

## Assessment of Gene Action to Develop Drought Tolerance Maize Inbred Lines

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**Abstract:** Drought is one of the most significant environmental pressures around the world. The climate changes and increasing population pose serious factor to crop improvement. It is one of the most serious production restraints for world agriculture and is estimated to get worse with anticipated climate change. It is thought that understanding of how plants reply to drought at the molecular level are useful for developing improved genotypes which would accomplish well under drought. Maize (*Zea mays* L.), one of the most important food crops in the world, is very sensitive to drought, especially during flowering, pollination and embryo enlargement. Inter-disciplinary scientists have been trying to understand and dismember the mechanisms of plant tolerance to drought stress using a variety of tactics; however, success has been inadequate. Recent genomics and genetic approaches coupled with developments in particular phenotyping and breeding methodologies are expected to be more efficiently unravel the genes and metabolic pathways that discuss drought tolerance in maize. Topics enclosed by this review include the theoretical framework for improvement of traits accompanying with yield comeback to drought and how to overcome the drought conditions.

**Key words:** Breeding • Drought • Maize • Combining ability • Yield

### INTRODUCTION

Maize (*Zea mays* L.) is world's leading cereal crop with added importance for countries like Pakistan where population is rapidly increasing. Maize is the third important cereal in Pakistan after wheat and rice. Maize is a tropical plant but it is also adapted to subtropical and temperate regions of the world. It becomes the significant crop of the world due to multi-locational adaptability. Maize accounts for 2.20 % of value of agriculture and 0.5% to expanded at 1<sup>st</sup> GDP. Its area of production in Pakistan is 1085 thousand hectares with annual production of 4631 thousand tons and yield per hectare is 4.268 tons. Production increased 6.8 % over last years due to use of hybrid varieties at large area [1]. Maize is dual purpose crop such as food for human and feed for livestock and poultry and also used as industrial raw material for manufacture of different products in different food industries. It has highest crude protein (6.0-10%) from early stages to maturity, starch 72 %, protein 10 %, oil 4.80 %, sugar 3.0 % and endosperm 82 % [2].

Maize is grown twice in a year, i.e., spring and autumn. The production per hectare is low in spring season because of high temperature that affects the pollination and seed setting in maize. Its main contribution to fulfill the dietary needs of country especially the summer season due to short duration crop and large production of grains per unit area. It contains protein 10%, starch 72%, oil 1.4% and ashes 1.7% [3, 4]. Crop productivity is limited due to abiotic stresses [5]. Among different abiotic stresses drought is one of the most undesirable factors affecting the growth and yield of crop plant. The crop production with improved tolerance under stresses especially drought is one of the vital force for world food security [6]. Extra maize production from water scarce "marginal" areas of Pakistan is the need of time, which requires development of drought tolerant maize varieties producing comparatively better yield in drought conditions [7-11]. Production of maize in Pakistan is low as compared to other countries due to biotic and abiotic stresses. Drought is major problem for low production in Pakistan as well as in the world. The yield of maize hybrid

is higher than the open pollinated varieties. But the farmers in most countries do not use hybrid seed due to high cost of hybrid seed. It is needed to increase the production by producing local low cost hybrids that perform better under water deficit conditions. To produce hybrids it is needed to collect information about germplasm diversity, combining ability and heterotic pattern that is essential in maximizing the effectiveness of the breeding programs. Combining abilities and heritability analysis are useful tools to select better inbred lines for the development of desirable hybrids. General combining ability (GCA) indicate average performance of parental lines as reflected in its hybrid combinations and specific combining ability (SCA) indicates average performance of a specific cross. Higher GCA indicates additive gene effects and higher SCA indicates the dominance gene effects. If both GCA and SCA are non-significant for some traits then epistatic gene effects plays role for such traits [12]. General combining ability and specific combining ability could also be evaluated by using Line x tester analysis [13].

**Seedling and Physiological Parameters under Normal Condition:** Akbar *et al.*, (2009) reported that the inheritance of some traits was controlled by non-additive genes like grain yield. Additive genes were responsible for days to 50% maturity. The *F1* hybrids were evaluated at normal and high temperature for various physiological and yield related traits. The SCA were highly significant for the traits that were under study and GCA was also significant for all traits except stomatal conductance and transpiration rate at high temperature [14]. Alam *et al.*, (2008) estimated the combining abilities for yield and yield related traits in maize in  $5 \times 5$  diallel cross. The cross  $P2 \times P3$  showed highest heterosis. The  $P1 \times P3$  and  $P1 \times P5$  showed negative heterosis for days to maturity. The SCA effects were high for plant height, ear height, days to 50% silking and days to maturity. The grains per ear and 1000 kernel weight showed high GCA effects [15]. GCA and SCA showed significant differences for plant height, days to 50% silking and 50% tasseling [16]. Dadheech and Joshi (2007) conducted the experiment for yield contributing traits in maize in early maturing genotypes of maize (*Zea mays L.*) concluded that dominant genes have more importance for inheritance of traits in maize like protein contents, starch contents and grain yield. The inbred line L9 was a good general combiner and the hybrid  $L15 \times T1$  showed high SCA effects for traits like oil content and starch content [17]. Mhike *et al.*, (2011) revealed significant results for GCA effects for yield

contributing traits except plant height and stem lodging. They also showed that non additive genes were predominant for all traits such as plant height, anthesis dates and grain yield [18]. Pavan *et al.*, (2011) showed that SCA variances were higher than GCA variances for specific traits as plant height, days to 50% silking, ear girth, ear length, number of kernel in ear, grain yield per plant, 100 grains weight, which revealed predominant relationship of non-additive gene effects in maize [19]. Dawod *et al.*, (2012) studied the nature and magnitude of the gene action by estimating genetic components and graphic analysis for different traits like plant height, number of grains /row, number of rows per ear, ear height, 300 grain weight and grain yield per plant. Dominance variance was dominated than the additive variance for all studied traits. The graphical analysis showed epistatic gene effects for plant height, days to tasseling, days to silking, grain yield per plant and kernels per row [20]. Muraya *et al.*, (2006) evaluated seven maize inbred lines to study the heterosis and inheritance of days to 50% flowering, cob length, number of lines per cob, 100-grain weight, number of seeds per line, plant height, ear height, leaf angle, number of leaves per plant, leaf area index, cob diameter and grain yield. Their study suggested existence of both additive and non-additive gene effects for all parameters. The cob diameter and 100 seeds weight indicated preponderance of additive gene effects for inheritance of these traits [21]. Haddadi *et al.*, (2012) revealed that number of rows per ear, kernel weight, days to silking and cob to ear ratio had more GCA variance than SCA variances indicated that additive gene effect has more importance for these traits in maize. There was significant positive correlation between kernel yield and other yield components as kernel length, number of kernels per ear row and kernel weight. Therefore these are suitable selection criteria for improvement in yield [22].

Amiruzzaman *et al.*, (2013) studied heterosis and (GCA, SCA) for different traits like plant height, grain yield, days to tasseling and ear height of different maize inbred lines. The general and specific combining abilities variances were high for all traits that were under study indicating that additive and dominance variance were important for these traits. For grain yield the inbred line Q7 was a best general combiner and Q1 was the best general combiner for lateness maturity and grain yield. The crosses like  $Q1 \times Q7$ ,  $Q6 \times Q7$ ,  $Q4 \times Q6$  and  $Q2 \times Q3$  showed high specific combining ability for grain yield [23]. Mehmood *et al.*, (2004) estimated heritability and genetic advance for days taken to tasseling, Plant height, kernel rows per ear, 100 grains weight and grain

yield/plant. The plant height and grain yield per plant had high heritability of 0.993, 0.990, respectively. The genetic advance for grain yield per plant ranged between 1.33 to 43.80. The high genetic advance and high heritability showed the importance of additive genes for the traits [24].

#### **Seedling and Physiological Parameters under Drought**

**Condition:** The significant differences in varietal means for all the traits like leaf area per plant, plant height, root dry weight and shoot dry weight under drought conditions in maize. The root dry weight was considered as a best indicator for drought tolerance in maize [25]. When plants were re-watered after short period of water stress leaf elongation rate was very rapid for a short time but rate of growth after re-watering did not return to normal in severely stressed plants [26].

Khan *et al.*, (2001) studied the effect of water stress on growth and yield of maize. Their experiment was conducted by using different irrigation levels. Due to increase in water stress, the traits like plant height, days to complete flowering, leaf area and yield were decreased. Yield components like 100 grain weight and number of grains per ear were also decreased [27]. Mansouri-Far *et al.*, (2010) evaluated the yield response of two maize hybrids at vegetative and reproductive stage under water stress and normal conditions. Water stress minimized the leaf greenness, relative water content, grain yield and 100 kernel weight but maximized proline content. The 100 kernel weight was considered highly sensitive to water stress. The interaction between environment and genotype and additive gene effects were significant for plant height, ear height and grain yield, while non-additive effects were also significant for above mentioned traits [28]. Tasseling and cob formation were considered as highly sensitive stages to water stress. A 40% losses in grain yield and 32% losses in dry weight were shown [29].

Sasidharan (2005) conducted genetic analysis for yield and quality attributes in castor un-irrigated and irrigated conditions and concluded that yield and yield components excelled under normal conditions, while quality traits like fatty acid and oil showed increase under drought conditions [30]. Abdelmula and Sabiel (2007) found that the effects of drought stress was significant for traits like plant height, time to 25% silking and grain yield. Plant height showed high genotypic coefficient of variation, genetic advance and heritability [31]. Farooq (2008) conducted an experiment on maize for developing the combining ability of different physiological parameters for drought by making 6 × 6 diallel mating system. His

results revealed that 20P2-1 had high GCA and considered as good general combiner for kernels per ear row and grain yield and the line 150P1 was the good general combiner for stomata size and 100 grain weight. The crosses 20P2-1 × 70NO2-2, 20P2-1 × L7-2 and L5 × 70NO2-2 have high specific combining ability for kernels per ear row and grain yield per plant [32]. Ahsan *et al.*, (2011) reported that fresh shoot length and fresh root weight were significantly and positively correlated with fresh shoot weight. Stomatal frequency and epidermal cell size were also significantly and negatively correlated with fresh shoot weight, therefore fresh shoot length and fresh root weight, stomatal frequency and epidermal cell size could be used as best selection criteria for high yield of fresh shoot weight under drought conditions [33]. Rahmati and Farshadfar (2012) studied the effects of drought stress on growth of *Agropyron trichophorum*. There was a significant decreasing effects of osmotic stress on germination percentage, radical length, radical number and plumule length [34]. Ahsan *et al.*, (2013) conducted an experiment for the selection of inbred lines that showed best performance under drought conditions. He selected six inbred lines and used complete diallel mating design. All the characters showed significant variances except leaf venation. Some characters showed complete dominance like stomatal size and some characters showed additive gene action like leaf venation. The range of broad sense heritability was from 32 to 78% while narrow sense heritability was from 35 to 80% [35].

**Agronomic Parameters under Normal Condition:** The non-additive variance is higher in magnitude than additive variances for number of grains per row, 100 grain weight, number of ear per plant and grain yield per plant. So the non-additive genes are more important for above mentioned traits in maize [36]. The significant differences among different top crosses for some traits as kernels per ear row, kernels rows per ear, plant height, ear length, ear weight and grain yield. Some inbred lines like MO-17 showed high GCA and were good combiners. Similarly some crosses like CML-3 × Sultan showed high SCA for traits under study [37]. Srdic *et al.*, (2007) found inheritance of maize grain yield and grain yield components such as number kernel rows, 1000-kernel weight and number of kernels per row. General and specific combining abilities were highly significant for all observed parameters. Dominant gene effects were more significant in maize grain yield and number of kernel per rows, while additive gene effects were more important for number of kernel rows and 1000-kernel weight [38].

Ahsan *et al.*, (2008) revealed that there were significant differences between maize genotypes for leaf Area, leaf venation and grain yield [39]. Jabeen (2010) performed an experiment to estimate the combining ability of maize inbred lines. He concluded from his experiment that the specific combining ability was higher for some traits like 100-grain weight, stomatal size, ear length, cob diameter, Plant height and grain yield per plant. The line Soneri was considered good combiner for the traits like plant height and 100-grain weight. Ev6089 × Agaiti85 had high specific combining ability for grain yield [40]. Khalil *et al.*, (2010) performed an experiment to evaluate single cross hybrids of maize for the development of double cross hybrids in maize and concluded that grain yield depends on both general combining ability and specific combining ability, so it shows both additive and non additive effects of gene [41]. Wali *et al.* (2010) revealed that variance due to single crosses was significant for yield and yield contributing traits like number of kernels per row, 100 grains weight, number of kernel rows per ear and grain yield. GCA effects was less than the SCA effects for kernels per row and 100 grains weight and reported predominance of non additive gene effects for inheritance of these traits in maize [42].

Wasif (2008) conducted an experiment that was based on 8 × 8 diallel crosses in maize. Some traits showed high GCA like kernels per ear row, 100-grain weight and ear length which showed additive gene action for all above mentioned traits. The SCA effects were highly significant for the traits like ear diameter and grain yield which show dominance gene action for these traits [43]. Kabdal *et al.*, (2003) studied seven maize genotypes in half diallel mating design and produced 21 different crosses They observed that GCA was higher than SCA for most of traits. They concluded that the expression was controlled by the additive genes except ear height which showed more SCA than GCA. So non additive genes were more important for ear height [44].

Unay *et al.*, (2003) estimated the inheritance, combining abilities and heterosis for grain yield in different maize genotypes by making half diallel among 9 inbred parental lines. The results of this experiment revealed that dominance genes controlled the grain yield. The parents that were useful for higher yield were DNB and 552. The useful heterosis was observed for A619 × A632 and N7A × ALKD90-1. The crosses like N7A × ALKD90-1, N7A × IDRN Cornell, N7A × DNB showed high SCA effects and used as promising hybrids [45].

Zivanovic *et al.*, (2010) estimated the combining abilities for different traits as grain yield cob length, kernels per ear row, cob diameter and kernels per ear by

using full diallel mating design. Both SCA and GCA were highly significant for all the traits. Results showed the importance of additive and dominance gene action in expression of above parameters. They concluded that the inheritance of grain yield, ear diameter and ear length was controlled by dominant genes and kernel rows per ear were controlled by additive genes [46]. Zare *et al.* (2011) studied the gene action in different maize inbred lines that were crossed in a complete diallel design. They concluded that the traits like number of rows per ear, plant height, grain yield and kernel depth showed over dominance. The traits like ear length and leaf area showed partial dominance and their inheritance was under the control of additive genes. Kernels per row showed complete dominance, so reciprocal recurrent selection was most effective for kernels per row [47]. Choukan and Mosavat (2005) studied grain yield and yield related traits by using line × tester analysis. This analysis indicated that the additive genes and dominance genes were important for grain yield and yield related traits in maize. The useful testers were MO17 and B73 and they concluded that these testers were useful for screening the germplasm [48]. Kanagarasu *et al.*, (2010) conducted an experiment by using line × tester mating design. They used twenty four lines and three testers and produced seventy two hybrids. They reported that GCA variances were less than SCA variances for the traits like cob girth, plant height, 100 grain weight, plant yield, cob length, rows per ear and leaf length in maize. This showed that dominance was predominant for the traits. The interaction of lines and testers was highly significant for all the traits under study except no. of leaves per plant. The cross UMI1044-7 × UMI61 showed high specific combining ability for cob length and grain yield per plant [49].

Abrha *et al.*, (2013) conducted an experiment and evaluated parents and crosses by line x tester analysis and reported that different genotypes showed significant mean squares for different traits like kernels per row, rows per ear, number of ears per plant, plant height and grain yield and also mentioned that general combining ability of lines showed significant differences in mean squares for all traits but general combining ability of testers showed significant mean squares only for ear height and grain yield [50]. Abuali *et al.*, (2012) reported high SCA than GCA for yield and yield contributing traits except number of kernels per row, cob girth, number of rows per ear and harvest index for maize [51]. Afshar *et al.*, (2012) explained that the specific combining ability for some traits as plant height, grain yield, ear length and showed the predominance of non-additive gene action and epistatic

gene effects for the traits in maize [52]. Masekha and Ishaq (2012) reported high general combining ability effects for some traits like plant height, cob length and grain yield in maize [53].

Nouman (2012) evaluated six genotypes by estimating combining abilities for different yield related traits such as ear per plant, row of kernels per ear, number of kernels /row ear length, days to maturity, ear diameter, 100 grains weight and grain yield per plant. According to his results the line A545 was the best general combiner and WFTMS × PB77 showed highest SCA for most traits that were under study [54]. Deitos *et al.*, (2006) studied the yield and combining abilities of different maize genotypes in different environments. The line AG1051 and hybrid AG4051 × AL30 were very good performer in different locations. The best combinations were different in different locations like AG4051 × AL25 was best in Florestal site and AG4051 × AL30 was best in Viosa site [55].

**Agronomic Parameters under Drought Condition:** Cakir (2004) conducted an experiment to study the effect of drought stress on the growth of maize. According his results the 100 kernel weight, grain yield per hectare, number of ears per plant, plant height, leaf area index and grain yield per cob were affected significantly by water stress [29]. Malik *et al.*, (2004) concluded that plant height, ear height, leaf area, ears per plant, ear weight and kernels per ear row were prominent characters for contributing towards high grain yield for genotypes QPM-1, QPM-3 and QPM-5. Water decrease the number of kernels per ear row and ear weight. Temperate lines showed high general combining ability for leaf area but all the other lines showed negative GCA for leaf area [56]. Plant height, leaf area and number of leaves per plant were positively correlated with grain yield. They found that Plant height, number of leaves per plant and stem diameter might best selection criteria for improvement in maize [31]. Moser *et al.*, (2006) studied the effect of water stress on the yield and harvest index of four maize cultivars viz; DK888, Sunwani, La postasequia and KTX2602. The number of kernel rows, number of kernels per row and 1000 kernels weight was minimized with an increase in harvest index under water stress conditions. A significant interaction was observed between water stress and varieties. For grain yield La posta was considered as drought tolerant variety and KTX2602 was susceptible [57]. Olaoye *et al.*, (2009) evaluated fourteen corn varieties under normal condition and water stress imposed by the withdrawl number of irrigations from pre-anthesis to

maturity. Water stress minimized the grain yield 53% and upto 22% reduction in number of ears per plant. Dogona-1, Douana-1 and Bondokuy-1 varieties had higher grain yield under water stress conditions. They also observed between high grain yield with lower leaf senescence [58].

Hussain *et al.*, (2009) found that different maize genotypes have significant differences for leaf area, plant height and grain yield and they also show partial dominance with additive gene effects under normal and water stress conditions [59]. The genetic variation in the degree of drought tolerance is better manifested under severe conditions of water deficit in the soil [60]. Therefore global food security depends on development of crop with increased the resistance to abiotic stresses such as drought and salinity. The solution of this problem is the development of drought tolerant varieties.

## CONCLUSIONS

It was concluded that non-additive genes are more important for above mentioned traits in maize and due to increase in water stress plant height, days to complete flowering, leaf area and yield were decreased. It was indicated that additive and dominance variance were important for these traits. It was also predicted that plant height, number of leaves per plant and stem diameter might be considered best selection criteria for improvement in maize. Some traits showed high GCA like kernels per ear row, 100-grain weight and ear length which showed additive gene action for quantitative traits. It was also concluded that SCA effects were highly significant for the traits like ear diameter, protein contents and grain yield which show dominance gene action for these traits.

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