL4) to 1.53 (IL1) under partially irrigated condition. The parental inbred line IL4 (-3.59) exhibited lowest gca effects tracked by parental inbred lines IL9 (-1.04), IL5 (-0.69) and IL8 (-0.03) under partially irrigated condition. Alternatively, the parental inbred line IL1 (1.53) exhibited highest gca effects tracked by parental inbred lines IL7 (1.32), IL10 (1.24) and IL3 (0.50) under partially irrigated condition (Table 19).

The estimates of sca effects for shelling (%) varied between -20.65 (IL5 × IL7) to 8.08 (IL5 × IL12) under partially irrigated condition. The hybrid IL5 × IL7 (-20.65) demonstrated high positive significant sca effects tracked by IL10 × IL11 (-10.54), IL4 × IL5 (-7.69) and IL8 × IL9 (-7.48). The hybrid IL5 × IL12 (8.08) demonstrated high negative significant sca effects tracked by IL1 × IL7 (7.83), IL5 × IL11 (7.8) and IL7 × IL11 (7.67) (Table 20 b).

4.3.2.2.14 Canopy temperature (at reproductive stages)

The estimates of gca effects for canopy temperature ranged between -0.57 (IL7) to 0.59 (IL1) under partially irrigated condition. The parental inbred line IL7 (-0.57) displayed lowest gca effects followed by parental inbred lines IL4 (-0.52), IL6 (-0.47) and IL2 (-0.45) under partially irrigated condition. Alternatively, the

parental inbred line IL1 (0.59) demonstrated highest gca effects followed by parental inbred lines IL9 (0.55), IL10 (0.42) and IL12 (0.40) under partially irrigated condition (Table 19).

The estimates of sca effects for canopy temperature arrayed between -3.66 (IL2 $\times$ IL9) to 2.92 (IL9 $\times$ IL11) under partially irrigated condition. The hybrid IL2 $\times$ IL9 (-3.66) exhibited high negative significant sca effects followed by IL7 $\times$ IL11 (-2.94), IL4 $\times$ IL12 (-2.07) and IL3 $\times$ IL12 (-1.87). The hybrid IL9 $\times$ IL11 (2.92) demonstrated high positive significant sca effects tracked by IL2 $\times$ IL3 (2.49), IL5 $\times$ IL8 (2.13) and IL10 $\times$ IL11 (2.10) (Table 20 b).

4.3.2.2.15 Turgid weight (g)

The estimates of gca effects for Turgid weight (g) ranged from -20.19 (IL1) to 15.35 (IL7) under partially irrigated condition. The parental inbred line IL1 (-20.19) disclosed lowest gca effects tracked by parental inbred lines IL3 (-10.51), IL6 (-5.40) and IL2 (-4.90) under partially irrigated condition. Conversely, the parental inbred line IL7 (15.35) exhibited highest gca effects followed by parental inbred lines IL9 (10.32), IL12 (6.99) and IL5 (6.49) under partially irrigated condition (Table 19).

The estimates of sca effects for Turgid weight (g) ranged from -33.91 (IL3 $\times$ IL4) to 50.08 (IL4 $\times$ IL8) under partially irrigated condition. The hybrid IL3 $\times$ IL4 (-33.91) showed high negative significant sca effects tracked by IL11 $\times$ IL12 (-32.66), IL8 $\times$ IL11 (-32.66) and IL2 $\times$ IL3 (-28.44). The hybrid IL4 $\times$ IL8 (50.08) exhibited high positive significant sca effects tracked by IL1 $\times$ IL7 (34.48), IL3 $\times$ IL5 (33.16) and IL5 $\times$ IL12 (31.66) (Table 20 b).

4.3.2.2.16 Relative water content

The estimates of gca effects for Relative water content ranged between -38.96 (IL4) to 33.13 (IL12) under partially irrigated condition. The parental inbred line IL4 (-38.96) exhibited lowest gca effects tracked by parental inbred lines IL11 (-24.44), IL6 (-9.62) and IL8 (-7.92) under partially irrigated condition. Alternatively,

the parental inbred line IL12 (33.13) demonstrated highest gca effects tracked by parental inbred lines IL10 (17.91), IL2 (16.83) and IL5 (16.76) under partially irrigated condition (Table 19).

The estimates of sca effects for Relative water content ranged from -95.67 (IL3 × IL10) to 143.28 (IL2 × IL3) under partially irrigated condition. The hybrid IL3 × IL10 (-95.67) showed high negative significant sca effects tracked by IL3 × IL4 (-89.13), IL1 × IL8 (-87.77) and IL7 × IL9 (-84.67). The hybrid IL2 × IL3 (143.28) exhibited high positive significant sca effects followed by IL8 × IL11 (103.53), IL6 × IL8 (92.88) and IL1 × IL4 (91.26) (Table 20 b).

4.3.2.2.17 Saturation water deficit

The estimates of gca effects for Saturation water deficit arrayed between -33.16 (IL12) to 38.94 (IL4) under partially irrigated condition. The parental inbred line IL12 (-33.16) demonstrated lowest gca effects tracked by parental inbred lines IL10 (-17.89), IL2 (-16.85) and IL5 (-16.69) under partially irrigated condition. Alternatively, the parental inbred line IL4 (38.94) exposed highest gca effects followed by parental inbred lines IL11 (24.42), IL6 (9.60) and IL8 (7.90) under partially irrigated condition (Table 19).

The estimates of sca effects for Saturation water deficit varied between -71.72 (IL10 × IL11) to 64.65 (IL7 × IL9) under partially irrigated condition. The hybrid IL10 × IL11 (-71.72) exhibited high negative significant sca effects tracked by IL6 × IL8 (-62.87), IL8 × IL10 (-46.95) and IL9 × IL10 (-43.84). The hybrid IL7 × IL9 (64.65) exhibited high positive significant sca effects tracked by IL4 × IL11 (52.12), IL3 × IL12 (51.95) and IL5 × IL10 (51.69) (Table 20 b).

4.3.2.2.18 Membrane stability index

The estimates of gca effects for Membrane stability index ranged from -6.56 (IL1) to 5.39 (IL3) under partially irrigated condition. The parental inbred line IL1 (-6.56) exposed lowest gca effects tracked by parental inbred lines IL11 (-5.48), IL10 (-2.59) and IL9 (-2.14) under partially irrigated condition. Alternatively, the

parental inbred line IL3 (5.39) exhibited highest gca effects followed by parental inbred lines IL6 (3.75), IL2 (3.27) and IL8 (2.02) under partially irrigated condition (Table 19).

The estimates of sca effects for Membrane stability index ranged between -25.86 (IL3 $\times$ IL7) to 38.13 (IL1 $\times$ IL9) under partially irrigated condition. The hybrid IL3 $\times$ IL7 (-25.86) exposed high negative significant sca effects tracked by IL5 $\times$ IL8 (-23.65), IL5 $\times$ IL12 (-23.62) and IL6 $\times$ IL7 (-22.93). The hybrid IL1 $\times$ IL9 (38.13) exhibited high positive significant sca effects tracked by IL2 $\times$ IL7 (36.31), IL8 $\times$ IL12 (35.52) and IL7 $\times$ IL12 (29.58) (Table 20 b).

Table 17. Estimation of general combining ability effects for different characters studied in maize (*Zea mays* L.) under irrigated condition

Parents	DFT	DFS	ASI	PH	CL	NKRC	NKR	HGW	SYP
IL1	22.44	2.28	0.83	-7.15**	-0.43**	-0.89	0.72**	-12.52**	-2.36
IL2	-0.30	-0.27**	-3.10**	3.94	0.11	2.26	0.92**	-8.45**	-0.97
IL3	-25.42**	-2.52**	-0.06	4.33**	-0.29	-7.88**	-1.08**	2.65**	-2.96**
IL4	-30.77**	-2.85**	2.44**	1.80	0.61**	-7.82**	0.11**	0.56	-5.00**
IL5	36.73	3.41	-2.92	1.88	-0.38	-4.08**	-1.27**	-10.14**	-9.16**
IL6	-19.35**	-2.08**	-1.67**	0.70	0.34**	-3.53**	1.50**	13.74**	2.21**
IL7	14.23	1.14	-2.74	14.89**	0.19**	3.89	-0.04	13.67**	9.47**
IL8	-6.13**	-0.27	3.51	-2.77	-0.40**	4.63**	-0.68**	-2.95	-3.06**
IL9	-1.13**	0.17	-2.80**	-19.55**	0.51**	1.49**	0.09	21.02**	3.44**
IL10	-11.13**	-0.95	1.73	-3.48**	-0.02	2.18	0	-9.84**	4.64**
IL11	-20.06**	-2.06**	0.42	4.75**	-0.37**	5.11**	-0.15**	-5.43	1.61
IL12	40.3	4.01	-0.42	0.66	0.14	4.65**	-0.14	-2.32	2.13

* and ** significant at 5% and 1% level of significance, respectively

Parents	NCP	DM	CG	SP	CT	TW	RWC	SWD	MSI
IL1	0.48**	4.41	3.27**	-0.14	-0.34**	-17.62	-1.37**	1.16**	32.01**
IL2	0.72**	5.48**	-4.05**	0.02	-0.51**	-5.87	2.16**	-2.16**	55.29**
IL3	2.12**	-17.74**	-5.61**	0.04	0.40**	-10.33	0.61	-0.61	121.26**
IL4	0.35**	-15.24**	-4.66**	-4.06**	0.12	-0.8	-4.07**	4.07**	6.71
IL5	-0.67**	8.69**	-3.12**	-0.86**	0.13**	6.74**	1.45**	-1.45**	1.26
IL6	-1.00**	-2.02	1.66**	-0.62**	-0.08	-5.69	-0.86	0.86	-46.41**
IL7	-0.08	7.62**	0.49	0.41	-0.24**	15.52**	-0.54	0.54	-36.64**
IL8	0.15	-0.24	5.38**	1.29**	-0.02	2.99	-0.89**	0.90**	15.96**
IL9	-0.29	-5.95**	5.08**	-0.19**	0.50**	10.81**	-0.1	0.1	-18.84
IL10	-0.24	-4.17**	-0.81	2.10**	0.19**	-1.33	2.36**	-2.36**	-27.31**
IL11	-0.32**	3.33	1.17	1.50**	-0.25**	-0.94	-2.28**	2.45**	-24.55
IL12	-1.22**	15.83**	1.21	0.51**	0.11	6.52**	3.52**	-3.52**	-78.75**

* and ** significant at 5% and 1% level of significance, respectively

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob, NKRC = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm), SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

Table 18 (a). Estimation of specific combining ability effects for different characters studied in maize (*Zea mays* L.) under irrigated condition

Hybrid	DFT	DFS	ASI	PH	CL	NKRC	NKR	HGW	SYP
IL1 × IL2	27.198	2.103	-6.841	-8.243	1.554	-16.454	-1.977	6.88	-0.312
IL1 × IL3	-17.088	-1.147	5.124	11.214	0.319	-1.722	-0.825	-12.424	-0.562
IL1 × IL4	-26.731	-3.826	-12.376	-37.04**	2.24**	14.374	2.809	29.412	26.768
IL1 × IL5	-79.231	-7.57**	2.981	5.341	-0.046	4.481	2.518	-1.885	6.399
IL1 × IL6	46.841	4.407	-3.269	8.951	0.501	-5.62	-2.905	-8.761	-32.18**
IL1 × IL7	-86.731**	-8.308	2.80**	10.035	-2.07**	16.16	5.313	38.005	39.62**
IL1 × IL8	33.626	2.103	-13.44**	-6.817	2.061	1.026	-1.328	2.371	-14.877
IL1 × IL9	-41.374	-3.593	4.766	-5.865	-0.87	-3.537	0.337	-8.392	-1.259
IL1 × IL10	-26.374	-2.718	0.838	5.306	-0.464	10.317	1.713	-7.681	8.243
IL1 × IL11	-17.445	-3.111	-12.019	3.3	-0.157	5.288	-3.727	11.601	-1.836
IL1 × IL12	-12.802	-1.933	-7.019	16.09**	-0.828	-14.747	-4.98**	-46.05**	-14.938
IL2 × IL3	-34.945	-3.093	4.052	4.377	-0.015	11.281	-1.572	24.515	-1.302
IL2 × IL4	-39.588	-2.272	16.55**	8.576	-1.142	-13.772	-2.835	19.551	-24.26**
IL2 × IL5	32.912	2.228	-10.591	-2.396	-0.705	10.935	-1.681	-18.695	-20.436
IL2 × IL6	-41.016	-4.04	0.659	-10.359	-0.423	1.783	6.71**	1.078	17.623
IL2 × IL7	-69.588	-6.254	6.731	-24.12**	2.30**	-0.987	3.129	-49.50**	21.814
IL2 × IL8	-39.231	-3.093	7.981	6	0.617	-25.97**	-1.11	-8.74	17.163
IL2 × IL9	-34.231	-3.04	3.695	14.783	3.78**	3.417	2.678	39.498	7.476
IL2 × IL10	-19.231	-3.415	-12.73**	-1.131	0.216	-0.779	-0.334	-35.09**	-4.712
IL2 × IL11	4.698	-1.558	-20.59**	-9.168	0.019	0.592	-3.90**	-21.96	-18.876
IL2 × IL12	54.341	5.121	-3.091	1.235	-1.29**	5.906	-0.491	-26.117	-19.563
IL3 × IL4	16.126	0.728	-8.984	-16.828	1.353	1.46	-3.768	-44.30**	-10.507
IL3 × IL5	-26.374	-3.272	-6.126	5.7	-0.953	-4.358	3.046	-24.674	-6.85
IL3 × IL6	44.698	4.21	-2.376	-6.05	0.474	0.04	1.473	-20.101	-4.826
IL3 × IL7	31.126	2.746	-3.805	18.72**	0.316	-3.204	1.334	60.49**	17.665
IL3 × IL8	-23.516	-1.593	7.445	20.81**	-1.41**	10.937	-1.993	-8.319	2.948
IL3 × IL9	-48.516	-5.29	-4.341	6.701	-0.31	8.549	3.92	3.644	0.026
IL3 × IL10	51.484	5.585	4.231	3.193	0.396	9.653	4.505	-0.345	38.88**
IL3 × IL11	-9.588	-1.308	-3.626	0.119	1.979	3.674	-0.422	-20.113	25.62

* and ** significant at 5% and 1% level of significance, respectively

Contd.....

Table 18 (a). Contd.....

Hybrid	DFT	DFS	ASI	PH	CL	NKRC	NKR	HGW	SYP
IL3 × IL12	75.055	6.621	-8.626	5.224	0.745	-27.63**	-0.544	-21.295	-20.58**
IL4 × IL5	78.984	8.29**	3.874	8.288	-0.572	16.76**	4.15	-17.863	5.234
IL4 × IL6	100.055	9.03**	-9.876	-18.497	0.095	8.362	2.325	-13.84	31.67**
IL4 × IL7	-28.516	-2.183	6.195	-11.993	-1.71**	-6.533	-4.10**	6.501	-32.33**
IL4 × IL8	-18.159	-3.522	-12.555	-19.973	-0.597	-5.567	4.114	-4.533	-0.788
IL4 × IL9	-53.159	-4.968	3.159	12.144	0.799	13.496	4.239	-27.62	2.436
IL4 × IL10	-38.159	-4.593	-8.269	-3.052	-0.245	-1.001	3.382	-6.01	-4.253
IL4 × IL11	0.769	0.764	6.374	15.767	-0.538	-6.329	3.679	-7.727	27.039
IL4 × IL12	-24.588	-3.058	-6.126	-9.881	1.876	9.535	2.858	1.165	11.411
IL5 × IL6	-52.445	-6.218	-9.519	-6.574	-1.59**	-7.381	-0.914	56.31**	0.275
IL5 × IL7	53.984	4.317	-10.948	6.752	2.69**	-17.00**	-3.283	3.58	-27.51**
IL5 × IL8	89.341	8.47**	-4.698	-10.473	-0.413	-19.53**	-5.64**	-49.45**	-13.176
IL5 × IL9	54.341	5.782	3.51	8.744	1.113	-12.422	-0.109	42.80**	16.362
IL5 × IL10	-85.65**	-7.093	14.58**	8.403	0.851	25.30**	-0.809	11.744	18.304
IL5 × IL11	-81.73**	-6.236	19.23**	9.439	1.436	14.503	5.184	15.601	18.355
IL5 × IL12	22.912	2.192	-0.769	16.44**	0.035	6.867	5.43**	17.644	24.318
IL6 × IL7	-24.945	-2.701	-2.198	-12.5	0.683	5.647	-1.528	-18.247	24.53
IL6 × IL8	-34.588	-2.04	14.05**	10.923	-0.362	8.913	-2.66	-7.481	2.098
IL6 × IL9	-14.588	-0.236	12.26**	-23.03**	-0.638	16.001	-5.59**	3.606	-17.049
IL6 × IL10	-4.588	-0.361	0.838	23.53**	0.493	-12.545	1.338	10.067	12.463
IL6 × IL11	-15.659	-2.254	-7.019	12.37	2.43**	-17.92**	0.831	-17.951	-11.04
IL6 × IL12	-51.016	-4.326	7.981	-8.775	1.364	19.09**	1.922	-24.858	23.107
IL7 × IL8	-43.159	-3.754	5.124	-14.769	0.643	18.89**	5.33**	-22.565	28.66**
IL7 × IL9	106.841	10.54**	-1.662	12.871	-0.641	-7.694	-0.277	6.498	-3.048
IL7 × IL10	-18.159	-3.076	-13.09**	-4.73	1.048	-5.915	2.166	-31.617	-12.446
IL7 × IL11	-44.231	-3.968	4.052	15.731	-0.455	6.856	1.431	36.165	11.58
IL7 × IL12	30.412	2.96	-0.948	3.401	0.279	9.321	4.69	-9.842	23.208
IL8 × IL9	82.198	6.71**	-15.41**	-25.24**	-1.02	5.672	4.202	-4.686	6.496
IL8 × IL10	62.198	6.585	3.159	3.327	1.171	1.426	1.932	65.32**	-5.313
IL8 × IL11	-18.874	-1.808	0.302	-3.395	-0.942	3.297	5.38**	54.35**	-4.441

* and ** significant at 5% and 1% level of significance, respectively

Contd.....

Table 18 (a). Contd.....

Hybrid	DFT	DFS	ASI	PH	CL	NKRC	NKR	HGW	SYP
IL8 × IL12	-84.23**	-8.37**	0.302	12.308	0.639	18.68**	2.566	0.624	10.296
IL9 × IL10	-32.802	-3.611	-3.626	-30.49**	0.817	4.938	-2.57	-31.913	8.681
IL9 × IL11	-8.874	-2.254	-11.484	2.244	-0.973	-12.315	6.37**	-11.556	-15.388
IL9 × IL12	15.769	1.924	3.516	2.022	-0.687	12.724	0.054	-9.238	-6.68
IL10 × IL11	-38.874	-2.879	9.588	-22.47	-0.382	-1.912	2.173	7.805	-5.371
IL10 × IL12	-94.23**	-9.95**	-5.412	-14.792	-0.876	-12.672	1.057	20.823	-14.229
IL11 × IL12	-80.30**	-7.84**	1.731	-13.614	-0.554	-11.501	4.239	30.655	45.65**

* and ** significant at 5% and 1% level of significance, respectively

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob, NKRC = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g)

Table 18 (b). Estimation of specific combining ability effects for different characters studied in maize (*Zea mays* L.) under irrigated condition

Hybrid	NCP	DM	CG	SP	CT	TW	RWC	SWD	MSI
IL1 × IL2	0.326	-26.291	-5.957	-9.96	-0.307	-6.679	1.023	-1.021	-74.691
IL1 × IL3	-1.701	-28.07**	0.347	0.27	-1.695	-9.214	0.407	-0.414	-160.01**
IL1 × IL4	0.692	-15.577	4.804	-0.873	-0.435	-17.75	9.63**	-9.624	188.14**
IL1 × IL5	2.594	15.495	-4.639	4.226	0.499	-13.286	1.905	-1.904	95.141
IL1 × IL6	-2.04	-18.791	-6.773	-6.71	0.014	-15.857	-4.191	4.193	-19.189
IL1 × IL7	1.13**	56.57**	-15.95	10.80**	1.577	45.93**	1.526	-1.525	144.791
IL1 × IL8	-0.977	14.423	0.263	-16.82**	-1.002	14.464	-7.315	7.307	-69.01
IL1 × IL9	1.335	15.137	30.165	4.518	-0.864	9.143	-3.125	3.127	238.39**
IL1 × IL10	5.782	28.35**	5.647	4.49	-0.307	-4.214	1.694	-1.692	44.383
IL1 × IL11	0.121	15.852	-1.228	2.555	0.057	-10.607	8.896	-8.895	-40.726
IL1 × IL12	4.514	23.352	-0.971	1.934	0.574	-4.071	-5.998	5.999	-5.25
IL2 × IL3	3.933	45.85**	21.168	1.127	1.81**	-26.464	13.37**	-13.377	54.49
IL2 × IL4	0.451	-6.648	11.525	-1.978	1.539	-14.5	-7.85**	7.86**	13.334
IL2 × IL5	1.478	9.423	-16.718	-1.775	0.273	-7.036	-1.419	1.421	46.713
IL2 × IL6	-0.817	20.137	-17.202	5.204	-0.612	-9.607	-5.506	5.507	166.73**
IL2 × IL7	-0.361	0.495	0.422	-3.279	-1.049	-0.321	-4.011	4.012	-98.362
IL2 × IL8	0.657	-16.648	-3.066	3.589	-0.978	1.214	-5.529	5.522	2.636
IL2 × IL9	0.469	-10.934	6.586	-6.712	-3.74**	-8.607	0.195	-0.194	50.34
IL2 × IL10	4.041	-22.72	-4.382	-0.62	-0.363	-5.464	4.602	-4.6	61.729
IL2 × IL11	1.13	-15.22	-6.457	-2.74	0.921	14.643	-0.303	0.305	150.795
IL2 × IL12	-3.477	7.28	-2.9	1.281	0.518	10.679	5.653	-5.651	-7.928
IL3 × IL4	-3.701	21.566	-12.421	-10.15**	-2.45**	-34.03**	-8.87**	8.86**	4.518
IL3 × IL5	1.576	47.63**	-11.089	2.543	0.3	29.929	4.7	-4.707	1.947
IL3 × IL6	0.407	8.352	-13.723	0.38	0.515	31.35**	-0.634	0.627	219.62**
IL3 × IL7	-2.763	-21.291	2.725	4.821	1.613	26.143	-3.686	3.679	-143.20**
IL3 × IL8	-0.245	1.566	4.413	6.93**	2.74**	-18.821	-3.78	3.889	82.32
IL3 × IL9	1.192	-12.72	0.14	3.868	0.732	-25.643	-4.178	4.171	-120.951
IL3 × IL10	-0.361	-9.505	12.822	4.632	0.258	-8.5	-9.58**	9.57**	82.363
IL3 × IL11	1.978	-27.005	3.197	-5.137	0.403	-2.893	-0.797	0.789	230.88**

* and ** significant at 5% and 1% level of significance, respectively

Contd.....

Table 18 (b). Contd.....

Hybrid	NCP	DM	CG	SP	CT	TW	RWC	SWD	MSI
IL3 × IL12	-0.62	-14.505	-12.221	-3.606	-2.54**	30.14**	-5.826	5.818	-17.069
IL4 × IL5	2.719	-14.863	0.193	5.623	0.095	23.893	7.98	-7.979	110.241
IL4 × IL6	3.82	-9.148	0.409	2.477	0.63	-13.679	-2.324	2.325	-82.289
IL4 × IL7	-4.25	-18.791	11.507	1.628	0.808	1.107	4.554	-4.553	1.541
IL4 × IL8	7.023	-10.934	3.07	2.709	0.429	50.64**	-2.462	2.455	-2.76
IL4 × IL9	1.46	4.78	4.097	-8.895	0.682	10.821	-2.398	2.399	-128.532
IL4 × IL10	-2.593	-32.00**	-2.121	3.302	0.488	1.964	1.872	-1.87	140.033
IL4 × IL11	0.246	15.495	-1.296	8.72**	-1.167	-9.929	-4.221	4.222	41.249
IL4 × IL12	1.639	7.995	-7.039	-4.241	-1.86	-6.393	-5.148	5.149	45.35
IL5 × IL6	0.201	-18.077	0.466	4.87	2.44**	-21.714	2.511	-2.51	-39.66
IL5 × IL7	-1.71	-22.72	-21.01	-20.32**	-1.043	-15.429	-1.678	1.68	140.12
IL5 × IL8	-5.701	10.137	-17.248	-3.945	1.528	-11.893	-4.172	4.165	-90.157
IL5 × IL9	-4.013	10.852	18.029	-5.283	-1.559	-27.21**	-5.918	5.919	-97.453
IL5 × IL10	-0.067	-5.934	34.186	3.451	-0.927	-3.571	-5.681	5.682	-82.039
IL5 × IL11	-2.977	11.566	17.686	3.103	-1.208	0.536	-2.349	2.35	-134.048
IL5 × IL12	-3.584	-25.934	7.443	6.93**	1.439	33.07**	-1.42	1.421	-17.45**
IL6 × IL7	-1.388	27.10**	11.606	-1.179	-0.558	-25	0.535	-0.534	-94.06
IL6 × IL8	-5.12	5.852	49.118	1.894	0.193	-8.464	9.48**	-9.484	46.838
IL6 × IL9	2.817	11.566	-1.93	0.626	0.201	13.214	1.799	-1.797	130.166
IL6 × IL10	-0.986	4.78	5.402	3.535	-0.363	-2.143	-9.65**	9.66**	-6.944
IL6 × IL11	-1.647	-32.72**	-0.173	-12.86**	-1.468	-14.536	5.137	-5.136	-107.103
IL6 × IL12	1.246	14.78	-8.166	-3.591	-1.511	1	-4.591	4.593	-42.076
IL7 × IL8	6.46**	11.209	4.241	5.233	-1.644	4.321	-5.403	5.396	-131.08**
IL7 × IL9	-5.602	-13.077	6.968	3.565	-1.421	-10	-8.19**	8.19**	-81.553
IL7 × IL10	-6.281	-9.863	-13.475	-10.24**	-0.789	-16.857	5.228	-5.227	-48.339
IL7 × IL11	1.308	-2.363	8.15	5.159	-1.87**	1.25	0.953	-0.951	68.527
IL7 × IL12	2.826	-54.86**	16.157	5.793	0.102	-28.71**	9.02**	-9.02	-53.271
IL8 × IL9	-3.834	-35.22**	-5.519	4.568	1.65	-20.464	0.692	-0.7	-65.505
IL8 × IL10	-2.888	2.995	-6.487	-2.868	-2.14**	-6.321	5.972	-5.979	-18.216
IL8 × IL11	3.201	0.495	10.138	1.812	1.001	-30.21**	9.41**	-9.416	35.15

* and ** significant at 5% and 1% level of significance, respectively

Contd.....

Table 18 (b). Contd.....

Hybrid	NCP	DM	CG	SP	CT	TW	RWC	SWD	MSI
IL8 × IL12	1.469	-22.005	2.87	1.626	-1.137	9.821	2.062	-2.07	16.752
IL9 × IL10	2.049	8.709	-2.16	-7.062	-0.44	26.857	6.694	-6.692	-72.962
IL9 × IL11	2.139	1.209	1.69	2.684	2.13**	-10.536	7.996	-7.995	-173.90**
IL9 × IL12	-0.968	8.709	-2.278	1.363	2.11**	-20	7.365	-7.363	-92.244
IL10 × IL11	-0.415	-0.577	-4.078	1.445	0.236	-1.893	7.773	-7.771	-53.507
IL10 × IL12	-2.272	1.923	6.104	-0.073	-0.502	19.143	1.326	-1.325	-35.305
IL11 × IL12	1.93**	-10.577	5.529	6.74**	-1.158	-33.25**	4.721	-4.72	-13.789

* and ** significant at 5% and 1% level of significance, respectively

NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm), SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI=Membrane stability index

Table 19. Estimation of general combining ability effects for different characters studied in maize (*Zea mays* L.) under partially irrigated condition

Parents	DFT	DFS	ASI	PH	CL	NKRC	NKR	HGW	SYP
IL1	4.88**	4.7**	-0.8**	-10.6**	-0.1	-3.35**	0.75**	-123.4**	-0.69
IL2	-0.48	-0.3	-0.45	4.68**	0.27**	4.65**	1.09**	-128.4**	0.4
IL3	-18.3**	-16.2**	-0.98**	2.35	-0.27	-1.63	0.82**	-121.78	0.8
IL4	-30.5**	-27.1**	2.95**	-1.74**	0.37**	-11.2**	-0.7**	102.68**	-6.42**
IL5	42.02**	38.63**	-03.66**	1.52	-0.31**	-3.38**	-0.59**	-123.2	-6.4**
IL6	-26.91**	-28.16**	-0.63	-1.98**	-0.07	-4.5**	0.39	107.01**	-3.47**
IL7	16.67**	17.38**	0.63	11.67**	-0.37**	4.7**	-0.28	90.12**	6.1**
IL8	-6.19	-3.69	2.77**	-0.53	-0.27**	2.97	-1.14**	-123.8**	-4.16**
IL9	-1.91	-4.23	-1.52**	-13.24**	0.68**	4.85**	0.29	98.14**	6.11**
IL10	-10.48	-9.23	1.16**	-1.46	0.28**	4.86**	0.5**	-123.23	9.2**
IL11	-19.76**	-19.94**	-0.45	5.9**	-0.35**	-0.3	-0.46	-133.35**	-2.76
IL12	50.95**	50.24**	0.98**	3.4**	0.15	2.28	-0.68**	-117.62	1.3**

* and ** significant at 5% and 1% level of significance, respectively

Parents	NCP	DM	CG	SP	CT	TW	RWC	SWD	MSI
IL1	-0.33**	15.54**	1.22	1.53**	0.59**	-20.19**	-4.96	4.94	-6.56**
IL2	-0.1	0.18	-0.17	0.29	-0.45**	-4.9**	16.83**	-16.85**	3.27**
IL3	0.4**	-15.54**	-3.93**	0.5**	-0.3	-10.51**	6.36	-6.29	5.39**
IL4	0.23	-20.18**	-6.8**	-3.59**	-0.52**	-0.94	-38.96**	38.94**	0.84
IL5	-0.51**	-1.96	-1.76**	-0.69**	-0.02	6.49**	16.76**	-16.69**	1.92
IL6	-0.77**	-5.18**	0.48	0.38	-0.47**	-5.4**	-9.62**	9.6**	3.75**
IL7	0.83**	6.25**	3.32**	1.32**	-0.57**	15.35**	-6.56	6.57	0.5
IL8	1.31**	-0.54	1.53**	-0.03**	0.33	2.99	-7.92**	7.9**	2.02**
IL9	0.12	3.75	4.22**	-1.04**	0.55**	10.32**	1.47	-1.49	-2.14**
IL10	-0.1	-9.82**	1.12	1.24**	0.42**	-0.04	17.91**	-17.89**	-2.59**
IL11	0.35**	9.46**	-1.17**	0.01	0.04	-0.19	-24.44**	24.42**	-5.48**
IL12	-1.44**	18.04**	1.95**	0.08	0.4**	6.99**	33.13**	-33.16**	-0.94

* and ** significant at 5% and 1% level of significance, respectively

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob, NKRC = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm), SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

Table 20 (a). Estimation of specific combining ability effects for different characters studied in maize (*Zea mays* L.) under partial irrigated condition

Hybrid	DFT	DFS	ASI	PH	CL	NKRC	NKR	HGW	SYP
IL1 × IL2	48.92	67	17.88	-0.87	0.3	-20.85**	-2.65	104.53	-4.17
IL1 × IL3	31.78	37.54	3.42	-31.69**	0.13	-7.07	-1.1	101.36	-6.72
IL1 × IL4	-11.07	-11.2	1.992	0.53	0.14	23.34	-0.97	-75.54	23.13**
IL1 × IL5	-83.57	-74.42	13.599	8.92	-0.66	-19.72	-3.43	89.23	1.47
IL1 × IL6	-4.64	14.86	15.56	-1.28	0.39	-0.55	-1.6	-11.32	-23.18**
IL1 × IL7	-83.21**	-70.67	16.81	11.65	-0.62	1.33	1.78	107.44	28.35**
IL1 × IL8	44.64	40.39	-13.5**	2.64	1.71**	-1.03	0.97	114.03	-13.5
IL1 × IL9	-39.64	-34.06	3.95	22.58	0.56	6.78	1.3	135.77	9.97
IL1 × IL10	-21.07	-31.56	-11.22	-4.05	-0.54	4.28	2.3	103.66	-0.27
IL1 × IL11	-6.78	-8.35	0.38	9.82	-0.44	3.03	-4.51**	136.23	-4.11
IL1 × IL12	7.5	-3.53	-11.04	-3.74	-1.87	-12.88	-4.51	107.25	-13.55
IL2 × IL3	-42.85	-44.95	-1.93	14.48	-0.17	8.17	-1.03	140.27	3.84
IL2 × IL4	-15.71	-6.2	16.55**	-9.44	-1.53**	-10.65**	-5.30**	-94.84**	-18.78
IL2 × IL5	31.78	30.57	-4.25	7.33	-0.18	3.52	-5.25**	79.43	-21.62**
IL2 × IL6	-34.28	-42.63	-4.79	-2.94	0.25	4.64	7.73**	-11.67	22.1
IL2 × IL7	-67.85	-63.17	6.45	-7.86	2.05	-5.66	4.09	74.74	22.22
IL2 × IL8	-35	-27.1	6.81	-18.52**	0.79	-23.03	0.36	105.54	16.71
IL2 × IL9	-49.28	-46.56	1.099	-17.141	2.852	3.539	3.144	146.63**	4.974
IL2 × IL10	-20.71	-19.06	0.92	5.222	-0.563	-6.118	-0.689	69.47	-11.317
IL2 × IL11	-41.42	-58.35	-12.5**	8.587	-0.144	2.489	-2.825	96.841	-11.963
IL2 × IL12	47.85	41.47	-6.401	18.84	0.428	12.718**	0.024	90.409	-20.57**
IL3 × IL4	12.143	9.32	-2.83	0.478	0.796	0.975	-2.788	-19.863	4.822
IL3 × IL5	-25.35	-31.38	-1.223	-2.727	-0.313	-1.468	2.478	101.891	-8.063
IL3 × IL6	63.57	60.39	-1.758	3.174	0.662	8.102	0.579	-27.318	-0.821
IL3 × IL7	40	37.36	-5.508	-26.34**	0.93	-8.679	2.068	171.073**	-1.148
IL3 × IL8	-27.14	-39.06	-7.651	7.965	-0.839	6.377	-0.727	96.296	0.885
IL3 × IL9	-56.42	-61.03	-3.365	9.03	0.013	3.421	5.7	83.009	1.83
IL3 × IL10	37.14	36.47	-1.044	-0.292	-0.478	1.314	3.31	126.948	49.709**
IL3 × IL11	-18.57	-5.31	8.063	8.543	0.296	6.971	0.584	84.47	6.008

* and ** significant at 5% and 1% level of significance, respectively

Contd.....

Table 20 (a). Contd.....

Hybrid	DFT	DFS	ASI	PH	CL	NKRC	NKR	HGW	SYP
IL3 × IL12	65.71	54.5	-8.365	13.753**	0.14	-18.23**	-2.304	125.162	-19.563
IL4 × IL5	71.78	67.36	-2.651	21.778**	1.051	9.575**	6.149**	-23.145	12.728
IL4 × IL6	100.71**	89.14	-10.687	-2.209	1.121	6.344	0.862	131.246	19.275
IL4 × IL7	-32.85	-33.88	0.563	9.514	-0.481	-5.586	-4.091	-35.913	-25.91**
IL4 × IL8	-25	-22.81	0.92	4.642	-0.197	7.894	0.501	-90.914**	-3.398
IL4 × IL9	-49.28	-47.28	0.206	1.108	0.899	8.989	1.671	-16.802	7.312
IL4 × IL10	-40.71	-42.28	-2.473	5.241	-0.011	5.132	3.488	-19.063	-3.904
IL4 × IL11	-6.42	5.93	11.635	6.589	-0.543	-2.961	6.408**	-83.891**	11.934
IL4 × IL12	-42.14	-49.24	-4.794	6.901	1.399	23.668	5.354	-21.523	13.739
IL5 × IL6	-56.78	-54.06	3.42	1.961	-1.82**	-1.773	-0.269	-44.925	3.19
IL5 × IL7	49.64	45.39	-7.83	-4.489	2.515	1.771	-0.09	95.191	-4.087
IL5 × IL8	87.50**	88.97	-2.473	12.217	-0.186	-8.898	-2.9	48.989	-17.829
IL5 × IL9	63.21	57	-3.187	12.853	-0.44	-11.354	-1.2	132.852	8.126
IL5 × IL10	-88.21**	-87.99	14.58**	-3.686	1.177**	21.314**	-0.896	113.016	7.78
IL5 × IL11	-78.92	-79.78	-19.2**	-0.446	0.834	15.596	3.799	119.012	13.184
IL5 × IL12	40.35	35.04	-8.187	-15.387	-0.045	8.325	6.228**	121.48	21.038
IL6 × IL7	-21.42	-17.81	4.135	3.22	-0.87	-1.809	-2.947	-13.818	3.61
IL6 × IL8	-23.57	-21.74	14.05**	1.681	-2.73**	4.121	-2.287	-14.82	1.923
IL6 × IL9	-17.85	-3.7	13.777	7.831	-1.618	-8.959**	-5.77**	-18.082	-20.437
IL6 × IL10	10.71	-6.2	-13.901	4.582	1.122	-6.566	1.31	-88.793**	4.303
IL6 × IL11	-15	-15.49	-4.794	5.439	1.156	-7.159	2.01	-22.072	-2.224
IL6 × IL12	-55.71	-53.17	1.277	8.054	2.822**	16.419**	-0.416	-34.754	6.51
IL7 × IL8	-52.14	-54.78	-4.258	5.923	0.529	19.566	3.547	124.596	18.546
IL7 × IL9	103.5**	98.255	-2.473	0.099	-0.724	-11.19**	-2.71	114.259	-2.464
IL7 × IL10	-17.85	-21.74	-13.1**	20.009**	0.603	-0.422	0.867	70.773	-7.72
IL7 × IL11	-43.57	-38.53	3.956	4.917	-0.458	8.735	1.014	111.645	11.469
IL7 × IL12	35.71	41.29	0.027	1.029	-0.071	22.664	2.355	117.112	22.878**
IL8 × IL9	96.42**	84.32	-17.12	5.14	0.794	10.641**	2.915	100.057	4.589
IL8 × IL10	65	74.32	5.206	18.781	-0.271	8.284	2.674	156.896**	12.184
IL8 × IL11	-20.71	-24.95	-3.187	26.763	0.168	8.141	2.967	164.768	9.852

* and ** significant at 5% and 1% level of significance, respectively

Contd.....

Table 20 (a). Contd.....

Hybrid	DFT	DFS	ASI	PH	CL	NKRC	NKR	HGW	SYP
IL8 × IL12	-81.43**	-70.13	10.385	-7.06	1.162	17.244**	2.113	100.261	11.327
IL9 × IL10	-29.28	-30.13	-0.508	8.971	0.41	-15.772	-3.043	96.259	-5.251
IL9 × IL11	-20	-26.92	-6.401	7.521	-1.12**	7.21	4.959	95.905	-1.308
IL9 × IL12	14.28	25.39	9.67	11.681	-0.669	6.514	-1.77	81.298	1.032
IL10 × IL11	-36.42	-39.42	-1.58	9.302	2.056**	-1.897	0.711	133.595	3.607
IL10 × IL12	-97.14**	-97.1**	1.99	7.036	-0.625	-0.093	2.437	117.737	9.241
IL11 × IL12	-57.85	-56.38	1.099	-17.46**	-0.511	2.064	3.477	136.909	20.424

* and ** significant at 5% and 1% level of significance, respectively

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob, NKRC = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g)

Table 20 (b). Estimation of specific combining ability effects for different characters studied in maize (*Zea mays* L.) under partial irrigated condition.

Hybrid	NCP	DM	CG	SP	CT	TW	RWC	SWD	MSI
IL1 × IL2	0.05	-8.98	-6.34	-3.31	0.15	-3.26	-3.24	3.26	-11.27
IL1 × IL3	-3.19	-23.26	1.36	-1.908	-0.47	-10.66	3.02	-3.09	-16.59
IL1 × IL4	-3.76	-8.62	6.63	7.13	-0.02	-16.23	91.26**	-41.24	-9.4
IL1 × IL5	2.21	-16.84	-5.15	4.05	0.02	-15.16	32.34	-32.41	-6.66
IL1 × IL6	1.34	-63.62**	-9.74	-5.88	0.47	-13.76	-48.29	48.31	-16.86
IL1 × IL7	3.37	-10.05	-5.7	7.83**	1.57	34.48**	32.11	-32.12	-11.77
IL1 × IL8	1.65	-3.26	3.2	-5.73	-1.32	18.83	-87.77**	8.79	-3.82
IL1 × IL9	-0.78	-2.55	11.61	-6.91	-0.25	10.01	-31.81	31.83	38.13
IL1 × IL10	4.30**	21.01	2.76	3.58	-1.31	-5.62	28.22	-28.23	24.29
IL1 × IL11	2.6	11.73	-3.39	1.86	-0.56	-9.48	85.16	-25.15	18.04
IL1 × IL12	0.14	13.15	-5.21	-0.14	0.75	-5.16	-51.12	21.14	-14.04
IL2 × IL3	0.94	22.08	9.1	1.65	2.49**	-28.44**	143.28**	-43.35	2.58
IL2 × IL4	-1.25	-38.26**	-1.82	1.89	1.41	-14.01	-80.47	50.49	3.19
IL2 × IL5	2.48	18.51	-10.66**	-1	0.7	-6.94	-15.79	15.72	21.19
IL2 × IL6	0.74	1.73	-1.5	4.19	0.1	-11.05	-48.23	48.25	7.76
IL2 × IL7	0.64	-4.69	-4.54	-5.94	-0.53	-1.3	-31.87	31.85	36.31
IL2 × IL8	2.66	-12.91	1.8	3.48	-0.88	-1.44	-43.03	43.05	5.06
IL2 × IL9	-3.144	-42.2**	3.252	-7.429	-3.662**	-7.269	-5.326	5.345	1.736
IL2 × IL10	1.57	-18.626	0.852	-2.297	-1.107	-4.412	36.933	-36.95	0.848
IL2 × IL11	-1.376	32.088	-1.051	-0.55	-0.19	10.731	13.306	-13.287	11.782
IL2 × IL12	-1.466	38.516**	-3.619	-1.029	-0.233	11.552	53.583	-23.564	-22.836
IL3 × IL4	-4.25**	42.445**	0.884	-2.214	-1.172	-33.912**	-89.127**	9.057	11.092
IL3 × IL5	-2.894	29.231	-2.826	-0.117	-0.158	33.159**	33.301	-32.21	25.562
IL3 × IL6	-1.885	32.445**	-14.57**	-2.838	-0.158	30.052	0.558	-0.628	8.402
IL3 × IL7	-4.11**	-23.984	10.518	1.243	-0.12	26.802	-35.456	35.35	-25.858
IL3 × IL8	0.918	7.802	5.386	6.75	0.048	-18.341	-40.119	40.048	1.589
IL3 × IL9	0.856	-16.484	-5.087	0.639	1.317	-25.662	-39.556	39.486	-21.713
IL3 × IL10	1.07	-27.912	3.113	2.274	0.222	-8.305	-95.672**	5.566	19.331
IL3 × IL11	4.624**	-42.2**	-1.341	3.923	-1.202	-4.162	-1.724	1.654	24.272

* and ** significant at 5% and 1% level of significance, respectively

Contd.....

Table 20 (b). Contd.....

Hybrid	NCP	DM	CG	SP	CT	TW	RWC	SWD	MSI
IL3 × IL12	1.784	-5.769	-10.184	0.832	-1.879**	29.159	-52.022	51.952**	22.937
IL4 × IL5	5.659**	-6.126	14.366**	-7.693**	0.072	24.088	78.394	-8.464	19.183
IL4 × IL6	-3.332	-2.912	1.225	0.759	0.443	-12.019	-30.649	30.668	-8.529
IL4 × IL7	2.195	-24.341	5.761	-2.005	0.76	1.231	47.212	-17.228	-1.247
IL4 × IL8	7.347**	-17.555	-2.846	4.974	0.263	50.088**	-22.076	22.095	-6.55
IL4 × IL9	3.534	-6.841	0.381	-6.907	-0.598	8.266	-14.188	14.207	-15.775
IL4 × IL10	-1.251	1.731	12.581	2.053	0.237	2.124	17.421	-17.437	7.007
IL4 × IL11	0.177	2.445	13.477	6.045	-0.886	-7.734	-52.106	52.125**	-14.547
IL4 × IL12	2.588	-16.126	1.959	-7.036	-2.068**	-8.912	-40.604	40.623	2.858
IL5 × IL6	1.4	3.874	17.34**	5.223	1.821	-21.448	22.08	-22.15	-19.082
IL5 × IL7	-2.698	2.445	-7.95	-20.648**	-0.926	-13.698	-21.785	21.679	17.135
IL5 × IL8	-4.05**	19.231	-10.66**	-0.711	2.127**	-9.841	-51.372	31.302	-23.653
IL5 × IL9	-2.734	19.945	11.87	5.815	-0.774	-23.662	-75.285	45.215	-17.363
IL5 × IL10	-1.144	-21.484	19.345**	2.602	-0.014	-2.305	-61.801	51.695**	-19.316
IL5 × IL11	-1.966	-5.769	1.566	7.807**	-1.263	-1.162	-17.927	17.857	-16.792
IL5 × IL12	-1.055	5.659	1.599	8.083**	-0.455	31.659**	-7.601	7.531	-23.628
IL6 × IL7	-0.189	5.659	7.759	2.686	0.194	-22.805	-5.202	5.186	-22.932
IL6 × IL8	-4.16**	12.445	6.102	6.287	-0.023	-8.448	92.885**	-62.866**	22.175
IL6 × IL9	0.775	3.159	-4.046	3.319	-0.579	11.731	24.848	-24.828	7.835
IL6 × IL10	0.99	11.731	5.754	1.271	-0.514	-4.912	-83.669	33.652	-3.278
IL6 × IL11	-1.957	-7.555	1	-0.489	-1.387	-12.769	39.855	-9.835	13.223
IL6 × IL12	2.954	8.874	0.483	-5.668	-0.819	-0.448	-37.944	37.963	1.165
IL7 × IL8	1.74	31.016	-1.987	5.521	-0.27	7.302	-61.454	5.438	-21.101
IL7 × IL9	-2.698	26.731	-5.01	3.628	-0.261	-8.519	-84.667**	64.65**	26.027
IL7 × IL10	-3.734	-4.698	-11.44**	-2.81	-0.251	-15.662	48.142	-27.694	-7.516
IL7 × IL11	2.695	-13.984	0.511	7.674	-2.945**	2.981	4.065	-4.082	-22.517
IL7 × IL12	-1.644	-22.555	19.143**	5.446	0.233	-26.698	79.942	-9.959	29.585
IL8 × IL9	-3.796	-31.484	2.283	-7.481**	1.592	-20.662	7.171	-7.152	-3.651
IL8 × IL10	-3.582	17.088	9.383	-4.013	-1.673	-6.305	56.93	-46.946**	14.111
IL8 × IL11	-1.528	2.802	10.929	0.561	2.003	-32.662**	103.528**	-13.509	9.475

* and ** significant at 5% and 1% level of significance, respectively

Contd.....

Table 20 (b). Contd.....

Hybrid	NCP	DM	CG	SP	CT	TW	RWC	SWD	MSI
IL8 × IL12	1.508	-10.769	4.086	2.943	0.376	11.159	14.005	-13.985	35.524
IL9 × IL10	0.731	32.802**	-0.791	4.46	0.916	27.874	63.467	-43.484**	-14.143
IL9 × IL11	0.284	13.516	13.581	1.125	2.927**	-12.484	87.215	-7.196	-14.31
IL9 × IL12	-0.305	4.945	1.238	0.866	1.71	-17.662	59.717	-9.698	17.56
IL10 × IL11	-1.376	-27.912	-5.519	-10.54**	2.102**	-1.626	71.699	-71.716**	19.157
IL10 × IL12	-0.716	13.516	-0.262	-3.929	0.475	20.695	7.076	-7.093	-12.816
IL11 × IL12	-2.537	-20.769	-3.566	4.663	0.302	-32.662**	39.224	-39.205	-12.172

* and ** significant at 5% and 1% level of significance, respectively

NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm), SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI=Membrane stability index

4.4. Components of genetic variance

The data recorded for the parents and their hybrids for each trait were subjected to component analysis where additive-dominance model was found adequate as revealed by non-significant differences of t value (Hayman 1954b). Therefore for such characters are used to computation of components of genetic variances.

Table 21. Estimates of components of genetic variance for various characters

S.No.	Source	DFT	DM	SYP	RWC	SWD
1	D +SE	15.18**	21.45**	0.56**	0.21**	0.25**
2	F +SE	10.47**	21.49**	0.34**	0.12**	0.36**
3	H1 +SE	21.16**	25.46**	1.56**	0.45**	0.86**
4	H2 +SE	-21.16	-26.46	2.16**	0.36**	0.76**
5	h* +SE	-15.44	-6.69	1.16**	0.54**	-1.64
6	E +SE	1.39**	1.95	0.41**	0.01**	0.03**
7	H1/D	1.05	1.03	2.13	1.49	1.91
8	H2/4H1	-0.38	-0.12	0.23	0.22	0.24
9	Proportion of dominant recessive alleles	1.01	1.02	1.13	1.99	2.35
10	Number of gene blocks	-0.16	-0.06	0.11	0.28	-0.42
11	Heritability (NS)	0.87	0.68	0.05	0.08	0.02

* and ** significant at 5% and 1% level of significance, respectively

4.4.1 Days to 50% tasseling

The component analysis revealed that both additive (D) and dominance component (H1) of genetic variance were found significant and dominance component (H2) of genetic variance was investigated non-significant that indicates that alleles are asymmetrically distributed. This indicated that both additive and dominance (H1) components were operating in the expression of this trait. The value of F was found significant and positive which suggested that dominant alleles in excess over recessive alleles in parents. Environment component of variance (E) was found highly significant suggesting influence of the environment in the expression of this trait. The ratio of mean degree of dominance as measured by (H1/D) was more than unity, indicating over

dominance. The value of $(H2/4H1)$ was -0.38 indicating asymmetric distribution of positive and negative alleles. The ratio of dominant to recessive alleles was more than unity, indicating accumulation of dominant alleles. The heritability in narrow sense was noticed 0.87.

4.4.2 Days to maturity

The additive dominance model for this character was found adequate. The component analysis revealed that both additive (D) and dominance component (H1) of genetic variance were significant but dominance component (H2) of genetic variance was non-significant that indicates that alleles are asymmetrically distributed (Table 21). This indicated that both additive and dominance components (H1) were operating in the expression of this trait. The value of F was found significant and positive which suggested existence of dominant alleles in excess of recessive allele in parents. Environment component of variance (E) was found non-significant suggesting absence of influence of the environment in the expression of this trait. The ratio of mean degree of dominance as measured by $(H1/D)$ was more than unity indicating over dominance. The value of $(H2/4H1)$ was -0.12 indicating asymmetric distribution of positive and negative alleles. The ratio of dominant to recessive alleles was more than unity indicating preponderance of dominant alleles. The heritability in narrow sense was found 0.68.

4.4.3 Yield per plant (g)

The component analysis revealed that both additive (D) and dominance component (H1) of genetic variance were significant (Table 21). Dominance component (H2) of genetic variance was also found significant which indicate that alleles are symmetrically distributed. This designated that both additive and non-additive component operating in the expression of this trait. The value of F was investigated significant and positive which suggested that dominance allele in excess over recessive allele in parents. Environment component of variance (E) was found significant suggesting that influence of the environment in the expression of this trait. The ratio of mean degree of dominance as measured by $(H1/D)$ was more than unity indicating over dominance. The value of $(H2/4H1)$

was 0.23 indicating symmetric distribution of positive and negative alleles. The ratio of dominant to recessive alleles was noticed more than unity indicating accumulation of dominant alleles. The heritability in narrow sense was estimated 0.05.

4.4.4 Relative water content

The additive-dominance model for this character also was found adequate. The component analysis revealed that both additive (D) and dominance component (H1) of genetic variance were highly significant (Table 4.9). Dominance component (H2) of genetic variance was also found significant which indicated that alleles are symmetrically distributed. This emphasized that both additive and non-additive components of gene action are operating in the expression of this trait. The value of F was found highly significant and positive that suggested that dominance allele in excess over recessive allele in parents. Environment component of variance (E) was found significant signifying that impact of the environment in the expression of this trait. The ratio of mean degree of dominance as measured by (H1/D) was more than unity indicating over dominance. The value of (H2/4H1) was 0.22 indicating symmetric distribution of positive and negative alleles. The ratio of dominant to recessive alleles was more than unity indicating accumulation of dominant alleles. The heritability in narrow sense was found 0.08.

4.4.5 Saturation water deficit

The additive dominance model for this character was found adequate. The component analysis revealed that both additive (D) and dominance component (H1) of genetic variance were highly significant (4.4). Dominance component (H2) of genetic variance was also found highly significant which indicated that alleles are symmetrically distributed (Table 21). Therefore, both additive and non-additive components were important in the expression of this trait. The value of F was found significant and positive which suggested that dominant alleles are in excess over recessive alleles in parents. Environment component of variance (E) was investigated significant suggesting influence of the environment in the

expression of this trait. The ratio of mean degree of dominance as measured by ($H1/D$) was investigated more than unity indicating presence of over dominance. The value of ($H2/4H1$) was found 0.24 indicating asymmetric distribution of positive and negative alleles. The ratio of dominant to recessive alleles was more than unity indicating accumulation of dominant alleles. The heritability in narrow sense was noticed 0.02.

4.5. Estimation of heterosis

The magnitude of heterosis, measured as percent increase or decrease of 66 hybrids value over 12 parents and two commercial checks (standard heterosis) for 18 characters are presented in Table 22 (a-f) and Table 23 (a-f) for the characters like days to 50 percent flowering, days to maturity and plant height the low scoring hybrids were considered as better cross combinations for estimation of heterosis. The results are summarized character wise in the following sections.

4.5.1 Days to 50% tasseling

The mid parent heterosis was ranged from -195.00 (IL11 $\times$ IL12) to -92.50 (IL5 $\times$ IL8) with a mean heterosis of cross -56.50 percent under irrigated condition (Table 22 a). Under partially irrigated condition, it ranged from -193.73 (IL11 $\times$ IL12) to -93.77 percent (IL5 $\times$ IL8) with a mean mid parent heterosis of cross -41.98 percent (Table 23 a).

The hetrobeltiosis was ranged from -220.00 (IL10 $\times$ IL12) to -90.00 (IL8 $\times$ IL9) with a mean heterosis of cross -102.05 percent under irrigated condition (Table 22 a). Under partially irrigated condition, it ranged from -168.73 (IL3 $\times$ IL11) to -91.27 percent (IL8 $\times$ IL9) with a mean hetrobeltiosis of cross -21.10 percent (Table 23 a).

The percent heterosis over commercial check was ranged between -240.00 (IL4 $\times$ IL9) to -35.00 (IL5 $\times$ IL8 and IL7 $\times$ IL9) with a mean heterosis of cross -163.56 percent under irrigated condition (Table 22 a). Under partially irrigated condition, it ranged between -228.73 (IL3 $\times$ IL9) to -3.83 percent (IL3 $\times$ IL4) with a mean heterosis of cross combination -62.69 percent (Table 23 a).

4.5.2 Days to 50 % silking

The mid parent heterosis was varied between -20.50 (IL10 × IL12) to -8.63 (IL5 × IL8 and IL7 × IL9) with a mean heterosis of cross combination -6.33 percent under irrigated condition (Table 22 a). Under partially irrigated condition, it ranged from -19.23 (IL10 × IL12) to -9.90 percent (IL5 × IL8/ IL7 × IL9) with a mean mid parent heterosis of cross -5.05 percent (Table 23 a).

The hetrobeltiosis was varied from -23.25 (IL10 × IL12) to 7.00 (IL8 × IL9) with a mean heterosis of cross combination -10.98 percent under irrigated condition (Table 22 a). Under partially irrigated condition, it arrayed from -21.98 (IL10 × IL12) to -8.27 percent (IL8 × IL9) with a mean hetrobeltiosis of cross -9.71 percent (Table 23 a).

The percent heterosis over commercial check was ranged between -24.75 (IL4 × IL10) to -4.52 (IL7 × IL9) with a mean heterosis of cross -17.33 percent under irrigated condition (Table 22 a). Under partially irrigated condition, it ranged from -23.48 (IL4 × IL10) to -3.23 percent (IL7 × IL9) with a mean heterosis of cross -16.04 percent (Table 23 a).

4.5.3 Anthesis silking interval (ASI)

The mid parent heterosis was ranged from -27.50 (IL1 × IL4/ IL2 × IL11) to 16.25 (IL5 × IL11) with a mean heterosis of cross -7.46 percent under irrigated condition (Table 22 a). Under partially irrigated condition, it ranged from -26.23 (IL1 × IL4/IL2× IL11) to -17.52 percent (IL5 × IL11) with a mean mid parent heterosis for cross -6.19 percent (Table 23 a).

The hetrobeltiosis was ranged between -32.50 (IL1 × IL11) to 10.00 (IL5 × IL11) with a mean heterosis for cross -12.12 percent under irrigated condition (Table 22 a). Under partially irrigated condition, it ranged between -31.23 (IL1 × IL11) to -11.27 percent (IL5 × IL11) with a mean hetrobeltiosis for cross -10.85 percent (Table 23 a).

The percent heterosis over commercial check was ranged between -45.00 (IL2 × IL11) to -5.00 (IL2 × IL4), (IL5 × IL11) and IL6 × IL8) with a mean heterosis

of cross -22.05 percent under irrigated condition (Table 22 a). Under partially irrigated condition, it ranged between -43.72 (IL2 × IL11) to -3.73 percent (IL6 × IL8) with a mean heterosis for cross combination -20.76 percent (Table 23 a).

4.5.4 Plant height (cm)

The mid parent heterosis was varied between -24.51 (IL1 × IL10) to 58.05 (IL2 × IL4) with a mean heterosis for cross 17.72 percent under irrigated condition (Table 22 b). While, under partially irrigated condition, it ranged between -23.15 (IL2 × IL4) to 59.41 percent (IL1 × IL10) with a mean mid parent heterosis for cross 19.08 percent (Table 23 b).

The hetrobeltiosis was ranged between -44.97 (IL1 × IL10) to -48.69 (IL7 × IL9) with a mean heterosis for cross 2.63 percent under irrigated condition (Table 22 b). Under partially irrigated condition, it ranged between -43.61 (IL7 × IL9) to 50.05 percent (IL1 × IL10) with a mean hetrobeltiosis for cross 4.00 percent (Table 23 b).

The percent heterosis over commercial check was ranged from -48.58 (IL2 × IL4) to 18.14 (IL4 × IL7) with a mean heterosis for cross -14.55 percent under irrigated condition (Table 22 b). Under partially irrigated condition, it ranged between -47.22 (IL2 × IL4) to -19.50 percent (IL4 × IL7) with a mean heterosis for cross -13.20 percent (Table 23 b).

4.5.5 Cob length (cm)

The mid parent heterosis was ranged between -0.74 (IL2 × IL9) to 5.35 (IL1 × IL7) with a mean heterosis of cross 1.32 percent under irrigated condition (Table 22 b). However, under partially irrigated condition, it ranged between 0.62 (IL1 × IL7) to 6.71 percent (IL2 × IL9) with a mean mid parent heterosis for cross 2.70 percent (Table 23 b).

The hetrobeltiosis was ranged from -1.36 (IL2 × IL9) to 4.07 (IL4 × IL7) with a mean heterosis for cross 0.79 percent under irrigated condition (Table 22 b). Under partially irrigated condition, it ranged between 0.00 (IL4 × IL7) to 5.43 percent (IL2 × IL9) with a mean hetrobeltiosis for cross 2.15 percent (Table 23 b).

The percent heterosis over commercial check ranged between -2.76 (IL1 × IL4) to -3.96 (IL2 × IL9) with a mean heterosis of cross 0.23 percent under irrigated condition (Table 22 b). Under partially irrigated condition, it ranged between -1.40 (IL1 × IL7) to 5.32 percent (IL2 × IL9) with a mean heterosis of cross 1.20 percent (Table 23 b).

4.5.6 Number of kernel rows per cob (NKRC)

The mid parent heterosis was ranged from -27.54 (IL5 × IL10) to 34.05 (IL2 × IL8) with a mean heterosis for cross 6.80 percent under irrigated condition (Table 22 b). While, under partially irrigated condition, it ranged from -26.18 (IL2 × IL8) to 35.41 percent (IL3 × IL5) with a mean mid parent heterosis for cross 8.16 percent (Table 23 b).

The heterobeltiosis was ranged from -35.88 (IL5 × IL10) to 27.45 (IL2 × IL4) with a mean heterosis of cross 1.64 percent under irrigated condition (Table 22 b). Under partially irrigated condition, it varied between -34.52 (IL2 × IL4) to 28.81 percent (IL5 × IL10) with a mean heterobeltiosis for cross -0.28 percent (Table 23 b).

The percent heterosis over commercial check ranged between -48.98 (IL3 × IL12) to 9.85 (IL8 × IL12) with a mean heterosis for cross -17.06 percent under irrigated condition (Table 22 b). While, under partially irrigated condition, it ranged between -47.62 (IL3 × IL12) to 11.21 percent (IL8 × IL12) with a mean heterosis for cross 15.70 percent (Table 23 b).

4.5.7 Numbers of kernel per rows (NKR)

The mid parent heterosis was ranged between -3.42 (IL1 × IL6) to 14.99 (IL9 × IL11) with a mean heterosis for cross 5.77 percent under irrigated condition (Table 22 c). While under partially irrigated condition, it varied between -2.59 (IL1 × IL6) to 15.83 percent (IL9 × IL11) with a mean mid parent heterosis for cross combination 6.61 percent (Table 23 c).

The heterobeltiosis was ranged from -7.38 (IL1 × IL12) to 12.75 (IL9 × IL11) with a mean heterosis for cross 3.17 percent under irrigated condition (Table 22

c). However, under partially irrigated condition, it varied between -6.88 (IL1 × IL12) to 13.59 percent (IL9 × IL11) with a mean heterobeltiosis for cross 4.05 percent (Table 23 c).

The percent heterosis over commercial check was from -10.57 (IL5 × IL8) to 6.16 (IL2 × IL6) with a mean heterosis for cross -2.08 percent under irrigated condition (Table 22 c). While, under partially irrigated condition, it ranged from -9.73 (IL5 × IL8) to 7.79 percent (IL2 × IL6) with a mean heterosis for cross 1.23 percent (Table 23 c).

4.5.8 100 grain weight (g)

The mid parent heterosis was ranged between -76.35 (IL3 × IL4) to 77.80 (IL8 × IL11) with a mean heterosis for cross combination -7.20 percent under irrigated condition (Table 22 c). Whereas, under partially irrigated condition, it varied between -75.51 (IL3 × IL4) to 78.64 percent (IL8 × IL11) with a mean mid parent heterosis for cross 6.36 percent (Table 23 c).

The heterobeltiosis was ranged between -89.50 (IL1 × IL12) to 66.80 (IL8 × IL10) with a mean heterosis for cross -27.05 percent under irrigated condition (Table 22 c). While, under partially irrigated condition, it varied between -88.66 (IL1 × IL12) to 67.72 percent (IL8 × IL10) with a mean heterobeltiosis for cross 24.84 percent (Table 23 c).

The percent heterosis over commercial check was arrayed from -110.10 (IL5 × IL8) to 29.25 (IL3 × IL7) with a mean heterosis for cross -48.67 percent under irrigated condition (Table 22 c). While under partially irrigated condition, it ranged between -107.61 (IL1 × IL12) to 30.09 percent (IL3 × IL7) with a mean heterosis for cross combination 45.59 percent (Table 23 c).

4.5.9 Yield per plant (g)

The mid parent heterosis was ranged between -22.51 (IL2 × IL4) to 78.97 (IL11 × IL12) with a mean heterosis for cross 20.83 percent under irrigated condition (Table 22 c). However, under partially irrigated condition, it varied between -

21.67 (IL2 × IL4) to 79.81 percent (IL11 × IL12) with a mean mid parent heterosis for cross 21.66 percent (Table 23 c).

The heterobeltiosis was ranged between -41.32 (IL2 × IL5) to 76.13 (IL11 × IL12) with a mean heterosis for cross 13.11 percent under irrigated condition (Table 22 c). While under partially irrigated condition, it ranged from -40.48 (IL2 × IL5) to 76.97 percent (IL1 × IL12) with a mean heterobeltiosis for cross 13.98 percent (Table 23 c).

The percent heterosis over commercial check was varied between -43.08 (IL1 × IL6) to 38.67 (IL11 × IL12) with a mean heterosis for cross -7.54 percent under irrigated condition (Table 22 c). While under partially irrigated condition, it ranged between -42.24 (IL1 × IL6) to 39.47 percent (IL11 × IL12) with a mean heterosis for cross combination 6.71 percent (Table 23 c).

4.5.10 Number of cobs per plant (NCP)

The mid parent heterosis was ranged from -8.06 (IL5 × IL8) to 9.13 (IL4 × IL8) with a mean heterosis of cross 0.52 percent under irrigated condition (Table 22 d). However, under partially irrigated condition, it varied between -6.87 (IL5 × IL8) to 10.32 percent (IL4 × IL8) with a mean mid parent heterosis for cross combination 1.72 percent (Table 23 d).

The heterobeltiosis ranged from -9.63 (IL5 × IL8) to 7.25 (IL4 × IL8) with a mean heterosis for cross -1.28 percent under irrigated condition (Table 22 d). While, under partially irrigated condition, it arrayed from -8.44 (IL5 × IL8) to 8.44 percent (IL4 × IL8) with a mean heterobeltiosis for cross combination -0.09 percent (Table 23 d).

The percent heterosis over commercial check varied from -10.38 (IL7 × IL10) to 3.75 (IL4 × IL8) with a mean heterosis of cross -3.70 percent under irrigated condition (Table 22 d). Under partially irrigated condition, it ranged between -9.19 (IL7 × IL10) to 4.94 percent (IL4 × IL8) with a mean heterosis for the cross-combination 2.51 percent (Table 23 d).

4.5.11 Days to maturity

The mid parent heterosis was ranged from -82.50 (IL7 × IL12) to 65.00 (IL1 × IL7) with a mean heterosis for cross combination -9.16 percent under irrigated condition (Table 22 d). While under partially irrigated condition, it ranged between -81.31 (IL7× IL12) to 66.15 (IL1 × IL7) percent with a mean mid parent heterosis value for cross combination -7.98 percent (Table 23 d).

The hetrobeltiosis was ranged from -95.00 (IL7 × IL12) to 30.00 (IL3 × IL5/ IL1 × IL7) with a mean heterosis for cross -26.21 percent under irrigated condition (Table 22 d). Whereas, under partially irrigated condition, it ranged from -93.87 (IL7 × IL12) to 31.19 percent (IL1 × IL7) with a mean hetrobeltiosis for cross -24.83 percent (Table 23 d).

The percent heterosis over commercial check varied between -115.00 (IL4 × IL10) to 5.00 (IL1 × IL7) with a mean heterosis of cross -65.00 percent under irrigated condition (Table 22 d). However, under partially irrigated condition, it arrayed from -103.18 (IL1 × IL3) to 6.19 percent (IL1 × IL7) with a mean heterosis value for cross combination 57.92 percent (Table 23 d).

4.5.12 Cob girth (cm)

The mid parent heterosis was ranged from -19.14 (IL2 × IL5) to 64.33 (IL6 × IL8) with a mean heterosis of cross 9.90 percent under irrigated condition (Table 22 d). Whereas, under partially irrigated condition, it varied from -17.95 (IL2× IL5) to 65.52 (IL6 × IL8) percent with a mean mid parent heterosis for cross 11.09 percent (Table 23 d).

The hetrobeltiosis was ranged between -24.28 (IL2 × IL5) to 62.35 (IL6 × IL8) with a mean heterosis for cross combination -5.61 percent under irrigated condition (Table 22 d). While under partially irrigated condition, it ranged between -23.09 (IL2 × IL5) to 63.54 percent (IL6 × IL8) with a mean hetrobeltiosis for cross combination -6.80 percent (Table 23 d).

The percent heterosis over commercial check ranged between -27.58 (IL2 × IL5) to 52.48 (IL6 × IL8) with a mean heterosis for cross -2.16 percent under irrigated condition (Table 22 d). However, under partially irrigated condition, it

ranged from -26.39 (IL2 × IL5) to 53.67 percent (IL6 × IL8) with a mean heterosis for cross -0.97 percent (Table 23 d).

4.5.13 Shelling (%)

The mid parent heterosis was ranged from -19.96 (IL5 × IL7) to 13.14 (IL11 × IL12) with a mean heterosis for cross 0.10 percent under irrigated condition (Table 22 e). Under partially irrigated condition, it ranged from -17.53 (IL5 × IL7) to 15.58 (IL11 × IL12) percent with a mean mid parent heterosis for cross combination 2.54 percent (Table 23 e).

The hetrobeltiosis ranged between -20.59 (IL5 × IL7) to 11.49 (IL11 × IL12) with a mean heterosis for cross combination -2.43 percent under irrigated condition (Table 22 e). However, under partially irrigated condition, it ranged from -18.16 (IL5 × IL7) to 13.93 percent (IL11 × IL12) with a mean hetrobeltiosis of cross 0.02 percent (Table 23 e).

The percent heterosis over commercial check arrayed from -28.74 (IL5 × IL7) to 3.09 (IL1 × IL7) with a mean heterosis for cross -7.97 percent under irrigated condition (Table 22 e). Under partially irrigated condition, it ranged from -26.31 (IL5 × IL7) to 5.53 percent (IL1 × IL7) with a mean heterosis for cross -5.54 percent (Table 23 e).

4.5.14 Canopy temperature (at reproductive stages)

The mid parent heterosis was ranged from -4.36 (IL2 × IL9) to 3.34 (IL3 × IL8) with a mean heterosis for cross combination -0.84 percent under irrigated condition (Table 22 e). However, under partially irrigated condition, it ranged between -1.93 (IL2 × IL9) to 5.78 (IL3 × IL8) percent with a mean mid parent heterosis for cross combination 1.59 percent (Table 23 e).

The hetrobeltiosis ranged from -5.00 (IL2 × IL9) to 3.19 (IL2 × IL8) with a mean heterosis of cross -1.46 percent under irrigated condition (Table 22 e). However, under partially irrigated condition, it ranged between -2.57 (IL2 × IL9) to 5.63 percent (IL3 × IL8) with a mean hetrobeltiosis for cross combination 0.97 percent (Table 23 e).

The percent heterosis over commercial check was ranged between -6.56 (IL2 × IL9) to 0.32 (IL3 × IL8) with a mean heterosis of cross -2.94 percent under irrigated condition (Table 22 e). While under partially irrigated condition, it varied between -4.13 (IL2 × IL9) to 2.76 percent (IL2 × IL8) with a mean heterosis of cross -0.50 percent (Table 23 e).

4.5.15 Turgid weight (g)

The mid parent heterosis was ranged from -58.50 (IL8 × IL11) to 44.75 (IL4 × IL8) with a mean heterosis for cross -16.79 percent under irrigated condition (Table 22 e). However, under partially irrigated condition, it ranged from -56.07 (IL8 × IL11) to 47.19 (IL4 × IL8) percent with a mean mid parent heterosis of cross -14.35 percent (Table 23 e).

The hetrobeltiosis was ranged from -76.00 (IL3 × IL9) to 39.00 (IL4 × IL8) with a mean heterosis of cross -31.18 percent under irrigated condition (Table 22 e). Under partially irrigated condition, it ranged from -75.57 (IL3 × IL9) to 41.44 percent (IL4 × IL8) with a mean hetrobeltiosis for cross -28.75 percent (Table 23 e).

The percent heterosis over commercial check was from -98.00 (IL2 × IL4) to 12.44 (IL4 × IL8) with a mean heterosis of cross -55.23 percent under irrigated condition (Table 22 e). While, under partially irrigated condition, it ranged between -95.57 (IL3 × IL4) to 2.44 percent (IL4 × IL8) with a mean heterosis for cross -52.54 percent (Table 23 e).

4.5.16 Relative water content

The mid parent heterosis was ranged from -15.89 (IL3 × IL4) to 19.64 (IL10 × IL11) with a mean heterosis for cross 0.83 percent under irrigated condition (Table 22 f). Whereas under partially irrigated condition, it ranged between -15.48 (IL3 × IL4) to 20.06 (IL10 × IL11) percent with a mean mid parent heterosis value for cross 1.25 percent (Table 23 f).

The hetrobeltiosis was ranged between -22.98 (IL3 × IL4) to 10.20 (IL1 × IL11) with a mean heterosis for cross -3.36 percent under irrigated condition

(Table 22 f). While, under partially irrigated condition, it ranged between -22.54 (IL3 × IL4) to 11.55 percent (IL4 × IL10) with a mean heterobeltiosis for cross - combination 2.76 percent (Table 23 f).

The percent heterosis over commercial check ranged between -22.98 (IL3 × IL4) to 5.48 (IL2 × IL3) with a mean heterosis for crosses -10.53 percent under irrigated condition Table 22 (f). While under partially irrigated condition, it ranged between -21.84 (IL3 × IL4) to 6.62 percent (IL2 × IL3) with a mean heterosis for crosses -9.39 percent (Table 23 f).

4.5.17 Saturation water deficit

The mid parent heterosis was ranged between -19.64 (IL10 × IL11) to 15.89 (IL3 × IL4) with a mean heterosis of cross 0.83 percent under irrigated condition (Table 22 f). while under partially irrigated condition, it ranged from -18.50 (IL10 × IL11) to 17.03 percent (IL3 × IL4) with a mean heterobeltiosis for crosses 0.30 percent (Table 23 f).

The heterobeltiosis was ranged from -31.02 (IL10 × IL11) to 8.81 (IL3 × IL4) with a mean heterosis of cross -5.02 percent under irrigated condition (Table 22 f). Under partially irrigated condition, it ranged from -29.88 (IL10 × IL11) to 9.95 percent (IL3 × IL4) with a mean heterobeltiosis of cross 3.88 percent (Table 23 f).

The percent heterosis over commercial check was varied between -39.32 (IL2 × IL3) to -10.85 (IL3 × IL4) with a mean heterosis for cross -23.30 percent under irrigated condition (Table 22 f). While under partially irrigated condition, it ranged between -38.18 (IL2 × IL3) to 9.71 percent (IL3 × IL4) with a mean heterosis for cross -22.17 percent (Table 23 f).

4.5.18 Membrane stability index

The mid parent heterosis was ranged from -276.56 (IL9 × IL11) to 356.34 (IL1 × IL4) with a mean heterosis of cross 13.25 percent under irrigated condition (Table 22 f). However, under partially irrigated condition, it ranged from -275.42 (IL9 × IL11) to 357.48 percent (IL1 × IL4) with a mean heterobeltiosis for cross 24.72 percent (Table 23 f).

The heterobeltiosis was ranged from -386.70 (IL9 × IL11) to 333.83 (IL1 × IL4) with a mean heterosis of cross -54.95 percent under irrigated condition (Table 22 f). Under partially irrigated condition, it ranged from -358.11 (IL9 × IL12) to 93.72 percent (IL1 × IL5) with a mean heterobeltiosis of cross -5.84 percent (Table 23 f).

The percent heterosis over commercial check was from -386.70 (IL9 × IL11) to 158.18 (IL3 × IL11) with a mean heterosis of cross -163.38 percent under irrigated condition (Table 22 f). Under partially irrigated condition, it ranged from -241.21 (IL5 × IL8) to 62.77 percent (IL2 × IL3) with a mean heterosis of cross -29.36 percent (Table 23 f).

Table 22 (a). Estimation of mid parent, better parent and standard heterosis studied for Days to 50 % tasseling, Days to 50 % silking and Anthesis silking interval in maize (*Zea mays* L.) under irrigated condition.

Hybrid	DFT			DFS			ASI		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	-62.50**	-95	-105.00**	-8.13**	-12.25**	-12.25	-20.00**	-30.00**	-30
IL1 × IL3	-52.5	-165	-175	-6.00**	-17.75**	-17.75	-8.75	-15.00**	-15
IL1 × IL4	-85.00**	-180	-190	-11.13**	-20.75**	-20.75	-27.5	-30.00**	-30
IL1 × IL5	-127.50**	-165	-175.00**	-13.25**	-18.25**	-18.25	-6.25	-20	-20
IL1 × IL6	-15.00*	-95	-105.00**	-2.63**	-11.75**	-11.75	-12.5	-25	-25
IL1 × IL7	-160	-195	-205	-16.63**	-21.25**	-21.25**	-8.75	-20	-20
IL1 × IL8	-15.00*	-95	-105.00**	-3.88**	-12.25**	-12.25	-25	-30	-30
IL1 × IL9	-85.00**	-165.00**	-175	-9.00**	-17.50**	-17.5	-6.25	-12.5	-12.5
IL1 × IL10	-137.50**	-160.00**	-170	-15.00**	-17.75**	-17.75	-11.25	-17.5	-17.5
IL1 × IL11	-145	-160	-170	-17.13**	-19.25**	-19.25	-25	-32.5	-32.5
IL1 × IL12	-100.00**	-105.00**	-105	-12.00**	-12.00**	-12	-21.25	-27.50**	-27.50**
IL2 × IL3	-60.00**	-140	-215.00**	-6.38**	-14.00**	-22.25	-3.75	-7.5	-20.00**
IL2 × IL4	-87.50**	-150.00**	-225.00**	-8.00**	-13.50**	-21.75	7.50*	-1.32	-5
IL2 × IL5	-5	-10	-85.00**	-1.88**	-2.75**	-11	-13.75**	-17.50**	-37.50**
IL2 × IL6	-92.50**	-140.00**	-215	-9.50**	-14.50**	-22.75	-2.5	-5	-25.00**
IL2 × IL7	-132.50**	-135.00**	-210	-13.00**	-13.50**	-21.75	1.25	1.43	-20.00**
IL2 × IL8	-77.50**	-125	-200.00**	-7.50**	-11.75**	-20	2.5	-2.5	-12.50**
IL2 × IL9	-67.50**	-115	-190.00**	-6.88**	-11.25**	-19.5	-1.25	-5	-17.50**
IL2 × IL10	-120.00**	-130	-185.00**	-14.13**	-15.50**	-21	-18.75	-22.50**	-35.00**
IL2 × IL11	-112.50**	-130	-170.00**	-14.00**	-16.00**	-20.25	-27.50**	-30.00**	-45.00**
IL2 × IL12	-22.50**	-60.00**	-60.00**	-3.38**	-7.50**	-7.5	-11.25**	-15.00**	-27.50**
IL3 × IL4	22.50**	5	-195.00**	0.38	-1.75*	-21	-18.75	-22.50**	-27.50**
IL3 × IL5	-10	-85.00**	-170	-2.00**	-8.75**	-18.75**	-10.00**	-17.50**	-30.00**
IL3 × IL6	47.50**	15.00*	-155.00**	4.13**	1.5	-16.75	-6.25	-12.50**	-25.00**
IL3 × IL7	22.50**	-55.00**	-135.00**	1.38*	-5.75**	-15	-10.00**	-15.00**	-27.50**
IL3 × IL8	-7.5	-40.00**	-210.00**	-0.63	-4.00**	-20.75	1.25	0	-10.00*
IL3 × IL9	-27.50**	-60.00**	-230.00**	-3.75**	-7.00**	-24	-10.00**	-10.00*	-22.50**
IL3 × IL10	5	-85.00**	-140.00**	0.25	-8.75**	-14.25	-2.5	-2.5	-15.00**
IL3 × IL11	-72.50**	-170.00**	-210.00**	-8.38**	-18.00**	-22.25	-11.25**	-12.50**	-25.00**
IL3 × IL12	52.50**	-65.00**	-65.00**	3.50**	-8.25**	-8.25**	-17.50**	-17.50**	-30.00**
IL4 × IL5	72.50**	15.00*	-70.00**	7.13**	2.50**	-7.50**	-1.25	-12.50**	-17.50**
IL4 × IL6	80.00**	65.00**	-105.00**	6.50**	6.00**	-12.25	-15.00**	-25.00**	-30.00**
IL4 × IL7	-60.00**	-120.00**	-200.00**	-6.00**	-11.00**	-20.25	-1.25	-10.00*	-15.00**
IL4 × IL8	-25.00**	-40.00**	-210.00**	-5.00**	-6.25**	-23	-20.00**	-22.50**	-27.50**
IL4 × IL9	-55.00**	-70.00**	-240.00**	-5.88**	-7.00**	-24	-3.75	-7.5	-12.50**

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 22 (a). Contd.....

Hybrid	DFT			DFS			ASI		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	-107.50**	-180.00**	-235.00**	-12.38**	-19.25**	-24.75	-16.25**	-20.00**	-25.00**
IL4 × IL11	-85.00**	-165.00**	-205.00**	-8.75**	-16.25**	-20.5	-2.5	-7.5	-12.50**
IL4 × IL12	-70.00**	-170.00**	-170.00**	-8.63**	-18.25**	-18.25	-16.25**	-20.00**	-25.00**
IL5 × IL6	-62.50**	-105.00**	-190.00**	-7.13**	-11.25**	-21.25**	-8.75**	-10.00*	-35.00**
IL5 × IL7	32.50**	30.00**	-50.00**	2.13**	1.75*	-7.5	-12.50**	-15.00**	-37.50**
IL5 × IL8	92.50**	50.00**	-35.00**	8.63**	5.25**	-4.75	-6.25	-15.00**	-25.00**
IL5 × IL9	62.50**	20.00**	-65.00**	6.50**	3.00**	-7	2.5	-5	-17.50**
IL5 × IL10	-145.00**	-160.00**	-215.00**	-13.25**	-15.50**	-21	12.50**	5	-7.5
IL5 × IL11	-157.50**	-180.00**	-220.00**	-14.13**	-17.00**	-21.25	16.25**	10.00*	-5
IL5 × IL12	-12.50*	-55.00**	-55.00**	-1.75**	-6.75**	-6.75**	-5	-12.50**	-25.00**
IL6 × IL7	-60.00**	-105.00**	-185.00**	-6.25**	-10.75**	-20	-3.75	-5	-27.50**
IL6 × IL8	-45.00**	-45.00**	-215.00**	-3.25**	-4.00**	-20.75	12.50**	5	-5
IL6 × IL9	-20.00**	-20.00**	-190.00**	-0.88	-1.5	-18.50**	11.25**	5	-7.5
IL6 × IL10	-77.50**	-135.00**	-190.00**	-7.88**	-14.25	-19.75**	-1.25	-7.5	-20.00**
IL6 × IL11	-105.00**	-170.00**	-210.00**	-11.50**	-18.5	-22.75	-10.00**	-15.00**	-30.00**
IL6 × IL12	-100.00**	-185.00**	-185.00**	-9.63**	-18.75	-18.75	3.75	-2.5	-15.00**
IL7 × IL8	-65.00**	-110.00**	-190.00**	-6.25**	-10	-19.25	1.25	-5	-15.00**
IL7 × IL9	90.00**	45.00**	-35.00**	8.63**	4.75	-4.5	-5	-10.00*	-22.50**
IL7 × IL10	-102.50**	-115.00**	-170.00**	-11.88**	-13.75	-19.25	-17.50**	-22.50**	-35.00**
IL7 × IL11	-145.00**	-165.00**	-205.00**	-14.50**	-17	-21.25	-1.25	-5	-20.00**
IL7 × IL12	-30.00**	-70.00**	-70.00**	-3.63**	-8.25**	-8.25	-7.50*	-12.50**	-25.00**
IL8 × IL9	90.00**	90.00**	-80.00**	7.13**	7.00**	-9.75	-18.75**	-20.00**	-30.00**
IL8 × IL10	2.5	-55.00**	-110.00**	0.13	-5.5	-11	-1.25	-2.5	-12.50**
IL8 × IL11	-95.00**	-160.00**	-200.00**	-10.00**	-16.25	-20.5	-5	-7.5	-17.50**
IL8 × IL12	-120.00**	-205.00**	-205.00**	-12.63**	-21	-21	-6.25	-7.5	-17.50**
IL9 × IL10	-87.50**	-145.00**	-200.00**	-9.50**	-15.25	-20.75	-7.50*	-7.5	-20.00**
IL9 × IL11	-80.00**	-145.00**	-185.00**	-9.88**	-16.25	-20.5	-16.25**	-17.50**	-30.00**
IL9 × IL12	-15.00*	-100.00**	-100.00**	-1.75**	-10.25	-10.25	-2.5	-2.5	-15.00**
IL10 × IL11	-177.50**	-185.00**	-225.00**	-17.38**	-18	-22.25**	3.75	2.5	-10.00*
IL10 × IL12	-192.50**	-220.00**	-220.00**	-20.50**	-23.25	-23.25**	-12.50**	-12.50**	-25.00**
IL11 × IL12	-195.00**	-215.00**	-215.00**	-20.13**	-22.25**	-22.25**	-6.25	-7.5	-20.00**
Mean	-56.06	-102.05	-163.56	-6.33	-10.98	-17.33	-7.46	-12.12	-22.05
SE	0.29	0.84	0.27	0.48	0.87	0.24	0.64	0.9	0.23
Min.	-195	-220	-240	-20.5	-23.25	-24.75	-27.5	-32.5	-45
Max.	92.5	90	-35	8.63	7	-4.5	16.25	10	-5
CD @ 5%	3.26	12.54	3.92	5.28	6.86	8.23	5.23	3.34	2.23
CD @ 1%	4.45	13.45	4.25	6.35	7.76	9.45	6.36	4.45	3.56

* and ** significant at 5% and 1% level of significance, respectively,

DFT=, DFS= Days to 50 % silking, ASI = Anthesis silking interval

Table 22 (b). Estimation of mid parent, better parent and standard heterosis studied for Plant height (cm), Cob length (cm) and Number of kernel rows per cob in maize (*Zea mays* L.) under irrigated condition.

Hybrid	PH			CL			NKRC		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	31.03**	3.12*	-14.52**	3.34**	3.22	0.79	-20.08**	-31.63**	-33.20**
IL1 × IL3	15.37**	-19.24**	-23.48**	1.60*	1.58	-0.85	2.84	-3.93	-28.60**
IL1 × IL4	37.04**	15.56**	-14.93**	3.19**	1.98	1.98*	24.46**	12.23	-12.45
IL1 × IL5	27.06**	-7.06**	-12.28**	0.98	0.83	-1.3	11.41*	6.08	-18.60**
IL1 × IL6	24.01**	-1.48	-23.94**	1.82**	1.24	-0.03	0.86	-3.48	-28.15**
IL1 × IL7	37.78**	1.05	1.05	-0.74	-1.15	-2.76**	22.44**	19.15**	1.05
IL1 × IL8	30.11**	12.18**	-25.41**	2.72**	2.22**	0.79	7.86	4.4	-13.35*
IL1 × IL9	45.46**	41.38**	-32.08**	0.03	-1.13	-1.24	6.06	3.62	-21.05**
IL1 × IL10	58.05**	48.69**	-6.04**	0.85	0.64	-1.36	16.91**	15.65*	-6.5
IL1 × IL11	45.50**	23.89**	-6.35**	0.87	0.71	-1.4	3.74	-8.6	-8.6
IL1 × IL12	31.69**	9.75**	-19.83**	-0.09	-1.05	-1.56*	-8.46	-12.5	-29.10**
IL2 × IL3	13.15**	6.44**	2.21	1.94**	1.84*	-0.64	7.44	-10.88	-12.45
IL2 × IL4	-24.51**	-30.94**	-48.58	0.48	-0.86	-0.86	-12.09*	-35.88**	-37.45**
IL2 × IL5	5.32**	-0.89	-6.11**	0.99	0.71	-1.41	9.46	-7.43	-9
IL2 × IL6	16.36**	13.95**	-3.69**	1.56*	0.86	-0.41	-0.14	-16.03*	-17.60**
IL2 × IL7	20.41**	11.59**	11.59**	4.31**	3.78**	2.17**	-3.11	-11.38	-12.95*
IL2 × IL8	4.69**	-5.29**	-22.93	1.94**	1.32	-0.11	-27.54**	-35.63**	-37.20**
IL2 × IL9	10.88**	-21.11**	-38.75	5.35**	4.07**	3.96**	4.61	-9.38	-10.95
IL2 × IL10	24.67**	6.13**	-11.51**	2.20**	1.86*	-0.13	-2.59	-12.88*	-14.45*
IL2 × IL11	18.66**	12.36**	-5.28**	1.71*	1.43	-0.68	-9.36	-10.15	-10.15
IL2 × IL12	27.02**	21.06**	3.42**	0.11	-0.97	-1.48	3.79	-3.73	-5.3
IL3 × IL4	14.80**	1.67	-2.56*	2.47**	1.23	1.23	11.33*	5.85	-32.35**
IL3 × IL5	-8.73**	-9.22**	-13.46	0.23	0.06	-2.06**	2.35	0.92	-34.43**
IL3 × IL6	-9.26**	-18.37**	-22.61	1.95**	1.35	0.08	6.3	3.87	-29.48
IL3 × IL7	-20.07**	-22.18**	-22.18	1.81**	1.38	-0.23	2.85	-7.2	-25.3
IL3 × IL8	11.20**	-5.48**	-9.72	-0.6	-1.12	-2.55**	17.55**	7.32	-10.43
IL3 × IL9	25.22**	-13.48**	-17.71	0.75	-0.43	-0.54	17.93**	13.60*	-15.95*
IL3 × IL10	11.93**	-13.32**	-17.55**	1.88**	1.64*	-0.36	16.03**	8	-14.15*
IL3 × IL11	-0.12	-13.13**	-17.36**	3.17**	2.99**	0.88	1.9	-17.20**	-17.2
IL3 × IL12	5.85**	-6.82**	-11.05**	1.64*	0.66	0.15	-21.58**	-32.38**	-48.98
IL4 × IL5	9.97**	-2.66*	-7.89**	0.28	-0.78	-0.78	29.00**	22.10**	-13.25*
IL4 × IL6	5.65**	1.63	-20.83	1.24	0.61	0.61	20.15**	12.25	-21.1
IL4 × IL7	33.39**	18.14**	18.14	-0.56	-1.36	-1.36	5.05	-10.48	-28.58**
IL4 × IL8	36.62**	33.07**	2.57*	-0.11	-0.83	-0.83	6.57	-9.13	-26.88**
IL4 × IL9	27.74**	2.18	-28.32	1.53*	1.48	1.48	28.40**	18.60**	-10.95

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 22 (b). Contd.....

Hybrid	PH			CL			NKRC		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	26.85**	14.74	-15.76**	0.9	-0.1	-0.1	10.9	-2.6	-24.75**
IL4 × IL11	19.77**	19.64	-10.60**	0.32	-0.74	-0.74	-2.58	-27.15**	-27.15**
IL4 × IL12	20.45**	19.99	-9.59**	2.44**	2.19**	2.19**	21.13**	4.85	-11.75
IL5 × IL6	-19.35**	-27.97	-33.2	-0.38	-0.8	-2.07**	1.25	0.25	-33.1
IL5 × IL7	-9.89**	-12.5	-12.5	3.93**	3.68**	2.07**	-8.58	-17.20**	-35.3
IL5 × IL8	-16.73**	-32.92	-38.14	0.15	-0.2	-1.63*	-10.55	-19.35**	-37.1
IL5 × IL9	20.62**	-17.57	-22.80**	1.92**	0.91	0.8	-0.67	-3.57	-33.13
IL5 × IL10	8.05**	-16.7	-21.93**	2.07**	2.01*	0.01	34.05**	27.45**	5.3
IL5 × IL11	22.86**	10.35	5.13**	2.37**	2.36**	0.25	15.10**	-2.57	-2.57
IL5 × IL12	-7.22**	-19.39	-24.62	0.67	-0.13	-0.64	15.30**	5.92	-10.68
IL6 × IL7	16.29**	5.06	5.06**	2.21**	2.04**	0.77	13.63*	6	-12.1
IL6 × IL8	0.2	-7.37**	-29.83**	0.49	0.41	-0.86	17.45**	9.65	-8.1
IL6 × IL9	24.65**	-4.93**	-27.38	0.46	-0.12	-0.23	27.30**	25.40**	-4.15
IL6 × IL10	26.94**	10.80**	-11.66**	2.01**	1.65*	0.38	-4.25	-9.85	-32.00**
IL6 × IL11	23.96**	20.07**	-2.39	3.65**	3.24**	1.97*	-17.78**	-34.45**	-34.45**
IL6 × IL12	26.54**	22.98**	0.53	2.30**	1.92*	1.41	27.08**	18.70**	2.1
IL7 × IL8	24.56**	5.76**	5.76**	1.51*	1.42	-0.01	27.23**	27.05**	9.3
IL7 × IL9	-4.16**	-44.97	-44.97**	0.47	-0.28	-0.39	3.4	-2.32	-20.43**
IL7 × IL10	45.03	17.67	17.67**	2.58**	2.39**	0.78	2.18	0.15	-17.95**
IL7 × IL11	29.86	14.74	14.74	0.78	0.54	-1.08	6.8	-2.25	-2.25
IL7 × IL12	4.28	-10.51	-10.51	1.23	0.68	0.17	17.10**	16.35*	-0.25
IL8 × IL9	32.88	10.87	-26.73	-0.58	-1.24	-1.35	17.33**	11.43	-6.32
IL8 × IL10	17.9	9.33	-28.26**	2.02**	1.74*	0.31	10.08	7.88	-9.88
IL8 × IL11	34.35	30.68	0.44	-0.38	-0.72	-2.15**	3.8	-5.07	-5.07
IL8 × IL12	17.59	13.59	-15.99**	0.91	0.45	-0.06	27.03**	26.45**	9.85
IL9 × IL10	31.19	17.75	-36.98**	1.92**	0.98	0.87	16.35**	12.65	-9.5
IL9 × IL11	20.46	-5.22	-35.47	-0.16	-1.16	-1.27	-9.05	-23.83	-23.83**
IL9 × IL12	31.74**	5.72	-23.86	-0.17	-0.37	-0.48	23.83**	17.35**	0.75
IL10 × IL11	28.73**	16.48	-13.76	0.84	0.78	-1.21	-1.65	-12.73*	-12.73*
IL10 × IL12	24.08**	11.5	-18.08	0.05	-0.69	-1.2	-4.57	-7.35	-23.95**
IL11 × IL12	3.25**	2.92*	-26.66*	0.09	-0.71	-1.22	-11.55*	-19.85**	-19.85**
Mean	17.72	2.63	-14.55	1.33	0.79	-0.24	6.81	-1.65	-17.06
Min.	-24.51	-44.97	-48.58	-0.74	-1.36	-2.76	-27.54	-35.88	-48.98
SE	0.54	0.72	0.05	0.65	0.29	0.42	0.84	0.91	0.14
Max.	58.05	48.69	18.14	5.35	4.07	3.96	34.05	27.45	9.85
CD @ 5%	4.34	2.34	5.65	7.23	8.23	9.12	7.23	6.48	2.32
CD@ 1%	5.24	3.43	6.34	8.19	9.49	10.12	8.84	8.39	3.29

* and ** significant at 5% and 1% level of significance, respectively, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob

Table 22 (c). Estimation of mid parent, better parent and standard heterosis studied for Numbers of kernel per rows, 100 grain weight (g) and Seed Yield per plant (g) in maize (*Zea mays* L.) under irrigated condition.

Hybrid	NKR			HGW			SYP		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	-3.09*	-3.31*	-3.31*	-9.5	-31.48**	-61.65**	-2.89**	-14.40**	-14.40**
IL1 × IL3	-0.3	-4.16**	-4.16**	-27.39**	-59.05**	-69.85**	13.34**	6.38	-16.63**
IL1 × IL4	6.26**	0.67	0.67	13.86*	-16.30*	-30.10**	38.64**	31.67	8.65
IL1 × IL5	3.73**	-1	-1	7.66	2.03	-72.10**	15.49**	7.14	-15.87
IL1 × IL6	-3.42**	-3.66*	-3.66*	-18.04**	-55.10**	-55.10**	-16.75**	-20.07	-43.08
IL1 × IL7	8.10**	3.02*	3.02*	43.64**	21.55**	-8.4	66.34**	59	35.99
IL1 × IL8	0.61	-4.26**	-4.26**	7.36	1.25	-60.65**	-3.84**	-8.04**	-31.05
IL1 × IL9	2.88*	-1.82	-1.82	-6.96	-40.60**	-47.45**	2.02*	-8.03**	-10.94
IL1 × IL10	4.59**	-0.54	-0.54	-6.14	-8.8	-77.60**	22.08**	21.37	-0.23
IL1 × IL11	0.82	-6.13**	-6.13**	31.59**	20.23**	-53.90**	19.76**	9.67**	-13.34**
IL1 × IL12	-1.55	-7.38**	-7.38**	-61.91**	-89.50**	-108.45**	4.33**	-2.92**	-25.93**
IL2 × IL3	-0.63	-4.26**	-4.70**	-8.36	-18.05**	-28.85**	2.48**	-15.98**	-15.98**
IL2 × IL4	1.03	-4.34**	-4.78**	-13.91*	-22.10**	-35.90**	-22.51**	-40.99**	-40.99**
IL2 × IL5	-0.05	-4.56**	-5.00**	-27.06	-54.68**	-84.85**	-21.47**	-41.32**	-41.32
IL2 × IL6	6.62**	6.60**	6.16**	-26.11	-41.20**	-41.20**	22.95**	8.12**	8.12
IL2 × IL7	6.34**	1.47	1.03	-61.79**	-61.90**	-91.85**	38.41**	19.57**	19.57**
IL2 × IL8	1.24	-3.40*	-3.84**	-21.66**	-37.53**	-67.70**	18.09**	2.38*	2.38*
IL2 × IL9	5.64**	1.16	0.72	23.01**	11.35	4.5	0.64	-0.81	-0.81
IL2 × IL10	2.96*	-1.95	-2.39	-51.46	-70.78**	-100.95**	-1	-11.79**	-11.79
IL2 × IL11	1.06	-5.66**	-6.10**	-19.89	-53.23**	-83.40**	-7.40**	-28.99**	-28.99**
IL2 × IL12	3.36**	-2.25	-2.69	-59.89	-65.50**	-84.45**	-10.41**	-29.16**	-29.16**
IL3 × IL4	1.73	0	-7.71**	-76.35**	-77.85**	-88.65**	7.73**	7.71**	-29.22
IL3 × IL5	6.31**	5.43**	-2.28	-31.63**	-68.93**	-79.73**	8.60**	7.21**	-29.72
IL3 × IL6	3.01*	-0.61	-1.08	-45.88**	-51.28**	-51.28**	16.97**	13.34**	-16.32**
IL3 × IL7	6.17**	4.95**	-2.76	49.63**	40.05**	29.25**	50.73**	50.36**	13.43**
IL3 × IL8	2	0.98	-6.73**	-19.83	-45.38**	-56.18**	20.35**	17.59**	-13.82
IL3 × IL9	8.52**	7.67**	-0.04	-11.43	-13.40*	-20.25**	9.67**	-7.34**	-10.25**
IL3 × IL10	9.43**	8.16**	0.45	-15.3	-44.30**	-55.10**	59.08**	51.42**	29.83**
IL3 × IL11	6.18**	3.08*	-4.62**	-16.63	-59.65**	-70.45**	53.57**	50.45**	13.52
IL3 × IL12	4.95**	2.97*	-4.74**	-53.65	-57.73**	-68.53**	5.05**	4.77**	-32.16**
IL4 × IL5	10.34**	9.48**	0.02	-25.40**	-61.20**	-75.00**	18.66**	17.29**	-19.68
IL4 × IL6	6.79**	1.44	0.96	-40.20**	-47.10**	-47.10**	51.45**	47.80**	18.14**
IL4 × IL7	3.66**	3.16*	-7.01**	-4.95	-13.03*	-26.83**	-1.29	-1.65	-38.62**
IL4 × IL8	11.03**	10.3	0.57	-16.63**	-40.68**	-54.48**	14.59**	11.81**	-19.60**
IL4 × IL9	11.76**	10.88**	1.47	-43.28**	-46.75**	-53.60**	10.05**	-6.97**	-9.88

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 22 (c). Contd.....

Hybrid	NKR			HGW			SYP		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	11.23**	10.77**	0.52	-21.55**	-49.05**	-62.85**	13.92**	6.23**	-15.36
IL4 × IL11	13.20**	11.85**	0.67	-4.83	-46.35**	-60.15**	52.97**	49.86**	12.9
IL4 × IL12	11.27**	11.03**	-0.15	-31.78**	-34.35**	-48.15**	35.02**	34.75**	-2.22*
IL5 × IL6	1.31	-3.18*	-3.66*	55.05**	12.35	12.35	17.26**	12.24**	-17.42
IL5 × IL7	2.24	1.89	-7.57**	17.23**	-10.5	-40.45**	0.74	-0.27	-37.95
IL5 × IL8	-0.97	-1.11	-10.57**	-36.45**	-48.20**	-110.10**	-0.59	-4.74**	-36.14
IL5 × IL9	5.18	5.15**	-4.26**	52.25**	12.98*	6.13	21.19**	2.79*	-0.11
IL5 × IL10	4.8	4.41**	-5.05**	21.30**	13.00*	-55.80**	33.69**	24.63**	3.04**
IL5 × IL11	12.47	10.25**	0.79	43.60**	37.88**	-47.53**	41.50**	39.76**	0.05
IL5 × IL12	11.61	10.51	1.05	9.8	-23.43**	-42.38**	45.14**	44.04**	6.54**
IL6 × IL7	2.27	-2.57	-3.05*	-23.43**	-38.40**	-38.40**	59.14**	55.13**	25.47**
IL6 × IL8	0.29	-4.34**	-4.82**	-13.30*	-44.25**	-44.25**	21.04**	20.17**	-9.50**
IL6 × IL9	-2.04	-6.51**	-6.98**	-5.77	-9.2	-9.2	-5.87**	-19.25**	-22.15**
IL6 × IL10	5.23**	0.34	-0.14	0.8	-33.60**	-33.60**	34.20**	30.16**	8.57
IL6 × IL11	6.39**	-0.32	-0.79	-8.78	-57.20**	-57.20**	18.45	11.69**	-17.97
IL6 × IL12	6.37**	0.78	0.3	-51.53**	-61.00**	-61.00**	50.28	46.36**	16.7
IL7 × IL8	11.58**	11.37**	1.63	-13.48*	-29.45**	-59.40**	58.88	55.74**	24.34
IL7 × IL9	6.59**	6.21**	-3.20*	12.03*	0.48	-6.38	19.4	2.01	-0.89
IL7 × IL10	9.36**	9.31**	-0.85	-25.98**	-45.40**	-75.35**	20.56	12.51**	-9.08**
IL7 × IL11	10.29**	8.43**	-1.74	60.25**	26.80**	-3.15	52.34	49.59**	11.91
IL7 × IL12	12.44	11.69	1.53	-21.60**	-27.10**	-46.05**	61.65**	61.56**	24.06**
IL8 × IL9	10.21	10.05**	0.64	0.2	-27.33**	-34.18**	13.28**	-0.97	-3.88**
IL8 × IL10	8.27	8.01	-1.72	70.33**	66.88**	4.97	12.02**	7.11	-14.48**
IL8 × IL11	13.4	11.32	1.59	77.80**	60.33**	-1.58	20.65**	14.76	-16.64**
IL8 × IL12	9.47**	8.50**	-1.23	-11.78*	-33.25**	-52.20**	33.07**	30.02	-1.39
IL9 × IL10	4.38**	3.96**	-5.45**	-30.48**	-61.45**	-68.30**	18.26**	8.92	6.01**
IL9 × IL11	14.99**	12.75	3.34*	8.32	-36.68**	-43.53**	1.95*	-18.19	-21.1
IL9 × IL12	7.57**	6.44**	-2.97*	-25.20**	-31.25**	-38.10**	8.33**	-8.97	-11.87
IL10 × IL11	11.12**	9.30**	-0.95	27.80**	13.78*	-55.03**	22.52**	11.72**	-9.87**
IL10 × IL12	8.9	8.19	-2.06	4.97	-19.95**	-38.90**	11.34**	3.38**	-18.21**
IL11 × IL12	13.75	12.64**	0.97	33.25**	-5.7	-24.65**	78.97**	76.13**	38.63**
Mean	5.78	3.17	-2.09	-7.2	-27.05	-48.67	20.83	13.11	-7.55
SE	0.36	0.56	0.39	0.32	0.48	0.29	0.94	0.39	0.31
Min.	-3.42	-7.38	-10.57	-76.35	-89.5	-110.1	-22.51	-41.32	-43.08
Max.	14.99	12.75	6.16	77.8	66.88	29.25	78.97	76.13	38.63
CD @ 5%	4.23	2.19	6.49	4.35	5.94	6.84	2.48	5.84	4.34
CD @ 1%	6.28	4.39	7.39	5.94	7.93	7.94	3.94	6.94	5.34

* and ** significant at 5% and 1% level of significance, respectively,

NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g)

Table 22 (d). Estimation of mid parent, better parent and standard heterosis studied for Number of cobs per plant, Days to maturity and Cob girth (cm) in maize (*Zea mays* L.) under irrigated condition.

Hybrid	NCP			DM			CG		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	6.25**	4.00**	-2.25*	-10	-35.00**	-80.00**	-8.78	-10.43	-10.43
IL1 × IL3	2.50**	-2.88**	-2.88**	-5	-10	-105.00**	0.61	-5.68	-5.68
IL1 × IL4	6.75**	5.00**	-2.25*	-10	-25.00**	-90.00**	9.41	-0.27	-0.27
IL1 × IL5	4.19**	-1	-1.38	40.00**	20.00**	-35.00**	-1.39	-8.18	-8.18
IL1 × IL6	4.25**	0	-2.25*	5	-5	-80.00**	-0.59	-5.52	-5.52
IL1 × IL7	4.56**	0.63	-2.25*	65.00**	30.00**	5	-11.69*	-15.88*	-15.88*
IL1 × IL8	3.00**	-0.63	-4.13**	25.00**	0	-45.00**	12.14*	5.23	5.23
IL1 × IL9	4.56**	0.63	-2.25*	32.50**	20.00**	-50.00**	45.54**	34.83**	34.83**
IL1 × IL10	8.75**	4.50**	2.25*	40.00**	20.00**	-35.00**	14.94**	4.43	4.43
IL1 × IL11	4.88**	2.50*	-3.50**	25.00**	-5	-40.00**	8.49	-0.48	-0.48
IL1 × IL12	8.50**	6.25**	0	27.50**	-20.00**	-20.00**	1.59	-0.17	-0.17
IL2 × IL3	6.13**	3.00**	3.00**	45.00**	15.00*	-30.00**	15.76**	11.13	7.83
IL2 × IL4	4.50**	4.00**	-2.25*	-25.00**	-35.00**	-80.00**	10.46	2.42	-0.88
IL2 × IL5	1.06	-1.88	-2.25*	10	5	-40.00**	-19.14**	-24.28**	-27.58**
IL2 × IL6	-0.63	-2.63*	-4.88**	20.00**	5	-40.00**	-16.69**	-19.98**	-23.28**
IL2 × IL7	1.06	-0.63	-3.50**	-15.00*	-25.00**	-50.00**	-0.99	-3.53	-6.83
IL2 × IL8	2.63**	1.25	-2.25*	-30.00**	-30.00**	-75.00**	3.14	-2.13	-5.43
IL2 × IL9	1.69	0	-2.88**	-17.50**	-30	-75.00**	16.29**	7.22	3.93
IL2 × IL10	5.00**	3.00**	0.75	-35.00**	-40.00**	-85.00**	-0.76	-9.63	-12.93*
IL2 × IL11	3.88**	3.75**	-2.25*	-30.00**	-35	-70.00**	-2.41	-9.73	-13.03*
IL2 × IL12	-1.5	-1.5	-7.75**	-12.50*	-35.00**	-35.00**	-6.01	-6.13	-9.43
IL3 × IL4	-1.38	-5.00**	-5.00**	10	-10	-75.00**	-10.4	-13.80*	-26.38**
IL3 × IL5	-0.56	-0.75	-0.75	55.00**	30	-25.00**	-10.43	-10.93	-23.50**
IL3 × IL6	-1.13	-2.25*	-2.25*	15.00*	0	-75.00**	-10.13	-11.48	-21.35**
IL3 × IL7	-3.06**	-4.50**	-4.50**	-30.00**	-70	-95	4.4	2.3	-6.08
IL3 × IL8	0	-1.75	-1.75	-5	-35.00**	-80	13.70*	13.08*	0.5
IL3 × IL9	0.69	-0.75	-0.75	-12.50*	-30.00**	-100	12.93*	8.5	-4.08
IL3 × IL10	-1.13	-2.25*	-2.25*	-15.00*	-40	-95.00**	19.53**	15.30*	2.73
IL3 × IL11	3.00**	0	0	-35.00**	-70	-105.00**	10.33	7.65	-4.93
IL3 × IL12	0.88	-2.25*	-2.25*	-27.50**	-80.00**	-80.00**	-12.25*	-16.78**	-20.30**
IL4 × IL5	2.44**	-1	-1.38	-25.00**	-30.00**	-85.00**	5.2	2.3	-11.28
IL4 × IL6	-3.50**	-6.00**	-8.25**	-20.00**	-25.00**	-90.00**	8.35	3.6	-6.28
IL4 × IL7	5.81**	3.63**	0.75	-45.00**	-65.00**	-90.00**	17.53**	12.03	3.65
IL4 × IL8	9.13**	7.25**	3.75**	-35.00**	-45.00**	-90.00**	16.70**	13.93*	0.1
IL4 × IL9	2.81**	0.63	-2.25*	-12.50*	-15.00*	-80.00**	21.23**	20.20**	0.83

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 22 (d). Contd.....

Hybrid	NCP			DM			CG		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	-1.5	-4.00**	-6.25**	-55.00**	-60.00**	-115.00**	8.93	8.1	-11.28
IL4 × IL11	3.13**	2.50*	-3.50**	-10	-25.00**	-60.00**	10.18	9.45	-8.48
IL4 × IL12	3.75**	3.25**	-3.00**	-22.50**	-55.00**	-55.00**	-2.72	-10.65	-14.18*
IL5 × IL6	-3.94**	-4.88**	-5.25**	-10	-20.00**	-75.00**	7.05	5.2	-4.68
IL5 × IL7	-4.63**	-5.88**	-6.25**	-30.00**	-45.00**	-70.00**	-16.35**	-18.95**	-27.33**
IL5 × IL8	-8.06**	-9.63**	-10.00**	5	0	-45.00**	-4.97	-5.1	-18.68**
IL5 × IL9	-7.13**	-8.38**	-8.75**	12.50*	5	-50.00**	33.80**	29.88**	16.30*
IL5 × IL10	-3.44**	-4.38**	-4.75**	-10	-10	-65.00**	43.88**	40.15**	26.58**
IL5 × IL11	-4.56**	-7.38**	-7.75**	5	-5	-40.00**	27.80**	25.63**	12.05
IL5 × IL12	-5.94**	-8.88**	-9.25**	-37.50**	-65.00**	-65.00**	10.4	5.37	1.85
IL6 × IL7	-3.69**	-4.00**	-6.25**	20.00**	-5	-30.00**	19.20**	18.45**	10.08
IL6 × IL8	-6.88**	-7.50**	-9.75**	0	-15.00*	-60.00**	64.33**	62.35**	52.48**
IL6 × IL9	0.31	0	-2.25*	12.50*	10	-60.00**	16.78**	11	1.12
IL6 × IL10	-3.75**	-3.75**	-6.00**	0	-10	-65.00**	18.03**	12.45	2.58
IL6 × IL11	-2.63**	-4.50**	-6.75**	-40.00**	-60.00**	-95.00**	12.88*	8.85	-1.03
IL6 × IL12	-0.5	-2.50*	-4.75**	2.5	-35.00**	-35.00**	-2.28	-5.45	-8.98
IL7 × IL8	5.94**	5.63**	2.75**	-10	-20.00**	-45.00**	17.53**	14.80*	6.43
IL7 × IL9	-6.88**	-6.88**	-9.75**	-27.50**	-50.00**	-75.00**	23.75**	17.23**	8.85
IL7 × IL10	-7.81**	-8.13**	-10.38**	-30.00**	-45.00**	-70.00**	-2.77	-9.1	-17.48**
IL7 × IL11	1.56	0	-2.88**	-25.00**	-30.00**	-55.00**	19.28**	14.50*	6.12
IL7 × IL12	2.31*	0.63	-2.25*	-82.50**	-95.00**	-95.00**	20.13**	17.70**	14.18*
IL8 × IL9	-4.56**	-4.88**	-7.75**	-47.50**	-60.00**	-105.00**	18.88**	15.08*	1.25
IL8 × IL10	-3.88**	-4.50**	-6.75**	-15.00*	-20.00**	-65.00**	11.83*	8.23	-5.6
IL8 × IL11	4.00**	2.75**	-0.75	-20.00**	-25.00**	-60.00**	28.88**	26.83**	13.00*
IL8 × IL12	1.5	0.13	-3.38**	-47.50**	-70.00**	-70.00**	14.45**	9.3	5.77
IL9 × IL10	0.31	0	-2.25*	-2.5	-10	-65.00**	19.65**	19.45**	-1.58
IL9 × IL11	2.19*	0.63	-2.25*	-12.50*	-30.00**	-65.00**	23.93**	22.18**	4.25
IL9 × IL12	-1.69	-3.38**	-6.25**	-10	-45.00**	-45.00**	12.80*	3.85	0.33
IL10 × IL11	-0.63	-2.50*	-4.75**	-20.00**	-30.00**	-65.00**	12.08*	10.53	-7.4
IL10 × IL12	-3.25**	-5.25**	-7.50**	-22.50**	-50.00**	-50.00**	15.10**	6.35	2.83
IL11 × IL12	-1.13	-1.25	-7.25**	-37.50**	-55.00**	-55.00**	14.95**	7.75	4.23
Mean	0.52	-1.28	-3.7	-9.17	-26.21	-65	9.91	5.61	-2.16
SE	0.93	0.37	0.62	0.82	0.19	0.32	0.83	0.9	0.24
Min.	-8.06	-9.63	-10.38	-82.5	-95	-115	-19.14	-24.28	-27.58
Max.	9.13	7.25	3.75	65	30	5	64.33	62.35	52.48
CD @ 5%	3.54	2.54	2.76	3.67	4.65	5.38	4.54	2.92	3.83
CD@ 1%	4.39	3.93	3.42	4.94	5.93	6.64	5.93	3.84	4.93

* and ** significant at 5% and 1% level of significance, respectively,

NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm),

Table 22 (e). Estimation of mid parent, better parent and standard heterosis studied for Shelling %, Canopy temperature and Turgid weight (g) in maize (*Zea mays* L.) under irrigated condition.

Hybrid	SP			CT			TW		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	-15.32**	-18.06**	-18.06**	-1.28	-1.43	-3.96**	-22.75**	-44.50**	-83.00**
IL1 × IL3	0.29	-2.34	-7.81**	-1.74	-1.91	-4.44**	-14.25**	-20.50**	-90.00**
IL1 × IL4	-2.69	-7.58**	-13.05**	-1.22	-1.51	-3.46**	-22.75**	-38.50**	-89.00**
IL1 × IL5	2.69	0.72	-4.75	0.49	0.03	-2.51*	-19.50**	-44.00**	-77.00**
IL1 × IL6	-9.44**	-9.97**	-15.44**	-0.59	-0.68	-3.21**	-35.25**	-60.50**	-92.00**
IL1 × IL7	9.90**	8.56**	3.09	0.04	-0.65	-1.81	38.50**	4.00**	-9.00**
IL1 × IL8	-17.03**	-18.17**	-23.64**	-1.31	-1.63	-4.16**	7.50**	-14.00**	-53.00**
IL1 × IL9	1.43	1.18	-3.79	-1.46	-1.95	-3.51**	-9.50**	-50.50**	-50.50**
IL1 × IL10	3.1	2.24	-1.52	-1.99*	-3.26**	-3.26**	-7.50**	-21.00**	-76.00**
IL1 × IL11	4.03	1.41	-4.06	-0.94	-1.08	-3.34**	-38.00**	-76.00**	-82.00**
IL1 × IL12	4.08	-0.2	-5.67*	-0.89	-1.85	-2.46*	-4.25**	-22.50**	-68.00**
IL2 × IL3	-1.42	-6.79**	-6.79**	1.74	1.73	-1.11	-41.50**	-57.00**	-95.50**
IL2 × IL4	-6.37**	-13.99**	-13.99**	0.73	0.29	-1.66	-29.50**	-35.50**	-74
IL2 × IL5	-5.88**	-10.59**	-10.59**	0.24	-0.07	-2.91**	-23.25**	-26.00**	-59
IL2 × IL6	-0.1	-3.37	-3.37	-1.24	-1.3	-4.01**	-39.00**	-42.50**	-74
IL2 × IL7	-6.75**	-10.83**	-10.83**	-2.61**	-3.45**	-4.61**	-17.75**	-30.50**	-43.5
IL2 × IL8	0.8	-3.07	-3.07	-1.31	-1.48	-4.31**	-15.75**	-16.00**	-54.5
IL2 × IL9	-12.37**	-14.85**	-14.85**	-4.36**	-5.00**	-6.56**	-37.25**	-56.50**	-56.5
IL2 × IL10	-4.59*	-6.47*	-6.47*	-2.07*	-3.49**	-3.49**	-18.75**	-27.00**	-65.5
IL2 × IL11	-3.84	-9.19**	-9.19**	-0.1	-0.39	-2.65*	-22.75**	-39.00**	-45
IL2 × IL12	0.85	-6.16*	-6.16*	-0.97	-2.08	-2.69*	0.5	-3.00**	-41.5
IL3 × IL4	-9.16**	-11.42**	-22.16**	-2.34*	-2.79*	-4.74**	-38.00**	-47.50**	-98.0*
IL3 × IL5	3.82	3.15	-6.25*	1.19	0.88	-1.98	24.75**	6.50**	-26.50**
IL3 × IL6	0.46	-1.65	-8.18**	0.81	0.73	-1.98	13.00**	-6.00**	-37.50**
IL3 × IL7	6.73**	5.44*	-2.71	0.97	0.12	-1.04	19.75**	-8.50**	-21.50**
IL3 × IL8	9.53**	8.03**	0.28	3.34**	3.19**	0.32	-24.75**	-40.00**	-79.00**
IL3 × IL9	3.6	0.71	-4.26	1.03	0.38	-1.18	-43.25**	-78.00**	-78.00**
IL3 × IL10	6.05**	2.56	-1.2	-0.53	-1.96	-1.96	-10.75**	-18.00**	-73.00**
IL3 × IL11	-0.85	-0.87	-11.57**	0.3	0	-2.26*	-29.25**	-61.00**	-67.00**
IL3 × IL12	1.35	-0.3	-11.03**	-3.10**	-4.23**	-4.84**	31.00**	19.00**	-26.50**
IL4 × IL5	5.06*	2.13	-7.27**	0.25	-0.51	-2.46*	18.75**	10.00**	-23.00**
IL4 × IL6	0.72	-3.65	-10.18**	0.19	-0.19	-2.14	-32.00**	-41.50**	-73.00**
IL4 × IL7	1.7	-1.85	-10.00**	-0.57	-0.97	-2.13	-5.25**	-24.00**	-37.00**
IL4 × IL8	3.47	-0.28	-8.03**	0.28	-0.32	-2.28*	44.75**	39.00**	12.44
IL4 × IL9	-11.01**	-16.15**	-21.12**	0.25	0.05	-1.51	-6.75**	-32.00**	-32.00**

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 22 (e). Contd.....

Hybrid	SP			CT			TW		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	2.88	-2.86	-6.63*	-1.04	-2.01	-2.01	-0.25	-2.50**	-53.00**
IL4 × IL11	11.17**	8.89**	-1.81	-2.01*	-2.16*	-4.11**	-36.25**	-58.50**	-64.50**
IL4 × IL12	-1.13	-1.74	-15.76**	-3.16**	-3.83**	-4.44**	-5.50**	-8.00**	-53.50**
IL5 × IL6	3.39	1.95	-4.58	2.78**	2.40*	-0.31	-41.25**	-42.00**	-73.50**
IL5 × IL7	-19.96**	-20.59**	-28.74**	-1.65	-2.80*	-3.96**	-23.00**	-33.00**	-46.00**
IL5 × IL8	-2.91	-3.73	-11.48**	2.15*	2	-1.16	-19.00**	-22.00**	-55.00**
IL5 × IL9	-7.12**	-9.33**	-14.30**	-1.23	-2.18*	-3.74**	-46.00**	-62.50**	-62.50**
IL5 × IL10	3.31	0.49	-3.28	-1.68	-3.41**	-3.41**	-7.00**	-18.00**	-51.00**
IL5 × IL11	5.83**	5.18*	-4.22	-1.28	-1.88	-4.14**	-27.00**	-40.50**	-46.50**
IL5 × IL12	10.32**	8.01**	-1.39	0.91	-0.52	-1.13	32.75**	26.50**	-6.50**
IL6 × IL7	-2.02	-2.84	-9.36**	-1.76	-2.53*	-3.69**	-45.75**	-55.00**	-68.00**
IL6 × IL8	1.74	1.13	-5.40*	0.23	0	-2.71*	-28.75**	-32.50**	-64.00**
IL6 × IL9	-2.4	-3.18	-8.15**	-0.05	-0.63	-2.19*	-18.75**	-34.50**	-34.50**
IL6 × IL10	2.19	0.81	-2.95	-1.71	-3.06**	-3.06**	-18.75**	-30.50**	-62.00**
IL6 × IL11	-11.34**	-13.43**	-19.95**	-2.13*	-2.35*	-4.61**	-55.25**	-68.00**	-74.00**
IL6 × IL12	-1.39	-5.14*	-11.67**	-2.63**	-3.68**	-4.29**	-12.50**	-19.50**	-51.00**
IL7 × IL8	6.91**	6.71**	-1.04	-2.55**	-3.55**	-4.71**	-4.00**	-17.00**	-30.00**
IL7 × IL9	2.37	0.78	-4.19	-2.62**	-2.82*	-3.98**	-30.00**	-36.50**	-36.50**
IL7 × IL10	-9.74**	-11.94**	-15.70**	-3.07**	-3.65**	-3.65**	-21.50**	-42.50**	-55.50**
IL7 × IL11	8.52**	7.25**	-0.91	-3.46**	-4.01**	-5.17**	-27.50**	-31.00**	-37.00**
IL7 × IL12	9.83**	6.89**	-1.26	-1.96*	-2.23*	-2.84*	-30.25**	-46.50**	-59.50**
IL8 × IL9	4.06	2.67	-2.3	1.69	0.89	-0.68	-40.00**	-59.50**	-59.50**
IL8 × IL10	-1.69	-3.68	-7.44**	-3.20**	-4.78**	-4.78**	-10.50**	-18.50**	-57.50**
IL8 × IL11	5.86**	4.38	-3.37	0.64	0.18	-2.08	-58.50**	-75.00**	-81.00**
IL8 × IL12	6.35**	3.21	-4.54	-1.97*	-3.24**	-3.85**	8.75**	5.50**	-33.50**
IL9 × IL10	-8.75**	-9.36**	-13.12**	-1.78	-2.56*	-2.56*	11.00**	-16.50**	-16.50**
IL9 × IL11	3.86	1	-3.97	1.49	1.14	-0.43	-50.50**	-53.50**	-53.50**
IL9 × IL12	3.21	-1.32	-6.29*	0.99	0.52	-0.09	-32.75**	-55.50**	-55.50**
IL10 × IL11	4.31	0.84	-2.92	-1.51	-2.64*	-2.64*	-26.50**	-51.00**	-57.00**
IL10 × IL12	3.46	-1.67	-5.43*	-2.71**	-3.01**	-3.01**	21.75**	17.00**	-28.50**
IL11 × IL12	13.14**	11.49**	0.78	-2.68**	-3.50**	-4.11**	-54.75**	-74.50**	-80.50**
Mean	0.11	-2.44	-7.96	-0.84	-1.46	-2.94	-16.79	-31.19	-55.23
SE	0.76	0.43	0.94	0.26	0.95	0.38	0.27	0.27	0.85
Min.	-19.96	-20.59	-28.74	-4.36	-5	-6.56	-58.5	-78	-98
Max.	13.14	11.49	3.09	3.34	3.19	0.32	44.75	39	12.44
CD @ 5%	2.43	4.54	7.39	4.93	3.94	2.92	1.93	4.12	2.23
CD @ 1%	3.45	5.94	8.84	5.93	4.93	3.92	2.93	5.93	3.92

* and ** significant at 5% and 1% level of significance, respectively,

SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g)

Table 22 (f). Estimation of mid parent, better parent and standard heterosis studied for Relative water content, Saturation water deficit and Membrane stability index in maize (*Zea mays* L.) under irrigated condition.

Hybrid	RWC			SWD			MSI		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	2.19**	-2.40**	-8.84**	-2.19**	-6.77**	-24.99**	102.25**	84.93**	-156.80**
IL1 × IL3	-3.20**	-11.01**	-11.01**	3.20**	-4.61**	-22.83**	-15.79**	-131.80**	-176.15**
IL1 × IL4	8.43**	7.71**	-6.47**	-8.43**	-9.15**	-27.36**	356.34**	333.83**	57.45**
IL1 × IL5	1.63*	-3.68**	-8.67**	-1.63*	-6.95**	-25.16**	163.98**	92.58**	-41.00**
IL1 × IL6	-4.94**	-8.42**	-17.08**	4.94**	1.47	-16.75**	109.31**	73.38**	-203.00**
IL1 × IL7	2.35**	0.13	-11.04**	-2.35**	-4.58**	-22.80**	156.56**	66.00**	-29.25**
IL1 × IL8	-6.47**	-8.32**	-20.23**	6.47**	4.62**	-13.60**	-31.78**	-149.48**	-190.45**
IL1 × IL9	-1.78*	-3.93**	-15.25**	1.78*	-0.37	-18.58**	220.34**	82.15**	82.15**
IL1 × IL10	5.36**	3.09**	-7.97**	-5.37**	-7.64**	-25.86**	132.68**	109.30**	-120.33**
IL1 × IL11	19.31**	10.20**	-5.41**	-19.31**	-28.42**	-28.42**	45.65**	17.60**	-202.68**
IL1 × IL12	-3.10**	-7.30**	-14.50**	3.10**	-1.11	-19.33**	24.68**	-5.63	-221.40**
IL2 × IL3	8.71**	5.48**	5.48**	-8.71**	-11.93**	-39.32**	204.66**	105.98**	61.63**
IL2 × IL4	-10.11**	-13.98**	-20.42**	10.11**	6.25**	-13.41**	187.49**	147.65**	-94.07**
IL2 × IL5	-2.75**	-3.48**	-8.47**	2.75**	2.02*	-25.37**	121.50**	67.43**	-66.15**
IL2 × IL6	-7.31**	-8.42**	-14.87**	7.31**	6.21**	-18.97**	301.19**	247.93**	6.2
IL2 × IL7	-4.24**	-6.60**	-13.05**	4.24**	1.89*	-20.79**	-80.64**	-153.88**	-249.13**
IL2 × IL8	-5.74**	-8.47**	-14.92**	5.74**	3.00**	-18.91**	45.83**	-54.55**	-95.52**
IL2 × IL9	0.48	-1.95*	-8.40**	-0.48	-2.92**	-25.43**	38.24**	-82.62**	-82.62**
IL2 × IL10	7.22**	4.91**	-1.54	-7.22**	-9.52**	-32.30**	155.98**	149.93**	-79.70**
IL2 × IL11	9.06**	-4.64**	-11.09**	-9.06**	-22.75**	-22.75**	243.13**	232.40**	12.13*
IL2 × IL12	7.50**	7.12**	0.67	-7.50**	-7.88**	-34.51**	27.95**	14.98**	-200.80**
IL3 × IL4	-15.89**	-22.98**	-22.98**	15.89**	8.81**	-10.85**	145.95**	7.42	-36.93**
IL3 × IL5	-1.4	-3.90**	-3.90**	1.4	-1.09	-29.94**	44.01**	-0.6	-44.95**
IL3 × IL6	-7.21**	-11.55**	-11.55**	7.21**	2.88**	-22.29**	321.35**	169.40**	125.05**
IL3 × IL7	-8.69**	-14.27**	-14.27**	8.69**	3.11**	-19.56**	-158.20**	-183.65**	-228.00**
IL3 × IL8	-8.76**	-14.72**	-14.72**	8.89**	2.93**	-18.99**	92.79**	91.10**	50.13**
IL3 × IL9	-8.66**	-14.33**	-14.33**	8.66**	3.00**	-19.51**	-165.78**	-187.95**	-187.95**
IL3 × IL10	-11.74**	-17.27**	-17.27**	11.74**	6.21**	-16.56**	143.89**	51.25**	6.9
IL3 × IL11	3.79**	-13.13**	-13.13**	-3.79**	-20.71**	-20.71**	290.49**	202.53**	158.18**
IL3 × IL12	-8.75**	-12.35**	-12.35**	8.75**	5.15**	-21.48**	-13.91**	-99.63**	-143.98**
IL4 × IL5	4.29**	-0.31	-5.30**	-4.29**	-8.88**	-28.54**	176.29**	82.38**	-51.20**
IL4 × IL6	-6.50**	-9.25**	-17.92**	6.50**	3.74**	-15.92**	43.43**	30.00**	-291.40**
IL4 × IL7	1.96*	0.45	-10.71**	-1.96*	-3.47**	-23.12**	10.53*	-102.55**	-197.80**
IL4 × IL8	-5.04**	-6.16**	-18.08**	5.04**	3.91**	-15.75**	31.69**	-108.53**	-149.50**
IL4 × IL9	-4.47**	-5.90**	-17.23**	4.47**	3.05**	-16.61**	-149.38**	-310.08**	-310.08**

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 22 (f). Contd.....

Hybrid	RWC			SWD			MSI		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	2.12**	0.56	-10.50**	-2.12**	-3.68**	-23.34**	225.54**	179.65**	-49.98**
IL4 × IL11	2.77**	-7.05**	-21.23**	-2.77**	-12.60**	-12.60**	124.84**	74.28**	-146.00**
IL4 × IL12	-5.67**	-9.15**	-16.36**	5.67**	2.18*	-17.48**	72.49**	19.68**	-196.10**
IL5 × IL6	-0.73	-2.57**	-7.56**	0.73	-1.1	-26.27**	-13.31**	-120.65**	-254.23**
IL5 × IL7	-3.35**	-6.44**	-11.43**	3.35**	0.26	-22.41**	49.74**	30.58**	-64.67**
IL5 × IL8	-5.82**	-9.29**	-14.27**	5.82**	2.36**	-19.56**	-155.08**	-201.38**	-242.35**
IL5 × IL9	-7.07**	-10.24**	-15.23**	7.07**	3.90**	-18.61**	-217.66**	-284.45**	-284.45**
IL5 × IL10	-4.51**	-7.54**	-12.53**	4.51**	1.47	-21.30**	-95.90**	-143.93**	-277.50**
IL5 × IL11	5.57**	-8.85**	-13.84**	-5.57**	-19.99**	-19.99**	-149.83**	-193.18**	-326.75**
IL5 × IL12	-1.01	-2.12*	-7.11**	1.01	-0.09	-26.73**	-89.68**	-130.78**	-264.35**
IL6 × IL7	-1.61*	-2.86**	-11.53**	1.61*	0.36	-22.31**	-124.78**	-251.28**	-346.53**
IL6 × IL8	7.35**	5.73**	-2.94**	-7.35**	-8.98**	-30.90**	41.59**	-112.05**	-153.03**
IL6 × IL9	0.17	-1.16	-9.82**	-0.17	-1.5	-24.01**	69.63**	-104.50**	-104.50**
IL6 × IL10	-8.96**	-10.16**	-18.82**	8.96**	7.76**	-15.01**	38.86**	-20.45**	-250.08**
IL6 × IL11	12.58**	0	-8.67**	-12.58**	-25.17**	-25.17**	-63.21**	-127.20**	-347.48**
IL6 × IL12	-4.66**	-5.39**	-12.59**	4.66**	3.93**	-21.24**	-54.64**	-120.88**	-336.65**
IL7 × IL8	-5.95**	-6.33**	-17.49**	5.95**	5.58**	-16.34**	-253.06**	-280.20**	-321.18**
IL7 × IL9	-8.24**	-8.32**	-19.48**	8.24**	8.16**	-14.35**	-258.83**	-306.45**	-306.45**
IL7 × IL10	7.50**	7.45**	-3.61**	-7.50**	-7.55**	-30.22**	-119.26**	-186.45**	-281.70**
IL7 × IL11	9.97**	-1.36	-12.53**	-9.97**	-21.31**	-21.31**	-4.31	-66.83**	-162.08**
IL7 × IL12	10.53**	8.55**	1.35	-10.53**	-12.51**	-35.18**	-182.56**	-242.83**	-338.08**
IL8 × IL9	0.66	0.37	-10.96**	-0.66	-0.96	-22.88**	-217.31**	-237.80**	-237.80**
IL8 × IL10	8.27**	7.84**	-3.22**	-8.27**	-8.70**	-30.61**	-63.68**	-158.00**	-198.98**
IL8 × IL11	18.45**	7.49**	-4.43**	-18.45**	-29.41**	-29.41**	-12.23*	-101.88**	-142.85**
IL8 × IL12	3.59**	1.23	-5.97**	-3.59**	-5.95**	-27.87**	-87.08**	-174.48**	-215.45**
IL9 × IL10	9.49**	9.36**	-1.71	-9.49**	-9.62**	-32.13**	-173.71**	-288.53**	-288.53**
IL9 × IL11	17.53**	6.28**	-5.05**	-17.53**	-28.79**	-28.79**	-276.56**	-386.70**	-386.70**
IL9 × IL12	9.39**	7.33**	0.13	-9.39**	-11.45**	-33.96**	-251.36**	-359.25**	-359.25**
IL10 × IL11	19.64**	8.25**	-2.81**	-19.64**	-31.02**	-31.02**	-49.83**	-54.50**	-274.78**
IL10 × IL12	5.68**	3.75**	-3.45**	-5.68**	-7.61**	-30.38**	-88.08**	-95.00**	-310.78**
IL11 × IL12	15.82**	2.50**	-4.70**	-15.82**	-29.13**	-29.13**	-68.48**	-70.73**	-286.50**
Mean	0.83	-3.36	-10.53	-0.83	-5.03	-23.3	13.26	-54.95	-167.38
SE	0.87	0.37	0.56	0.24	0.98	0.54	0.87	0.18	0.35
Min.	-15.89	-22.98	-22.98	-19.64	-31.02	-39.32	-276.56	-386.7	-386.7
Max.	19.64	10.2	5.48	15.89	8.81	-10.85	356.34	333.83	158.18
CD @ 5%	5.12	4.25	3.23	6.45	4.43	5.82	3.66	5.43	4.23
CD @ 1%	6.43	5.23	4.65	7.65	5.76	6.28	4.51	6.76	5.22

* and ** significant at 5% and 1% level of significance, respectively,

RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

Table 23 (a). Estimation of mid parent, better parent and standard heterosis studied for Days to 50 % tasseling, Days to 50 % silking and Anthesis silking interval in maize (*Zea mays* L.) under partial irrigated condition.

Hybrid	DFT			DFS			ASI		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	-61.23**	-93.73	-103.34**	-6.86	-10.98	-10.98	-18.73	-28.65	-28.45
IL1 × IL3	-51.23**	-13.73**	-13.26	-4.73	-16.48	-16.44	-7.48	-13.74	-13.76
IL1 × IL4	-83.73**	-18.73	-18.65	-9.86	-19.48	-19.32	-26.23	-28.7	-28.12
IL1 × IL5	-126.23	-13.73	-13.61	-11.98	-16.98	-16.65	-4.98	-18.73	-18.16
IL1 × IL6	-13.73	-93.73	-13.73	-1.36	-10.48	-10.11	-11.23	-23.73	-23.71
IL1 × IL7	-18.33	-19.73**	-23.43**	-15.36**	-19.98	-19.65	-7.48	-18.73	-18.73
IL1 × IL8	-13.71	-93.73	-103.43	-2.61**	-10.98**	-10.98	-23.73	-28.73	-28.73
IL1 × IL9	-83.65**	-13.73**	-173.63	-7.73**	-16.23	-16.12	-4.98	-11.23	-11.22
IL1 × IL10	-136.49**	-18.73**	-168.51	-13.73	-16.48	-16.48	-9.98	-16.23	-16.23
IL1 × IL11	-13.73**	-18.73	-158.51	-15.86	-17.98	-17.98	-23.73	-31.23	-31.29**
IL1 × IL12	-98.73**	-13.73	-103.62	-10.73*	-10.73	-10.73	-19.98	-26.23	-26.23**
IL2 × IL3	-58.73**	-18.73	-21.65**	-5.11	-12.75	-20.98	-2.48	-6.23	-18.7
IL2 × IL4	-86.23	-18.73	-23.53	-6.73	-12.23	-20.48	8.77	1.27	-3.73
IL2 × IL5	-3.73	-8.73	-83.85	-0.61**	-1.48**	-9.73	-12.48**	-16.23	-36.22
IL2 × IL6	-91.23	-18.73**	-13.73	-8.23**	-13.23	-21.48	-1.23**	-3.73	-23.73
IL2 × IL7	-11.23	-13.33	-28.77	-11.73**	-12.23	-20.48	2.52	1.27	-18.73
IL2 × IL8	-6.23	-13.73	-18.39**	-6.23**	-10.48**	-18.73	3.77	-1.23	-11.23
IL2 × IL9	-66.23	-13.73*	-18.28	-5.61**	-9.98**	-18.23	0.02	-3.73	-16.23
IL2 × IL10	-18.73*	-18.73	-13.39	-12.86	-14.23	-19.73	-17.48	-21.23	-33.71
IL2 × IL11	-11.23*	-18.73	-168.92	-12.73	-14.73	-18.98	-26.23	-28.73*	-43.72
IL2 × IL12	-21.23	-58.73	-58.83	-2.11	-6.23	-6.23	-9.98	-13.73	-26.11
IL3 × IL4	23.77	6.27	-3.83	1.65	-0.48	-19.73	-17.48	-21.23	-26.23
IL3 × IL5	-8.73	-83.73	-18.84**	-0.73	-7.48	-17.48	-8.73**	-16.23	-28.73
IL3 × IL6	48.77**	16.27**	-13.73**	5.4**	2.77	-15.48	-4.98**	-11.23	-23.73
IL3 × IL7	23.77	-53.73	-133.73	2.65	-4.48	-13.73	-8.73	-13.73	-26.23
IL3 × IL8	-6.23**	-38.73	-28.73	0.64	-2.73	-19.48	2.52	1.27	-8.73**
IL3 × IL9	-26.23	-58.73	-228.73	-2.48*	-5.73*	-22.73	-8.73	-8.73	-21.23
IL3 × IL10	6.27	-83.73	-18.73	1.52	-7.48	-12.98	-1.23	-1.23	-13.73
IL3 × IL11	-71.23	-168.73	-208.73**	-7.11	-16.73	-20.98	-9.98	-11.23	-23.77
IL3 × IL12	53.77	-63.73**	-63.73**	4.77	-6.98	-6.98	-16.23**	-16.23	-28.7
IL4 × IL5	73.77	16.27	-68.73**	8.4	3.77	-6.23	0.02	-11.23	-16.23
IL4 × IL6	81.27	66.27**	-103.73	7.77**	7.27	-10.98	-13.73	-23.73	-28.73
IL4 × IL7	-58.73	-11.73*	-198.73	-4.73	-9.73	-18.98	0.02	-8.73	-13.73
IL4 × IL8	-23.73	-38.73**	-28.7	-3.73**	-4.98	-21.73**	-18.73	-21.23	-26.23
IL4 × IL9	-5.73	-8.73	-8.73**	-4.61**	-5.73	-22.73	-2.48	-6.23	-11.23

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 23 (a). Contd.....

Hybrid	DFT			DFS			ASI		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	-106.23	-18.73	-23.73	-11.11**	-17.98	-23.48	-14.98**	-18.73	-23.73**
IL4 × IL11	-83.73	-13.73**	-23.73	-7.48**	-14.98	-19.23	-1.23	-6.23	-11.23
IL4 × IL12	-68.73**	-18.73*	-16.73**	-7.36**	-16.98	-16.98**	-14.98	-18.73	-23.83
IL5 × IL6	-61.23**	-13.73	-18.73**	-5.86**	-9.98	-19.98	-7.48	-8.73	-33.73
IL5 × IL7	33.77**	31.27	-48.73**	3.4**	3.02	-6.23**	-11.23	-13.73	-36.23
IL5 × IL8	93.77	51.27	-33.73**	9.9**	6.52	-3.48**	-4.98**	-13.73	-23.73
IL5 × IL9	63.77**	21.27	-63.73**	7.77**	4.27**	-5.73	3.77	-3.73	-16.27
IL5 × IL10	-143.73	-18.73**	-213.73**	-11.98	-14.23	-19.73	13.77	6.27	-6.23
IL5 × IL11	-156.23	-18.73	-28.73	-12.86	-15.73	-19.98	17.52	11.27	-3.73
IL5 × IL12	-11.23	-53.73	-53.73	-0.48	-5.48	-5.48**	-3.73	-11.23	-23.79
IL6 × IL7	-12.56**	-13.73	-13.75	-4.98**	-9.48	-18.73	-2.48	-3.73	-26.23
IL6 × IL8	-43.73	-43.73	-23.73	-1.98	-2.73	-19.48	13.77	6.27	-3.73
IL6 × IL9	-18.73	-18.73	-18.73	0.39	-0.23	-17.23	12.52	6.27	-6.23
IL6 × IL10	-76.23	-13.73	-18.73**	-6.61	-12.98	-18.48	0.02	-6.23	-18.73
IL6 × IL11	-13.73	-18.73	-28.73	-10.23	-17.23	-21.48	-8.73	-13.73	-28.73
IL6 × IL12	-98.73	-13.73	-13.73**	-8.36**	-17.48	-17.48	5.02	-1.23	-13.73**
IL7 × IL8	-63.73	-108.73	-188.73**	-4.98**	-8.73	-17.98	2.52	-3.73	-13.76
IL7 × IL9	91.27	46.27	-33.73**	9.9**	6.02	-3.23	-3.73	-8.73	-21.23
IL7 × IL10	-101.23	-11.73	-168.73	-10.61**	-12.48	-17.98	-16.23	-21.23	-33.77
IL7 × IL11	-143	-163.73	-23.73	-13.23	-15.73	-19.98	0.02	-3.73	-18.76
IL7 × IL12	-28.73**	-68.73	-68.73	-2.36**	-6.98	-6.98	-6.23	-11.23	-23.79
IL8 × IL9	91.27**	91.27**	-78.73	8.4**	8.27	-8.48	-17.48**	-18.73	-28.73
IL8 × IL10	3.77**	-53.73	-18.79	1.4**	-4.23	-9.73	0.02	-1.23	-11.23
IL8 × IL11	-93.73	-18.73	-18.73	-8.73**	-14.98**	-19.23	-3.73	-6.23	-16.23
IL8 × IL12	-118.73	-23.73	-23.73	-11.36	-19.73	-19.73	-4.98	-6.23	-16.23
IL9 × IL10	-86.23	-13.73**	-18.73	-8.23	-13.98	-19.48	-6.23	-6.23	-18.73
IL9 × IL11	-78.73	-14.73	-18.73**	-8.61	-14.98	-19.23	-14.98**	-16.23	-28.73**
IL9 × IL12	-13.73	-98.73	-98.73	-0.48**	-8.98	-8.98	-1.23	-1.23	-13.93**
IL10 × IL11	-176.23	-13.73	-223.73	-16.11	-16.73	-20.98	5.02	3.77	-8.83
IL10 × IL12	-191.23	-28.73	-28.3**	-19.23	-21.98	-21.98	-11.23**	-11.23	-23.73
IL11 × IL12	-193.73	-13.73**	-12.73**	-18.86	-20.98	-20.98	-4.98	-6.23**	-18.73
Mean	-41.99	-27.1	-62.69	-5.06	-9.71	-16.04	-6.19	-10.85	-20.76
SE	0.34	0.56	0.76	0.16	0.42	0.79	0.17	0.45	0.31
Min.	-193.73	-168.73	-228.73	-19.23	-21.98	-23.48	-26.23	-31.23	-43.72
Max.	93.77	91.27	-3.83	9.9	8.27	-3.23	17.52	11.27	-3.73
CD @ 5%	3.65	5.43	8.65	4.65	2.45	3.78	6.71	2.32	5.34
CD @ 1%	4.65	6.23	8.86	5.71	3.29	4.46	7.63	3.76	6.28

* and ** significant at 5% and 1% level of significance, respectively,

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval

Table 23 (b). Estimation of mid parent, better parent and standard heterosis studied for Plant height (cm), Cob length (cm) and Number of kernel rows per cob in maize (*Zea mays* L.) under partial irrigated condition.

Hybrid	PH			CL			NKRC		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	32.39	4.48**	-13.16**	4.78**	4.58**	2.15**	-18.72**	-30.27	-31.84
IL1 × IL3	16.73**	-17.88**	-22.12**	2.96**	2.94**	0.51	4.2**	-2.57	-27.24
IL1 × IL4	38.4**	16.92**	-13.57**	4.55**	3.34**	3.34	25.82**	13.59**	-11.09
IL1 × IL5	28.42	-5.7**	-10.92**	2.34	2.19**	0.06	12.77**	7.44**	-17.24
IL1 × IL6	25.37	-0.12**	-22.58**	3.18	2.6	1.33	2.22**	-2.12**	-26.79
IL1 × IL7	39.14**	2.41**	2.41**	0.62	0.21**	-1.4**	23.8**	20.51**	2.41**
IL1 × IL8	31.47	13.54**	-24.05**	4.08**	3.58**	2.15	9.22**	5.76	-11.99
IL1 × IL9	46.82	42.74**	-30.72**	1.39	0.23**	0.12	7.42**	4.98	-19.69
IL1 × IL10	59.41	50.05**	-4.68**	2.21**	2**	4.87**	18.27**	17.01	-5.14
IL1 × IL11	46.86	25.25**	-4.99**	2.23	2.07	-0.04**	5.1**	-7.24	-7.24
IL1 × IL12	33.05	11.11**	-18.47**	1.27**	0.31	-0.2**	-7.1**	-11.14	-27.74
IL2 × IL3	14.51	7.8**	3.57**	3.3	3.29	0.72**	8.8**	-9.52	-11.09**
IL2 × IL4	-23.15	-29.58**	-47.22**	1.8	0.5**	0.5**	-10.73**	-34.52	-36.09**
IL2 × IL5	6.68**	0.47**	-4.75**	2.35	2.07**	-0.05**	10.82**	-6.07	-7.64**
IL2 × IL6	17.72	15.31	-2.33**	2.92**	2.22	0.95	1.22**	-14.67	-16.24**
IL2 × IL7	21.77	12.95	12.95**	5.67**	5.14**	3.53	-1.75**	-10.02	-11.59**
IL2 × IL8	6.05**	-3.93**	-21.57**	3.3	2.68**	1.25**	-26.18**	-34.27	-35.84**
IL2 × IL9	12.24**	-19.75**	-37.39**	6.71*	5.43	5.32	5.97	-8.02**	-9.59**
IL2 × IL10	26.03**	7.49**	-10.15**	3.56	3.22	1.23**	-1.23	-11.52	-13.09**
IL2 × IL11	20.02**	13.72**	-3.92**	3.07	2.79	0.68**	-8**	-8.79**	-8.79**
IL2 × IL12	28.38**	22.42**	4.78**	1.47**	0.39	-0.12**	5.15**	-2.37**	-3.94**
IL3 × IL4	16.16**	3.03**	-1.2**	3.83**	2.59	2.59**	12.69**	7.21**	-30.99**
IL3 × IL5	-7.37**	-7.86**	-12.1**	1.59**	1.42	-0.76**	3.71**	2.28**	-33.07**
IL3 × IL6	-7.9**	-17.01**	-21.25**	3.31**	2.71	1.44	7.66**	5.23**	-28.12**
IL3 × IL7	-18.71**	-20.82	-20.82	3.17	2.74**	1.13	4.21**	-5.84	-23.94**
IL3 × IL8	12.56**	-4.12	-8.36	0.76	0.24	-1.19	18.91**	8.68	-9.07**
IL3 × IL9	26.58**	-12.12	-16.35	2.11**	0.93	0.82**	19.29**	14.96	-14.59**
IL3 × IL10	13.29**	-11.96**	-16.19	3.24**	3.00**	1**	17.39**	9.36**	-12.79**
IL3 × IL11	1.24**	-11.77	-16.51**	4.53**	4.35	2.24**	3.26**	-15.84	-15.84
IL3 × IL12	7.21**	-5.46**	-9.69**	3.98**	2.02	1.51	-20.22**	-31.02**	-47.62
IL4 × IL5	11.33**	-1.30**	-6.53**	1.64	0.58	0.58	30.36**	23.46**	-11.89
IL4 × IL6	7.01**	2.99	-19.47**	2.6**	1.97**	1.97**	21.51**	13.61	-19.74
IL4 × IL7	34.75**	19.5**	19.5**	0.8**	0**	0**	6.41**	-9.12**	-27.22
IL4 × IL8	37.98**	34.43	3.93**	1.25**	0.53**	0.53**	7.93**	-7.77	-25.52
IL4 × IL9	29.1**	3.54**	-26.96	2.89**	2.84**	2.84	29.76**	19.96**	-9.59

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 23 (b). Contd.....

Hybrid	PH			CL			NKRC		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	28.21**	16.1**	-14.4**	2.26**	1.26	1.26	12.26**	-1.24**	-23.39
IL4 × IL11	21.13**	21.54**	-9.24	1.68	0.62	0.62	-1.22**	-25.79	-25.79
IL4 × IL12	21.81**	21.35	-8.23**	3.8**	3.55	3.55	22.49**	6.21**	-10.39
IL5 × IL6	-17.99**	-26.61	-31.84	0.98**	0.56	-0.71	2.61**	1.61	-31.74
IL5 × IL7	-8.53**	-11.14	-11.14	5.29	5.04	3.43	-7.22**	-15.84**	-33.94
IL5 × IL8	-15.37**	-31.56	-36.78**	1.51	1.16	-0.27	-9.19**	-17.99	-35.74**
IL5 × IL9	21.98**	-16.21	-21.44**	3.28	2.27	2.16	0.69**	-2.21	-31.77
IL5 × IL10	9.41**	-15.34	-20.57**	3.43	3.37	1.37	35.41**	28.81	6.66
IL5 × IL11	24.22**	11.71**	6.49**	3.73	3.72	1.61	16.46**	-1.21	-1.21
IL5 × IL12	-5.86**	-18.03	-23.26**	2.03	1.23**	0.72	16.66**	7.28	-9.32
IL6 × IL7	17.65**	6.42	6.42**	3.57	3.4**	2.13	14.99**	7.36	-10.74
IL6 × IL8	1.56**	-6.01	-28.47**	1.85	1.77**	0.5	18.81**	11.01**	-6.74
IL6 × IL9	26.01**	-3.57	-26.02	1.82	1.24**	1.13	28.66**	26.76	-2.79
IL6 × IL10	28.3**	12.16	-10.3**	3.37	3.01**	1.74	-2.89**	-8.49**	-30.64
IL6 × IL11	25.32**	21.43**	-1.03**	5.01	4.6**	3.33	-16.42**	-33.09	-33.09
IL6 × IL12	27.9**	24.34**	1.89**	3.66	3.28**	2.77**	28.44**	20.06	3.46
IL7 × IL8	25.92	7.12**	7.12**	2.87**	2.78**	1.35	28.59**	28.41	10.66
IL7 × IL9	-2.8**	-43.61	-43.61**	1.83**	1.08**	0.97	4.76**	-0.96**	-19.07**
IL7 × IL10	46.39	19.03**	19.03**	3.94**	3.75**	2.14	3.54**	1.51	-16.59
IL7 × IL11	31.22	16.1**	16.1**	2.14	1.9**	0.28	8.16**	-0.89	-0.89
IL7 × IL12	5.64**	-9.15**	-9.15**	2.59	2.04**	1.53	18.46**	17.71	1.11
IL8 × IL9	34.24**	12.23**	-25.37**	0.78	0.12**	0.01	18.69**	12.79	-4.96
IL8 × IL10	19.26	10.69**	-26.9**	3.38	3.1**	1.67	11.44**	9.24	-8.52
IL8 × IL11	35.71	32.04**	1.8**	0.98*	0.64**	-0.79**	5.16**	-3.71	-3.71**
IL8 × IL12	18.95**	14.95**	-14.63**	2.27**	1.81**	1.3	28.39**	27.81*	11.21
IL9 × IL10	32.55**	19.11	-35.62**	3.28	2.34	2.23	17.71**	14.01	-8.14**
IL9 × IL11	21.82**	-3.86**	-34.11**	1.2**	0.2**	0.09	-7.69**	-22.47*	-22.47
IL9 × IL12	33.1**	7.08**	-22.5**	1.19	0.99**	0.88	25.19**	18.71	2.11**
IL10 × IL11	30.09**	17.84**	-12.4**	2.2	2.14**	0.15**	-0.29	-11.37	-11.37
IL10 × IL12	25.44**	12.86**	-16.72**	1.41	0.67**	0.16**	-3.21**	-5.99	-22.59
IL11 × IL12	4.61**	4.28**	-25.3**	1.45	0.65**	0.14**	-10.19	-18.49	-18.49**
Mean	19.08	4	-13.2	2.7	2.15	1.2	8.17	-0.29	-15.7
SE	0.56	0.24	0.87	0.37	1.05	0.76	0.64	0.87	0.24
Min.	-23.15	-43.61	-47.22	0.62	0	-1.4	-26.18	-34.52	-47.62
Max.	59.41	50.05	19.5	6.71	5.43	5.32	35.41	28.81	11.21
CD @ 5%	5.54	2.34	4.02	5.65	2.93	4.76	7.12	3.54	4.23
CD@ 1%	6.12	3.26	4.91	6.29	3.54	5.24	8.76	4.23	5.91

* and ** significant at 5% and 1% level of significance, respectively,

PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob

Table 23 (c). Estimation of mid parent, better parent and standard heterosis studied for Numbers of kernel per rows, 100 grain weight (g) and Seed Yield per plant (g) in maize (*Zea mays* L.) under partial irrigated condition.

Hybrid	NKR			HGW			SYP		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	-2.25	-2.47**	-1.47**	-8.67	-30.64	-60.81	-2.05	-12.16	-13.56**
IL1 × IL3	0.54	-3.32	-3.32**	-26.55	-58.21	-69.01	14.18	7.22	-15.79
IL1 × IL4	7.1**	1.67	1.51	14.7	-15.46	-29.26	39.48	32.51	9.49
IL1 × IL5	4.57**	-0.16	-0.16	8.55	2.85	-71.26	16.33	7.98	-15.03
IL1 × IL6	-2.58	-2.78	-2.82**	-17.29	-54.26	-54.26	-15.91	-19.23	-42.24**
IL1 × IL7	8.94	3.22	3.86**	44.48**	22.39	-7.56	67.18**	59.84	36.83**
IL1 × IL8	1.45	-3.65	-3.42**	8.28	2.09	-59.81	-3.86	-7.27	-30.21
IL1 × IL9	3.72	-0.91	-0.98	-6.12**	-39.76	-46.61	2.86	-7.19	-10.17
IL1 × IL10	5.43	1.72	0.38	-5.36	-7.96	-76.76	22.92	22.21	0.61
IL1 × IL11	1.66	-5.54	-5.29**	32.43**	21.07	-53.06	20.69	10.51	-12.59
IL1 × IL12	-0.71	-6.88	-6.54**	-61.07**	-88.66	-107.61	5.17	-2.08	-25.09**
IL2 × IL3	0.21	-3.42	-3.86	-7.52**	-17.21	-28.01	3.32**	-15.14	-15.14**
IL2 × IL4	1.87	-3.51**	-3.94	-13.07**	-21.26	-35.06	-21.67	-40.15	-40.15
IL2 × IL5	0.79**	-3.72	-4.16	-26.22**	-53.84	-84.01**	-20.63	-40.48	-40.48
IL2 × IL6	7.46	7.44	7.79	-25.27	-40.36	-40.36	23.79	8.96**	8.96
IL2 × IL7	7.18	2.31	1.87	-60.95	-61.06	-51.01**	39.25	20.41	20.41
IL2 × IL8	2.08	-2.56	-3.87	-20.82	-36.69	-66.86	18.93	3.22	3.22
IL2 × IL9	6.48	2.67**	1.56	23.85	12.19	5.33	1.48	0.03	0.039
IL2 × IL10	3.8**	-1.11	-1.55	-50.62	19.94	-12.11**	-0.1	-10.95	-10.95
IL2 × IL11	1.9**	-4.82	-5.26	-19.05**	-52.39	-82.56**	-6.56	-28.15	-28.15
IL2 × IL12	4.2**	-1.41	-1.85	-59.05	-64.66	-83.61	-9.57	-28.32	-28.32
IL3 × IL4	2.5	0.84	-6.87	-75.51	-77.01	-87.81	8.57	8.55	-28.38
IL3 × IL5	7.15	6.27	-1.44	-30.79	-68.09	-78.89	9.44	8.05**	-28.88
IL3 × IL6	3.85	0.23**	-0.24	-45.04	-50.44	-50.44	17.81	14.18	-15.48
IL3 × IL7	7.01	5.79	-1.92	50.47	40.89	30.09	51.57	51.28	14.27
IL3 × IL8	2.84	1.82	-5.89	-18.99	-44.54	-55.34	21.19	18.43	-12.98
IL3 × IL9	9.36	8.51	0.88	-10.59	-12.56	-19.41	10.51	-6.5**	-9.41
IL3 × IL10	10.27	9.87	1.29	-14.46	-43.46	-54.26	59.92	52.26	30.67
IL3 × IL11	7.02	3.92**	-3.78	-15.79	-58.81	-69.61	54.41	51.29	14.36
IL3 × IL12	5.79	3.81	-3.98	-52.81	-56.89	-67.69	5.89**	5.61	-31.32
IL4 × IL5	11.18	10.32	0.86	-24.56**	-60.36	-74.16	19.5**	18.13	-18.84
IL4 × IL6	7.63	2.28	1.89	-39.36**	-46.26	-46.26	52.29**	48.64	18.98
IL4 × IL7	4.5**	4.98	-6.15	-4.11**	-12.19	-25.99	-0.45	-0.81	-37.78
IL4 × IL8	11.87	11.14	1.41	-15.79	-39.84	-53.64	15.43	12.65	-18.76
IL4 × IL9	12.6	11.72	2.31	-42.44	-45.91	-52.76	10.89	-6.13	-9.04

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 23 (c). Contd.....

Hybrid	NKR			HGW			SYP		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	12.07	11.61	1.36	-20.71	-48.21	-62.01**	14.76	7.07	-14.52
IL4 × IL11	14.04	12.69**	1.51	-3.99**	-45.51	-59.31	53.81	50.7	13.74
IL4 × IL12	12.11**	11.87	0.69	-30.94	-33.51	-47.31	35.86**	35.59	-1.38
IL5 × IL6	2.15	-2.34	-2.82	55.89	13.19	13.19	18.1	13.08	-16.58
IL5 × IL7	3.08	2.73	-6.73**	18.07	-9.66**	-39.61	1.58	0.57	-37.11
IL5 × IL8	-0.13	-0.27	-9.73**	-35.61	-47.36	-89.26*	0.25	-3.99	-35.38
IL5 × IL9	6.02**	5.99	-3.42**	53.09	13.82	6.97**	22.03	3.63	0.73
IL5 × IL10	5.64	5.25	-4.21**	22.14**	13.84**	-54.96**	34.5	25.47	3.88
IL5 × IL11	13.31	11.09	1.63	44.44	38.72	-46.69	42.34*	40.69	0.89
IL5 × IL12	12.45	11.35	1.89	10.64	-22.59	-41.54**	45.98	44.88	7.38
IL6 × IL7	3.11	-1.73	-2.21	-22.59	-37.56	-37.56	59.98	55.97	26.31
IL6 × IL8	1.13	-3.59	-3.98	-12.46	-43.41	-43.41	21.88	21.01	-8.66
IL6 × IL9	-1.2*	-5.67**	-6.14**	-4.93	-8.36	-8.36**	-5.03	-18.41	-21.31
IL6 × IL10	6.07	1.18	0.79	1.64	-32.76	-32.76	35.04	31.78	9.41
IL6 × IL11	7.23	0.52	0.05	-7.94	-56.36	-56.36	19.29	12.53	-17.13
IL6 × IL12	7.21	1.62	1.14	-50.69	-60.16	-60.16	51.12	47.2	17.54**
IL7 × IL8	12.42	12.21**	2.47	-12.64	-28.61	-58.56	59.72	56.58	25.18
IL7 × IL9	7.43**	7.05	-2.36	12.87	1.32	-5.54**	20.24	2.85	-0.05
IL7 × IL10	10.2**	10.15**	-0.01**	-25.14	-44.56	-74.51	21.48	13.35	-8.24
IL7 × IL11	11.13	9.27	-0.99	61.09	27.64	-2.31**	53.18	50.43	12.75**
IL7 × IL12	13.28**	12.53**	2.37	-20.76	-26.26	-45.21**	62.49	62.47	24.9
IL8 × IL9	11.05**	10.89**	1.48	1.04	-26.49	-33.34**	14.12	-0.13	-3.04
IL8 × IL10	9.11	8.85	-0.88	71.17**	67.72	5.81	12.86	7.95	-13.64
IL8 × IL11	14.24**	12.16**	2.43	78.64**	61.17	-0.74	21.49	15.6	-15.89
IL8 × IL12	10.31	9.34	-0.39	-10.94	-32.41	-51.36	33.91	30.86	-0.55
IL9 × IL10	5.22*	4.87	-4.61	-29.64	-60.61	-67.46	19.19	9.76	6.85
IL9 × IL11	15.83**	13.59**	4.18**	9.16	-35.84	-42.69	2.79	-17.35	-20.26
IL9 × IL12	8.41	7.28**	-2.13	-24.36	-30.41	-37.26	9.17	-8.13	-11.03
IL10 × IL11	11.96	10.14**	-0.11	28.64	14.62	-54.19	23.36	12.56	-9.03
IL10 × IL12	9.74	9.03	-1.22	5.81	-19.11	-38.06	12.18	4.22	-17.37
IL11 × IL12	14.59	13.48**	1.81	34.09	-4.86	-23.81	79.81	76.97	39.47
Mean	6.62	4.05	-1.23	-6.36	-24.85	-45.59	21.66	13.99	-6.71
SE	0.62	0.74	0.13	0.87	0.92	0.54	0.43	0.98	0.25
Min.	-2.58	-6.88	-9.73	-75.51	-88.66	-107.61	-21.67	-40.48	-42.24
Max.	15.83	13.59	7.79	78.64	67.72	30.09	79.81	76.97	39.47
CD @ 5%	4.36	5.26	6.26	6.21	2.15	3.61	4.28	8.24	5.23
CD@ 1%	5.1	6.34	7.65	7.23	4.65	4.32	5.43	8.21	6.21

* and ** significant at 5% and 1% level of significance, respectively,

NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g)

Table 23 (d). Estimation of mid parent, better parent and standard heterosis studied for Number of cobs per plant, Days to maturity and Cob girth (cm) in maize (*Zea mays* L.) under partial irrigated condition.

Hybrid	NCP			DM			CG		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	7.44	5.19	-1.06	-8.81**	-33.81	-78.81**	-7.59	-9.24**	-9.24**
IL1 × IL3	3.69	-1.69	-1.69	-3.71**	-8.81	-103.18**	1.67	-4.49	-4.49
IL1 × IL4	7.94	6.19	-1.06	-8.81**	-23.81	-88.11	10.6	0.92	0.92
IL1 × IL5	5.38**	0.19	-0.16	41.19**	21.19**	-33.81**	-0.2	-6.99	-6.99**
IL1 × IL6	5.44	1.19	-1.06	6.19**	-3.81	-78.13**	0.6**	-4.33**	-4.33**
IL1 × IL7	5.75	1.82	-1.06	66.15**	31.19	6.19**	-10.5	-14.6	-14.69**
IL1 × IL8	4.19	0.56**	-2.94**	26.19**	1.19	-43.21	13.33	6.42	6.42
IL1 × IL9	5.75	1.82	-1.06	33.69**	21.19	-48.84	46.73	36.02	36.02
IL1 × IL10	9.94	5.69	3.44	41.19**	21.17	-33.83	16.13**	5.62	5.62
IL1 × IL11	6.07	3.69	-2.31**	26.19**	-3.81**	-38.81	9.68**	0.71**	0.71
IL1 × IL12	9.69**	7.44**	1.19	28.69**	-18.81	-18.81*	2.78	1.02**	1.02
IL2 × IL3	7.34	4.19	4.19	46.19**	16.19	-28.12	16.95	12.32**	9.02
IL2 × IL4	5.69	5.19	-1.06	-23.81**	-33.81	-78.11**	11.65	3.61	0.31
IL2 × IL5	2.25	-0.69**	-1.06	11.19**	6.76	-38.15**	-17.95**	-23.09	-26.39
IL2 × IL6	0.56	-1.44*	-3.69	21.19**	6.19	-38.81	-15.5**	-18.79**	-22.09**
IL2 × IL7	2.25	0.56	-2.31**	-13.86**	-23.81**	-48.1**	0.2	-2.34**	-5.64**
IL2 × IL8	3.82	2.44	-1.06	-28.81**	-26.86**	-73.12	4.33	-0.94**	-4.24**
IL2 × IL9	2.88	1.19	-1.69	-16.31**	-24.61	-71.14	17.48**	8.41	5.12
IL2 × IL10	6.19	4.19	1.94	-33.81**	-38.66	-83.86	0.43**	-8.44	-11.74
IL2 × IL11	5.07	4.94	-1.06	-28.81**	-33.81	-68.14	-1.22	-8.54	-11.84**
IL2 × IL12	-0.31	-0.31	-6.56**	-11.31**	-33.55	-33.85	-4.82	-4.94	-8.24**
IL3 × IL4	-0.19	-3.81	-3.81	11.19**	-8.81*	-73.83	-9.21	-12.61	-25.19**
IL3 × IL5	0.63	0.44	0.44	56.19**	31.19*	-23.81**	-9.24*	-9.74	-22.31
IL3 × IL6	0.06	-1.06	-1.06**	16.19**	1.19**	-73.87	-8.94	-10.29	-20.16
IL3 × IL7	-1.87	-3.31	-3.31**	-28.71	-68.86	-93.84**	5.59	3.49	-4.89
IL3 × IL8	1.19	-0.56	-0.56**	-3.81**	-33.56	-78.44	14.89	14.27	1.69**
IL3 × IL9	1.88	0.44	0.44	-11.37	-28.67	-98.33	14.12**	9.69	-2.89**
IL3 × IL10	0.06	-1.06	-1.06	-13.87	-38.67	-93.85	20.72	16.49	3.92**
IL3 × IL11	4.19	1.19	1.19**	-33.84	-68.51**	-13.81**	11.52**	8.84	-3.74**
IL3 × IL12	2.07	-1.06	-1.06	-26.31**	-78.81	-78.55	-11.06	-15.59	-19.11*
IL4 × IL5	3.63	0.19	-0.19	-23.84	-28.35	-83.84	6.39	3.49	-10.09
IL4 × IL6	-2.31	-4.81	-7.06	-18.81	-23.45	-98.55	9.54	4.79	-5.09
IL4 × IL7	7	4.82	1.94**	-43.81	-63.11	-18.56	18.72	13.22	4.84
IL4 × IL8	10.32	8.44	4.94	-33.81	-43.71	-58.44	17.89	15.12	1.29
IL4 × IL9	4.78	1.82**	-1.06	-11.31	-13.51**	-78.16**	22.42	21.39	2.02

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 23 (d). Contd.....

Hybrid	NCP			DM			CG		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	-0.31	-2.81	-5.06	-53.81	-58.88**	-13.81**	10.12	9.29**	-10.09
IL4 × IL11	4.32	3.69	-2.31	-8.81	-23.54	-58.86**	11.37	10.64**	-7.29
IL4 × IL12	4.94	4.44	-1.81**	-21.31	-53.81	-53.81	-1.53	-9.46	-12.99
IL5 × IL6	-2.75	-3.69**	-4.06**	-8.81	-18.86	-73.83	8.24*	6.39	-3.49*
IL5 × IL7	-3.44	-4.69**	-5.06	-28.81	-43.71	-68.81**	-15.16**	-17.76	-26.14*
IL5 × IL8	-6.87	-8.44	-8.81**	6.19**	1.19**	-43.81	-3.78**	-3.91	-17.49
IL5 × IL9	-5.94	-7.19	-7.56**	13.69	6.19**	-48.44**	34.99**	31.07	17.49
IL5 × IL10	-2.25	-3.19	-3.56**	-8.81	-8.51	-63.41**	45.07	41.34	27.77
IL5 × IL11	-3.37**	-6.19	-6.56**	6.19	-3.81	-38.84	28.99	26.82	13.24**
IL5 × IL12	-4.75	-7.69	-8.06**	-36.31	-63.81	-63.65	11.59	6.56	3.04**
IL6 × IL7	-2.5**	-2.81	-5.06**	21.19	-3.81	-28.81	20.39**	19.64	11.27**
IL6 × IL8	-5.69	-6.31	-8.56	1.19	-13.81	-58.1**	65.52	63.54	53.67
IL6 × IL9	1.5**	1.19	-1.06	13.69**	11.19	-58.81**	17.97	12.19	2.31
IL6 × IL10	-2.56	-2.56	-4.81	1.19	-8.81	-63.14	19.22	13.64	3.77
IL6 × IL11	-1.44	-3.31	-5.56	-38.81**	-58.85	-93.13	14.07	10.04	0.16
IL6 × IL12	0.69	-1.31	-3.56	3.69	-33.87	-33.14	-1.09**	-4.26	-7.79
IL7 × IL8	7.13	6.82	3.94**	-8.81	-18.61	-43.81	18.72	15.99	7.62**
IL7 × IL9	-5.69	-5.69	-8.56**	-26.31	-48.89	-73.15**	24.94	18.42	10.04
IL7 × IL10	-6.62	-6.94	-9.19	-28.81	-43.81	-68.13	-1.58	-7.91	-16.29
IL7 × IL11	2.75	1.19	-1.69	-23.81	-28.89	-53.81	20.47**	15.69	7.31**
IL7 × IL12	3.56	1.82	-1.06	-81.31	-93.87	-93.81	21.32	18.89	15.37**
IL8 × IL9	-3.37	-3.69	-6.56**	-46.31	-58.31	-13.1**	20.07	16.27	2.44*
IL8 × IL10	-2.69	-3.31	-5.56**	-13.81	-18.81	-63.55	13.02	9.42	-4.41
IL8 × IL11	5.19	3.94	0.44	-18.81	-23.85	-58.45	30.07	28.02	14.19
IL8 × IL12	2.69	1.32	-2.19	-46.71	-68.84	-68.83	15.64	10.49**	6.96
IL9 × IL10	1.54*	1.19	-1.06	-1.31	-8.98	-63.84**	20.84	20.64	-0.39
IL9 × IL11	3.38	1.82	-1.06**	-11.31	-28.34	-63.84	25.12**	23.37	5.44
IL9 × IL12	-0.52	-2.19	-5.06**	-8.81	-43.57	-43.52	13.99	5.04	1.52**
IL10 × IL11	0.56	-1.31	-3.56	-18.81	-28.13	-63.36	13.27	11.72	-6.21**
IL10 × IL12	-2.06**	-4.06	-6.31	-21.31	-48.22**	-48.63	16.29	7.54	4.02
IL11 × IL12	0.06	-0.06	-6.06	-36.31	-53.87	-53.83	16.14	8.94	5.42
Mean	1.73	-0.09	-2.51	-7.98	-24.83	-57.92	11.1	6.81	-0.97
SE	0.76	0.83	0.34	0.82	0.84	0.54	0.69	0.62	0.86
Min.	-6.87	-8.44	-9.19	-81.31	-93.87	-103.18	-17.95	-23.09	-26.39
Max.	10.32	8.44	4.94	66.15	31.19	6.19	65.52	63.54	53.67
CD @ 5%	6.21	2.15	1.43	3.65	4.12	5.72	3.12	4.87	5.74
CD @ 1%	7.54	3.18	2.76	4.82	5.87	6.83	4.8	4.26	6.24

* and ** significant at 5% and 1% level of significance, respectively,

NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm)

Table 23 (e). Estimation of mid parent, better parent and standard heterosis studied for Shelling %, Canopy temperature and Turgid weight (g) in maize (*Zea mays* L.) under partial irrigated condition.

Hybrid	SP			CT			TW		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	-12.89	-15.63**	-15.63	1.16	1.01	-1.53	-20.32	-42.07**	-50.57
IL1 × IL3	2.73	0.1	-5.38	0.7	0.53	-2.01	-11.82	-18.07	-87.57
IL1 × IL4	-0.34	-5.15	-10.62	1.22	0.93	-1.03	-20.32	-36.07	-86.57**
IL1 × IL5	5.13	3.16	-2.32	2.93	2.47	-0.07	-17.07	-41.57	-74.57**
IL1 × IL6	-7.01	-7.54	-13.01	1.85	1.76	-0.78	-32.82**	-58.07**	-89.57
IL1 × IL7	12.34	11.76	5.53	2.48	1.79	0.63	40.94**	6.44	-6.57
IL1 × IL8	-14.6**	-15.74	-21.21	1.1	0.81	-1.73	9.94	-11.57	-50.57**
IL1 × IL9	3.8	3.62	-1.36	0.98	0.49	-1.08	-7.07	-48.07	-48.07**
IL1 × IL10	5.54**	4.68**	0.92**	0.45	-0.83**	-0.83	-5.07**	-18.57	-73.57
IL1 × IL11	6.47**	3.85**	-1.63	1.5	1.36	-0.91	-35.57	-73.57**	-79.57
IL1 × IL12	6.52	2.24	-3.24**	1.55**	0.59	-0.02	-1.82	-20.07	-65.5
IL2 × IL3	1.02	-4.36	-4.36	4.18	4.17	1.33	-39.07	-54.57	-93.07
IL2 × IL4	-3.94	-11.56	-11.56	3.17	2.73**	0.78	-27.07	-33.07	-71.57
IL2 × IL5	-3.45	-8.16	-8.16	2.68	2.37**	-0.48	-20.82	-23.57	-56.57
IL2 × IL6	2.34	-0.94	-0.94**	1.2**	1.14**	-1.58	-36.57	-40.07	-71.57
IL2 × IL7	-4.32**	-8.4	-8.4**	-0.18**	-1.02	-2.18	-15.32	-28.07	-41.07
IL2 × IL8	3.24	-0.64	-0.64	1.13	0.96	-1.88	-13.32	-13.57**	-52.07**
IL2 × IL9	-9.94	-12.42	-12.42	-1.93	-2.57	-4.13	-34.82	-54.07	-54.07
IL2 × IL10	-2.16	-4.04	-4.04	0.37	-1.06**	-1.06	-16.32	-24.57	-63.07
IL2 × IL11	-1.41	-6.76	-6.76**	2.34	2.05**	-0.22	-20.32	-36.57**	-42.57
IL2 × IL12	3.29	-3.73	-3.73	1.47	0.36	-0.26	2.94	-0.57	-39.07
IL3 × IL4	-6.73	-8.99	-19.73	0.1	-0.36	-2.31	-35.57	-45.07	-95.57
IL3 × IL5	6.26**	5.59	-3.82	3.63	3.32	0.46**	27.19	8.94	-24.07**
IL3 × IL6	2.9**	0.79	-5.75	3.25	3.17	0.46**	15.44	-3.57	-35.07**
IL3 × IL7	9.17	7.88	-0.28**	3.41	2.56	1.4	22.19	-6.07	-19.07
IL3 × IL8	11.97	10.47	2.72**	5.78**	5.63	2.76	-22.32	-37.57**	-76.57
IL3 × IL9	6.04	3.15**	-1.83	3.47	2.82	1.26	-40.82	-75.57**	-75.57
IL3 × IL10	8.49	5.98	1.24	1.91	0.48	0.48	-8.32	-15.57**	-70.57
IL3 × IL11	1.59	1.57	-9.14	2.7	2.44	0.18	-26.82	-58.57	-64.57
IL3 × IL12	3.79	2.14	-8.6	-0.67	-1.8	-2.41	33.44	21.44	-24.07
IL4 × IL5	7.5	4.57	-4.84**	2.69	1.93	-0.02	21.19	12.44**	-20.57**
IL4 × IL6	3.16	-1.22	-7.75	2.63	2.25	0.3	-29.57	-39.07	-70.57**
IL4 × IL7	4.14	0.59	-7.57	1.87	1.47	0.31	-2.82	-21.57	-34.57**
IL4 × IL8	5.9	2.16	-5.6**	2.72	2.12	0.16	47.19	41.44	2.44
IL4 × IL9	-8.58	-13.72	-18.69	2.69	2.49	0.93	-4.32	-29.57**	-29.57

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 23 (e). Contd.....

Hybrid	SP			CT			TW		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	5.32	-0.43	-4.2**	1.4	0.43	0.43**	2.19	-0.06**	-50.57
IL4 × IL11	13.61	11.33	0.63**	0.43	0.28	-1.68**	-33.82**	-56.07**	-62.07**
IL4 × IL12	1.31**	0.7	-13.33*	-0.73	-1.4	-2.01	-3.07**	-5.57	-51.07**
IL5 × IL6	5.83	4.39	-2.15	5.22**	4.84	2.13	-38.82	-39.57	-71.07**
IL5 × IL7	-17.53	-18.16	-26.31	0.79	-0.37	-1.53	-20.57	-30.57	-43.57**
IL5 × IL8	-0.48**	-1.3**	-9.09	4.59**	4.44	1.28	-16.57	-19.57	-52.57
IL5 × IL9	-4.69**	-6.9	-11.87	1.21	0.26	-1.31**	-43.57**	-60.07**	-60.07
IL5 × IL10	5.75	2.93	-0.85	0.76**	-0.98	-0.98	-4.57	-15.57**	-48.57
IL5 × IL11	8.27	7.62	-1.79	1.16**	0.56	-1.71	-24.57**	-38.07**	-44.07
IL5 × IL12	12.76	10.45	1.05	3.35**	1.92	1.31	35.19	28.94**	-4.07
IL6 × IL7	0.42	-0.41	-6.93**	0.68	-0.09	-1.26	-43.32**	-52.57	-65.57
IL6 × IL8	4.18	3.57	-2.97**	2.67**	2.44	-0.28	-26.32**	-30.07	-61.57**
IL6 × IL9	0.04	-0.75	-5.72**	2.39**	1.81	0.25	-16.32	-32.07	-32.07
IL6 × IL10	4.63**	3.25	-0.52	0.73**	-0.63	-0.63	-16.32	-28.07	-59.57
IL6 × IL11	-8.91	-11**	-17.52**	0.31	0.09	-2.18	-52.82	-65.57	-71.57
IL6 × IL12	1.05	-2.71**	-9.24**	-0.2	-1.25**	-1.86	-10.07	-17.07	-48.57**
IL7 × IL8	9.35	9.15**	1.4	-0.12	-1.12**	-2.28	-1.57**	-14.57	-27.57**
IL7 × IL9	4.81	3.22**	-1.76	-0.19	-0.39	-1.55	-27.57	-34.07	-34.07**
IL7 × IL10	-7.31	-9.51**	-13.27**	-0.64	-1.22	-1.22	-19.07	-40.07	-53.07
IL7 × IL11	10.96**	9.69**	1.53	-1.03	-1.58	-2.74	-25.07**	-28.57	-34.57
IL7 × IL12	12.27	9.33	1.18	0.48	0.21	-0.41	-27.82**	-44.07	-57.07
IL8 × IL9	6.5	5.11	0.14	4.13	3.33	1.76	-37.57**	-57.07	-57.07
IL8 × IL10	0.75	-1.25	-5.01	-0.77	-2.35	-2.35	-8.07	-16.07	-55.07
IL8 × IL11	8.3	6.82	-0.94	3.08	2.62	0.36	-56.07**	-72.57	-78.57
IL8 × IL12	8.79	5.65	-2.11	0.47	-0.81	-1.42	11.19	7.94	-31.07
IL9 × IL10	-6.32	-6.93	-10.69	0.66	-0.13	-0.13	13.44	-14.07	-14.07
IL9 × IL11	6.3	3.44	-1.54	3.93	3.58	2.01	-48.07	-51.07	-51.07
IL9 × IL12	5.65	1.12	-3.86	3.43	2.96	2.35	-30.32	-53.07	-53.07
IL10 × IL11	6.75	3.28	-0.49	0.93	-0.21	-0.21	-24.07	-48.57	-54.57
IL10 × IL12	5.9	0.77	-3.77	-0.28	-0.58	-0.58	24.19	19.44	-26.07
IL11 × IL12	15.58**	13.93	3.22	-0.25	-1.07	-1.68	-52.32**	-72.07	-78.07**
Mean	2.54	0.03	-5.54	1.59	0.97	-0.5	-14.36	-28.76	-52.53
SE	0.84	0.27	0.42	0.73	0.72	0.51	0.73	79	0.85
Min.	-17.53	-18.16	-26.31	-1.93	-2.57	-4.13	-56.07	-75.57	-95.57
Max.	15.58	13.93	5.53	5.78	5.63	2.76	47.19	41.44	2.44
CD @ 5%	5.23	4.12	6.27	4.72	1.43	2.61	2.15	1.34	3.76
CD@ 1%	6.76	5.17	7.23	5.76	2.54	3.65	3.16	2.65	4.29

* and ** significant at 5% and 1% level of significance, respectively,

SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g)

Table 23 (f). Estimation of mid parent, better parent and standard heterosis studied for Relative water content, Saturation water deficit and Membrane stability index in maize (*Zea mays* L.) under partial irrigated condition.

Hybrid	RWC			SWD			MSI		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL1 × IL2	2.61	-1.96	-7.7	-1.05	-5.63	-23.85	103.39	86.07	-15.66
IL1 × IL3	-2.79	-10.57	-9.87	4.34	-3.47	-21.69	-14.65	-10.66	-15.01
IL1 × IL4	8.85	8.15	-5.33	-7.29	-8.01	-26.22**	357.48	34.97	58.59
IL1 × IL5	2.05	-3.24	-7.53	-0.49**	-5.81	-24.02*	165.12	93.72	-39.86
IL1 × IL6	-4.53	-7.98	-15.94**	6.08**	2.61	-15.61*	110.45	74.52	-1.86**
IL1 × IL7	2.77	0.57	-9.9	-1.21	-3.44**	-21.66	157.7	67.14**	-2.11
IL1 × IL8	-6.06	-7.88	-19.09**	7.61	5.76	-12.46	-30.64	-14.34	-19.31
IL1 × IL9	-1.37	-3.49	-14.11**	2.92	0.77	-17.44**	2.48**	8.29**	3.29**
IL1 × IL10	5.78**	3.53	-6.83	-4.23	-6.5	-24.72**	13.82	10.44**	-19.19**
IL1 × IL11	19.73	10.64	-4.2	-18.17	-27.28	-27.28	46.79	18.74	-21.54
IL1 × IL12	-2.69	-6.86	-13.36	4.24	0.03	-18.19	25.82	-4.49	-20.26
IL2 × IL3	9.13	5.92	6.62	-7.57	-10.79	-38.18	205.8	7.12**	62.77**
IL2 × IL4	-9.7	-13.54	-19.28**	11.25**	7.39**	-12.27	188.63	18.79	-92.93**
IL2 × IL5	-2.34	-3.04**	-7.33	3.89	3.16	-24.23**	122.64	68.57	-65.01
IL2 × IL6	-6.9**	-7.98**	-13.73**	8.45**	7.35	-17.83**	302.33*	9.07**	7.34**
IL2 × IL7	-3.83	-6.16	-11.91**	5.38**	3.03	-19.65	-79.5**	-12.74**	-27.99
IL2 × IL8	-5.33	-8.03	-13.78**	6.88**	4.14	-17.77	46.97**	-53.41	-94.38**
IL2 × IL9	0.9	-1.51	-7.26	0.6	-1.78**	-24.29	39.38**	-81.48	-81.48
IL2 × IL10	7.64	5.35	-0.47	-6.08*	-8.38	-31.16	157.12	11.07	-78.56
IL2 × IL11	9.48	-4.2	-9.95	-7.92**	-21.61	-21.61	244.27	3.54**	13.27
IL2 × IL12	7.92	7.56	1.81**	-6.36	-6.74	-33.37	29.09	16.12	-19.66
IL3 × IL4	-15.48	-22.54**	-21.84**	17.03	9.95	-9.71**	147.09	8.56	-35.79**
IL3 × IL5	-0.99	-3.46**	-2.76	2.54**	0.05**	-28.8**	45.15	0.54	-43.81**
IL3 × IL6	-6.8**	-11.11	-10.41**	8.35	4.02	-21.15	322.49	10.54**	12.19
IL3 × IL7	-8.28	-13.83	-13.13**	9.83	4.25**	-18.42**	-157.06	-12.51**	-26.86
IL3 × IL8	-8.35**	-14.28	-13.58	10.03**	4.07	-17.85	93.93	92.24**	51.27**
IL3 × IL9	-8.25**	-13.89	-13.19	9.8**	4.14	-18.37	-164.64	-16.81	-16.81**
IL3 × IL10	-11.33	-16.83**	-16.13**	12.88	7.35	-15.42	145.03	52.39	8.04**
IL3 × IL11	4.21	-12.69	-11.99**	-2.65	-19.57**	-19.57	291.63	3.67	15.32
IL3 × IL12	-8.34	-11.91	-11.21	9.89	6.29	-20.34	-12.77	-98.49*	-12.84
IL4 × IL5	4.71	0.13	-4.16	-3.15**	-7.74	-27.88	177.43	83.52	-50.06**
IL4 × IL6	-6.09	-8.81**	-16.78	7.64	4.88	-14.78	44.57	31.14**	-20.26
IL4 × IL7	2.38**	0.89	-9.57**	-0.82	-2.33	-21.98	11.67	-11.41	-16.66
IL4 × IL8	-4.63**	-5.72	-16.94**	6.18*	5.05	-14.61	32.83	-10.39**	-18.36**
IL4 × IL9	-4.06	-5.46	-16.09	5.61	4.19**	-15.47	-8.24	-8.94**	-8.91

* and ** significant at 5% and 1% level of significance, respectively,

Contd.....

Table 23 (f). Contd.....

Hybrid	RWC			SWD			MSI		
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
IL4 × IL10	2.54	11.55	-9.36	-0.98	-2.54	-22.2	6.68	10.79	-8.84
IL4 × IL11	3.19	-6.61	-20.09	-1.63	-11.46**	-11.46	25.98**	75.42	-14.86**
IL4 × IL12	-5.26	-8.71	-15.22	6.81	3.32	-16.34	73.63	20.82	-14.96**
IL5 × IL6	-0.32	-2.13	-6.42**	1.87	0.04	-25.13**	-12.17	-19.51**	-23.09
IL5 × IL7	-2.94	-6.33	-10.29	4.49	1.4	-21.27	50.88**	31.72**	-63.53**
IL5 × IL8	-5.41	-8.85	-13.13	6.96	3.5**	-18.42	-53.94	-20.24**	-241.21**
IL5 × IL9	-6.66	-9.8	-14.09	8.21	5.04	-17.47	-16.52	-23.31	-23.31
IL5 × IL10	-4.1	-7.1	-11.39	5.65	2.61	-20.16	-94.76	-12.79*	-26.36
IL5 × IL11	5.99	-8.41	-12.7	-4.43	-18.85**	-18.85**	-48.69	-12.04**	-35.61**
IL5 × IL12	-0.6	-1.68	-5.97**	2.15**	1.05	-25.59	-88.54**	-19.64	-23.21
IL6 × IL7	-1.2	-2.42	-10.39	2.75**	1.5	-21.17	-23.64	-20.14**	-35.39
IL6 × IL8	7.77	6.17	-1.8	-6.21	-7.84**	-29.76	42.73	-10.91	-151.89**
IL6 × IL9	0.59	-0.72	-8.68	0.97	-0.36	-22.87	70.77	-13.36	-13.36**
IL6 × IL10	-8.55	-9.72	-17.68	10.1	8.9	-13.87	40.76	-19.31	-8.94
IL6 × IL11	13.44	0.44	-7.53**	-11.44**	-24.03**	-24.03**	-62.07	-16	-36.34
IL6 × IL12	-4.25	-4.95	-11.45	5.8	5.07	-20.1	-53.5	-19.74	-35.51
IL7 × IL8	-5.54	-5.89	-16.35	7.09	6.72**	-15.2	-251.92	-29.06**	-30.04
IL7 × IL9	-7.83	-7.88	-18.34	9.38**	9.3	-13.21**	-27.69	-5.31**	-35.31
IL7 × IL10	7.92	7.89	-2.47	-6.36**	-6.41**	-29.08	-18.12	-15.31	-28.56**
IL7 × IL11	10.39	-0.92	-11.39	-8.83	-20.17**	-20.17	-3.17	-65.69	-16.94
IL7 × IL12	10.95	8.99	2.49	-9.39	-11.37**	-34.04	-11.42**	-21.69	-36.94
IL8 × IL9	1.08	0.81	-9.82	0.48	0.18	-21.74	-16.17	-26.66**	-26.66
IL8 × IL10	8.69	8.28	-2.08	-7.13	-7.56**	-29.47	-62.54	-16.86	-17.84
IL8 × IL11	18.87**	7.93	-3.29**	-17.31	-28.27	-28.27	-11.09**	-10.74**	-141.71
IL8 × IL12	4.01	1.67	-4.83**	-2.45	-4.81	-26.73	-85.94	-13.34	-24.31
IL9 × IL10	9.91	9.8	-0.57	-8.35**	-8.48	-30.99	-172.57	-27.39	-27.39**
IL9 × IL11	17.95*	6.72	-3.91	-16.39**	-27.65	-27.65	-275.42	-35.56	-35.56**
IL9 × IL12	9.81**	7.77	1.27	-8.25**	-10.31	-32.82	-250.22	-358.11	-38.11
IL10 × IL11	20.06**	8.69	-1.67**	-18.5	-29.88	-29.88	-48.69	-3.36	-23.64
IL10 × IL12	6.18	4.19	-2.31	-4.54	-6.47	-29.24	-86.94	-93.86	-39.64**
IL11 × IL12	16.24**	2.94	-3.56**	-14.68**	-27.99**	-27.99	-67.34	-69.59	-25.36**
Mean	1.26	-2.77	-9.39	0.31	-3.89	-22.17	24.73	-5.84	-29.36
SE	0.84	0.29	1.02	0.83	0.73	0.73	0.79	0.26	0.61
Min.	-15.48	-22.54	-21.84	-18.5	-29.88	-38.18	-275.42	-358.11	-241.21
Max.	20.06	11.55	6.62	17.03	9.95	-9.71	357.48	93.72	62.77
CD @ 5%	5.26	2.42	3.73	4.87	2.16	4.81	2.17	4.14	2.49
CD @ 1%	5.76	3.28	4.74	5.13	3.68	5.88	3.71	5.18	3.27

* and ** significant at 5% and 1% level of significance, respectively,

RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

4.6 Genetic variability, heritability, genetic advance and genetic advance as percent of mean

In the present investigation, an attempt was made to study the various genetic parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as percent of mean for 12 inbred lines and 66 hybrids and two checks for 18 parameters under irrigated and partial irrigated condition, which will help in formulating breeding strategies for maize improvement for various characters. These genetic parameters give an idea about variation present in the genotypes and extent of improvement that can be achieved. The results of these components for different characters are presented in Table 24.

4.6.1 Genotypic (GCV) and phenotypic (PCV) coefficients of variation

In general, phenotypic coefficient of variation was comparatively higher than that of the genotypic coefficient of variation (suggesting the influence of environmental factors on all characters). Among the eighty maize genotype the GCV and PCV revealed moderate to high variability for majority of the characters. membrane stability index (35.1% and 40.83%), days to 50 percent tasseling (0.99% and 21.47%), days to 50 percent silking (20.51% and 20.93%), Anthesis silking interval (20.57% and 25.2%), days to 50% maturity (19.82% and 19.84%), Seed Yield per plant (17.98% and 21.03%) and Canopy temperature (3.06% and 4.02%) showed low GCVs and PCVs respectively under irrigated condition. On the other hand, under partially irrigated condition, GCV and PCV revealed moderate to high variability for majority of the characters. 100 grain weight (27.95% and 48.33%), Membrane stability index (42.05% and 48.33%), Days to 50 percent tasseling (18.22% and 18.74%), days to 50 percent silking (18.32% and 18.76%), Anthesis silking interval (17.19% and 19.42%), days to 50% maturity (19.41% and 19.44%) and showed low GCVs and PCVs Canopy temperature (4.5% and 5.31%) respectively (Table 24).

4.6.2 Heritability in broad sense

In the present study, high heritability was observed for most of the traits and it was noted highest for days to maturity (99.80%) tracked by days to 50 % silking (96.00%), days to 50 % tasseling (95.50%) and plant height (91.70%), whereas shelling % (44.6%) displayed low heritability under irrigated condition. On the other hand, under partially irrigated condition high heritability exhibited for days to maturity (99.7%) tracked by days to 50 % silking (95.3%), days to 50 % tasseling (94.5%) and plant height (85.4%) and displayed low for shelling % (41.7%) (Table 24).

Table 24. Coefficient of variation, heritability and genetic advance as percent of mean among the inbred

Traits	GCV (%)		PCV (%)		Heritability (%)		Genetic Advance		Gen. Adv as % of Mean	
	I	PI	I	PI	I	PI	I	PI	I	PI
DFT	20.99	18.22	21.47	18.74	95.50	94.50	32.55	29.25	42.27	36.48
DFS	20.51	18.32	20.93	18.76	96.00	95.30	33.47	31.63	41.38	36.84
ASI	20.57	17.19	25.20	19.42	66.60	78.30	1.35	1.91	34.59	31.33
PH	20.50	15.14	21.40	16.39	91.70	85.40	55.92	38.22	40.44	28.83
CL	5.24	7.48	7.06	9.28	55.10	64.90	1.09	1.55	8.02	12.42
NKRC	6.88	8.53	8.05	10.33	73.00	68.20	1.61	1.75	12.11	14.50
NKR	12.60	16.03	15.00	18.03	70.50	79.00	4.62	5.44	21.79	29.35
HGW	7.33	279.55	9.85	48.33	55.40	66.70	2.38	156.56	11.25	470.26
SYP	17.98	17.55	21.03	20.86	73.10	70.80	22.80	20.45	31.65	30.43
NCP	10.59	11.13	13.25	13.80	63.90	65.10	0.32	0.30	17.44	18.50
DM	19.82	19.41	19.84	19.44	99.80	99.70	49.00	46.44	40.79	39.92
CG	8.44	7.70	9.60	8.98	77.20	73.40	1.84	1.57	15.27	13.58
SP	3.41	4.20	5.11	6.50	44.60	41.70	3.65	4.38	4.69	5.58
CT	3.06	4.50	4.02	5.31	57.80	71.80	1.29	2.10	4.79	7.86
TW	8.07	8.20	9.03	9.07	80.00	81.70	0.03	0.03	14.88	15.27
RWC	5.37	5.52	6.50	6.58	68.30	70.30	6.64	6.84	9.15	9.53
SWD	14.23	14.02	17.21	16.71	68.40	70.40	6.65	6.85	24.23	24.23
MSI	35.10	42.05	40.83	47.91	73.90	77.00	15.77	22.79	62.15	76.02

I = Irrigated condition, PI = Partial irrigated condition

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, DM= Days to maturity, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob, NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, ASI = Anthesis silking interval, CG = Cob girth (cm), SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

4.6.3 Genetic advance

Genetic advance was observed for most of the traits and it was noted highest for plant height (55.92%) tracked by days to maturity (49.00%), days to 50 % silking (33.47%) and days to 50 % tasseling (32.55%) and exhibited low for turgid weight (0.03%) under irrigated condition. On the other hand, under partially irrigated condition high genetic advance exhibited for hundred grain weight (156.56) tracked by days to maturity (46.44%), plant height (38.22%) and days to 50% silking (31.63%) and low for turgid weight (0.03%) (Table 24).

4.6.4 Genetic advance as percent of mean (GAM)

Among the eighty maize genotypes, the GAM values were observed for most of the traits and it was noted highest for membrane stability index (62.15) intimately followed by days to 50 % tasseling (42.27%), days to 50 % silking (41.38%), days to maturity (40.79%), and plant height (40.44%) and found low for shelling % (4.69%) under irrigated condition. Conversely, under partially irrigated condition, high GAM values documented for hundred grain weight (470.26%) tracked by membrane stability index (76.02), days to maturity (39.92%), days to 50 % silking (36.84%) and days to 50% tasseling (36.48%) and low in shelling % (5.58%) (Table 24).

4.7 Biochemical Analysis of the inbred lines and their hybrids

To discover drought-resistant genes by association analysis, physiological and biochemical traits were tested in eighty maize genotypes. The mean values of drought resistance indexes of proline content, total soluble sugar content, chlorophyll content, malondialdehyde content (MDA), H₂O₂ content, peroxidase activity, glutathione reductase activity and catalase activity were calculated in elite eighty maize genotypes subjected to drought treatment at the reproductive stage.

Extensive phenotypic variation was documented for proline content, total soluble sugar content, chlorophyll content, malondialdehyde content (MDA), H₂O₂ content, peroxidase activity, glutathione reductase activity and catalase activity during drought stress. The descriptive statistics for the phenotypes related to drought stress are presented in Table 25 a & b. Wide range of variation was observed among the accessions in terms of the drought resistance indexes for biochemical traits.

4.7.1 Proline content

The parental inbred line IL9 (23.9) showed lowest proline content followed by IL11 (24.9), IL3 (27.6) and IL7 (29.4) while the parental inbred line IL8 (43.6) demonstrated highest proline content tracked by IL5 (39.3), IL10 (36.6) and IL2 (36.5) under irrigated condition. Alternatively, the parental inbred line IL9 (25.9) exposed lowest proline content trailed by IL7 (31.2), IL3 (31.6) and IL4 (32.8) while the parental inbred line IL8 (47.7) disclosed highest proline content tracked by IL5 (41.3), IL2 (39.7) and IL10 (39.4) under partial irrigated condition (Table 25 a).

The hybrid IL5 × IL12 (17.3) demonstrated lowest proline content tracked by IL4 × IL8 (17.6), IL5 × IL7 (17.6) and IL6 × IL9 (18.4), while the parental inbred line IL8 (43.6) exhibited highest proline content tracked by IL5 (39.3), IL10 (36.6) and IL2 (36.5) under irrigated condition. Alternatively, the hybrid IL5 × IL7 (21.6) exposed lowest proline content tracked by IL4 × IL8 (22.7), IL8 × IL12 (23.5) and IL6 × IL10 (24.1). While, under partial irrigated condition hybrid IL7 × IL11 (62.5) exhibited highest proline content tracked by IL9 × IL10 (56.00), IL5 × IL11 (49.5) and IL1 × IL7 (43.3) (Table 25 a).

4.7.2 Total Soluble sugar content

The parental inbred line IL2 (0.9) displayed lowest total soluble sugar content followed by IL3 (0.91), IL4 (0.96) and IL11 (0.96), while the parental inbred line IL7 (1.23) exhibited highest total soluble sugar content tracked by IL8 (1.22), IL1 (1.2) and IL5 (1.20) under irrigated condition. Alternatively, the parental inbred

line IL9 (1.08) displayed lowest total soluble sugar content tracked by IL2 (1.2), IL7 (1.2) and IL3 (1.23). Whereas, under partial irrigated condition the parental inbred line IL8 (1.99) displayed highest total soluble sugar content tracked by IL12 (1.56), IL11 (1.52) and IL10 (1.48) under partial irrigated condition (Table 25 a).

The hybrids IL2 × IL9, IL4 × IL12, IL9 × IL12 (0.88) and IL6 × IL11 (0.9) showed lowest total soluble sugar content while the hybrid IL1 × IL4, IL3 × IL5, IL6 × IL9 along with check HKI 1128 (1.27) showed highest total soluble sugar content under irrigated condition. On the other hand, the hybrid IL2 × IL9 (0.94) demonstrated lowest total soluble sugar content tracked by IL2 × IL8 (0.99), IL1 × IL6 (1.01) and IL2 × IL10 (1.01). the hybrid IL2 × IL5 (1.93) showed highest total soluble sugar content followed by IL2 × IL11 (1.91), IL6 × IL10 (1.62) and IL7 × IL9 (1.62) under partial irrigated condition (Table 25 a).

4.7.3 Chlorophyll content

The parental inbred line IL5 (0.69) showed lowest chlorophyll content followed by IL1 (0.74), IL2 (0.75) and IL4 (0.75) while the parental inbred line IL10 (0.89) exhibited highest chlorophyll content tracked by IL6 (0.88), IL9 (0.84) and IL8 (0.81) under irrigated condition. Conversely, the parental inbred line IL5 (0.69) displayed lowest chlorophyll content tracked by IL1 (0.74), IL2 (0.75) and IL4 (0.75) while the parental inbred line IL10 (0.89) disclosed highest chlorophyll content tracked by IL6 (0.88), IL9 (0.84) and IL8 (0.81) under partial irrigated condition (Table 25 a).

The hybrid IL4 × IL5 (0.69) demonstrated lowest chlorophyll content tracked by IL6 × IL10 (0.69), IL3 × IL6 (0.71) and IL8 × IL11 (0.71) while the hybrid IL2 × IL10 (0.89) possessed high chlorophyll content trailed by IL7 × IL10 (0.89), IL2 × IL6 (0.88) and IL4 × IL6 (0.88) under irrigated condition. Alternatively, the hybrid IL2 × IL5 (0.69) demonstrated lowest chlorophyll content tracked by IL6 × IL10 (0.69), IL3 × IL6 (0.71) and IL8 × IL11 (0.71) and the hybrid IL2 × IL11(0.89) showed high chlorophyll content followed by IL7 × IL10 (0.89), IL2 × IL6 (0.88) and IL4 × IL6 (0.88) under partial irrigated condition (Table 25 a).

4.7.4 MDA TEST (Malondialdehyde content)

The parental inbred line IL2 (8.4) showed lowest malondialdehyde content followed by IL11 (8.4), IL5 (8.5) and IL6 (9.4) while the parental inbred line IL9 (10.4) demonstrated highest malondialdehyde content tracked by IL7 (10.3), IL4 (10.2) and IL8 (9.8) under irrigated condition. Conversely, the parental inbred line IL5 (11.6) exhibited lowest malondialdehyde content tracked by IL1 (12.5), IL10 (12.5) and IL12 (12.7). The parental inbred line IL8 (16.4) demonstrated highest malondialdehyde content tracked by IL6 (15.9), IL4 (15.8) and IL7 (15.5) under partial irrigated condition (Table 25 a).

The hybrid IL3 × IL4 (7.2) demonstrated lowest malondialdehyde content tracked by IL4 × IL7 (7.2), IL6 × IL12 (7.2) and IL8 × IL10 (7.3) while the hybrid IL1 × IL9 (14.6) demonstrated high malondialdehyde content tracked by IL4 × IL11 (14.6), IL10 × IL11 (14.6) and IL1 × IL8 (14.3) under irrigated condition. On the other hand, the hybrid IL3 × IL11 (10.3) showed lowest malondialdehyde content followed by IL8 × IL10 (10.3), IL3 × IL12 (10.5) and IL8 × IL11 (10.5). The hybrid IL1 × IL6 (17.4) demonstrated high malondialdehyde content tracked by IL4 × IL8 (17.4), IL9 × IL10 (17.4) and IL4 × IL11 (16.6) under partial irrigated condition (Table 25 a).

4.7.5 H₂O₂ content

The parental inbred line IL4 (33.9) showed lowest H₂O₂ content followed by IL9 (38.6), IL2 (38.8) and IL11 (39.6) while the parental inbred line IL3 (47.6) exhibited highest H₂O₂ content tracked by IL8 (46.5), IL10 (45.5) and IL5 (45.4) under irrigated condition. Alternatively, the parental inbred line IL4 (38.2) showed lowest H₂O₂ content tracked by IL9 (45.4), IL7 (50.7) and IL11 (54.3). The parental inbred line IL5 (68.2) showed highest H₂O₂ content followed by IL1 (64.4), IL3 (64.3) and IL8 (62.3) under partial irrigated condition (Table 25 b).

The hybrid IL4 × IL5 (34.9) showed lowest H₂O₂ content followed by IL3 × IL11 (35.7), IL3 × IL12 (36.3) and IL1 × IL6 (36.7) while the hybrid IL1 × IL8 (53.5) demonstrated high H₂O₂ content tracked by IL4 × IL10 (51.8), IL5 × IL8

(50.5) and IL3 × IL6 (50.2) under irrigated condition. Conversely, the hybrid IL1 × IL2 (42.1) demonstrated lowest H₂O₂ content tracked by IL9 × IL11 (44.2), IL3 × IL5 (46.9) and IL3 × IL9 (48.1). The hybrid IL8 × IL12 (76.9) demonstrated high H₂O₂ content tracked by IL9 × IL10 (73.1), IL7 × IL12 (70.8) and IL8 × IL11 (70.1) under partial irrigated condition (Table 25 b).

4.7.6 Peroxidase activity

The parental inbred line IL7 (13.2) demonstrated lowest peroxidase followed by IL12 (13.9), IL1 (14.1) and IL5 (14.4) while the parental inbred line IL2 (19.3) highest peroxidase tracked by IL6 (17.1), IL3 (16.3) and IL11 (15.9) under irrigated condition. Conversely, the parental inbred line IL6 (19.1) demonstrated lowest peroxidase tracked by IL5 (22.7), IL10 (24.2) and IL12 (25.5). The parental inbred line IL7 (31.9) demonstrated highest peroxidase tracked by IL11 (31.9), IL2 (29.8) and IL9 (29.4) under partial irrigated condition (Table 25 b).

The hybrid IL6 × IL11 (12.5) showed lowest peroxidase followed IL11 × IL12 (13.4), IL4 × IL6 (14.1) and IL9 × IL11 (14.2) while the hybrid IL1 × IL4 (23.1) demonstrated high peroxidase tracked by IL2 × IL9 (19.7), IL1 × IL8 (19.6) and IL3 × IL9 (19.6) under irrigated condition. Alternatively, the hybrid IL4 × IL7 (18.4) demonstrated lowest peroxidase tracked by IL7 × IL10 (19.1), IL6 × IL11 (19.9) and IL5 × IL12 (20.1). The check variety HKI 1128 (38.7) showed high peroxidase followed by hybrid IL1 × IL7 (31.8), IL1 × IL12 (31.4) and IL2 × IL10 (31.4) under partial irrigated condition (Table 25 b).

4.7.7 Glutathione reductase activity

The parental inbred line IL6 (0.227) showed lowest glutathione reductase activity followed by IL8 (0.257), IL3 (0.286) and IL11 (0.294) while the parental inbred line IL1 (0.37) demonstrated highest glutathione reductase tracked by IL9 (0.342), IL5 (0.33) and IL12 (0.33) under irrigated condition. On the other hand, the parental inbred line IL6 (0.225) showed lowest glutathione reductase trailed by IL8 (0.254), IL3 (0.284) and IL11 (0.293). The parental inbred line IL1 (0.369)

demonstrated highest Glutathione reductase followed by IL9 (0.342), IL12 (0.33) and IL5 (0.328) under partial irrigated condition (Table 25 b).

The check variety HKI 1128 (0.06) showed lowest glutathione reductase followed by hybrid IL1 × IL3 (0.213), IL3 × IL8 (0.23) and IL5 × IL6 (0.234) while the hybrid IL9 × IL12 (0.406) showed high glutathione reductase followed IL10 × IL11 (0.374), IL6 × IL12 (0.373) and IL2 × IL5 (0.369) under irrigated condition. Alternatively, the check variety HKI 1128 (0.06) demonstrated lowest glutathione reductase tracked by IL1 × IL3 (0.212), IL3 × IL8 (0.229) and IL3 × IL9 (0.233). The hybrid IL9 × IL12 (0.405) demonstrated high glutathione reductase tracked by IL6 × IL12 (0.373), IL10 × IL11 (0.373) and IL2 × IL5 (0.369) under partial irrigated condition (Table 25 b).

4.7.8 Catalase activity

The parental inbred line IL3 (6.5) showed lowest catalase followed by IL9 (6.5), IL4 (6.9) and IL10 (6.9) while the parental inbred line IL5 (7.8) exhibited highest catalase tracked by IL11 (7.8), IL7 (7.6) and IL6 (7.3) under irrigated condition. Alternatively, the parental inbred line IL4 (8.8) demonstrated lowest catalase tracked by IL5 (9.3), IL6 (9.6) and IL12 (9.6). The parental inbred line IL7 (11.9) exhibited highest catalase tracked by parental inbred lines IL8 (11.9), IL10 (11.2) and IL11 (10.8) under partial irrigated condition (Table 25 b).

The hybrid IL1 × IL3 (6.3) demonstrated lowest catalase tracked by IL1 × IL6 (6.3), IL3 × IL4 (6.3) and IL4 × IL10 (6.3) while the hybrid IL1 × IL8 (8.3) showed high catalase followed IL3 × IL5 (8.3), IL4 × IL11 (8.3) and IL6 × IL12 (8.3) under irrigated condition. Conversely, the hybrid IL2 × IL6 (8.8) showed lowest catalase tracked by IL4 × IL8 (8.8), IL7 × IL9 (8.8) and IL2 × IL7 (9.3). The hybrid IL2 × IL10 (11.9) demonstrated high catalase activity tracked by IL4 × IL12 (11.9), IL8 × IL9 (11.9) and IL1 × IL2 (10.7) under partial irrigated condition (Table 25b).

Table 25 (a) Nutritional, antinutritional and antioxidant profile of the inbred lines, their hybrids and check variety under irrigated condition and partial irrigated condition.

Genotype	Chlorophyll Content		Sugar Content		Proline Content		Malondialdehyde Content	
	I	PI	I	PI	I	PI	I	PI
IL1	0.74	0.74	1.2	1.27	29.8	32.9	9.7	12.5
IL2	0.75	0.75	0.9	1.2	36.5	39.7	8.4	13.5
IL3	0.77	0.77	0.91	1.23	27.6	31.6	9.7	12.7
IL4	0.75	0.75	0.96	1.36	29.5	32.8	10.2	15.8
IL5	0.69	0.69	1.2	1.47	39.3	41.3	8.5	11.6
IL6	0.88	0.88	1.1	1.3	33.5	38.3	9.4	15.9
IL7	0.76	0.76	1.23	1.2	29.4	31.2	10.3	15.5
IL8	0.81	0.81	1.22	1.99	43.6	47.7	9.8	16.4
IL9	0.84	0.84	0.97	1.08	23.9	25.9	10.4	14.5
IL10	0.89	0.89	0.97	1.48	36.6	39.4	9.7	12.5
IL11	0.76	0.76	0.96	1.52	24.9	36.7	8.4	13.5
IL12	0.77	0.77	0.99	1.56	31.8	34.5	9.7	12.7
IL1 × IL2	0.8	0.8	1.09	1.2	31.2	40.5	10.3	12.9
IL1 × IL3	0.82	0.82	1.23	1.4	34.4	37.3	9.5	15.2
IL1 × IL4	0.87	0.87	1.27	1.2	40.3	42.4	10.7	13.5
IL1 × IL5	0.78	0.78	1.2	1.27	36.6	42.1	9.2	11.7
IL1 × IL6	0.76	0.76	0.9	1.01	32.6	34.4	10.3	17.4
IL1 × IL7	0.77	0.77	0.91	1.11	41.6	43.3	10.4	15.1
IL1 × IL8	0.73	0.73	0.96	1.16	44.4	37.8	14.3	15.8
IL1 × IL9	0.78	0.78	1.2	1.21	38.9	41.7	14.6	16.6
IL1 × IL10	0.76	0.76	1.1	1.32	39.1	41.5	10.3	15.7
IL1 × IL11	0.74	0.74	1.23	1.37	31.4	34.8	9.6	12.8
IL1 × IL12	0.75	0.75	1.22	1.38	32.8	37.9	10.9	15.9
IL2 × IL3	0.77	0.77	0.97	1.17	33.5	38.7	10.2	14.6
IL2 × IL4	0.75	0.75	0.97	1.26	36.4	38.6	10.2	15.3
IL2 × IL5	0.69	0.69	0.96	1.93	37.5	41.1	9.6	12.7
IL2 × IL6	0.88	0.88	0.99	1.07	34.7	37.9	7.8	10.9
IL2 × IL7	0.76	0.76	0.95	1.12	32.9	36.4	9.9	10.8

I - Under irrigated condition, PI - partial irrigated condition

Contd.....

Table 25 (a). Contd.....

Genotype	Chlorophyll Content		Sugar Content		Proline Content		Malondialdehyde Content	
	I	PI	I	PI	I	PI	I	PI
IL2 × IL8	0.81	0.81	0.93	0.99	32.6	36.9	8.5	11.2
IL2 × IL9	0.84	0.84	0.88	0.94	35.2	37.4	8.2	12.9
IL2 × IL10	0.89	0.89	0.91	1.01	37.3	41.1	9.4	12.2
IL2 × IL11	0.76	0.76	0.96	1.91	32.9	39.2	7.9	13.3
IL2 × IL12	0.77	0.77	1.09	1.2	30.2	34.2	8.4	12.5
IL3 × IL4	0.76	0.76	1.23	1.39	20.7	30.3	7.2	13.7
IL3 × IL5	0.77	0.77	1.27	1.4	38.4	38.9	9.9	13.2
IL3 × IL6	0.71	0.71	1.2	1.41	37.6	39.1	7.4	12.8
IL3 × IL7	0.78	0.78	0.9	1.2	31.6	35.9	8.3	12.7
IL3 × IL8	0.76	0.76	0.91	1.03	32.7	36.1	7.3	13.8
IL3 × IL9	0.74	0.74	0.96	1.12	33.8	36.3	8.9	12.6
IL3 × IL10	0.75	0.75	1.2	1.32	20.3	24.3	7.5	10.9
IL3 × IL11	0.77	0.77	1.1	1.31	25.6	32.4	7.3	10.3
IL3 × IL12	0.75	0.75	1.23	1.36	29.4	38.4	8.2	10.5
IL4 × IL5	0.69	0.69	1.22	1.4	31.2	40.7	9.1	12.2
IL4 × IL6	0.88	0.88	0.97	1.1	29.8	32.2	8.4	13.6
IL4 × IL7	0.76	0.76	0.97	1.09	32.1	34.8	7.2	12.7
IL4 × IL8	0.81	0.81	0.96	1.29	17.6	22.7	10.3	17.4
IL4 × IL9	0.84	0.84	0.99	1.27	20.9	27.6	10.4	15.1
IL4 × IL10	0.8	0.8	0.95	1.09	27.2	35.8	14.3	15.8
IL4 × IL11	0.82	0.82	0.93	1.29	22.4	28.6	14.6	16.6
IL4 × IL12	0.87	0.87	0.88	1.27	22.4	28.2	10.3	15.7
IL5 × IL6	0.78	0.78	0.91	1.11	23.6	28.5	9.6	12.8
IL5 × IL7	0.76	0.76	0.96	1.22	17.6	21.6	10.9	15.9
IL5 × IL8	0.77	0.77	0.96	1.3	21.2	26.7	10.2	14.6
IL5 × IL9	0.73	0.73	0.91	1.56	28.3	37.5	10.2	15.3
IL5 × IL10	0.78	0.78	0.92	1.54	28.6	37.6	9.6	12.7
IL5 × IL11	0.76	0.76	0.93	1.11	29.6	49.5	7.8	10.9
IL5 × IL12	0.74	0.74	0.99	1.22	17.3	30.1	9.9	10.8

I - Under irrigated condition, PI - partial irrigated condition

Contd.....

Table 25 (a). Contd.....

Genotype	Chlorophyll Content		Sugar Content		Proline Content		Malondialdehyde Content	
	I	PI	I	PI	I	PI	I	PI
IL6 × IL7	0.75	0.75	1.09	1.25	26.6	30.4	8.5	11.2
IL6 × IL8	0.77	0.77	1.23	1.34	18.7	30.3	8.2	12.9
IL6 × IL9	0.75	0.75	1.27	1.53	18.4	36.8	9.4	12.2
IL6 × IL10	0.69	0.69	1.2	1.62	21.3	24.1	7.9	13.3
IL6 × IL11	0.88	0.88	0.9	1.54	21.5	38.8	8.4	12.5
IL6 × IL12	0.76	0.76	0.91	1.34	20.6	34.7	7.2	13.7
IL7 × IL8	0.81	0.81	0.96	1.53	21.2	32.4	9.9	13.2
IL7 × IL9	0.84	0.84	1.2	1.62	23.8	35.1	7.4	12.8
IL7 × IL10	0.89	0.89	1.1	1.54	23.3	41.2	8.3	12.7
IL7 × IL11	0.76	0.76	1.23	1.34	55.2	62.5	7.3	13.8
IL7 × IL12	0.77	0.77	1.22	1.53	21.1	32.7	8.9	12.6
IL8 × IL9	0.76	0.76	0.97	1.62	35.6	37.9	7.5	10.9
IL8 × IL10	0.77	0.77	0.97	1.54	26.6	32.6	7.3	10.3
IL8 × IL11	0.71	0.71	0.96	1.34	26.7	34.1	8.2	10.5
IL8 × IL12	0.8	0.8	0.99	1.53	19.8	23.5	9.1	12.2
IL9 × IL10	0.82	0.82	0.95	1.62	23.7	56	10.3	17.4
IL9 × IL11	0.87	0.87	0.93	1.54	22.2	30.3	10.4	15.1
IL9 × IL12	0.78	0.78	0.88	1.09	27.9	30.3	14.3	15.8
IL10 × IL11	0.76	0.76	0.91	1.23	29.8	36.1	14.6	16.6
IL10 × IL12	0.77	0.77	0.96	1.27	28.7	32.7	10.3	15.7
IL11 × IL12	0.73	0.73	1.09	1.2	28.9	29.5	10.3	15.5
HKI 1105	0.78	0.78	1.23	1.09	33.9	38.5	9.8	16.4
HKI 1128	0.76	0.76	1.27	1.23	28.4	32.9	10.4	14.5

I - Under irrigated condition, PI - partial irrigated condition

Table 25 (b). Nutritional, antinutritional and antioxidant profile of the inbred lines, their hybrids and check variety under irrigated condition and partial irrigated condition

Genotype	H ₂ O ₂ Content		Peroxidase		Glutathione		Catalase	
	I	PI	I	PI	I	PI	I	PI
IL1	42.4	64.4	14.1	25.8	0.37	0.369	7.2	10.4
IL2	38.8	57.5	19.3	29.8	0.321	0.32	7.1	9.8
IL3	47.6	64.3	16.3	28.4	0.286	0.284	6.5	9.8
IL4	33.9	38.2	14.8	29.2	0.305	0.301	6.9	8.8
IL5	45.4	68.2	14.4	22.7	0.33	0.328	7.8	9.3
IL6	44.3	56.5	17.1	19.1	0.227	0.225	7.3	9.6
IL7	43.5	50.7	13.2	31.9	0.321	0.322	7.6	10.9
IL8	46.5	62.3	15.5	26.7	0.257	0.254	7.1	11.9
IL9	38.6	45.4	14.7	29.4	0.342	0.342	6.5	10.7
IL10	45.5	58.7	15.1	24.2	0.316	0.316	6.9	11.2
IL11	39.6	54.3	15.9	31.9	0.294	0.293	7.8	10.8
IL12	40.5	56.4	13.9	25.5	0.33	0.33	7.3	9.6
IL1 × IL2	38.5	42.1	18.9	21.3	0.301	0.299	7.8	10.7
IL1 × IL3	37.9	53.3	15.7	28.9	0.213	0.212	6.3	11.2
IL1 × IL4	49.3	56.2	23.1	29.6	0.267	0.268	7.8	10.8
IL1 × IL5	38.6	63.6	15.9	30.9	0.265	0.265	6.5	9.6
IL1 × IL6	36.7	56.2	16.4	28.9	0.292	0.291	7.9	10.9
IL1 × IL7	41.1	59.4	18.7	31.8	0.325	0.324	6.3	10.2
IL1 × IL8	53.5	55.3	19.6	30.4	0.304	0.304	8.3	10.2
IL1 × IL9	46.9	55.7	17.2	27.6	0.285	0.285	7.8	10.8
IL1 × IL10	45.3	69.6	17.3	29.4	0.303	0.302	7.1	10.3
IL1 × IL11	44.4	66.4	19.1	27.8	0.279	0.277	7.7	11.7
IL1 × IL12	47.7	55.7	16.7	31.4	0.333	0.332	7.2	10.3
IL2 × IL3	49.4	55.7	17.2	27.3	0.342	0.341	7.1	10.4
IL2 × IL4	47.3	60.7	19.4	30.6	0.286	0.286	6.5	9.8
IL2 × IL5	45.6	53.7	16.6	21.8	0.369	0.369	6.9	9.8
IL2 × IL6	46.8	48.9	17.3	25.8	0.29	0.29	7.8	8.8
IL2 × IL7	47.1	53.9	16.5	24.2	0.255	0.254	7.3	9.3

I - Under irrigated condition, PI - partial irrigated condition

Contd.....

Table 25 (b). Contd.....

Genotype	H ₂ O ₂ Content		Peroxidase		Glutathione		Catalase	
	I	PI	I	PI	I	PI	I	PI
IL2 × IL8	46.9	51.6	17.7	28.3	0.286	0.286	7.6	9.6
IL2 × IL9	47.9	52.5	19.7	26.9	0.32	0.32	8.2	10.9
IL2 × IL10	42.1	59.5	16.9	31.4	0.29	0.29	7.8	11.9
IL2 × IL11	40.7	48.3	16.4	26.5	0.318	0.318	6.5	10.7
IL2 × IL12	46.2	49.8	15.3	24.8	0.285	0.284	7.9	11.2
IL3 × IL4	40.1	66.4	14.4	26.4	0.301	0.3	6.3	10.8
IL3 × IL5	39.8	46.9	17.8	27.1	0.301	0.299	8.3	9.6
IL3 × IL6	50.2	55.7	17.5	20.5	0.263	0.262	7.8	10.9
IL3 × IL7	42.7	50.5	17.1	25.1	0.249	0.249	7.1	10.2
IL3 × IL8	47.3	65.5	18.5	20.3	0.23	0.229	7.7	10.2
IL3 × IL9	42.4	48.1	19.6	23.1	0.235	0.233	7.2	10.8
IL3 × IL10	39.1	64.8	16.3	30.9	0.28	0.28	7.1	10.3
IL3 × IL11	35.7	54.6	16.7	26.6	0.26	0.26	6.5	11.7
IL3 × IL12	36.3	57.8	16.6	23.7	0.241	0.241	6.9	10.3
IL4 × IL5	34.9	54.3	16.2	23.3	0.239	0.24	7.8	10.4
IL4 × IL6	38.1	53.1	14.1	24.9	0.296	0.296	7.3	9.8
IL4 × IL7	42.2	57.9	15.9	18.4	0.321	0.321	7.6	9.8
IL4 × IL8	43.8	52.5	17.2	25.7	0.272	0.272	6.5	8.8
IL4 × IL9	45.5	54.2	18.6	24.2	0.275	0.275	7.9	9.3
IL4 × IL10	51.8	68.5	16.9	24.2	0.257	0.256	6.3	9.6
IL4 × IL11	39.8	61.4	16.6	21.6	0.302	0.301	8.3	10.9
IL4 × IL12	46.6	52.9	16.9	29.2	0.242	0.242	7.8	11.9
IL5 × IL6	48.1	55.4	16.6	23.7	0.234	0.233	7.1	10.7
IL5 × IL7	42.1	51.9	17.5	23.9	0.266	0.265	7.7	11.2
IL5 × IL8	50.5	57.1	16.3	21.5	0.347	0.345	7.2	10.8
IL5 × IL9	40.8	52.4	17.5	23.2	0.269	0.269	7.1	9.6
IL5 × IL10	42.9	50.4	17.1	23.8	0.299	0.299	6.5	10.9
IL5 × IL11	48.1	60.8	16.6	24.4	0.328	0.327	6.9	10.2
IL5 × IL12	44.6	63.4	17.3	20.1	0.282	0.281	7.8	10.2

I - Under irrigated condition, PI - partial irrigated condition

Contd.....

Table 25 (b). Contd.....

Genotype	H ₂ O ₂ Content		Peroxidase		Glutathione		Catalase	
	I	PI	I	PI	I	PI	I	PI
IL6 × IL7	36.8	59.7	15.3	20.6	0.341	0.341	7.3	10.8
IL6 × IL8	45.3	61.3	15.5	23.1	0.303	0.314	7.6	10.3
IL6 × IL9	49.3	68.4	16.9	24.9	0.303	0.301	6.5	11.7
IL6 × IL10	44.7	51.9	17.3	22.1	0.265	0.265	7.9	10.3
IL6 × IL11	42.2	60.7	12.5	19.9	0.287	0.286	6.3	10.4
IL6 × IL12	45.9	67.7	15.4	22.3	0.373	0.373	8.3	9.8
IL7 × IL8	45.5	59.6	16.6	24.5	0.354	0.353	7.8	9.8
IL7 × IL9	38.1	61.4	15.7	22.4	0.316	0.314	7.1	8.8
IL7 × IL10	38.7	66.2	17.1	19.1	0.314	0.314	7.7	9.3
IL7 × IL11	47.8	60.7	16.4	24.9	0.261	0.26	7.2	9.6
IL7 × IL12	42.9	70.8	16.2	23.8	0.244	0.242	7.1	10.9
IL8 × IL9	46.5	59.4	15.6	25.3	0.266	0.265	6.5	11.9
IL8 × IL10	45.3	62.6	16.4	22.5	0.304	0.302	6.9	10.7
IL8 × IL11	41.1	70.1	15.7	22.5	0.295	0.293	7.8	11.2
IL8 × IL12	47.7	76.9	16.1	30.5	0.283	0.282	7.3	10.8
IL9 × IL10	46.1	73.1	16.7	22.2	0.275	0.274	7.6	9.6
IL9 × IL11	38.3	44.2	14.2	20.1	0.266	0.265	6.5	10.9
IL9 × IL12	41.7	58.3	16.4	22.2	0.406	0.405	7.9	10.2
IL10 × IL11	44.3	50.5	15.8	23.1	0.374	0.373	6.3	10.2
IL10 × IL12	43.3	60.8	15.8	28.2	0.345	0.344	8.3	10.8
IL11 × IL12	43.4	57.8	13.4	23.5	0.349	0.347	7.8	10.3
HKI 1105	45.4	55.7	14.5	28.5	0.355	0.353	7.1	11.7
HKI 1128	46.5	58.7	15.7	38.7	0.06	0.06	7.7	10.3

I - Under irrigated condition, PI - partial irrigated condition

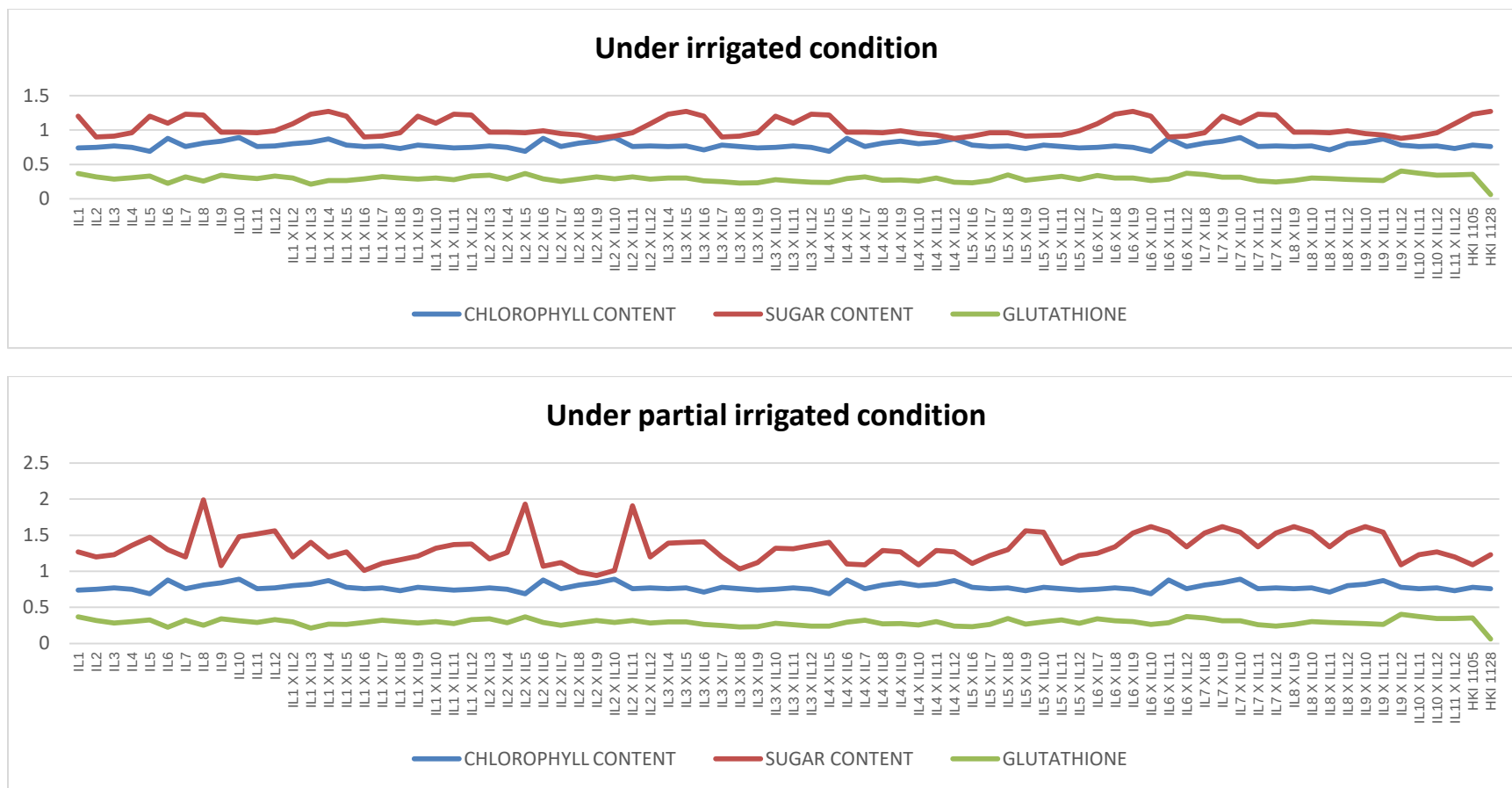


Fig 4. Line diagram of three important biochemical traits recorded in 80 maize genotypes under irrigated and partial irrigated condition.

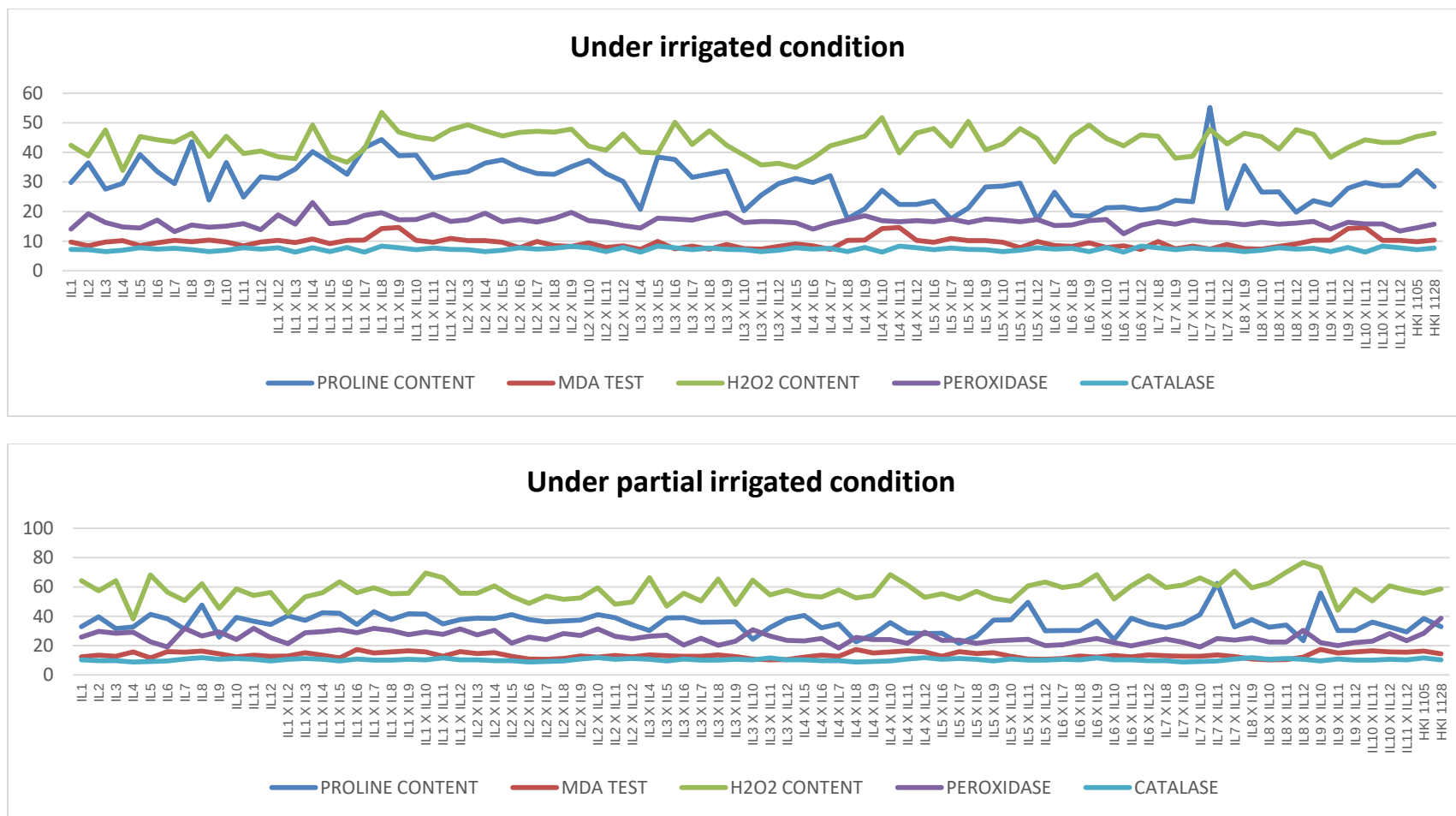


Fig 5. Line diagram of five important biochemical traits recorded in 80 maize genotypes under irrigated and partial irrigated condition

4.7. A Diversity and expression analysis among biochemical parameters

Phylogenetic analysis between 12 inbred lines, 66 hybrids along with two checks for nutritional, antinutritional and antioxidant profile revealed into different clusters Based on dendrogram (Fig 6). These clusters contained 80 genotypes that were divided mainly into five clusters, clusters I main group contained 39 genotypes, II clusters contained four genotypes, III clusters contained seven genotypes, IV clusters contained 23 genotypes, V clusters contained five genotypes and further division goes on. Genotype IL7 × IL11 and IL9 × IL10 was found most diverse.

Heat maps are used frequently in expression analysis studies for data visualization and quality control. Heat map analysis used for 80 genotypes using eight biochemical parameters such as proline content, total soluble sugar content, chlorophyll content, MDA TEST, H₂O₂ content, peroxidase activity, glutathione reductase activity, catalase activity, under irrigated and partial irrigated condition, using color key blue ranges from 0.69 to 76.9.

According to heat map analysis under irrigated condition the chlorophyll content expression seems to be maximum in IL10 and IL2 × IL10 for parent and hybrid respectively, while minimum in IL5 and IL6 × IL10 for parent and hybrid. The total soluble sugar content expression seems to be maximum in IL7 and IL1 × IL4 for parent and hybrid respectively, while minimum in IL2 and IL9 × IL12 for parent and hybrid. The proline content expression seems to be maximum in IL8 and IL7 × IL11 for parent and hybrid respectively while minimum in IL9 and IL5 × IL12 for parent and hybrid. The MDA test expression seems to be maximum in IL9 and IL1 × IL9 for parent and hybrid respectively, while minimum in IL2 and IL6 × IL12 for parent and hybrid. The H₂O₂ content expression seems to be maximum in IL3 and IL1 × IL8 for parent and hybrid respectively, while minimum in IL4 and IL4 × IL5 for parent and hybrid. The Peroxidase activity expression seems to be maximum in IL2 and IL1 × IL4 for parent and hybrid respectively while minimum in IL7 and IL6 × IL11 for parent and hybrid. The glutathione reductases activity expression seems to be maximum in IL1 and IL9 × IL12 for parent and hybrid respectively while minimum in IL6 and HKI 1128 for parent and

check variety. The catalase activity expression seems to be maximum in IL5 and IL1 × IL8 for parent and hybrid respectively while minimum in IL9 and IL10 × IL11 for parent and hybrid.

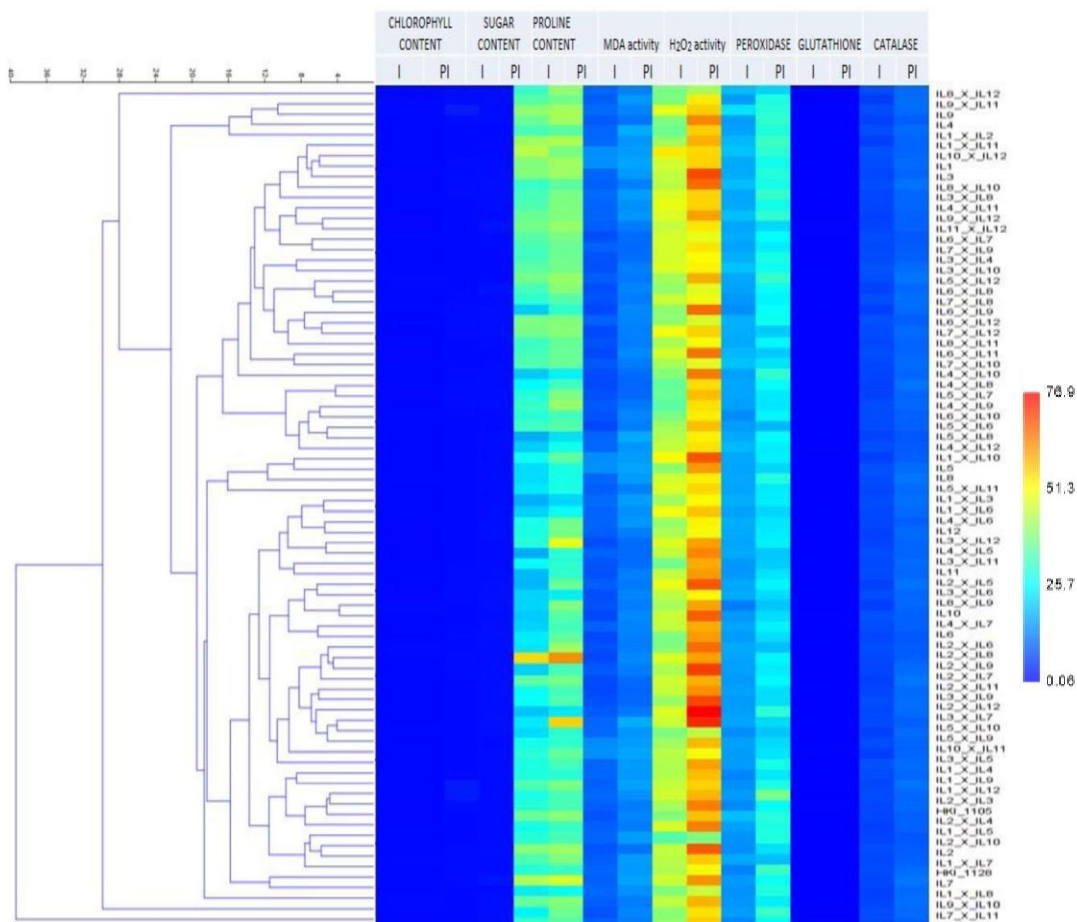


Fig 6. Dendrogram and Heat Map analysis of various Biochemical Parameter in inbred lines, their hybrids and check variety under irrigated (I) and partial irrigated condition (PI).

Under partial irrigated condition the chlorophyll content expression seems to be maximum in IL10 and IL2 × IL10 for parent and hybrid respectively while minimum in IL5 and IL6 × IL10 for parent and hybrid. The total Soluble sugar content expression seems to be maximum in IL8 and IL2 × IL5 for parent and hybrid respectively while minimum in IL9 and IL2 × IL9 for parent and hybrid. The proline content expression seems to be maximum in IL8 and IL7 × IL11 for parent and hybrid respectively while minimum in IL9 and IL5 × IL7 for parent and hybrid.

The MDA test expression seems to be maximum in IL8 and IL1 × IL6 for parent and hybrid respectively while minimum in IL5 and IL8 × IL10 for parent and hybrid. The H₂O₂ content expression seems to be maximum in IL5 and IL8 × IL12 for parent and hybrid respectively while minimum in IL4 and IL1 × IL2 for parent and hybrid. The Peroxidase activity expression seems to be maximum in IL7 and HKI 1128 for parent and Check variety respectively while minimum in IL6 and IL4 × IL7 for parent and hybrid. The Glutathione reductases activity expression seems to be maximum in IL1 and IL9 × IL12 for parent and hybrid respectively while minimum in IL6 and HKI 1128 for parent and Check variety. The Catalase activity expression seems to be maximum in IL8 and IL2 × IL10 for parent and hybrid respectively while minimum in IL4 and IL7 × IL9 for parent and hybrid.

4.8 Analysis of Genomic DNA of maize.

The amount of genomic DNA in all eighty maize genotypes ranged from 100 to 2000 ng/ul. In Nano-drop, the majority of the DNA samples had 260/280 and 260/230 values around 2.0, indicating high quality DNA. Genomic DNA with values less than 1.7 was sheared and isolated once more.

4.8.1 Screening of maize genotypes using gene-based markers against drought

A set of twenty gene-based markers was screen all eighty-maize genotype for drought resistance. For PCR amplification, high-quality genomic DNA was considered. Among the genotypes, all primers produced polymorphic bands. The scoring was done using a standard size ladder and a banding pattern. A data sheet was created in order to run in population structure and allele pattern A/A when the band was on the upper side, and when the band was on the lower side, pattern B/B was used. When the band was heterozygous, pattern A/B was used, and when there was no amplification, pattern -/- was used.

4.8.2 Phylogenetic cluster analysis and PIC information

Genetic variation

The variability among microsatellite loci was determined in terms of the major allelic frequency (MAF), number of allele (NA), gene diversity (GD) and polymorphic information content (PIC). Table 26.

Major allelic frequency (MAF)

Major allelic frequency ranged from 0.36 (bnlg2190) to 0.68 (bnlg1035) with mean value of 0.52.

Number of allele (AN)

Based on twenty polymorphic loci, 110 alleles were detected among 80 maize genotypes. Number of major alleles ranged from four to seven with an average of 5.5 alleles per locus. Markers (bnlg1083, bnlg1614, bnlg2190, bnlg2248 and bnlg439) showed maximum seven alleles per locus each.

Gene diversity (GD)

Gene diversity values ranged between 0.50-72.

Polymorphic information content (PIC)

The polymorphic information content was employed for each locus to assess the information of each marker and its discriminatory ability and it is a reflection of allele diversity and frequency among varieties. PIC values ranged between 0.47-0.67 with the mean value of 0.59.

All markers showing amplification in maize, 10 markers were highly polymorphic (>0.60). The highest PIC value was obtained for the molecular marker bnlg2190 (0.67) followed by respectively bnlg1614 and bnlg2248, phi053 and phi053 (0.64), whereas bnlg1083 and bnlg1136 (0.51) was the least. PIC value revealed that bnlg2190 was considered as best marker for test inbred lines and their hybrids. The polymorphic primers which have high PIC value can be used in further molecular studies like association mapping, tagging of gene of interest and the most called approach marker assisted selection (MAS).

Table 26. Details of diversity statistics for each microsatellite marker

Marker	MAF	GN	AN	GD	HZ	PIC
bnlg1028	0.57	6	6	0.6	0.62	0.54
bnlg1035	0.68	5	5	0.5	0.4	0.47
bnlg1063	0.55	5	5	0.61	0.38	0.56
bnlg1083	0.62	7	7	0.56	0.6	0.51
bnlg1136	0.63	6	6	0.55	0.58	0.51
bnlg1225	0.54	6	6	0.65	0.64	0.61
bnlg1297	0.41	5	5	0.69	0.62	0.63
bnlg1327	0.48	4	4	0.64	0.44	0.57
bnlg1346	0.56	4	4	0.62	0.6	0.58
bnlg1614	0.38	7	7	0.7	0.6	0.65
bnlg1812	0.42	5	5	0.68	0.52	0.62
bnlg1866	0.61	5	5	0.57	0.66	0.52
bnlg2190	0.36	7	7	0.71	0.58	0.67
bnlg2248	0.49	7	7	0.68	0.58	0.64
bnlg2252	0.55	5	5	0.64	0.5	0.6
bnlg2328	0.52	5	5	0.65	0.6	0.6
bnlg439	0.58	7	7	0.62	0.6	0.58
dupssr13	0.5	4	4	0.65	0.6	0.59
nc012	0.45	5	5	0.69	0.58	0.64
phi053	0.48	5	5	0.68	0.64	0.64
Mean	0.52	5.5	5.5	0.63	0.57	0.59

MAF= Major allelic frequency, GD = Gene diversity, AN = Number of alleles, GD = Gene diversity, HZ = Heterozygosity, PIC = Polymorphic information content

4.8.3 Neighbor-Joining UPGMA analyses

The genotypic data of SSRs were further used to study the genetic diversity based on NJ-UPGMA analysis. Interestingly, this analysis exhibited the similar pattern as structure analysis revealing eight different clusters. The

remarkably differences were observed among the inbred lines and their hybrids belonging to different considerable traits of drought.

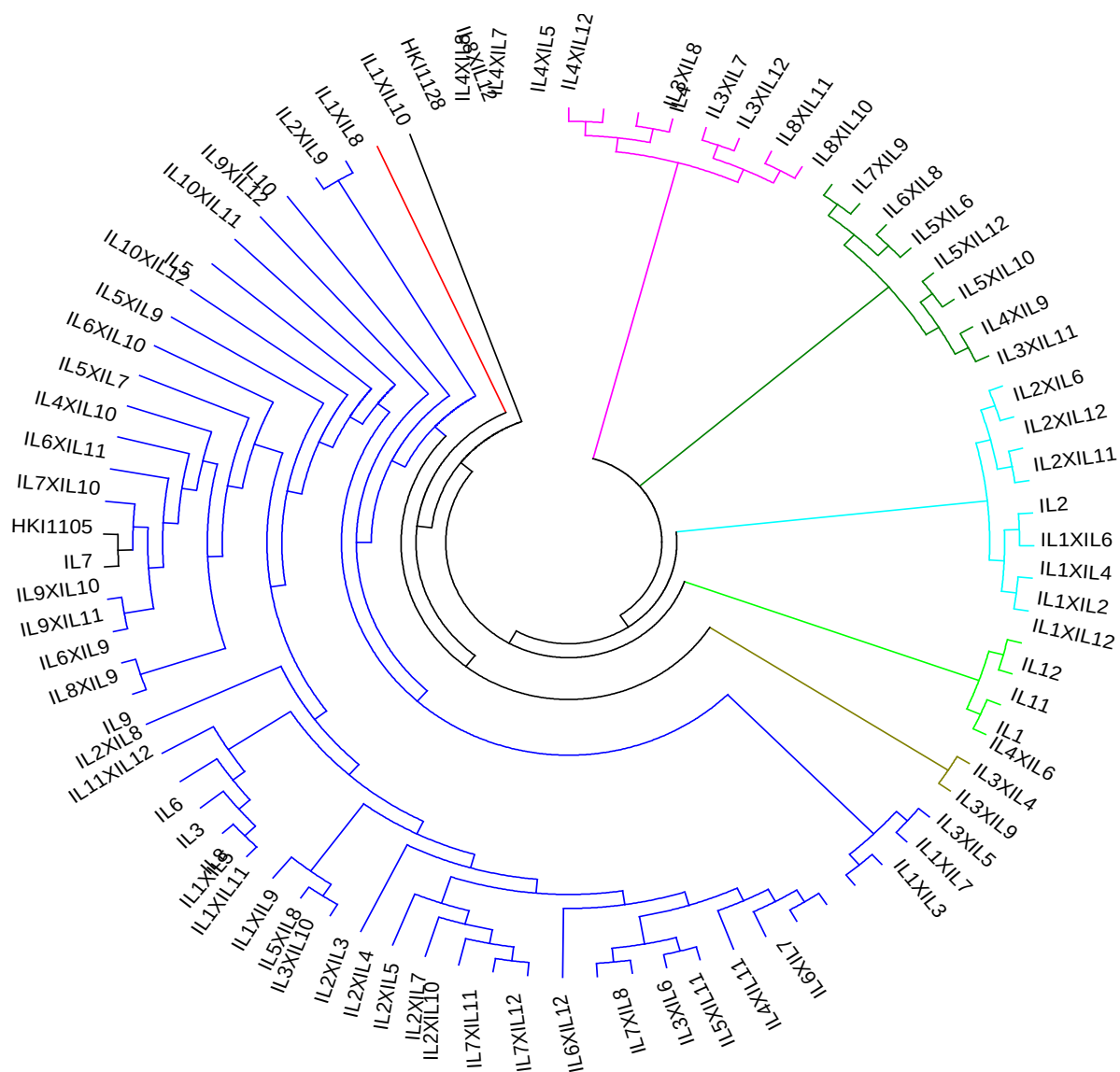


Fig 7. Phylogenetic UPGMA tree based on similarity index of SSR markers of maize genotypes.

Table 27. Clustering of twelve parents, two checks and 66 hybrids obtained from twenty SSR markers.

Cluster	No. of genotypes	Name of genotypes
I	8	IL4, IL3 × IL7, IL3 × IL8, IL3 × IL12, IL4 × IL5, IL4 × IL7, IL4 × IL8, IL4 × IL12
II	8	IL4 × IL9, IL5 × IL6, IL5 × IL10, IL5 × IL12, IL6 × IL8, IL7 × IL9, IL8 × IL10, IL8 × IL11
III	8	IL2, IL1 × IL2, IL1 × IL4, IL1 × IL6, IL2 × IL6, IL2 × IL11, IL2 × IL12, IL3 × IL11
IV	4	IL11, IL12, IL1, IL1 × IL11
V	2	IL3 × IL4, IL4 × IL6
VI	48	IL3, IL5, IL6, IL7, IL8, IL9, IL10, HK 1105, IL1 × IL3, IL1 × IL5, IL1 × IL7, IL1 × IL8, IL1 × IL9, IL1 × IL10, IL1 × IL12, IL2 × IL3, IL2 × IL4, IL2 × IL5, IL2 × IL7, IL2 × IL8, IL2 × IL9, IL2 × IL10, IL3 × IL5, IL3 × IL6, IL3 × IL9, IL3 × IL10, IL4 × IL10, IL4 × IL11, IL5 × IL7, IL5 × IL8, IL5 × IL9, IL5 × IL11, IL6 × IL7, IL6 × IL9, IL6 × IL10, IL6 × IL11, IL6 × IL12, IL7 × IL8, IL7 × IL10, IL7 × IL11, IL7 × IL12, IL8 × IL9, IL9 × IL10, IL9 × IL11, IL9 × IL12, IL10 × IL11, IL10 × IL12, IL11 × IL12
VII	1	HK1128
VIII	1	IL8 × IL12

Based on unweighted neighbor-joining cluster analysis put the eighty genotypes (Parents, Hybrids and Checks) into eight major clusters (Fig 7). Cluster VI comprised forty eight genotypes viz., IL3, IL5, IL6, IL7, IL8, IL9, IL10, HK 1105, IL1 × IL3, IL1 × IL5, IL1 × IL7, IL1 × IL8, IL1 × IL9, IL1 × IL10, IL1 × IL12, IL2 × IL3, IL2 × IL4, IL2 × IL5, IL2 × IL7, IL2 × IL8, IL2 × IL9, IL2 × IL10, IL3 × IL5, IL3 × IL6, IL3 × IL9, IL3 × IL10, IL4 × IL10, IL4 × IL11, IL5 × IL7, IL5 × IL8, IL5 × IL9, IL5 × IL11, IL6 × IL7, IL6 × IL9, IL6 × IL10, IL6 × IL11, IL6 × IL12, IL7 × IL8, IL7 × IL10, IL7 × IL11, IL7 × IL12, IL8 × IL9, IL9 × IL10, IL9 × IL11, IL9 × IL12, IL10 × IL11, IL10 × IL12, IL11 × IL12 evolving the maximum genotypes. The clusters I, II and III having eight genotypes each viz., IL4, IL3 × IL7, IL3 × IL8, IL3 × IL12, IL4 × IL5, IL4 × IL7, IL4 × IL8, IL4 × IL12; IL4 × IL9, IL5 × IL6, IL5

× IL10, IL5 × IL12, IL6 × IL8, IL7 × IL9, IL8 × IL10, IL8 × IL11 and IL2, IL1 × IL2, IL1 × IL4, IL1 × IL6, IL2 × IL6, IL2 × IL11, IL2 × IL12, IL3 × IL11 respectively. The cluster IV contains four genotypes (IL11, IL12, IL1, IL1 × IL11) and cluster V contains only two genotypes (IL3 × IL4, IL4 × IL6). Cluster VII and VIII comprised only one genotype each (HKI1128; IL8 × IL12). The pattern of group constellation proved the existence of significant amount of variability.

According to Jaccard's similarity coefficient, in cluster VI contained 48 genotypes the highest similarity was observed between IL1 × IL10, IL1 × IL8, HKI1105, IL7, IL9 × IL10, IL9 × IL11, IL6 × IL9, IL8 × IL9, IL3, IL8, IL1 × IL11, IL1 × IL9, IL2 × IL5, IL2 × IL7, IL7 × IL11, IL7 × IL12, IL6 × IL12, IL7 × IL8, IL4 × IL11, IL6 × IL7, IL3 × IL9, IL3 × IL5, IL1 × IL7, IL1 × IL3 and the highest genetic diversity was observed between IL1 × IL10 and IL3 × IL9. In cluster V contained two genotypes IL4 × IL6 and IL3 × IL4 they show highest similarity was observed. In cluster IV contained four genotypes IL1 × IL12, IL12, IL11 and IL1 they show highest similarity was observed. In cluster III contained eight genotypes IL3 × IL11, IL2 × IL6, IL2 × IL12, IL2 × IL11, IL2, IL1 × IL6, IL1 × IL4 and IL1 × IL2 they show highest similarity was observed. In cluster II contained eight genotypes IL8 × IL11, IL8 × IL10, IL7 × IL9, IL6 × IL8, IL5 × IL6, IL5 × IL12, IL5 × IL10 and IL4 × IL9 they show highest similarity was observed. In cluster I contained eight genotypes IL4 × IL8, IL4 × IL7, IL4 × IL5, IL4 × IL12, IL4, IL3 × IL8, IL3 × IL7 and IL3 × IL12 they show highest similarity was observed. Rest of the cluster VII and VIII both contained only one genotypes HKI1128 and IL8 × IL12. The drought tolerant genotypes HKI1105 fiend in group VI along with 47 genotypes, so all the genotypes show drought tolerance in nature. The drought susceptible HKI1128 only genotype fined in group VII. Rest of the group II, III, IV, V, VI, VIII show moderate drought tolerance in nature.

CHAPTER - 5

DISCUSSION

Exploitation of heterosis or hybrid vigor is an important method of crop improvement adopted in many of the cross-pollinated crops. This phenomenon of heterosis attracted the attention of plant breeders owing to its conspicuous effect on economic characters especially grain yield and this heterosis has been successfully exploited in many cross-pollinated crops among which maize is important.

In order to exploit heterosis, choice of suitable parents is an important step. The selection of parents depends on factors like *per se* performance of the parents and their combining ability. The concept of general and specific combining ability (Sprague and Tatum, 1942) helps the breeder in choosing the lines to be used as parents in the production of hybrids and also in identifying the superior hybrids having additive and non-additive genes. It is therefore necessary to assess the genetic potential of the parents in hybrid combination through systematic studies in relation to general and specific combining ability which are due to additive and non-additive gene actions. Thus, the information regarding heterosis, combining ability and nature of gene action are the basic requirements for a thorough understanding of genetic architecture of yield and its components.

Drought is the most pervasive limitation of yield potential in maize (Edmeades *et al.*, 2001). Moisture stress in maize affects both yield and yield stability. Within a given maize field, variation in soil depth and texture induce moisture stress. Besides this, the effect of climate change is looming large on agricultural production. Indian monsoon is known for unpredictable rainfall, which results into moisture stress at different growth stage of maize. One day of delay between pollen shed and silk emergence reduce the rate of fertilization and increase barrenness. Thus, developing drought tolerant varieties considering the ecosystem under which it is grown can stabilize maize productivity. The selection of tolerant lines for drought in maize depends largely on efficient selection criteria. Understanding of morphological, physiological and biochemical basis of

drought tolerance is pre-requisite for effective selection of genotypes and breeding for moisture stress condition.

5.1 Analysis of variance for experimental design

Analysis of variance was performed to test the difference amongst parents and hybrids for all the eighteen traits. The results revealed that the mean sum of squares due to genotypes were highly significant for all the characters studied. The mean sum of squares due to genotypes were further partitioned into parents, hybrids and parents vs. hybrids. The analysis of variance for experimental design in individual environment revealed significant differences among genotypes for all the characters in both under irrigated and partial irrigated environment.

Further partitioning of genotypic variance into parents, hybrids and parent's v/s hybrids revealed that for all the characters under study there were significant difference in all environments. The mean sum of squares of hybrids were also significant for all the characters in all the environments. This indicated the existence of appreciable amount of genetic variability in the experimental material of present study.

The analysis of variance for experimental design revealed the presence of significant amount of variability among parents in individual environment for most of the characters in the experiment. This suggested that the parental lines selected were quite variable for most of the characters under study. Further, the analysis of variance revealed that the variation due to moisture stress at two different times affect genotypes significantly for all the traits indicating the presence of sufficient variability in the experiment/study material. Presence of sufficient amount of variability encourages for screening of the genotypes for moisture stress tolerance.

Earlier workers like Dubey *et al.* (2001), Joshi *et al.* (2002), Abhirami *et al.* (2005), Dadheech and Joshi (2007), Luders *et al.* (2007), Suvana *et al.* (2008), Ngugi and Nielsen (2013), Rajesh *et al.* (2014), Kumar *et al.* (2016) and Ertiro *et al.* (2017) have also reported the significant differences among the genotypes for different traits.

5.2 *Per se* performance of morpho-physiological traits of parents, their hybrids and check varieties under irrigated and partially irrigated condition

Hybrid is one of the greater practical contributions of genetics and has its most significant expression in maize crop. The breeding strategy for exploitation of heterosis in maize (*Zea mays* L) through the cultivation of single cross hybrids is primarily development on the development and identification of high *per se* performance diverse, vigorous and productive inbred lines with good seed quality in cross combinations to identify single crosses with high heterotic effects.

Genetic parameters like heterosis and combining ability provide adequate guide lines for selection of parents/crosses for getting desirable segregants/exploitation of heterosis. Various mating design are available to derive information about the combining ability but for present study diallel mating design was used because in this design a greater number of parents and hybrids can be evaluated for their genetic worth.

In the present investigation, heterosis, combining ability effects, drought stress related parameters, early maturity and yield contributing parameters were studied to developed and identify suitable and stable single cross hybrids.

The mean data of days to 50% tasseling, days to 50% silking and anthesis silking interval revealed that the hybrids IL7 × IL8, IL1 × IL11, IL9 × IL12, IL9 × IL12 and IL5 × IL7 showed minimum value. On the basis of mean data, we can identify the early maturity hybrids.

Mean data of yield and its contributing traits revealed that the hybrids IL1 × IL8, IL7 × IL8, IL9 × IL10 and IL1 × IL3 showed maximum value. On the basis of mean data, we can identify the high yielding hybrids.

Mean data of drought tolerance indices revealed that the hybrids IL3 × IL5, IL8 × IL12, IL1 × IL10, IL3 × IL10 showed maximum value. On the basis of mean data, we can identify the hybrids with drought tolerance.

The importance of short ASI has also been documented by Kumari *et al.* (2004), Appunu *et al.* (2007), Nyombayire *et al.* (2011), Ali *et al.* (2012) and Ofori *et al.* (2015).

Physiological Traits

The relative water content (RWC) gives an idea of water retention capacity of a tissue. Many scientists have observed differences in RWC among the genotypes of crop species (Barrs and Weatherly, 1962; Parameshwara, 1978). Results of the present investigation indicated that the RWC decreased with a progress in crop growth in all genotypes and the decrease was more in stress situation. The parental inbred line IL6, IL4, IL12, IL10 and hybrid IL1 × IL12, IL1 × IL7, IL5 × IL8 and IL10 × IL12 recorded higher mean relative water content compared to other genotypes. Higher RWC in these genotypes may be attributed to their higher diffusion resistance or due to deeper root system under stress condition. Similar results were also documented by Patil *et al.* (1984), O'regan *et al.* (1993), Hiremath *et al.* (1994), Diouf *et al.* (2001), Li-Ping *et al.* (2006) and Guang-hua Yin *et al.* (2012).

Membrane stability index and relative water contents are very viable parameters that directly contribute to plant output (Lawlor, 2002). In the present study, drought caused a significant reduction in relative water contents and membrane stability index in all maize hybrids. The drought-tolerant varieties have higher water contents and membrane stability index (Khadem *et al.*, 2010). The maize parental inbred line viz., IL2, IL10, IL4, IL9 and hybrid IL1 × IL9, IL6 × IL7, IL5 × IL6 and IL2 × IL5 showed higher membrane stability index under drought stress conditions as compared to drought sensitive maize inbred line IL8 and hybrid IL7 × IL12. Higher relative water contents in water-stressed plants may be the result of lower rates of water loss owing to stomatal closure and developed variety (Valentovic *et al.* 2006). Cell membrane stability decreased by severe drought stress in other words in this condition destruction of cell wall increased (Pour *et al.* 2007).

5.3: Combining ability analysis:

The ultimate choice of parents to be used in a breeding programme is determined by *per se* performance and their behavior in hybrid combination. It is therefore, necessary to assess genetic potentialities of the parents in hybrid combination through systematic studies in relation to general and specific combining abilities. Sprague and Tatum (1942) developed the concept of combining ability and coined the two terms general combining ability (GCA) and specific combining ability (SCA). The combining ability elucidates the nature of gene action involved in the inheritance of a trait. The general combining ability is attributed to additive, additive $\times$ additive interactions and is fixable in nature. On the other hand, specific combining ability is attributed to non-additive (*i.e.* dominance, dominance $\times$ dominance and additive $\times$ dominance) gene action and it is non- fixable.

The Analysis of variance of combining ability for partitioning the total genetic variance into general combining ability, (gca representing additive type of gene action) and specific combining ability (sca, a measure of non-additive gene action) was carried out by the procedure suggested by Griffing (1956b) Method-2 and Model-I. Variance due to gca as well as sca was found significant for all the characters investigated. Magnitudes of gca variance component was higher than sca for all the characters.

Parents were classified as good, average and poor combiners on the basis of their GCA effects. Parents with desirable and significant GCA effects were considered good combiners while parents showing non-significant estimates but in desirable direction were classified as average combiners. Poor combiners had undesirable GCA effects. The parental inbred lines IL2, IL3, IL4, IL6, IL8, IL10 and IL11 showed negative significant gca effects under irrigated and partially irrigated condition.

GCA effects provides information about the additive gene action involved in expression of various traits *viz.*, days to 50% tasseling, days to 50 % silking, anthesis silking interval (ASI) and days to maturity and thus helps in deciding the

breeding procedure for genetic improvement of traits. The gca variance are higher sca variances, it means that there is pre-ponderance of additive gene action and progeny selection will be effective for the improvement of these traits.

The estimates of GCA effects for yield and yield contributing characters revealed that good general combiner inbred lines for grain yield per plant were IL6, IL7, IL9, IL10, IL11 and IL12.

The magnitude of SCA variance was greater than GCA variance for most of the traits indicating pre-ponderance of non-additive variance in controlling the expression of these traits. The majority of non-additive gene effects for grain yield in maize was also reported by Kanagarasu *et al.* (2010), Kose and Turgut (2011), Reddy *et al.* (2011), Lal and Kumar (2012), Abrha *et al.* (2013), Gautam *et al.* (2013), Kumara *et al.* (2013), Chandel *et al.* (2014), Kumar *et al.* (2014), Motamedi *et al.* (2014), Verma *et al.* (2014), Ruswandi (2015), Wuhiab *et al.* (2016) and Kuselan *et al.* (2017). Fu *et al.* (2008) reported that the variances of specific combining ability (SCA) were about double that of the general combining ability (GCA) for plant height, ASI and grain yield per plant.

The hybrid IL1 × IL11 showed high positive significant sca effect tracked by IL1 × IL7, IL3 × IL10, IL4 × IL6 and IL7 × IL8. The hybrid IL4 × IL7 showed high negative significant sca effect tracked by IL1 × IL6, IL5 × IL7, IL2 × IL4 and IL3 × IL12. The sca variance are higher gca variances, it means that there is preponderance of non-additive gene action and progeny heterosis will be effective for the for development of hybrids.

Similar findings for identification of superior hybrids based on SCA effects for grain yield and its components in maize were also reported by Premlatha *et al.* (2011), Kage *et al.* (2013), Kapoor *et al.* (2014), Jain and Bharadwaj (2014), Shah *et al.* (2015), Barh *et al.* (2016), Kuselan *et al.* (2017) and Lay and Razdan (2017). Zare *et al.* (2010), Gichuru *et al.* (2011), Lal and Kumar (2012), Singh *et al.* (2013), Tamirat *et al.* (2014), Ofori *et al.* (2015), Seyoum *et al.* (2016), Dar *et al.* (2017) and Vishwanath *et al.* (2018) reported similar findings for maturity related traits in maize.

5.4. Components of genetic variance

The data recorded for the parents and their F_1 generation for each trait were subjected to component analysis where additive-dominance model was found adequate as revealed by non-significant differences of t value (Hayman 1954b). Therefore, such characters are used to computation of components of genetic variances.

The additive dominance model for this early maturity related characters were found adequate. The component analysis revealed that both additive (D) and dominance component (H1) of genetic variance were significant but dominance component (H2) of genetic variance was non-significant that indicates that alleles are asymmetrically distributed. This indicated that both additive and dominance components (H1) were operating in the expression of this trait. The value of F was found significant and positive which suggested existence of dominant alleles in excess of recessive allele in parents. The ratio of mean degree of dominance as measured by $(H1/D)$ was more than unity indicating over dominance. The ratio of $(H2/4H1)$ indicating asymmetric distribution of positive and negative alleles. The ratio of dominant to recessive alleles was more than unity indicating preponderance of dominant alleles.

The additive-dominance model for yield and yield related characters also was found adequate. The component analysis revealed that both additive (D) and dominance component (H1) of genetic variance were highly significant. Dominance component (H2) of genetic variance was also found significant which indicated that alleles are symmetrically distributed. This indicated that both additive and non-additive components of gene action are operating in the expression of this trait. The value of F was highly significant and positive which suggested that dominance allele in excess of recessive allele in parents. The ratio of mean degree of dominance as measured by $(H1/D)$ was more than unity indicating over dominance. The value of $(H2/4H1)$ indicating symmetric distribution of positive and negative alleles. The ratio of dominant to recessive alleles was more than unity indicating accumulation of dominant alleles.

5.5: Heterosis

Heterosis is a complex genetical phenomenon depending upon the balance of additive, dominance and interaction components as well as the distribution of genes in the parental lines. The magnitude of heterotic effect is dependent on the genetical and ecological differences as well as diversity of origin of parents (Dhawan and Singh, 1961; Moll *et al.* 1965). The concept of heterosis was given by Shull (1914) refers to the superiority of the hybrid over better parent. In the present investigation, three types of heterosis viz., standard or economic heterosis, heterobeltiosis or better parent heterosis and average or mid parent heterosis have been studied.

A perusal of estimates of economic heterosis for yield and yield contributing characters along with quality traits revealed that hybrid IL4 × IL7, IL1 × IL6, IL5 × IL7 and IL2 × IL4 exhibited maximum estimates of significant positive economic heterosis for grain yield per plant under irrigated and partially irrigated condition.

Similar trends of results for yield and yield contributing traits in maize were also reported by Saleh *et al.* (2002), Marker *et al.* (2002), Venugopal *et al.* (2002), Betran *et al.* (2003), Tollenaar *et al.* (2004), Amiruzzaman *et al.* (2010), Sundararajan and Senthil (2011), Premlatha *et al.* (2011), Rajesh *et al.* (2014) and Verma *et al.* (2014), Ram and Agent (2015), Sharma *et al.* (2016) and Bisen *et al.* (2017) and Vishwanath *et al.* (2018). For quality traits, Netravati *et al.* (2013), Kumar and Babu (2016), Izhar *et al.* (2017) reported economic heterosis for protein and starch content. Marker (2000), Joshi *et al.* (2001), Mohan lal *et al.* (2007), Dadheech and Joshi (2007), Dubey *et al.* (2009), Premlatha and Kalamani (2010), Pavan *et al.* (2011), Singh *et al.* (2013), Sharma *et al.* (2016) and Bisen *et al.* (2017) reported economic heterosis for seed oil content and starch content in maize.

On the other hand, the traits viz., days to 50% tasseling, days to 50 % silking, anthesis silking interval and for maturity related traits, negative direction is desirable. The hybrid IL8 × IL9, IL5 × IL8, IL4 × IL6 and IL7 × IL9 showed high negative significant for days to 50% tasseling. The hybrids IL4 × IL5, IL5 × IL8,

IL4 × IL6 and IL7 × IL9 showed high negative significant for days to 50 % silking. The hybrids IL6 × IL8, L5 × IL11, IL2 × IL4 and IL5 × IL10 showed high negative significant for anthesis silking interval. The hybrids IL1 × IL12, IL4 × IL8, IL7 × IL8 and IL1 × IL10 showed high negative significant for days to maturity.

Similar results of economic heterosis for maturity related traits were also reported by Tollenaar *et al.* (2004), Mohanraj and Gopalan (2008), Muraya *et al.* (2006), Amanullah *et al.* (2011), Kumar *et al.* (2014), Reddy *et al.* (2015), Matin *et al.* (2017) and Gami *et al.* (2018). Singh (2003) also not observed negative significant economic heterosis for plant height in maize.

The majority of the hybrids of yield and yield related traits exhibited positive significant relative heterosis, thereby indicating that for these traits the genes with positive effect were dominant. While for maturity related traits, majority of the hybrids exhibited negative significant relative heterosis, thereby indicating that for these traits the genes with negative effect were dominant.

Similar findings for mid parent heterosis for yield and its contributing traits were also obtained by Rezaei *et al.* (2005), Bajaj and Prasanna (2006), Muraya *et al.* (2006), Appunu *et al.* (2007), Devi *et al.* (2007), Gissa *et al.* (2007), Rangel *et al.* (2007), Kumar (2008), Vieira *et al.* (2009), Yusuf *et al.* (2009), Vivek *et al.* (2009), Amanullah *et al.* (2011), Silva *et al.* (2011), Khanorkar *et al.* (2012) and Kage *et al.* (2013) Shah *et al.* (2016) and Bisen *et al.* (2017) and Chandana *et al.* (2018). Rezaei *et al.* (2005), Bajaj and Prasanna (2006), Appunu *et al.* (2007), Gissa *et al.* (2007), Kumar (2008), Assuncao *et al.* (2010), Amanullah *et al.* (2011), Amiruzzaman *et al.* (2013), Kumar *et al.* (2014) and Zeleke *et al.* (2015) reported relative heterosis for maturity type traits, whereas Bajaj and Prasanna (2006), Muraya *et al.* (2006), Appunu *et al.* (2007), Devi *et al.* (2007), Kumar (2008), Vieira *et al.* (2009), Iqbal *et al.* (2010), Amiruzzaman *et al.* (2013), Reddy *et al.* (2015) and Patil *et al.* (2017) for plant type traits.

Mid parent heterosis for quality traits was also reported by Assuncao *et al.* (2010) and Singh *et al.* (2013) for oil and starch content while Patel *et al.* (2009) and

Yusuf *et al.* (2009), Ikramullah *et al.* (2011) and Jain and Bharadwaj (2014) for protein content.

5.6: Genetic variability, heritability and genetic advance

The analysis of variance revealed the existence of significant differences among the genotypes for all the traits, indicating the presence of considerable genetic variability among the experimental material under study. Thus, there is plenty of area and scope for improvement of different quantitative and qualitative traits through selection. Similar finding on presence of significant variability for various characters in the maize genotypes was also reported by many researchers in their study (Kumar *et al.*, 2015; Kandel *et al.*, 2018)

The mean values, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean of all eighty maize genotypes were calculated for yield and yield attributes. For all the characters under study, phenotypic coefficient of variation values is slightly higher than the genotypic coefficient of variation values indicating that the characters were less influenced by the environment. Therefore, response to direct selection may be effective in improving these traits. In contrast to other traits, hundred grain weight, membrane stability index, days to 50% tasseling, days to 50% silking and days to maturity under irrigated and partial irrigated condition, the difference between phenotypic coefficient of variation and genotypic coefficient of variation was higher indicating that the characters were more influenced by the environment. The estimates of genotypic variation and phenotypic variation under irrigated condition (17.98%) and (21.03%), while under partial irrigated condition (17.55%) and (20.86%) were found to be high for grain yield. These findings are similar to the outcomes of Bhusal *et al.* (2017) and Sharma *et al.* (2018). ASI (20.57%, 25.2%) under irrigated condition and ASI (17.19%, 19.45%) under partial irrigated condition reported high genotypic and phenotypic coefficients of variations. Results were also supported by Kharel *et al.* (2017) and Sharma *et al.* (2018) who also reported higher variability for ASI.

Heritability and genetic advance

Among the maize genotype's heritability values found to be moderate to high, Mahmood *et al.* (2004) reported broad-sense heritability moderate to high for most of the trait. In the present study, high heritability was observed for most of the traits and it was noted highest for days to maturity (99.80%) tracked by days to 50 % silking (96.00%), days to 50 % tasseling (95.50%) and plant height (91.70%) and exhibited low in shelling % (44.6%) under irrigated condition. On the other hand, under partially irrigated condition high heritability showed for days to maturity (99.7%) tracked by days to 50% silking (95.3%), days to 50 % tasseling (94.5%) and plant height (85.4%) and showed low in shelling % (41.7%). Higher heritability values for these traits indicated that the variation observed was mainly under genetic control and less influenced by environment.

Genetic advance was observed for most of the traits and it was noted highest for plant height (55.92%) tracked by days to maturity (49.00%), days to 50 % silking (33.47%) and days to 50 % tasseling (32.55%) and disclosed low for turgid weight (0.03%) under irrigated condition. Conversely, under partially irrigated condition high genetic advance showed in hundred grain weight (156.56) tracked by days to maturity (46.44%), plant height (38.22%) and days to 50% silking (31.63%) and disclosed low for turgid weight (0.03%). All other traits under consideration expressed high heritability coupled with high genetic advance, which indicated the preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield.

5.7: Biochemical test

Analysis of the phenotypes of the inbred lines and their hybrids to discover drought-resistant genes by association analysis, physiological and biochemical traits were tested in eighty genotypes were analyzed under irrigated and partially irrigated conditions following biochemical parameters. Eight traits related to drought tolerance were measured, including proline content, total soluble sugar content, chlorophyll content, malondialdehyde content (MDA), H₂O₂ content,

peroxidase activity, glutathione reductase activity and catalase activity at the reproductive stage, the mean values of drought resistance indexes of proline content, total soluble sugar content, chlorophyll content, malondialdehyde content (MDA), H_2O_2 content, peroxidase activity, glutathione reductase activity and catalase activity were calculated in elite maize genotypes subjected to drought treatment.

Extensive phenotypic variation was evidenced for proline content, total soluble sugar content, chlorophyll content, malondialdehyde content (MDA), H_2O_2 content, peroxidase activity, glutathione reductase activity and catalase activity during drought stress. A wide range of variation was observed among the accessions in terms of the drought resistance indexes of biochemical traits.

Proline plays an important role, as a storage compound for carbon and nitrogen, detoxification of NH_3 and preserving the hydration of proteins in dehydrated tissues, thereby contributing to the maintenance of cellular functions. In the present study, a surge in proline content was observed in stress situation in all the genotypes and its accumulation was more in drought tolerant genotypes. The parental inbred line IL8, IL5, IL10, IL2 and hybrid IL7 $\times$ IL11 and IL1 $\times$ IL7 recorded higher proline content under irrigated and partial irrigated condition compared to other genotypes. Although, proline accumulation increased with an advancement of stress in other genotypes, the extent of increase was comparatively lower in drought susceptible genotypes. Similar results were reported by Navari *et al.* (1990), Tawat (1992), Udomprasert and Thiraporn (1994), Mohammadkhani *et al.* (2008), Guang-hua Yin *et al.* (2012). Li-Ping *et al.* (2006), Harrigan *et al.* (2007), Kaur *et al.* (2010) and Manasa *et al.* (2014).

Chlorophylls have been rightly designated as “pigments of life” because of their central role in living systems responsible for harvesting sunlight and transforming its energy into biochemical energy essential for life on earth. In the present investigation, among the genotypes, the parental inbred line IL10, IL6, IL9, IL8 and the hybrid IL2 $\times$ IL10, IL7 $\times$ IL10, IL2 $\times$ IL6 and IL4 $\times$ IL6 showed higher chlorophyll content under partial irrigated condition. The total chlorophyll

estimation based on chlorophyll 'a' and chlorophyll 'b' and the results were expressed as mg of chlorophyll/g of fresh weight. Estimation of chlorophyll was extracted in 80 per cent acetone and absorbance at 663 nm and 645 nm are read in a spectrophotometer. For chlorophyll content, Kumari *et al.* (2004) and Manasa *et al.* (2014) reported that under drought conditions, there is decrease in chlorophyll content.

It was found that the total sugar content in the leaves was higher under partial irrigated condition on reproductive stage with compare to under irrigated condition. The genotypes which had higher content of total sugars at reproductive stage and at harvest also performed better with respect to yield and yield components and other growth characters which could probably be because of the maintenance of leaf water status through osmoregulation. Soluble sugar may also function as a typical osmoprotectant, stabilizing cellular membranes and maintaining turgor pressure. In the present study, the parental inbred line IL8, IL12, IL11 and the hybrid IL2 × IL 5, IL2 × IL11 and IL6 × IL10 recorded higher total soluble sugar content compared to other genotypes. Similar results were also reported by Mohamed and Naglaa (2010), Guang-hua Yin *et al.* (2012) and Abid Ali *et al.* (2013).

The content of MDA is often employed as an indicator of lipid peroxidation in plant tissues, resulting from an oxidative stress induced by various abiotic stresses. Recently, an increase in MDA content under drought stress has been reported in leaves of drought sensitive genotype of maize, whereas no change is observed in tolerant genotypes (Moussa and Abdel-Aziz 2008; Chugh. *et al.* 2011). In present study, minimum change was observed in MDA content of leaves of tolerant genotypes under partial irrigated condition, indicating that parental inbred line IL5, IL1, IL10, IL12 and hybrid IL3 × IL11, IL8 × IL10, IL3 × IL12 and IL8 × IL11 were better equipped with efficient free radical quenching system than sensitive genotypes that offered protection against oxidative stress. The unchanged lipid peroxidation seemed to be a characteristic of tolerant plants that cope with environmental stresses like drought.

Tolerant genotypes did not accumulate more H_2O_2 under drought stress, indicating less severe oxidative damage. Accumulation of higher H_2O_2 content in leaf tissue of sensitive genotype of maize, as compared to tolerant ones under drought stress induced by polyethylene glycol has been reported (Kellos *et al.* 2008; Chugh. *et al.* 2011). Higher H_2O_2 content in the leaves of drought sensitive maize under drought stress as compared to drought tolerant maize has been observed (Moussa and Abdel-Aziz 2008; Chugh. *et al.* 2011). It might be assumed that parental inbred line IL4, IL9, IL7, IL11 and hybrid IL1 $\times$ IL2, IL9 $\times$ IL11, IL3 $\times$ IL5 and IL3 $\times$ IL9, H_2O_2 detoxification was effectively managed by combined action of APX, CAT and POX, as compared to sensitive genotypes.

Peroxidase is most important enzyme in the decomposition of H_2O_2 into water and oxygen in the cytosol and chloroplast. Changes in peroxidase activity have been frequently correlated to the response of resistance or susceptibility of plants to stresses (Zoz *et al.*, 2013). The data clearly shows that activity of peroxidase increased with increase in stress in roots and shoots of all the genotypes. Under partial irrigated condition parental line IL7, IL11, IL2, IL9 and hybrid IL1 $\times$ IL7, IL1 $\times$ IL12, IL2 $\times$ IL10 and drought resistance HKI 1105 had more peroxidase activity as compared to under irrigated condition. In agreement with our results, an increase in peroxidase activity in drought tolerant and sensitive genotypes of maize under water stress has also been reported by Kolarovic *et al* (2009). Abedi and Pakniyat (2010) observed that under water stress conditions, the peroxidase activity increased in the oilseed rape plants. Similar results were obtained by Chugh *et al* (2011), Moharramnejad *et al.* (2016) and Xie *et al.* (2018) in maize.

In present study, maximum GR activity was recorded in parental inbred line IL1 tracked by IL9, IL12, IL5 and hybrid IL9 $\times$ IL12, IL6 $\times$ IL12, IL10 $\times$ IL11, IL2 $\times$ IL5 under partial irrigated condition. GR activity was increased under drought in plant species such as maize (Jiang and Zhang 2002; Pastori and Trippi, 1992), wheat (Chen *et al.*, 2004; Sairam *et al.*, 1997), rice (Selote and Khanna-Chopra 2004; Sharma and Dubey, 2005). GR activity was increased with short-term drought treatment in leaves of wheat (Bartoli *et al.*, 1999). Total GR activity was increased in the drought-tolerant sugarcane genotype under severe water stress

but not mild stress, but was increased even under mild stress in non–drought-tolerant cultivars (Boaretto *et al.*, 2014). GR activity was increased in a drought-resistant wheat cultivar subjected to 100% oxygen and water stress (Pastori and Trippi, 1993). However, under continuous drought, dual-targeted GR transcripts were upregulated in the drought-sensitive cultivar but downregulated in the resistant cultivar (Contour-Ansel *et al.*, 2006).

Catalase (CAT) decomposes H_2O_2 into water and oxygen at different cellular locations (Mittler, 2002). A decline in CAT activity is considered as a common response to many stresses (Gunes *et al.*, 2008 and Liu *et al.*, 2008). During stress conditions, CAT activity is supposedly decreased due to the inhibition of enzyme synthesis or change in the assembly of enzyme subunits. It may also be associated with degradation caused by induced peroxisomal proteases or due to the photo-inactivation of the enzyme (Abedi and Pakniyat 2010). In the absence of natural scavengers such as CAT and POD, high level of H_2O_2 accumulates in tissues. Maximum activity of catalase was recorded in parental inbred line IL7 followed by IL8, IL10, IL11 and hybrid IL2 × IL10, IL4 × IL12, IL8 × IL9, IL1 × IL2 under partial irrigated condition. Under irrigated conditions, the maximum activity of catalase record in parental inbred line IL5, IL11, IL7, IL6 and hybrid IL1 × IL8, IL3 × IL5, IL4 × IL11 and IL6 × IL12. Catalase is heterogeneous in nature under drought stress. It might be increased and remain unchanged or decreased on exposure to water stress (Carvalho 2008). Similar to our results by Anjum *et al.* (2017) also observed that catalase activity decreased due to water deficiency as compared with well water conditions in maize hybrids. Xie *et al.* (2018) demonstrated a decline in the catalase enzyme activity in maize hybrids under drought stress conditions.

5.8 Molecular characterization

The 80 maize genotypes were also characterized employing 20 droughts linked SSR molecular markers and all SSR markers proved to be polymorphic. Polymorphic markers amplified a total of 110 alleles with a mean worth of 5.5 alleles per marker. The maximum number of seven alleles was amplified followed

by six and five alleles by markers. In accordance with our findings, Iboyi *et al.* (2021) also experimented in a range of 2-7 alleles by using twenty-three SSR markers for molecular diversity analysis in maize genotypes. The variable number of alleles per marker designated incidence of a higher level of genetic diversity among the genotypes. In the present study, 16 SSR loci with di-repeat motif were analyzed, while the SSRs with higher repeat motifs *i.e.*, tri repeat (one loci), tetra-repeat (one loci) and complex repeats (two loci).

The Polymorphism Information Content value of an SSR locus is prejudiced by the number of alleles (allele prosperity) along with dispersal of these alleles across the genotypes. The PIC value per marker pair arrayed from 0.47 for marker bnlg1035 to 0.66 for marker bnlg2190 with an average value of 0.58. Fifteen SSR loci exhibited PIC values >0.55 (bnlg1063, bnlg1225, bnlg1297, bnlg1327, bnlg1346, bnlg1614, bnlg1812, bnlg2190, bnlg2248, bnlg2252, bnlg2328, bnlg439, dupssr13, nc012 and phi053). Such loci could be highly useful in genotype differentiation and genetic diversity analysis. PIC is usually directly correlated to the repeat-type of the SSR locus. The 16 SSR loci with di-repeat motifs investigated a mean PIC value of 0.58, whilst the 4 SSR loci with other repeat motifs evidenced a slightly higher mean PIC value of 0.60. Significantly, four of the 8 SSR loci, *viz.*, bnlg2190, phi053, nc012 and bnlg2248, with high PIC values (>0.60) represent those with di and tetra repeat motifs. However, in an earlier investigation, Kumar *et al.* (2017) reported that the tri and tetra repeats had high polymorphism in comparison to di-repeats.

Based on unweighted neighbor-joining cluster analysis put the eighty genotypes (12 Parents, 66 Hybrids and 2 Checks) into eight clusters. Cluster VI comprised forty-eight genotypes evolving the maximum genotypes. The clusters I, II and III having eight genotypes each. The cluster IV contains four genotypes and cluster V contains only two genotypes. Cluster VI and VII comprised only one genotype each. The pattern of group constellation proved the existence of significant amount of variability. The drought tolerant genotype HKI1105 was in Cluster VI along with 47 genotypes, so possibility exist may all these genotypes be drought tolerant falling in this group. The drought susceptible genotype HKI1128 fallen in

group VII. Rest of the group II, III, IV, V, VI and VIII showed moderate drought tolerance.

As in the case of locus bnlg1083, the loci were shown to be linked with stomatal conductance and osmotic potential, which was previously reported to be associated with plant height (PH) and hundred kernel weight (HKW) (Guo et al., 2008). Likewise, locus bnlg2328, which were previously linked to the number of kernel rows and the drought resistance index, strongly correlated with leaf water potential (Guo et al., 2008). While past studies suggested a relationship between this marker and ASI, female flowering time, ear weight, grain weight, and RWC, the current study found that bnlg1035 is associated with seed yield (SY) as earlier reported by Nikolic *et al.* (2012). The current study also discovered relationships between loci phi053 and plant height and ASI, along with bnlg1812 with RWC. According to Sun *et al.* (2015) this kind of pleotropic relationship may be useful to find some significant genes connected to tolerance. Additional markers that are associated with many traits may be useful in marker-assisted selection to enhance multiple traits. Thus, throughout the water challenged and well-watered environments in the studied seasons, substantial relationships between a small number of SSR markers and water relations as well as yield contributing features were found. This correlation emphasizes the significance of intrinsic tolerance functioning mechanisms and cumulative features for maize drought tolerance.

CHAPTER - 6

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FURTHER WORK

Exploitation of heterosis or hybrid vigor is an important method of crop improvement adopted in many of the cross-pollinated crops. This phenomenon of heterosis attracted the attention of plant breeders due to its conspicuous effect on economic characters especially grain yield and this heterosis has been successfully exploited in many cross-pollinated crops among which maize is important.

In order to exploit heterosis, choice of suitable parents is an important step. The selection of parents depends on factors like *per se* performance of the parents and their combining ability. The concept of general and specific combining ability (Sprague and Tatum, 1942) helps the breeder in choosing the lines to be used as parents in the production of hybrids and also in identifying the superior hybrids having additive and non-additive genes. It is therefore necessary to assess the genetic potential of the parents in hybrid combination through systematic studies in relation to general and specific combining ability which are due to additive and non-additive gene actions. Thus, the information regarding heterosis, combining ability and nature of gene action are the basic requirements for a thorough understanding of genetic architecture of yield and its components.

Drought is the most pervasive limitation of yield potential in maize (Edmeades *et al.*, 2001). Moisture stress in maize affects both yield and yield stability. Within a given maize field, variation in soil depth and texture induce moisture stress. Besides this, the effect of climate change is looming large on agricultural production. Indian monsoon is known for unpredictable rainfall, which results into moisture stress at different growth stage of maize. One day of delay between pollen shed and silk emergence reduce the rate of fertilization and increase barrenness. Thus, developing drought tolerant varieties considering the ecosystem under which it is grown can stabilize maize productivity. The selection

of tolerant lines for drought in maize depends largely on efficient selection criteria. Understanding of morphological, physiological, biochemical and molecular basis of drought tolerance is pre-requisite for effective selection of genotypes and breeding for moisture stress condition.

The analysis of variance for experimental design revealed the presence of significant amount of variability among parents in individual environment for most of the characters in the experiment. This suggested that the parental lines selected were quite variable for most of the characters under study. Further, the analysis of variance revealed that the variation due to moisture stress at two different times affect genotypes significantly for all the traits indicating the presence of sufficient variability in the experiment/study material. Presence of sufficient amount of variability encourages for screening of the genotypes for moisture stress tolerance.

Hybrid is one of the greater practical contributions of genetics and has its most significant expression in maize crop. The breeding strategy for exploitation of heterosis in maize (*Zea mays* L) through the cultivation of single cross hybrids is primarily development on the development and identification of high *per se* performance diverse, vigorous and productive inbred lines with good seed quality in cross combinations to identify single crosses with high heterotic effects.

Genetic parameters like heterosis and combining ability provide adequate guide lines for selection of parents/crosses for getting desirable segregants/ exploitation of heterosis. Various mating design are available to derive information about the combining ability but for present study diallel mating design was used because in this design a greater number of parents and hybrids can be evaluated for their genetic worth.

In the present investigation, heterosis, combining ability effects and drought stress related parameters were studied for various traits to developed and identify suitable and stable single cross hybrids.

The *per se* performance of days to 50% tasseling, days to 50 % silking and anthesis silking interval revealed that the hybrids IL7 × IL8, IL1 × IL11, IL9 ×

IL12, IL9 × IL12 and IL5 × IL7 showed minimum value. On the basis of mean data, we can identify the early maturity hybrids. Mean data revealed that yield and yield contributing traits revealed that the hybrids IL1 × IL8, IL7 × IL8, IL9 × IL10 and IL1 × IL3 showed maximum value. On the basis of mean data, we can identify the high yielding genotypes hybrids.

Mean data revealed that drought tolerance indices revealed that the hybrids IL3 × IL5, IL8 × IL12, IL1 × IL10 and IL3 × IL10 showed maximum value. On the basis of mean data, we can identify the hybrids with drought tolerance.

The ultimate choice of parents to be used in a breeding programme is determined by *per se* performance and their behavior in hybrid combination. It is therefore, necessary to assess genetic potentialities of the parents in hybrid combination through systematic studies in relation to general and specific combining abilities. The combining ability elucidates the nature of gene action involved in the inheritance of a trait. The general combining ability is attributed to additive, additive × additive interactions and is fixable in nature. On the other hand, specific combining ability is attributed to non-additive (*i.e.* dominance, dominance × dominance and additive × dominance) gene action and it is non-fixable.

Parents were classified as good, average and poor combiners on the basis of their GCA effects. Parents with desirable and significant GCA effects were considered good combiners while parents showing non-significant estimates but in desirable direction were classified as average combiners. Poor combiners had undesirable GCA effects. The parental inbred lines IL2, IL3, IL4, IL6, IL8, IL10 and IL11 showed negative significant gca effects under irrigated and partially irrigated condition.

GCA effects provides information about the additive gene action involved in expression of various traits viz., days to 50% tasseling, days to 50 % silking, anthesis silking interval (ASI) and days to maturity and thus helps in deciding the breeding procedure for genetic improvement of traits. The gca variance are higher sca variances, it means that there is preponderance of additive gene

action and progeny selection will be effective for the improvement of these traits. The estimates of GCA effects for yield and yield contributing characters revealed that good general combiner inbred lines for grain yield per plant were IL7, IL10, IL9, IL6, IL12 and IL11.

The magnitude of SCA variance was greater than GCA variance for most of the traits indicating preponderance of non-additive variance in controlling the expression of these traits.

The hybrid IL11 $\times$ IL1 showed high positive significant sca effect followed IL1 $\times$ IL7, IL3 $\times$ IL10, IL4 $\times$ IL6 and IL7 $\times$ IL8. The hybrid IL4 $\times$ IL7 showed high negative significant sca effect followed by IL1 $\times$ IL6, IL5 $\times$ IL7, IL2 $\times$ IL4 and IL3 $\times$ IL12. The sca variance are higher gca variances, it means that there is preponderance of non-additive gene action and progeny heterosis will be effective for the development of hybrids.

Heterosis is a complex genetical phenomenon depending upon the balance of additive, dominance and interaction components as well as the distribution of genes in the parental lines. The magnitude of heterotic effect is dependent on the genetical and ecological differences as well as diversity of origin of parents. A perusal of estimates of economic heterosis for yield and yield contributing characters along with quality traits revealed that hybrid IL4 $\times$ IL7, IL1 $\times$ IL6, IL5 $\times$ IL7 and IL2 $\times$ IL4 exhibited maximum estimates of significant positive economic heterosis for grain yield per plant in irrigated and partially irrigated condition.

On the other hand, the traits viz., days to 50% tasseling, days to 50 % silking, anthesis silking interval and for maturity related traits, negative direction is desirable. The hybrid IL8 $\times$ IL9, IL5 $\times$ IL8, IL4 $\times$ IL6 and IL7 $\times$ IL9 showed high negative significant for days to 50% tasseling. The hybrids IL4 $\times$ IL5, IL5 $\times$ IL8, IL4 $\times$ IL6 and IL7 $\times$ IL9 showed high negative significant for days to 50 % silking. The hybrids IL6 $\times$ IL8, L5 $\times$ IL11, IL2 $\times$ IL4 and IL5 $\times$ IL10 showed high negative significant for anthesis silking interval. The hybrids IL1 $\times$ IL12, IL4 $\times$ IL8, IL7 $\times$ IL8 and IL1 $\times$ IL10 showed high negative significant for days to maturity.

The majority of the hybrids of yield and its related traits exhibited positive significant relative heterosis, thereby indicating that for these traits the genes with positive effect were dominant. While for maturity related traits, majority of the hybrids exhibited negative significant relative heterosis, thereby indicating that for these traits the genes with negative effect were dominant.

To discover drought-resistant genes by association analysis, physiological and biochemical traits were tested in 80 maize genotypes. Eight traits related to drought tolerance were measured, including proline content, total soluble sugar content, chlorophyll content, malondialdehyde content (MDA), H_2O_2 content, peroxidase activity, glutathione reductase activity and catalase activity at the reproductive stage, the mean values of drought resistance indexes of proline content, total Soluble sugar content, chlorophyll content, malondialdehyde content (MDA), H_2O_2 content, peroxidase activity, glutathione reductase activity and catalase activity were calculated in elite inbred maize lines subjected to drought treatment.

A perusal of estimation of biochemical parameters for drought tolerance, finding information about proline content, total soluble sugar content and chlorophyll content value in parental line IL6, IL8, IL10, IL11 and hybrid IL7 × IL11, IL2 × IL11, IL6 × IL10, IL2 × IL10, IL2 × IL6 showed high value in partial irrigated condition. The parental line IL9, IL10, IL11, IL12 and hybrid IL3 × IL12, IL3 × IL9, IL8 × IL11, IL9 × IL11 showed minimum value in partial irrigated condition for malondialdehyde content (MDA) and H_2O_2 content. On the other hand, study of the Antioxidant enzyme activity (peroxidase activity, glutathione reductase activity and catalase activity) in partial irrigated condition these parental line IL7, IL9, IL11, IL12 and hybrid IL1 × IL12, IL2 × IL10, IL9 × IL12, IL6 × IL12 showed highest activity. Extensive physiological variation was documented for proline content, total soluble sugar content, chlorophyll content, malondialdehyde content (MDA), H_2O_2 content, peroxidase activity, glutathione reductase activity and catalase activity during drought stress. A wide range of variation was investigated among the accessions in terms of the drought resistance indexes of physiological and biochemical traits.

The polymorphic information content was employed for each locus to assess the information of each marker and its discriminatory ability and it is a reflection of allele diversity and frequency among varieties. All markers showing amplification in maize, 10 markers were highly polymorphic. The highest PIC value was obtained for the molecular marker bnlg2190 followed by respectively bnlg1614, bnlg2248, nc012 and phi053, whereas bnlg1083 and bnlg1136 was the least. PIC value revealed that bnlg2190 was considered as best marker for test inbred lines and their hybrids. The polymorphic primers which have high PIC value can be used in further molecular studies like association mapping, tagging of gene of interest and the most called approach marker assisted selection (MAS).

Based on unweighted neighbor-joining cluster analysis put the eighty genotypes (12 Parents, 66 Hybrids and 2 Checks) into eight clusters. Cluster VI comprised forty-eight genotypes evolving the maximum genotypes. The clusters I, II and III having eight genotypes each. The cluster IV contains four genotypes and cluster V contains only two genotypes. Cluster V and VII comprised only one genotype each. The pattern of group constellation proved the existence of significant amount of variability. The drought tolerant genotype HKI1105 was in Cluster VI along with 47 genotypes, so possibility exist maybe all these genotypes to be drought tolerant. The drought susceptible genotype HKI1128 fallen in group VII. Rest of the cluster II, III, IV, V, VI and VIII showed moderate drought tolerance.

Suggestion for further work:

The highlight of the results obtained and inferences drawn from the different aspects of the study have given rise to some directions for future line of work. They are as follows:

1. There is a need to screening of large number of germplasm lines for drought tolerant traits that will be utilized for breeding programme.
2. The potential single cross hybrids obtained in diallel fashion are to be tested further under various water regimes at different locations especially

under rainfed conditions for their drought tolerance, stability, disease resistance and yielding ability. This could be done by testing the hybrids under rainfed and productive environments in farmers' fields as a part of participatory varietal selection scheme.

3. Comprehensive study on biochemical parameters like proline, soluble sugar content, relative water content, total chlorophyll content and antioxidant enzyme activities to be taken up to develop drought tolerant germplasm lines.
4. Similar work may be taken up using other promising inbred lines that show wider molecular and morphological variation among them.

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APPENDICES

A. Morphological mean data of *rabi* season 2019-20 under irrigated (I) and partial irrigation (PI) condition.

Genotype	DFT		DFS		ASI		PH		CL		NKRC	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL1	111.5	115.5	116	122.5	4.5	7	112.22	76.42	12.4	10.95	12	12.46
IL2	109.5	112.5	113	117	3.5	4.5	106.77	125.47	10.7	10.55	13.9	13.8
IL3	80	81	86	89.5	6	8.5	143.75	125.05	10.75	9.75	10.6	10.9
IL4	86.5	86.5	93	94	6.5	7.5	100.06	90.16	14.53	13.4	10.3	8.6
IL5	107	109	110.5	116.5	3.5	7.5	111.65	107.45	11.75	10.95	11	10.3
IL6	88	88	90.5	93.5	2.5	5.5	94.25	95.35	12.15	10.4	11.13	10.46
IL7	106	108	109	114	3.5	6	172.2	157.4	12.45	11.15	13.13	12.5
IL8	88.5	88.5	94	97	5.5	9	101.7	78.8	12.85	11.98	13.3	11.55
IL9	87	89	93.5	95.5	6.5	7	64.25	63.65	13.95	12.45	12.2	12.6
IL10	110	112	116.5	121	6.5	9	107.96	100.06	12.33	11.98	12.6	12.3
IL11	112	115	117.5	122.5	5.5	7.5	124.25	102.35	12.15	10.4	14.6	12.6
IL12	118.5	119.5	124	126.5	5.5	7.5	116.3	139	13.85	11.9	13.3	9.46
IL1 X IL2	99.5	102.5	103	111.5	3.5	9	140.75	119.55	14.75	13.45	11.6	10.6
IL1 X IL3	83	94	88.5	101.5	5.5	7.5	125.47	104.37	13.31	12.4	12.13	11.05
IL1 X IL4	85	86	87	92.5	2	6.5	107.75	118.05	16.15	14.55	13.6	13.13
IL1 X IL5	85.5	86.5	89	94	3.5	7.5	116.8	137.7	12.65	11.98	12.8	11.6
IL1 X IL6	99	86	102.5	93.5	3.5	7.5	104.4	106.2	14.45	13.25	12.46	11.68
IL1 X IL7	84.5	84.5	89.5	92.5	5	8	111.8	120.4	11.45	10.85	14.46	12.4
IL1 X IL8	98	100	101	107	3	7	106.55	112.65	15.55	14.45	14.13	12.13
IL1 X IL9	85.5	84.5	91	91	5.5	6.5	88.85	129.95	12.95	12.75	12.46	11.3
IL1 X IL10	84	84	88.5	90.5	5	6	135.85	136.95	13.15	12.4	14.13	12.6
IL1 X IL11	85	86	88.5	93.5	4	7.5	122.67	128.87	13.31	12.85	13.8	11.3
IL1 X IL12	96	100	100	106.5	4	6.5	131	80.2	12.45	10.9	11.6	10.2
IL2 X IL3	83.5	84.5	87	89.5	3.5	5	124.1	127.1	12.85	11.9	13.46	12.13
IL2 X IL4	82	84	88.5	91.5	6.5	7.5	79.45	97.6	13.45	12.25	11.1	10.46

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob

Contd.....

Genotype	DFT		DFS		ASI		PH		CL		NKRC	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL2 X IL5	98	100	100.5	106	2.5	6	134.75	130.05	12.75	11.45	14.1	13.5
IL2 X IL6	83.5	84.5	89	90	5.5	5.5	123.25	100.15	13.75	13.45	13.13	12.6
IL2 X IL7	84	86	88.5	93.5	4.5	7.5	140.4	118.2	15.85	15.15	14.2	12.13
IL2 X IL8	84.5	86.5	90.5	95	6	8.5	116.05	96.25	13.75	13.55	11.3	10.46
IL2 X IL9	88.5	88.5	92.5	96	4	7.5	95.95	74.85	18.35	15.9	14	13.4
IL2 X IL10	85.5	86.5	87.5	93.5	2.5	7	130.97	123.97	14.31	12.45	13.46	12.3
IL2 X IL11	86.5	87.5	87.5	92	1	4.5	146.66	129.66	13.53	12.31	13.6	11.6
IL2 X IL12	103	106	106.5	111.5	3.5	5.5	136.47	143.17	12.31	11.98	14.46	13.55
IL3 X IL4	83.5	84.5	88.5	92	5	7.5	129.37	108.67	15.31	13.45	12.05	10.46
IL3 X IL5	84.5	87.5	88	93	3.5	5.5	119.73	101.53	10.98	10.31	11.3	10.46
IL3 X IL6	93	97	96.5	103	3.5	6	105.13	104.53	13.98	12.45	12.46	11.6
IL3 X IL7	99	100	101.5	106.5	2.5	6.5	92.37	72.47	13.31	12.45	12.46	10.3
IL3 X IL8	82.5	82.5	88	88.5	5.5	6	128.93	115.03	10.98	10.75	13.6	11.2
IL3 X IL9	84	85	89	92.5	5	7.5	114.58	95.88	13.09	12.4	13.55	12.6
IL3 X IL10	100.5	102.5	106	110	5.5	7.5	108.4	96.8	13.85	13.55	13.46	11.3
IL3 X IL11	82	83	85.5	91.5	3.5	8	107.45	131.55	14.75	14.31	13.46	12.55
IL3 X IL12	109.5	110.5	113	117	3.5	6.5	112.17	132.47	13.9	13.31	10.3	9.6
IL4 X IL5	107	108	111	114.5	4	6.5	119.5	144.4	13.45	11.75	13.6	11.6
IL4 X IL6	105	105	108	110.5	3	5.5	82.17	102.97	14.31	12.31	13.13	12.46
IL4 X IL7	82	83	88.5	92.5	6.5	9.5	149.93	147.93	12.98	12.51	12.3	10.55
IL4 X IL8	81.5	81.5	86	89.5	4.5	8	141.53	143.13	12.98	12.85	12.46	11.2
IL4 X IL9	82.5	83.5	88	90.5	5.5	7	88.4	106.4	15.45	14.6	14.8	12.4
IL4 X IL10	82.5	82.5	86.5	90.5	4	8	111.4	139.4	14.05	12.45	12.6	11.6
IL4 X IL11	83.5	83.5	89	92	5.5	8.5	107.05	134.35	12.75	11.31	12.3	10.3
IL4 X IL12	85.5	86.5	89	94	3.5	7.5	112.17	113.47	17.31	15.15	14.13	13.55
IL5 X IL6	86	86	88.5	93.5	2.5	7.5	81.3	134.5	11.45	10.15	11.3	10.6
IL5 X IL7	113	115	115	120.5	2	5.5	95.8	106.8	16.65	14.98	12.13	11.75

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob

Contd.....

Genotype	DFT		DFS		ASI		PH		CL		NKRC	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL5 X IL8	111	113	114.5	119	3.5	6	95.8	125.7	12.05	11.98	10.8	10.3
IL5 X IL9	109.5	113.5	112.5	119	3	5.5	110.65	97.32	15.6	14.31	12.2	10.13
IL5 X IL10	81	84	87.5	89	6.5	5	105.95	119.95	14.75	14.65	15.3	13.4
IL5 X IL11	80.5	83.5	87	90	6.5	6.5	135.67	116.97	14.9	13.45	15.13	14.3
IL5 X IL12	111.5	115.5	115	122	3.5	6.5	110.73	119.63	12.98	12.4	13.55	11.4
IL6 X IL7	84	85	87.5	92.5	3.5	7.5	145.27	147.77	14.31	13.53	13.6	12.3
IL6 X IL8	83	84	88.5	91.5	5.5	7.5	116.9	129.1	12.45	9.85	14.13	13.55
IL6 X IL9	83	83	89	92	6	9	110.17	125.77	13.31	10.98	14.05	12.4
IL6 X IL10	84.5	85.5	90	92	5.5	6.5	121.95	128.65	14.75	14.53	12.3	11.6
IL6 X IL11	84	84	88.5	91.5	4.5	7.5	108.2	130.1	16.45	14.45	11.8	10.3
IL6 X IL12	86	87	91.5	95	5.5	8	124.97	139.37	16.31	15.75	15.8	14.46
IL7 X IL8	86	89	91	95.5	5	6.5	138.55	156.55	13.75	13.15	15.6	14.46
IL7 X IL9	115.5	116.5	118.5	121.5	3	5	85.135	124.13	13.98	12.48	13.13	12.13
IL7 X IL10	86	88	88.5	94.5	2.5	6.5	147.76	166.46	15.33	13.15	13.6	12.3
IL7 X IL11	82.5	83.5	88	91	5.5	7.5	140.79	156.09	13.27	12.6	14.55	13.4
IL7 X IL12	111	115	113.5	121	2.5	6	88.57	112.87	14.31	13.9	15.3	14.55
IL8 X IL9	113	116	116	120.5	3	4.5	108.78	110.88	12.48	11.15	14	13.4
IL8 X IL10	108	110	113.5	117.5	5.5	7.5	101.18	137.68	14.48	13.15	14.13	12.6
IL8 X IL11	83	85	87.5	91.5	4.5	6.5	142.63	169.93	10.98	9.75	14	12.46
IL8 X IL12	84	87	88	95.5	4	8.5	102.96	89.16	14.33	13.98	16	13.13
IL9 X IL10	83	85	89.5	93.5	6.5	8.5	96.55	117.45	15.35	13.98	14.3	12.6
IL9 X IL11	84.5	85.5	87.5	92.5	3.5	6.5	93.18	107.08	12.48	11.31	12.2	11.4
IL9 X IL12	108	110	112.5	118.5	4.5	8.5	100.97	120.77	13.31	11.98	15	13.55
IL10 X IL11	85	86	90.5	92.5	5.5	6.5	109.95	139.92	12.4	12.05	13.18	11.2
IL10 X IL12	84.5	87.5	88.5	95	4	7.5	105.9	133.2	12.45	11.05	12.3	11.1
IL11 X IL12	85	91	89.5	99.5	4.5	8.5	88.65	97.45	12.75	12.25	12.6	12.05
HKI 1105	86	86	91.5	92.5	5.5	6.5	68.85	123.85	13.15	11.4	13.13	13.6
HKI 1128	108.5	111.5	113	119	4.5	7.5	117.95	141.12	16.4	14.31	15	14.55

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob

Contd.....

Genotype	NKR		HGW		SYP		NCP		DM		CG	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL1	27.23	25.34	16.98	18.42	65.65	60.17	1	1.3	151.5	140.5	11.65	12.19
IL2	21.61	20.42	21.31	20.5	79.27	72.35	1.6	1.5	145.5	138.5	11.45	12.2
IL3	14.8	15.9	23.55	22.58	43.24	44.77	2.15	2	137	134	10.15	10.03
IL4	13.25	14.1	24.15	23.6	43.34	40.66	1.5	1.15	143.5	137.5	9.98	9.15
IL5	13.8	13.05	17.75	18.87	45.49	41.1	2.25	1.75	144	134	10.45	8.15
IL6	21.43	21.08	24.4	22.93	54.8	50.98	2	1.5	141	132	10.53	10.25
IL7	13.53	14.11	22.03	21.84	48.58	48.85	1.87	2	150	145	10.98	11.31
IL8	13.5	12.63	20.08	20.95	52.63	51.35	2	2	144.5	135.5	10.75	11.43
IL9	14.46	12.15	18.95	20.31	77.19	74.53	2	2	142	140	10.45	10.4
IL10	12.8	12.7	18.05	18.4	63.76	61.49	2	1.75	142	133	9.75	9.4
IL11	9.93	9.26	16.25	15.03	42.9	42.9	1.5	2	144	142	11.15	10.45
IL12	11.91	11.13	23.85	23.15	44.5	47.18	1.6	1.2	151.5	140.5	12.15	11.45
IL1 X IL2	19.9	17.4	20.03	18.03	66.48	61.28	2	1.55	141.5	141.5	11.05	10.98
IL1 X IL3	19.23	18.49	18.45	19.05	63.25	57.88	1.87	1.3	139	138	11.45	10.85
IL1 X IL4	23.2	21.45	23.15	22.22	88.26	84	2	1.3	138	135	12.1	11.1
IL1 X IL5	21.3	20.16	19.05	16.95	65.3	63.23	2.3	1.75	150.5	139.5	10.95	11.65
IL1 X IL6	19.87	18.37	19.95	21.09	42.11	44.61	2	1.67	144	137	12.05	10.78
IL1 X IL7	26.07	25.32	24.03	21.87	113.73	104.98	2	2	153.5	137.5	9.98	10.155
IL1 X IL8	20.23	20.23	20.1	20.75	53.73	51.97	1.87	1.75	147	140	12.75	11.83
IL1 X IL9	21.47	19.87	20.31	21.03	70.1	67.21	2	1.6	148.5	135.5	15.05	13.05
IL1 X IL10	22.13	21.58	17.98	20.09	82.5	79.03	2.6	2	150	141	12.45	11.31
IL1 X IL11	17.38	16.3	20.75	18.31	69.2	68.01	1.75	1.75	145	139	12.05	10.15
IL1 X IL12	16.6	14.45	14.85	14.98	58.4	62.32	2.15	1.3	150	142	11.95	10.98
IL2 X IL3	18.5	16.57	22.45	19.75	65.18	67.94	2.6	1.6	150.5	142.5	12.75	11.09
IL2 X IL4	18.15	16.7	21.85	21.1	43.78	47.66	2	1.4	144	134	11.98	12.13

NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm),

Contd.....

Genotype	NKR		HGW		SYP		NCP		DM		CG	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL2 X IL5	17.51	17.95	17.15	18.03	45.46	46	2	2	149	142	9.45	10.02
IL2 X IL6	28.08	25.99	20.98	19.95	87.18	82.75	1.67	1.6	152.5	143.5	9.98	11.1
IL2 X IL7	24.13	23.13	17.45	19.13	99.15	94.13	1.75	1.75	149	137	12.05	11.81
IL2 X IL8	18.65	17.58	18.98	19.45	84.64	80.24	2	2	141.5	136.5	11.55	11.87
IL2 X IL9	24.3	21.78	25.87	24.4	82.27	79.93	2	1.15	144.5	133.5	12.45	11.75
IL2 X IL10	20.77	18.36	15.78	14.95	69.5	63.43	2.3	1.75	141.5	137.5	11.31	12.98
IL2 X IL11	17.4	17.48	17.98	17.09	55.73	60.71	2	1.5	144.5	144.5	11.05	11.75
IL2 X IL12	18.92	19.1	17.31	18.53	55.41	54.47	1.3	1.12	147	144	10.98	11.05
IL3 X IL4	17.07	14.44	17.85	18.55	56.8	53.62	2.15	1.25	140.5	135.5	10.31	11.15
IL3 X IL5	20.75	19.65	17.76	18.85	53.77	51.73	2.3	1.5	148.5	137.5	9.55	9.95
IL3 X IL6	22.07	20.17	20.53	19.87	63.39	59.88	2	1.4	141	139	10.31	9.75
IL3 X IL7	20.97	19.57	28.75	27.45	91.69	85.13	1.67	1.25	139	133	11.03	12.1
IL3 X IL8	16.35	16.2	19.8	18.25	71.03	67.01	2.3	2.5	141.5	139.5	11.85	10.95
IL3 X IL9	23.45	22.97	22.98	21.3	74.1	68.51	2	1.5	138	135	11.45	10.05
IL3 X IL10	23.57	21.92	20.9	21.95	106.6	98.23	2	1.5	137.5	135.5	12.4	9.85
IL3 X IL11	16.97	15.67	19.15	17.31	93.29	90.25	2.15	2.3	137	134	11.98	10.95
IL3 X IL12	19.95	18.35	18.75	18.55	51.85	55.79	2	1.62	140.5	139.5	10.65	10.98
IL4 X IL5	23.6	21.54	18.25	20.75	63.07	62.12	2.42	2.3	141	138	11.4	13.15
IL4 X IL6	20.03	19.66	21.45	20.65	99.35	91.45	1.3	1.3	141	136	11.98	12.1
IL4 X IL7	15.95	14.15	22.4	21.13	46.13	42.56	2.3	2.25	135	133	12.31	12.81
IL4 X IL8	22.97	20.22	19.45	19.3	61.34	62.40	2.6	2.5	136.5	131.5	12.1	11.03
IL4 X IL9	21.67	20.42	21.15	18.88	71.24	65.61	2	2	137.5	133.5	12.98	10.92
IL4 X IL10	23.02	23.35	19.75	18.83	67.02	64.26	1.6	1.5	134.5	132.5	11.53	12.21
IL4 X IL11	23.55	21.95	19.25	17.87	93.29	85.95	2.3	1.87	142.5	134.5	11.4	12.28
IL4 X IL12	23.16	19.98	19.7	17.75	77.94	70.81	1.55	1.75	143.5	137.5	11.05	11.35
IL5 X IL6	20.05	18.52	26.13	24.15	63.76	60.77	1.6	1.5	141	139	11.55	12.4
IL5 X IL7	16.49	16.63	22.95	21.45	43.15	40.33	1.6	1.25	144	143	10.45	10.18

NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm),

Contd.....

Genotype	NKR		HGW		SYP		NCP		DM		CG	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL5 X IL8	13.2	13.83	14.9	14.08	43.82	40.68	1.3	1.37	146	143	10.05	9.48
IL5 X IL9	19.1	17.9	26.05	25.31	81.82	75.96	1.4	1.3	144.5	143.5	13.85	12.13
IL5 X IL10	18.61	17.55	20.98	20.5	85.73	80.43	1.75	1.5	142	132	14.98	12.25
IL5 X IL11	23.51	22.68	21.87	21.6	81.53	79.38	1.6	1.5	149.5	139.5	13.95	11.31
IL5 X IL12	24.02	22.55	21	21.03	90.43	86.34	1.3	1.37	143.5	142.5	12.25	10.98
IL6 X IL7	20.6	19.55	20.95	19.85	104.84	95.72	1.6	1.75	148	137	13.1	12.1
IL6 X IL8	18.03	15.89	22.06	19.14	71.46	65.7	1.37	1.25	141	138	16.15	13.81
IL6 X IL9	15.67	14.55	24.13	22.03	60.07	56.68	2	1.5	144	139	12.31	10.75
IL6 X IL10	23.41	24.5	23	21.87	89.49	88.99	1.5	1.5	141.5	137.5	12.98	12.65
IL6 X IL11	23.1	22.85	19.05	18.82	63.33	64.38	1.6	1.25	139	136	12.31	11.75
IL6 X IL12	23.4	19.49	19.45	18.8	95.47	92.9	1.5	1.5	148	141	11.85	11.7
IL7 X IL8	24.48	23.43	20.05	20.71	103.47	100.27	2.5	2	147	143	12.45	11.25
IL7 X IL9	19.83	18.99	24.65	23.65	80.23	75.375	1.25	1.62	143.5	141.5	13.05	12.13
IL7 X IL10	22.6	19.58	18.25	16.05	75.41	69.71	1.25	1.37	143	137	11.1	11.07
IL7 X IL11	21.30	20.92	24.55	22.4	91.67	84.99	2	2	144.5	138.5	12.45	10.13
IL7 X IL12	23.65	22.02	20.87	22.28	103.21	95.27	2	1.25	143	143	13.65	13
IL8 X IL9	23	20.58	22.45	20.88	77.20	72.20	1.4	1.5	144	139	11.75	9.98
IL8 X IL10	21.43	19.46	25.95	24.9	66.31	60.42	1.6	1.5	144	143	12.05	10.95
IL8 X IL11	24.2	21.3	24.45	24.05	66.09	65.10	2.3	1.5	144	142	12.85	12.05
IL8 X IL12	21.18	20	20.05	19.44	79.58	76.67	1.87	1.75	143	140	12.75	12.81
IL9 X IL10	17.41	16.25	19.05	20.15	86.4	82.23	2	1.62	142	142	12.45	11.05
IL9 X IL11	26.9	26.13	20.85	19.83	63.76	60.76	2	1.75	143.5	143.5	12.31	12.03
IL9 X IL12	19.75	17.55	21.03	18.98	69.14	68.49	1.6	1.5	146	142	12.15	12.1
IL10 X IL11	21.69	18.71	21.05	21.25	72.38	70.35	1.75	1.5	142	136	11.31	9.75
IL10 X IL12	21.08	17.35	22.31	21.31	62.33	64.14	1.45	1.37	146.5	141.5	12.05	9.95
IL11 X IL12	23.78	22.26	22.33	19.18	113.21	105.17	1.5	1.25	145	139	12.48	10.98
HKI 1105	21.43	22.55	20.08	18	62.93	60.04	1.3	1.5	144	139	11.75	12.05
HKI 1128	24.4	23.51	19.75	20.33	71.42	73.20	1.3	2.3	145.5	143.5	13.53	12.32

NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm),

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Genotype	SP		CT		TW		RWC		SWD		MSI	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL1	80.22	80.66	27.87	25.87	0.173	0.172	69.18	69.66	30.81	30.34	19.85	18.31
IL2	83.75	81.20	26.72	26.72	0.219	0.225	77.28	74.39	22.71	25.61	12.67	12.97
IL3	72.46	67.26	26.6	26.5	0.186	0.188	84.83	83.53	15.17	16.47	30.77	15.48
IL4	68.17	82.79	27.61	24.91	0.21	0.214	68.24	66.67	31.76	33.33	9.11	38.14
IL5	79.16	70.26	25.8	25.7	0.228	0.227	77.17	77.6	22.83	22.4	36.99	56.23
IL6	80.83	72.95	26.7	25.6	0.225	0.228	75.44	74.14	24.56	25.86	11.33	43.12
IL7	81.54	82.30	28.25	25.55	0.248	0.244	71.13	72.63	28.86	27.36	27.75	26.16
IL8	79.24	78.65	26.55	25.25	0.221	0.221	70.52	70.52	29.47	29.47	36.52	22.10
IL9	79.24	80.43	27.9	24.2	0.261	0.259	71.00	71.72	28.99	28.28	33.16	12.22
IL10	84.15	89.32	29.21	25.21	0.202	0.204	72.84	71.95	27.16	28.04	16.84	11.12
IL11	79.18	73.46	27.1	24.9	0.255	0.257	48.81	48.35	51.18	51.64	26.11	10.67
IL12	71.06	80.29	28.65	26.45	0.215	0.217	74.92	74.07	25.07	25.92	23.46	21.59
IL1 X IL2	66.29	75.94	26.1	27.4	0.177	0.18	73.61	72.11	26.39	27.89	37.74	16.83
IL1 X IL3	75.96	76.57	25.42	27.42	0.164	0.167	73.00	71.37	26.99	28.62	21.00	17.15
IL1 X IL4	71.20	84.03	25.8	26.4	0.168	0.170	77.33	76.2	22.66	23.8	46.67	12.87
IL1 X IL5	79.92	84.69	26.85	26.95	0.182	0.179	74.05	75.62	25.95	24.38	47.99	13.23
IL1 X IL6	73.19	80.34	26.45	27.65	0.166	0.164	66.16	67.18	33.84	32.82	18.69	9.425
IL1 X IL7	86.83	91.21	27.65	27.65	0.233	0.235	75.41	74.59	24.59	25.40	33.16	8.84
IL1 X IL8	63.83	77.30	25.1	26.2	0.207	0.209	62.42	61.68	37.57	38.32	3.29	21.77
IL1 X IL9	80.88	69.03	25.7	28.1	0.208	0.210	68.08	67.27	31.91	32.73	40.85	55.71
IL1 X IL10	84.23	87.25	26.4	26.5	0.183	0.186	75	73.47	25	26.53	30.00	43.08
IL1 X IL11	81.57	84.23	26.42	26.92	0.177	0.181	77.26	75.09	22.74	24.91	25.38	47.67
IL1 X IL12	81.47	81.81	27.15	29.15	0.192	0.19	68.03	68.97	31.97	31.03	23.01	10.02
IL2 X IL3	77.88	78.17	28.65	28.15	0.162	0.161	89.43	90.17	10.56	9.83	55.27	41.74
IL2 X IL4	74.06	83.43	27.55	25.95	0.185	0.187	62.59	61.7	37.41	38.3	37.42	37.81

SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

Contd.....

Genotype	SP		CT		TW		RWC		SWD		MSI	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL2 X IL5	80.33	85.45	26.6	27.2	0.201	0.203	73.76	72.79	26.23	27.20	30.77	56.97
IL2 X IL6	80.5	81.45	25.4	25.5	0.185	0.188	68.12	66.67	31.88	33.33	54.04	58.25
IL2 X IL7	73.54	73.31	25.05	25.35	0.217	0.214	69.37	70.59	30.63	29.40	3.62	78.55
IL2 X IL8	82.44	82.32	25	25.3	0.201	0.2	69.57	70	30.43	30	31.43	41.78
IL2 X IL9	71.13	71.05	23.1	23.3	0.201	0.205	75.1	73.04	24.9	26.95	38.29	34.37
IL2 X IL10	78.35	76.29	26.02	25.12	0.194	0.198	81.12	78.91	18.87	21.08	36.96	31.26
IL2 X IL11	78.36	81.92	26.61	25.31	0.215	0.212	70.09	71.38	29.91	28.61	58.58	37.97
IL2 X IL12	81.33	84.28	26.82	25.02	0.214	0.217	85.08	83.66	14.92	16.33	21.80	10.50
IL3 X IL4	66.37	65.08	24.62	23.82	0.163	0.165	59.09	58.21	40.91	41.79	32.53	44.21
IL3 X IL5	80.24	76.63	27.58	24.78	0.23	0.235	80.23	78.02	19.77	21.98	37.37	63.19
IL3 X IL6	75.5	73.80	27.68	23.38	0.219	0.221	72.34	71.47	27.66	28.52	54.27	49.07
IL3 X IL7	80.86	85.35	28.62	23.02	0.238	0.239	68.57	68.18	31.43	31.82	24.53	13.99
IL3 X IL8	87.59	87.55	30.08	23.88	0.180	0.181	68.04	67.58	31.95	32.42	53.23	44.83
IL3 X IL9	82.59	74.17	28.53	28.23	0.177	0.174	70.68	72.31	29.32	27.68	31.86	14.78
IL3 X IL10	82.08	73.03	27.25	26.25	0.186	0.188	65.50	64.60	34.49	35.39	45.59	53.74
IL3 X IL11	72.8	87.00	26.9	22.9	0.19	0.186	70.83	72.86	29.16	27.14	58.90	53.23
IL3 X IL12	75.91	86.14	24.62	24.22	0.230	0.233	71.47	70.3	28.53	29.7	37.98	59.79
IL4 X IL5	78.53	63.34	27.25	24.85	0.233	0.231	78.79	79.66	21.21	20.33	37.30	66.54
IL4 X IL6	74.90	86.08	27.12	24.62	0.185	0.188	65.54	64.24	34.45	35.75	10.65	13.41
IL4 X IL7	77.99	76.16	27.08	24.98	0.223	0.224	71.91	71.51	28.09	28.49	30.18	43.61
IL4 X IL8	76.41	85.34	27.38	25.48	0.259	0.259	66.03	66.03	33.96	33.96	28.7	28
IL4 X IL9	65.10	62.06	27.95	24.35	0.225	0.224	66.67	67.05	33.33	32.94	13.31	15.25
IL4 X IL10	78.91	76.95	27.55	25.65	0.207	0.208	71.82	71.38	28.17	28.61	39.03	35.85
IL4 X IL11	82.78	83.81	25.3	24.9	0.195	0.198	61.59	60.39	38.41	39.61	29.14	7.9
IL4 X IL12	68.61	65.11	25.12	23.82	0.204	0.202	67.09	67.94	32.91	32.05	23.69	32.39
IL5 X IL6	80.06	83.65	29.05	26.75	0.185	0.187	75.68	74.67	24.32	25.33	17.31	16.97
IL5 X IL7	55.63	45.08	25.65	25.95	0.212	0.212	72.03	72.03	27.97	27.97	36.71	59.94

SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index
Contd.....

Genotype	SP		CT		TW		RWC		SWD		MSI	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL5 X IL8	71.56	79.52	28.15	29.15	0.204	0.205	68.75	68.32	31.25	31.68	18.44	15.63
IL5 X IL9	71.02	83.2	25.4	26.77	0.194	0.198	68.92	67.11	31.08	32.89	17.47	16.78
IL5 X IL10	82.46	83.52	25.8	27.2	0.209	0.210	69.85	69.44	30.14	30.56	14.27	12.72
IL5 X IL11	80.83	91.59	25.52	25.32	0.21	0.21	70.26	70.26	29.73	29.73	4.79	13.77
IL5 X IL12	85.02	87.9	28.58	25.08	0.249	0.247	77.07	77.86	22.92	22.14	13.95	10.17
IL6 X IL7	74.98	87.14	25.62	24.92	0.189	0.193	72.52	70.37	27.47	29.62	1.85	14.11
IL6 X IL8	79.20	88.64	26.85	26.35	0.192	0.191	81.41	81.99	18.58	18.01	32.23	56.38
IL6 X IL9	77.24	88.90	27.42	25.22	0.225	0.223	72.99	73.84	27.01	26.16	33.24	40.15
IL6 X IL10	81.87	84.27	26.1	25.6	0.198	0.194	63.54	65.29	36.45	34.70	19.58	26.20
IL6 X IL11	64.87	83.09	24.85	24.85	0.183	0.186	75.35	73.79	24.65	26.21	7.25	40.57
IL6 X IL12	72.30	81.39	25.32	25.62	0.206	0.202	71.34	73.30	28.65	26.69	11.77	35.44
IL7 X IL8	83.13	87.59	24.4	27.2	0.228	0.23	65.93	65.2	34.07	34.8	2.44	13.94
IL7 X IL9	80.64	81.43	25.28	27.48	0.223	0.224	63.35	62.96	36.64	37.03	9.57	53.54
IL7 X IL10	71.17	75.17	25.91	27.11	0.202	0.206	80.13	78.13	19.86	21.87	16.23	19.67
IL7 X IL11	83.36	89.34	24.44	22.14	0.219	0.222	71.56	70.27	28.43	29.72	29.54	21.34
IL7 X IL12	82.92	84.25	26.72	27.52	0.198	0.2	85.15	84.01	14.85	15.98	8.24	57.33
IL8 X IL9	82.47	69.02	28.73	29.53	0.201	0.202	71.11	70.67	28.88	29.33	23.34	45.69
IL8 X IL10	77	64.13	24.73	27.13	0.199	0.205	81.08	77.92	18.91	22.07	20.28	40.13
IL8 X IL11	82.41	75.71	27.58	30.68	0.178	0.174	78.52	80.92	21.48	19.08	28.57	36.67
IL8 X IL12	80.19	82.15	25.51	29.71	0.222	0.227	78.42	76.11	21.57	23.88	18.64	65.55
IL9 X IL10	71.47	86.41	26.6	28.7	0.24	0.242	82.42	81.52	17.58	18.47	15.21	14.36
IL9 X IL11	83.52	73.1	29.23	30.83	0.207	0.205	76.81	77.89	23.18	22.10	6.98	6.66
IL9 X IL12	78.33	74.12	29.32	29.32	0.205	0.206	81.97	81.44	18.02	18.55	41.78	45.21
IL10 X IL11	82.53	65.29	26.67	29.97	0.199	0.204	81.53	78.78	18.46	21.21	19.3	40.77
IL10 X IL12	78.75	64.96	26.25	29.15	0.227	0.231	80.94	79.08	19.06	20.91	10.82	11.42
IL11 X IL12	83.4	84.77	25.6	28.7	0.18	0.181	77.37	76.81	22.62	23.18	14.07	15.62
HKI 1105	76.64	83.75	26.9	26.8	0.218	0.222	82.14	80.12	17.86	19.87	15.74	28.67
HKI 1128	66.70	80.37	24.87	24.97	0.197	0.203	79.88	76.79	20.12	23.21	23.64	55.76

SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

B. Morphological mean data *kharif* 2020 under irrigated (I) and partial irrigation (PI) condition.

Genotype	DFT		DFS		ASI		PH		CL		NKRC	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL1	62.5	67.5	65	72	2.5	5	96.12	87.82	13.07	12.32	13.13	12.80
IL2	60.5	65.5	65	71.5	4.5	6.5	169.1	160.7	12.07	11.43	15.98	15.32
IL3	58	64	61.5	69.5	3.5	5.5	158.93	153.13	12.43	12.98	11.96	12.6
IL4	58.5	65.5	63	71	4.5	6	150.1	122.9	13.59	10.41	10.07	4.41
IL5	61	67	64	71	3	5	189.05	125.45	12.13	10.86	12.13	10.8
IL6	63	67	67.5	72	4.5	6	171.98	132.38	13.43	13.82	12.4	10.6
IL7	63	68	67	72.5	4	5.5	138.95	136.75	12.45	8.97	13.45	11.45
IL8	62.5	66.5	67	70.5	4.5	5.5	134.27	124.07	12.41	11	13.35	8.85
IL9	64	69	67	73	3	5	83.67	78.87	13.95	14.3	12.09	13.5
IL10	64	68	67	73.5	3	6.5	93.74	88.14	11.81	11.26	13.17	12.84
IL11	65	72	68.5	76	3.5	5	126.42	116.8	11.76	11.91	15.6	7.2
IL12	66.5	73.5	70.5	78.5	4	6.5	135.7	116.1	13.25	11.55	13.58	7.75
IL1 X IL2	64.5	68.5	67	74.5	2.5	6.5	141.37	132.07	14.96	12.5	11.96	9.63
IL1 X IL3	67	70	70.5	75	3.5	5	138.73	80.93	13.12	12.11	12.35	10.68
IL1 X IL4	62	67	66	72.5	4	6.5	173.53	123.53	15.93	11.26	14.11	12.78
IL1 X IL5	64.5	66.5	69	71.5	4.5	6.5	169.78	127.18	12.88	10.85	13.68	7.25
IL1 X IL6	65	69	68.5	76.5	3.5	7.5	158.87	131.27	13.61	12.2	12.11	10.78
IL1 X IL7	59.5	63.5	62.5	69.5	3	7.5	201.45	170.25	11.15	11.95	15.95	12.28
IL1 X IL8	66	69	69	73	3	5	153.77	135.57	14.15	13.23	13.4	11.73
IL1 X IL9	64.5	68.5	68.5	74	4	6	158.15	132.75	12.7	14.53	13.53	14.5
IL1 X IL10	67	71	70.5	74	3.5	4	163.22	96.02	12.26	11.85	14.77	12.7
IL1 X IL11	66	70	67.5	73.5	1.5	4.5	175.78	146.58	12.02	10.35	14.68	12.72
IL1 X IL12	68	73	70.5	75.5	2.5	3.5	140.5	163.1	12.55	10.45	12.78	11.15
IL2 X IL3	58.5	63.5	63	69.5	4.5	6.5	191.47	181.07	14	12.75	14.25	14.25
IL2 X IL4	58	67	62.5	73.5	4.5	6.5	134.55	154.55	12.95	10.95	11.61	10.25

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob

Contd.....

Genotype	DFT		DFS		ASI		PH		CL		NKRC	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL2 X IL5	70	75	72	79.5	2	4.5	164.17	162.17	12.55	13.1	14.3	11.6
IL2 X IL6	58.5	63.5	60	67.5	1.5	5.5	180.52	164.52	13.55	12.46	13.55	12.5
IL2 X IL7	59	64	62.5	69	3.5	6	193.92	163.92	16.6	13.75	13.41	12.75
IL2 X IL8	60.5	65.5	64	70.5	3.5	5.5	149.25	140.15	14.15	13.05	11.46	10.6
IL2 X IL9	58.5	61.5	63	65.5	4.5	4.5	137.70	138.90	17.69	16.7	14.01	13.35
IL2 X IL10	62.5	67.5	65	72.5	2.5	5.5	157.16	158.06	13.55	12.52	13.85	12.52
IL2 X IL11	64.5	60.5	66.5	64	2	5	153.92	173.82	13.24	12.24	14.57	13.91
IL2 X IL12	70	74	73	78.5	3	5.5	181.51	175.81	12.85	14.72	14.68	14.52
IL3 X IL4	62.5	68.5	64	72.5	1.5	4.5	176.65	158.65	15.27	13.32	11.68	11.32
IL3 X IL5	66.5	72.5	69	76.5	2.5	5.5	164.5	165.9	13.01	12.88	12.01	12.38
IL3 X IL6	61	67	64.5	71.5	3.5	5.5	160.80	167.70	14.30	13.18	11.84	12.93
IL3 X IL7	59	68	63	72.5	4	4.5	174.41	168.01	14.35	13.12	12.68	12.72
IL3 X IL8	60.5	67.5	65	71	4.5	5	162.78	169.68	12.04	11.48	14.51	14.48
IL3 X IL9	55	60	57.5	62.5	2.5	3.5	161.15	165.55	13.96	13.43	13.46	12.87
IL3 X IL10	56.5	59.5	60	63.5	3.5	4.5	167.64	169.54	13.56	10.5	13.91	13.75
IL3 X IL11	61	66	64.5	71.5	3.5	5.5	168.98	167.18	15.13	10.03	13.3	12.6
IL3 X IL12	62.5	69.5	65	72	2.5	4	176.87	171.67	14.52	11.72	10.10	11.02
IL4 X IL5	64	69	68.5	73	4.5	5	175.87	163.87	13.11	15.45	13.95	11.55
IL4 X IL6	59	64	62	68	3	5	187.33	150.33	15.02	15.52	12.85	9.82
IL4 X IL7	63	68	65.5	70.5	2.5	3.5	197.5	156.1	12.41	11.51	12.18	11.18
IL4 X IL8	61.5	66.5	62.5	71.5	2	5.5	174.76	126.76	13.48	11.94	12.36	12.88
IL4 X IL9	54.5	60.5	58.5	65.5	4	5.5	166.11	131.01	15.62	14.28	13.61	12.28
IL4 X IL10	55.5	61.5	58.5	65.5	3	4.5	168.23	129.83	13.88	13.81	12.65	12.31
IL4 X IL11	60.5	65.5	64.5	71.5	4	6.5	182.9	152.3	13.9	12.63	12.47	10.96
IL4 X IL12	65.5	69.5	69	72.5	3.5	4.5	179.8	168.8	15.18	13.68	13.72	13.55
IL5 X IL6	61	66	63.5	69.5	2.5	4.5	163.46	133.66	12.53	10.45	12.28	11.61
IL5 X IL7	62	67	64.5	71.5	2.5	4.5	190.35	175.75	15.6	13.68	11.01	13.01

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob

Contd.....

Genotype	DFT		DFS		ASI		PH		CL		NKRC	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL5 X IL8	67	72	70.5	77.5	3.5	5.5	139.07	165.87	12.81	11.48	11.98	11.98
IL5 X IL9	62.5	67.5	68	71	5.5	5	154.9	170.1	14.12	10.53	11.37	12.03
IL5 X IL10	61	65	65	71	4	6	161.35	137.95	13.4	12.63	15.96	15.3
IL5 X IL11	60.5	65.5	65	69.5	4.5	4.5	185.72	162.12	13.72	11.88	14.55	12.22
IL5 X IL12	62.5	71.5	66	74.5	3.5	3.5	151.18	124.58	13.85	12.18	14.51	14.18
IL6 X IL7	64	69	67	73.5	3	5.5	176	143.2	15.35	8.85	14.18	11.52
IL6 X IL8	59	65	64.5	69.5	5.5	5.5	134.6	134.4	13.95	9.02	14.45	11.11
IL6 X IL9	64	68	68.5	72.5	4.5	5.5	146.21	124.61	14.35	12	15.32	10.02
IL6 X IL10	62.5	69.5	65	71	2.5	3	165.89	138.79	14.12	13.13	11.5	11.3
IL6 X IL11	59	64	60.5	67.5	1.5	3.5	198.17	153.77	15.6	12.02	11.51	11.45
IL6 X IL12	62	67	65.5	70.5	3.5	4.5	187.23	144.73	14.62	15.06	14.82	12.52
IL7 X IL8	61	63	65	68	4	5.5	184.12	142.72	14.35	11.63	16.46	15.13
IL7 X IL9	62.5	67.5	67	72.5	4.5	6.5	136.07	138.07	13.36	11.68	12.98	11.68
IL7 X IL10	65	70	67.5	74.5	2.5	5.5	198.72	159.12	14.34	12.87	13.01	13.67
IL7 X IL11	61.5	67.5	64	72.5	2.5	5.5	199.83	154.03	12.7	10.04	15.2	13.37
IL7 X IL12	60	66	64.5	72.5	4.5	6.5	201.57	184.47	14.14	10.52	14.85	15.52
IL8 X IL9	56	62	59	66.5	3	4.5	148.91	137.01	12.93	16.25	14.93	14.43
IL8 X IL10	55	60	59	66.5	4	6.5	153.45	161.05	14.26	11.32	14.09	14.76
IL8 X IL11	62	66	66	70.5	4	5.5	169.38	159.48	12.84	14.34	15.18	13.84
IL8 X IL12	60	66	64.5	71.5	4.5	6.5	176.21	167.61	13.67	13.11	16.17	15.51
IL9 X IL10	62	67	63.5	69.5	1.5	3.5	140.65	136.25	14.5	13.75	14	10.33
IL9 X IL11	63.5	66.5	66	69	2.5	4	147.03	158.43	13.09	12.09	13.23	15.09
IL9 X IL12	57	63	61.5	67.5	4.5	5.5	162.46	148.06	13.85	13.34	15.35	13.32
IL10 X IL11	55	61	59.5	65.5	4.5	5.5	173.71	152.71	13.30	16.91	14.47	13.47
IL10 X IL12	56.5	61.5	59.5	65.5	3	5.5	169.1	149.9	13.28	13.56	13.11	14.45
IL11 X IL12	57	64	60.5	67	3.5	4	169.18	151.38	12.93	11.33	13.63	12.9
HKI 1105	58	63	61	66.5	3	4.5	170.12	151.12	13.26	10.71	13.43	14.4
HKI 1128	59.5	65.5	63	68.5	3.5	3.5	180.94	162.54	15.63	9.79	14.65	12.65

DFT= Days to 50 % tasseling, DFS= Days to 50 % silking, ASI = Anthesis silking interval, PH= Plant height (cm), CL= Cob length (cm), NKRC= Number of kernel rows per cob

Contd.....

Genotype	NKR		HGW		SYP		NCP		DM		CG	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL1	25.27	22.97	18.97	18.57	68.63	59.35	1.3	1	96.5	93.5	12.97	12.57
IL2	25.82	23.42	24.47	23.58	86.27	82.25	1.6	1.5	98.5	95.5	12.65	12.32
IL3	18.1	17.7	26.11	16.96	48.46	62.05	2.3	2	95	93	12.1	11.9
IL4	12.71	8.91	24.91	12.08	48.29	27.11	1.5	1.4	96.5	94.5	10.91	6.01
IL5	15.6	17.05	16.99	25.13	40.66	51.8	2.12	1.75	98	93	11.6	11.4
IL6	25.93	18.35	27.42	21.09	51.43	55.28	2	1.75	97	98	12.26	12.1
IL7	14.45	15.95	23.8	28.33	41.61	44.2	2	2	98	94	12.11	12.45
IL8	15.35	9.75	19.36	15.54	50.12	25.12	1.75	1.87	99.5	95.5	11.25	9.55
IL9	15.03	20.9	31.5	30.9	82.55	75.95	1.87	2	97	94	10.03	11.5
IL10	15.01	13.91	20.01	18.84	58.61	51.34	2	1.75	100	96	10.81	10.61
IL11	10.6	7.4	16.2	10.87	36.29	23.6	1.75	1.4	102	100	10.03	9.6
IL12	13.08	10.25	24.18	22.25	46.05	39.91	1.6	1.32	101.5	98.5	11.91	11.9
IL1 X IL2	21.8	18.05	19.46	19.1	70.28	64.18	2	1.6	95.5	92.5	11.63	11.1
IL1 X IL3	20.77	19.52	19.4	18.77	69.04	63.29	2	1.3	93	90	12.18	12.02
IL1 X IL4	26.45	13.78	22.65	23.11	94.6	82.45	2	1.15	97	95	12.61	12.25
IL1 X IL5	25.01	10.35	18.35	18.16	68.51	59.95	1.87	1.75	95.5	92.5	12.18	10.35
IL1 X IL6	21.13	17.78	20.85	19.95	37.28	35.1	2	1.6	93	85	11.61	10.75
IL1 X IL7	28.28	16.25	26.11	20.17	123.8	96.95	2	2	100.5	97.5	11.61	12.75
IL1 X IL8	19.56	18	19.59	19.2	49.73	45.73	1.75	2	97	95	13.06	12.5
IL1 X IL9	23.2	21.9	22.02	28.4	73.58	98	2	1.42	94.5	100.5	16.68	13.5
IL1 X IL10	25.1	22.6	18.32	17.9	82.6	71.83	2.3	2	96	97	13.2	12.85
IL1 X IL11	18.68	12.32	20.29	24.17	69.67	51.28	2	2	100	101	12.62	12.32
IL1 X IL12	16.95	13.75	15.28	24.85	55.3	46.19	2.3	1.6	99	100	12.78	11.75
IL2 X IL3	20.41	22.25	23.6	24.85	68.41	76.55	2.45	1.87	96.5	91.5	13.58	13.05
IL2 X IL4	20.61	10.55	22.79	19.37	39.8	37.11	2	1.6	93	87	12.61	9.25

NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm),

Contd.....

Genotype	NKR		HGW		SYP		NCP		DM		CG	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL2 X IL5	20.8	9.6	17.7	14.12	37.46	33.15	2	1.6	96	94	9.8	10.6
IL2 X IL6	32.55	29.5	22.6	22.02	94.6	89.7	1.8	1.6	92.5	88.5	10.13	11.8
IL2 X IL7	26.25	23.75	16	15.37	105.53	97.7	2	1.75	94	96	11.35	11.05
IL2 X IL8	21.98	20.13	19.3	17.8	85.68	80.07	2	2	96.5	93.5	12.13	11.9
IL2 X IL9	25.45	24.35	26.85	26.2	81.66	77.44	1.87	1.45	93.5	91.5	13.1	12.85
IL2 X IL10	22.77	20.52	15.85	15.2	72.47	67.52	2.3	1.75	94.5	89.5	10.87	10.52
IL2 X IL11	18.71	15.21	17.16	16.51	51.84	45.04	2	1.5	94.5	96.5	11.11	10.91
IL2 X IL12	24.02	18.85	17.62	16.93	51.82	42.18	1.6	1.5	99	100	11.9	11.72
IL3 X IL4	15.82	17.3	16.24	18.24	50.32	79.18	1.3	1.25	97.5	98.5	9.18	10.02
IL3 X IL5	23.01	22.83	18.11	19.11	52.34	55.34	2	1.12	99.5	97.5	10.51	11.48
IL3 X IL6	24.08	20.48	21.03	18.29	69.51	67.52	2	1.37	97	96	10.18	9.78
IL3 X IL7	21.82	22.72	28.92	27.64	100.72	60.77	1.87	1.4	95	93	12.52	13.02
IL3 X IL8	18.51	18.78	20.78	18.47	66.88	62.43	1.8	1.25	95.5	91.5	13.01	12.78
IL3 X IL9	24.78	27.73	24.79	17.9	70.96	83.38	2.3	2	95	92	12.5	12.13
IL3 X IL10	25.65	24.42	19.9	21.02	118.6	155.58	2	2	96.5	86.5	12.91	13.35
IL3 X IL11	22.1	23.3	18.58	15.14	99.3	52.25	2.3	2	95	89	11.8	10.9
IL3 X IL12	18.88	14.40	19.36	25.18	49.37	43.67	2	1.75	96.5	92.5	10.05	9.72
IL4 X IL5	24.75	25.25	18.57	15.1	63.13	72.1	1.75	2	95	89	11.11	11.15
IL4 X IL6	30.2	18.52	20.95	20.12	102.47	61.71	1.5	1.15	94	91	11.53	10.02
IL4 X IL7	18.34	12.78	24.05	15.45	42.18	39.36	2.3	1.62	100	92	13.18	10.78
IL4 X IL8	26.48	14.18	21.47	22.87	65.01	44.03	2.6	2.5	98.5	93.5	12.68	10.48
IL4 X IL9	21.75	22.61	19.95	25.25	74.55	82.8	2	2	99.5	94.5	11.95	11.78
IL4 X IL10	26.33	20.31	19.5	21.83	67.81	67.88	1.6	1.5	95.5	94.5	10.98	12.31
IL4 X IL11	26.1	25.63	20.54	23.8	98.05	53.96	1.45	1.5	98.5	96.5	11.67	11.96
IL4 X IL12	24.85	25.05	22.49	19.54	83.18	80.82	2.3	1.75	98.5	91.5	10.88	11.21
IL5 X IL6	20.95	17.61	28.16	30.21	66.95	60.27	1.8	1.75	97	93	12.28	13.95
IL5 X IL7	16.68	18.51	20.78	18.18	46.5	85.3	1.6	1.5	95	91	8.85	11.68

NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm),

Contd.....

Genotype	NKR		HGW		SYP		NCP		DM		CG	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL5 X IL8	13.98	13.98	14.9	12.9	49.45	36.95	1.15	1.2	98	93	10.98	11.48
IL5 X IL9	20.69	16.17	26.99	23.57	83.50	74.12	1.3	1.3	98.5	93.5	14.17	13.87
IL5 X IL10	19.6	17.55	19.68	19.4	85.9	75.13	1.75	1.37	98	94	15.1	14.63
IL5 X IL11	26.38	19.88	20.44	17.47	84.12	63.07	1.3	1.3	95.5	93.5	13.22	11.55
IL5 X IL12	26.38	24.43	22.34	21.68	88.18	79.93	1.3	1.25	96.5	94.5	12.88	12.51
IL6 X IL7	21.62	11.85	23.19	24.02	111.64	51.15	1.6	1.45	99	97	13.68	13.35
IL6 X IL8	20.65	15.11	20.91	21.12	75.1	57.28	1.12	1.25	100	96	19.11	10.95
IL6 X IL9	18.68	12.35	25.85	22.71	61.18	42.13	2	1.75	97	94	12.68	12.52
IL6 X IL10	24.63	16.98	22.1	23.71	93.2	65.46	1.75	1.75	98.5	94.5	12.3	11.96
IL6 X IL11	23.63	18.11	21.33	18.08	66.28	53.11	1.5	1.5	95	96	12.25	11.45
IL6 X IL12	25.52	16.18	20.17	18.71	103.47	50.17	2	1.87	98	96	11.12	12.02
IL7 X IL8	27.1	17.9	19.89	24.68	110.75	75.1	2.5	2	97	97	13.6	12.46
IL7 X IL9	22.07	12.68	25.89	24.80	83.53	78.52	1.25	1.25	94.5	98.5	13.48	11.51
IL7 X IL10	24.01	19.67	18.5	18.69	71.98	79.84	1.12	1.25	96	94	10.17	10.67
IL7 X IL11	23.54	16.7	26.64	18.49	97.7	79.03	1.87	2	97.5	94.5	13.54	13.54
IL7 X IL12	27.72	17.85	21.74	22.85	110.45	99.68	2	1.52	91	90	13.95	15.02
IL8 X IL9	26.59	20.63	22.53	21.32	80.59	75.28	1.5	1.25	88	88	13.26	14.76
IL8 X IL10	23.43	21.68	26.86	23.65	70.28	108.41	1.5	1.25	96	91	11.59	14.59
IL8 X IL11	27.28	18.51	27.05	24.05	66.17	75.16	2	1.75	97	93	14.51	13.34
IL8 X IL12	24.67	17.67	21.33	18.91	83.2	74.66	1.9	1.75	96	94	13.17	11.84
IL9 X IL10	20	16.33	19.11	21.41	91.17	72.29	2	1.75	98	96	12	13
IL9 X IL11	28.09	20.53	22.26	19.63	59.59	77.73	2	1.62	96.5	94.5	13.30	14.43
IL9 X IL12	22.62	15.22	23.17	20.71	72.67	82.8	1.6	1.4	98	96	12.68	12.52
IL10 X IL11	24.72	19.87	19.76	20.73	73.42	84.13	1.75	1.5	98	91	11.97	12.27
IL10 X IL12	23.11	24.25	21.73	20.65	66.8	109.73	1.5	1.4	96.5	95.5	13.28	13.75
IL11 X IL12	26.48	19.5	24.56	24.59	129.6	67.16	1.5	1.25	97	95	13.13	11.6
HKI 1105	22.1	18.2	21.71	20.71	67.03	57.26	1.37	1.3	99	96	11.43	11.1
HKI 1128	27.68	19.15	18.35	20.62	77.42	75.96	2	1.62	95.5	97.5	13.45	11.65

NKR = Numbers of kernel per rows, HGW= 100 grain weight (g), SYP = Seed Yield per plant (g), NCP = Number of cobs per plant, DM= Days to maturity, CG = Cob girth (cm)

Contd.....

Genotype	SP		CT		TW		RWC		SWD		MSI	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL1	82.29	79.95	28.77	28.47	0.177	0.181	67.33	65.58	32.66	34.41	23.83	11.05
IL2	87.80	87.27	27.02	26.52	0.221	0.226	76.29	73.92	23.70	26.08	23.62	3.69
IL3	77.63	81.48	27.1	26.7	0.191	0.194	81.64	79.85	18.35	20.14	45	14.42
IL4	72.88	62.81	27.91	27.91	0.206	0.204	69.88	70.73	30.12	29.27	11.25	37.9
IL5	73.59	80.54	26.7	26.4	0.223	0.219	79.33	81.14	20.67	18.86	20.93	54.83
IL6	77.67	76.65	27.3	26.3	0.229	0.231	73.71	72.88	26.29	27.12	3.65	41.96
IL7	73.71	77.32	28.85	28.05	0.243	0.248	73.01	71.13	26.98	28.87	37.84	39.66
IL8	76.82	65.62	26.55	27.15	0.217	0.215	72.11	72.93	27.88	27.07	39.92	16.75
IL9	82.37	81.26	28.4	29	0.256	0.255	72.82	73.2	27.18	26.8	51.47	34.83
IL10	79.87	79.95	30.21	30.71	0.205	0.209	71.51	69.82	28.48	30.17	21.87	10.78
IL11	70.97	61.44	27.8	29.7	0.25	0.258	49.99	48.13	50.00	51.87	14.47	11.74
IL12	72.45	71.96	29.55	30.05	0.210	0.212	77.15	76.24	22.85	23.75	18.02	10.48
IL1 X IL2	69.15	78.03	25.4	26.5	0.174	0.178	75.18	73.10	24.82	26.89	15.54	13.98
IL1 X IL3	79.97	80.64	25.12	25.52	0.172	0.164	71.45	73	28.54	27	28.40	7.28
IL1 X IL4	74.25	83.1	26.7	27	0.170	0.169	76.2	76.76	23.8	23.24	49.45	16.84
IL1 X IL5	82.14	82.05	27.55	27.55	0.180	0.177	75.08	76.7	24.91	23.3	28.44	24.15
IL1 X IL6	67.48	68.67	26.55	26.85	0.166	0.171	66.15	63.73	33.84	36.26	25.35	11.17
IL1 X IL7	90.9	87.12	28.15	28.85	0.266	0.239	68.99	73.01	31.01	26.98	45.63	15.44
IL1 X IL8	60.44	71.19	26	26.3	0.204	0.209	63.58	61.68	36.41	38.32	13.26	21.45
IL1 X IL9	83.11	75.09	26.7	27	0.207	0.204	67.89	69.16	32.11	30.84	60.21	63.11
IL1 X IL10	84.28	82.43	26.5	26.2	0.182	0.177	75.53	78.25	24.47	21.74	30.57	47.14
IL1 X IL11	81.87	79.53	26.32	26.52	0.175	0.173	78.39	79.55	21.61	20.44	18.72	24.29
IL1 X IL12	78.75	78.08	27.35	27.65	0.189	0.188	69.44	69.93	30.56	30.07	17.34	6.85
IL2 X IL3	80.09	83.68	28.55	28.65	0.164	0.166	88.00	86.61	11.99	13.38	41.69	40.7
IL2 X IL4	69.51	70.73	28.55	28.25	0.184	0.188	63.04	61.27	36.96	38.73	28.4	36.76

SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

Contd.....

Genotype	SP		CT		TW		RWC		SWD		MSI	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL2 X IL5	70.05	68.7	27	26.6	0.197	0.200	75.77	74.25	24.22	25.74	40.64	55.75
IL2 X IL6	84.33	85.23	26	26.2	0.184	0.184	68.62	68.61	31.38	31.38	31.84	31.28
IL2 X IL7	76.37	74.98	25.15	24.85	0.213	0.219	71.01	68.57	28.99	31.42	31.19	61.57
IL2 X IL8	82.97	82.14	25.8	26	0.207	0.208	67.06	66.66	32.93	33.33	34.1	38.86
IL2 X IL9	70.72	69.56	23.2	22.9	0.202	0.205	74.57	73.04	25.43	26.96	29.85	31.32
IL2 X IL10	80.27	79.14	26.42	25.92	0.192	0.198	82.27	78.91	17.72	21.09	31.74	31.74
IL2 X IL11	74.82	74.54	27.51	26.81	0.211	0.213	74.21	73.24	25.78	26.75	28.48	41.13
IL2 X IL12	77.91	71.36	27.22	27.72	0.219	0.224	82.74	80.53	17.25	19.46	22.67	8.44
IL3 X IL4	60.87	81.28	25.32	25.52	0.158	0.159	61.42	60.93	38.58	39.06	44.72	50.39
IL3 X IL5	78.81	79.73	27.88	27.58	0.234	0.238	78.45	76.75	21.55	23.49	38.28	62.51
IL3 X IL6	79.71	79.24	27.78	28.08	0.222	0.221	71.04	71.47	28.95	28.52	55.38	45.97
IL3 X IL7	85.27	77.75	28.72	28.32	0.236	0.239	69.36	68.18	30.64	31.82	14.50	6.02
IL3 X IL8	84.53	83.86	29.98	29.58	0.178	0.181	68.99	67.57	31.26	32.42	41.43	33.11
IL3 X IL9	80.45	83.00	28.53	28.23	0.184	0.189	67.14	64.83	32.85	35.17	15.19	8.25
IL3 X IL10	87.07	91.96	28.25	27.75	0.184	0.188	66.43	64.60	33.57	35.39	40.42	50.46
IL3 X IL11	75.61	78.82	28	27.5	0.193	0.199	69.38	66.67	30.61	33.33	57.37	55.08
IL3 X IL12	73.58	73.64	25.12	25.52	0.233	0.232	70.3	70.68	29.7	29.31	17.86	54.94
IL4 X IL5	78.49	69.68	27.25	27.55	0.237	0.242	77.09	75.06	22.91	24.93	37.09	37.31
IL4 X IL6	76.30	65.98	28.02	27.62	0.186	0.19	65.1	63.4	34.9	36.6	15.70	38.67
IL4 X IL7	73.57	72.26	28.08	27.68	0.22	0.222	73.14	72.32	26.86	27.68	14.9	16.52
IL4 X IL8	79.08	74.34	27.48	27.98	0.257	0.259	64.27	63.66	35.72	36.33	26.04	24.57
IL4 X IL9	64.22	71.84	28.45	27.85	0.228	0.226	65.35	66.1	34.64	33.9	9.315	10.56
IL4 X IL10	79.39	79.43	27.85	27.95	0.203	0.208	73.65	71.38	26.34	28.62	35.61	34.61
IL4 X IL11	85.15	78.08	25.9	25.7	0.193	0.199	62.42	60	37.58	40	26.29	13.68
IL4 X IL12	71.42	70.76	25.42	25.12	0.205	0.206	66.67	66.26	33.32	33.74	21.73	33.08
IL5 X IL6	82.34	83.13	29.75	29.25	0.185	0.187	75.67	74.66	24.32	25.33	16.48	16.16
IL5 X IL7	58.44	71.85	25.85	24.35	0.213	0.219	71.59	69.14	28.40	30.85	34.99	39.12

SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD= Saturation water deficit, MSI= Membrane stability index
Contd.....

Genotype	SP		CT		TW		RWC		SWD		MSI	
	I	PI	I	PI	I	PI	I	PI	I	PI	I	PI
IL5 X IL8	77.03	74.59	28.95	29.05	0.203	0.209	69.18	66.66	30.82	33.33	17.72	4.89
IL5 X IL9	71.93	81.94	26.47	26.07	0.198	0.203	67.10	64.97	32.89	35.03	10.27	8.01
IL5 X IL10	82.54	79.75	26.8	26.9	0.205	0.212	71.56	68.62	28.44	31.37	14.86	7.25
IL5 X IL11	82.28	79.62	25.62	25.52	0.214	0.215	68.53	68.10	31.47	31.89	14.49	5.48
IL5 X IL12	83.75	84.01	28.58	28.08	0.254	0.257	75.18	74.09	24.81	25.91	17.82	4.5
IL6 X IL7	77.85	78.59	26.42	26.72	0.192	0.196	70.9	68.84	29.1	31.16	3.45	8.48
IL6 X IL8	81.55	81.59	27.15	26.65	0.196	0.201	79.18	76.57	20.81	23.43	21.80	59.45
IL6 X IL9	78.05	73.37	27.62	27.12	0.223	0.225	73.84	72.99	26.16	27.01	30.5	38.69
IL6 X IL10	83.78	78.46	27.2	26.6	0.194	0.199	65.29	63.12	34.71	36.88	15.04	29.51
IL6 X IL11	66.78	73.65	25.35	24.85	0.186	0.192	73.79	70.86	26.21	29.14	7.89	42.37
IL6 X IL12	75.92	65.14	25.52	25.92	0.209	0.215	69.94	67.3	30.05	32.7	5.53	32.47
IL7 X IL8	86.35	83	25.6	25.1	0.229	0.236	65.56	63.10	34.44	36.89	17.96	8.84
IL7 X IL9	82.53	83.35	26.18	25.28	0.221	0.225	64.15	62.57	35.84	37.42	13.77	55.18
IL7 X IL10	68.98	81.3	26.21	25.41	0.204	0.208	79.12	77.26	20.88	22.84	12.06	21.05
IL7 X IL11	86.39	85.63	24.64	24.24	0.223	0.228	69.85	67.83	30.14	32.17	22.68	3.61
IL7 X IL12	86.12	86.4	27.02	25.92	0.2	0.206	84.01	80.78	15.98	19.22	8.78	60.91
IL8 X IL9	84.49	70.85	29.33	28.73	0.196	0.197	73.44	72.96	26.55	27.03	13.74	6.71
IL8 X IL10	79.67	87.23	25.13	24.33	0.203	0.203	78.95	78.95	21.05	21.05	24.56	46.89
IL8 X IL11	82.41	82.33	27.68	27.38	0.177	0.181	79.10	76.80	20.89	23.19	27.49	35.3
IL8 X IL12	82.28	80.8	26.21	25.81	0.227	0.229	76.11	75.22	23.88	24.78	22.90	67.60
IL9 X IL10	73.84	79.88	27.7	28.4	0.244	0.249	80.64	78.53	19.35	21.46	11.72	7.83
IL9 X IL11	80.08	84.05	29.33	29.53	0.202	0.204	79.57	78.44	20.43	21.55	7.31	9.43
IL9 X IL12	80.66	82.66	29.92	29.32	0.200	0.207	84.75	80.91	15.24	19.09	11.01	43.70
IL10 X IL11	83.18	73.09	27.47	28.47	0.203	0.206	79.32	77.74	20.68	22.26	10.38	41.35
IL10 X IL12	81.94	86.78	27.15	26.75	0.232	0.238	78.63	76.03	21.37	23.97	11.66	15.84
IL11 X IL12	89.72	81.68	25.6	26.1	0.176	0.182	79.7	76.26	20.3	23.74	13.26	7.15
HKI 1105	79.54	81.32	27.6	27.2	0.223	0.230	79.64	76.39	20.36	23.61	6.68	39.56
HKI 1128	70.18	82.03	25.17	24.67	0.192	0.198	85.65	82.10	14.35	17.89	16.65	55.82

SP= Shelling %, CT= Canopy temperature, TW = Turgid weight (g), RWC = Relative water content, SWD = Saturation water deficit, MSI = Membrane stability index

THESIS ABSTRACT

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8. Total number of pages in the thesis : 226
9. Number of words in the abstract : 731

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“Genetic enhancement of maize (*Zea mays* L.) for drought using phenotyping, genotyping and conventional breeding approaches”

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ABSTRACT

In the present investigation, heterosis, combining ability effects and drought stress related parameters were studied for various traits to developed and identify suitable and stable single cross hybrids. The analysis of variance for experimental design revealed the presence of significant amount of variability among parents in individual environment for most of the characters in the experiment. This suggested that the parental lines selected were quite variable for most of the characters under study. Further, the analysis of variance revealed that the variation due to moisture stress under irrigated and partial irrigated condition affect genotypes significantly for all the traits indicating the presence of sufficient variability in the experiment/ study material. Presence of sufficient amount of variability encourages for screening of the genotypes for moisture stress tolerance.

GCA effects provides information about the additive gene action involved in expression of various traits viz., days to 50% tasseling, days to 50% silking, anthesis silking interval (ASI) and days to maturity and thus helps in deciding the breeding procedure for genetic improvement of traits. The gca variance are higher sca variances, it means that there is preponderance of additive gene action and progeny selection will be effective for the improvement of these traits. The estimates of GCA effects for yield and yield contributing characters revealed that good general combiner inbred lines for grain yield per plant were IL7, IL10, IL9, IL6, IL12 and IL11.

The hybrid IL11 X IL1 showed high positive significant sca effect tracked IL1 X IL7, IL3 X IL10, IL4 X IL6 and IL7 X IL8. The hybrid IL4 X IL7 showed high

negative significant sca effect followed by IL1 X IL6, IL5 X IL7, IL2 X IL4 and IL3 X IL12. The sca variance are higher gca variances, it means that there is preponderance of non-additive gene action and progeny heterosis will be effective for the for development of hybrids.

A perusal of estimation of biochemical parameters for drought tolerance, finding information about proline content, total Soluble sugar content and chlorophyll content value in parental line IL6, IL8, IL10, IL11 and hybrid IL7 X IL11, IL2 X IL11, IL6 X IL10, IL2 X IL10, IL2 X IL6 showed high value in partial irrigated condition. The parental line IL9, IL10, IL11, IL12 and hybrid IL3 X IL12, IL3 X IL9, IL8 X IL11, IL9 X IL11 showed minimum value in partial irrigated condition for malondialdehyde content (MDA) and H₂O₂ content. On the other hand, study of the Antioxidant enzyme activity in partial irrigated condition these parental line IL7, IL9, IL11, IL12 and hybrid IL1 X IL12, IL2 X IL10, IL9 X IL12, IL6 X IL12 showed highest activity. Extensive physiological variation was observed under partial irrigated condition. A wide range of variation was observed among the accessions in terms of the drought resistance indexes of physiological and biochemical traits.

In this study, all 80 genotypes (12 Parents, 66 Hybrids and 2 Checks) of maize were characterized using 20 droughts related polymorphic microsatellite/SSR markers. Genomic DNA was extracted with the CTAB method and PCR was performed based on the common method for microsatellite markers. PCR products were separated using 6% polyacrylamide denaturing gel. Polymorphic markers amplified a total of 110 alleles with an average of 5.5 alleles per marker. The polymorphic information content (PIC) per marker pair ranged from 0.47 for bnlg1035 to 0.66 for bnlg2190 with an average value of 0.58. 15 SSR loci recorded PIC values >0.55 (bnlg1063, bnlg1225, bnlg1297, bnlg1327, bnlg1346, bnlg1614, bnlg1812, bnlg2190, bnlg2248, bnlg2252, bnlg2328, bnlg439, dupssr13, nc012, phi053), such loci could be highly useful in genotype differentiation and genetic diversity analysis. Based on unweighted neighbor-joining cluster analysis put the eighty genotypes into eight major clusters. Cluster VI comprised forty-eight genotypes evolving the maximum

genotypes. The clusters I, II and III having eight genotypes each. The cluster IV contains four genotypes and cluster V contains only two genotypes. Cluster VI and VII comprised only one genotype each. The drought tolerant genotype HKI1105 was found in Cluster VI along with 47 genotypes, so possibility exist may all these genotypes be drought tolerant falling in this group. The drought susceptible genotype HKI1128 fallen in group VII. Rest of the group II, III, IV, V, VI and VIII showed moderate drought tolerance. The pattern of group constellation proved the existence of significant amount of variability.

Key words: Maize, GCA, SCA, Heterosis, biochemical parameter, Drought tolerance, simple sequence repeat (SSR).

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1. Yadav, P. K., Singh, A. K., Tripathi, M. K., Tiwari, Sushma and Rathore, Jaya (2022). Morpho-physiological characterization of Maize (*Zea mays* L.) genotypes against drought. *Biological Forum – An International Journal* 14(2): 0975-1130.
2. Yadav, P. K., Singh, A. K., Tripathi, M. K., Tiwari, S., Yadav, S. K., Solanki, R. and Tripathi, N. (2022). Assessment of maize (*Zea mays* L.) genotypes on the basis of biochemical contents in respect to drought. *The Pharma Innovation Journal* 11(6): 2349-8242.

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