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COMBING ABILITY ESTIMATES AND MODE OF INHERITANCE FOR DROUGHT RELATED TRAITS IN GENETICALLY DISTANT MAIZE ACCESSIONS (*Zea mays*)

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ABSTRACT

Ten genetically distant maize accessions with variable response to different levels of moisture were crossed following line × tester mating fashion. All the germplasm was evaluated at normal and stress moisture levels against some physiological and morphological parameters i.e. leaf temperature, leaf area, stomatal frequency, stomatal size, silk elongation rate, 100-grain weight and grain yield per plant for two years. General and specific combining abilities and heterotic effects were determined along with percent contribution of lines, testers and line × testers in the inheritance of traits. Using dominance and additive variance values, potence ratio was calculated for all the traits at both moisture levels. General combining ability (GCA) effects of lines and testers had variable magnitude and directions. On the basis of GCA effects accessions A50-2, M-14, WFTMS, and N48-1 could potentially be used in the hybridization programme. Crosses A50-2 × B-34, A50-2 × WFTMS, NC-9 × B-34, NC-9 × N48-1 and B-42 × WFTMS have high specific combining ability (SCA) effects for most of the parameters studied. There was variable magnitude and direction of heterotic effects at both the moisture levels shown by most of the traits. Partial dominance was found for all the traits under study except 100 grain weight and grain yield per plant.

Key words: Maize, moisture stress, line × tester, GCA and SCA.

INTRODUCTION

A plant may experience several distinct abiotic stresses like water shortage, salinity and temperature extremes either continuously or discontinuously at different times during the growing season, which limit crop productivity (Tester and Bacic, 2005). Drought affects humanity from personal inconvenience to nationhood level by reducing crop yields, pasture deterioration and livestock deaths. Food security at household to subcontinents level is under serious threat due to reduction in cereal production because of moisture stress. This destructive impact of drought may grow, as the climate change becomes a reality. There is broad consensus that stresses due to continued climatic changes will increase, and thus impose significant difficulties to plant and crop growth in most parts of the world (White, 2004).

Maize is a versatile high yielding C4 cereal and is used in both fresh and processed forms. According to Rosegrant *et al*., 1999, global demand for maize will increase up to 784 M tons in 2020, with most of the increased demand coming from developing countries. Assuming no increase in maize production area, approximately an annual growth rate of 1.5% will be needed; however, in the previous decade the yield growth rate was 1.2% worldwide, but only 1% in developed countries. At this rate of growth, demand for maize will be doubled after every 15 years (Duvick and Cassman, 1999). The projected rapid growth in demand implies that unless major production increase occurs, the completely Asian region will become a net importer of maize. Maize requires 500 – 800 mm of water during life cycle of 80 to 110 days. At tesseling, moisture demand is 135 mm/month (4.5 mm/day) which increases up to 195 mm/month (6.5 mm/day) during hot windy conditions (Jamieson *et al*. 1995).

World food security is dependent on continuous crop improvement with increased tolerance to abiotic stresses especially drought and salinity (Denby and Gehring, 2005). Yield stability can be insured by improving drought tolerance with the use of genetics. Improved genetics can be packaged in a seed and easily be adapted than improved agricultural practices. Availability of rich genetic diversity for drought tolerance in maize enables plant breeders to evolve drought tolerant maize lines.

Knowledge about the diversity patterns of genetic resources has great importance in maize breeding, which helps to maintain diversity among breeding lines and to maximize heterosis in hybrid combination (Warburton *et al*., 2002). The need of screening of parents before their use in breeding programme and combining ability analysis based on progeny test data is a useful method for evaluating parents and crosses for a wide range of quantitative characters. Plant breeders working with several species reported a direct relationship between the level of heterosis exhibited by F_1 and the divergence between their parents. Therefore, estimation of genetic distance can be useful for prediction of high performance crossings.

To evolve drought tolerant and high yielding varieties, there must be better understanding of physiological and genetic responses of germplasm, therefore germplasm evaluation is a decisive aspect in maize breeding programs. Information on the genetic architecture of traits related to drought tolerance and their mode of inheritance is a necessary step to move forward. Combining ability analysis provides useful information in this respect, a way out lies in the use of Line × Tester analysis of combining ability. The present study was designed to estimate GCA, SCA by using line × tester mating fashion and mode of inheritance for different drought related traits in maize accessions having variable responses at different moisture levels. This information may be useful to pick up best performing maize accessions and to plan further the breeding programs using these accessions as in parental combinations.

MATERIALS AND METHODS

Development of genetic material: In a line × tester mating, ten genetically distant maize accessions having variable response to different moisture stress levels were mated (Aslam *at el*., 2009). Out of ten maize accessions, five drought susceptible namely T-7, N48-1, B-34, USSR and WFTMS were used as testers and five drought tolerant namely NC-9, A50-2, M-14, B-42 and NC-3 (Aslam *et al*., 2006) were used as lines. Rows and plants were kept 75 cm and 25 cm apart respectively. Two seeds per hole were dibbled. After 15 days of sowing, thinning was done and one healthy seedling per hole was retained. All recommended agronomic and cultural practices were adopted uniformly.

Evaluation of genetic material: All the germplasm (25 crosses & 10 parents) were sown in the field under normal and moisture stress conditions. Following Kirda *et al.,* 2005;
Normal: Normal irrigations were applied.
Drought: 50% of the normal irrigations were applied.
two factor factorial triplicated randomized complete block design was followed. The data were recorded for the following traits at appropriate time.

Leaf temperature (LT): Three leaves equally exposed to sun from each of five selected plant per entry were used for readings with the help of infrared thermometer (RAYPRM30CFTRG, RAYTEK USA).

Leaf area (LA): Physiologically mature, fully expanded second leaf from the top of five plants in each entry was measured for LA. LA was recorded in cm^2 using leaf area meter (ΔT-MK2, England).

Stomatal frequency (SF): Two leaves from each entry at both the moisture levels were taken for data record. These leaf samples were placed in Carney's solution for 24 hours to arrest stomatal movement and to remove chlorophyll and then washed in acetone and stored in formalin solution. The cleaned leaves were examined from the upper surface of middle part of the leaf blades under 10X microscopic magnification and numbers of stomata were counted.

Stomatal size (SS): Stomatal size of the same samples used for the measurement of SF, was measured with the help of ocular micrometer by using medium power (40X) of microscope (NIKON-H-3, JAPAN). Ocular micrometer was calibrated with the help of stage micrometer. The length and width of the stomata was measured in microns. Three observations were recorded from different places of each leaf and area was calculated by using the following formula;

Area = Length × Width

Silk elongation rate (SER): SER was recorded following Anderson *et al.,* (2004). Five cobs from five plants of each genotype were selected to record the data in each entry. Silks from each cob were bundled into three groups, each containing ten to twelve silks. On the day of first silk appearance the silk length was marked as zero (DAFS = 0). Length of silks was recorded daily in the morning between 7.00 – 8.00 am regularly for 10 days. Silks were kept covered with butter paper bag to rule out any chance of pollination during this period.

Elongation rate = Total length of silk / Total no. of days after first silk appearance

100-grain weight (100GW): Grains harvested from five selected plants of each entry were bulked separately. 100 grains from each bulk were taken randomly and weighed in grams using an electronic balance (OHAUS-GT4000, USA).

Grain yield per plant (GYPP): The cobs from five selected plants of each entry per treatment were harvested and threshed separately. The grains from each plant were weighed in grams.

Data analysis: Means of the data were calculated on two yearly bases in order to have a single mean value of each parameter.

These data from parents and crosses were subjected to Line × Tester analysis of variance as outlined by Kempthorne (1957). Mean responses were compared using Duncan's Multiple Range Test (Statistica, StatSoft Inc.). GCA and SCA effects, genetic components and contribution of lines, testers and interactions to total variance were calculated following Singh and Chaudhary (1999). Heterosis over mid and better parent was estimated following Falconer and

Mackay (1996) and t-test was used to estimate significance of heterosis.

RESULTS AND DISCUSSION

Results pertaining to ANOVA for various traits measured at both moisture levels (Table-1) showed significant differences ($P \leq 0.01$) among genotypes, parents, crosses, lines, testers and line x tester interaction for all the traits except testers for SF. Crosses were significantly different ($P \leq 0.01$) from parents for LT, LA, 100 GW and GYPP at both moisture levels. These significant differences reflect that there are chances to improve the performance of genotypes, parents, crosses, lines, testers and line x tester interaction at both levels of moisture stress by exploiting the potential they possess.

GCA effects of lines and testers for various traits are given in Table-2. Among all the maize accessions M-14, A50-2, WFTMS and N48-1 had positive and significant GCA effects for most of the traits. Among lines, M14 showed positive and significant GCA effects for LA, SER and GYPP at both moisture levels and for 100GW at normal moisture level whereas A50-2 showed significant and positive GCA effects for LT and GYPP at both moisture levels and for SS and 100GW at moisture stress level. Among testers, WFTMS and N48-1 had significant and positive GCA effects for LA, SER, 100GW and GYPP at both the moisture levels except WFTMS for GYPP at both the moisture levels and N48-1 for GYPP at normal moisture level. High GCA value (positive or negative) indicates that the parental mean is superior or inferior to the general mean and gives information about the concentration of predominant genes with additive effects.

According to results presented in Table-3, variable magnitude and direction of SCA effects is evident. Crosses A50-2 × WFTMS, A50-2 × B-34, NC-9 × B-34, NC-9 × N48-1 and B-42 × WFTMS had positive and significant SCA effects for most of the traits studied. Crosses A50-2 × WFTMS and A50-2 × B-34 and NC-9 × B-34 showed positive and significant SCA effects for LA, SER, 100 GW and GYPP at both moisture levels. NC-9 × N48-1 had positive and significant SCA effects for LA, 100 GW and GYPP at both the moisture levels and for LT and SER at normal moisture level. SCA reflects non-additive interactions. For the selection of parents the combination of SCA, GCA and hybrid mean should be used. The frequency of favourable genes increases with the best combination of high mean, favourable SCA and high GCA effects and populations having high frequency of favourable alleles are good source for plant selection (Miranda and Viegas, 1987). Low GCA and SCA can be improved through inter and intra population selection procedures. Differences among GCA effects and SCA effects may be due to additive, additive × additive and higher order additive interactions while SCA may be due to non-additive genetic variances. Positive GCA effects mean that continuous improvement is possible through breeding. Some of the crosses with significant SCA involved both the parents with significant GCA effects e.g. A50-2 × WFTMS and in some crosses at least one parent had significant GCA effects e.g. NC-9 × N48-1 indicating the preponderance of additive genetic effects for that trait. Crosses in which none of the parent had significant GCA e.g. NC-9 × B-34 indicated the presence of non-additive genetic effects controlling that character. The cross combination with good mean, favourable SCA and at least one parent with high GCA, tend to increase favourable alleles. Hybrids were evolved through, High × high, low × low and low × high general combiners, such as A50-2 × WFTMS, NC-9 × B-34 and NC-3 × N48-1 for SER, M-14 × WFTMS, B-42 × USSR and NC-9 × N48-1 for 100GW and A50-2 × WFTMS, NC-9 × B-34 and B-42 × WFTMS for GYPP. These results reflected that the best hybrid combinations are not always due to parents with best GCA, both hybrid means and the GCA of parents therefore should be considered together. High mean hybrid with favourable SCA along with parents of high GCA is actually due to high concentration of favourable alleles, which is good for breeders. Both additive and non-additive effects have role in the control of LA, whereas predominantly additive gene effects were observed in case of 100GW and GYPP. In case of LT and SS non-additive effects were predominant.

Contribution of line × tester interaction in total inheritance was comparative to lines and testers in all the traits studied at both the moisture levels except in 100 GW at moisture stress level (Table-4). Lines contributed more than testers in the inheritance for all the traits except LA at both moisture levels, 100 GW at normal moisture level and in SS at moisture stress level.

Partial dominance was observed for LT, SF, SS, SER and LA at both moisture levels except LT at moisture stress level and SER at normal moisture level which showed no dominance. 100GW and GYPP showed over dominance at both moisture levels.

Variable heterosis in both magnitude and direction was observed at both moisture levels (Table-6). For LA all the crosses had negative and significant heterosis at both moisture levels except A50-2 × WFTMS at both moisture levels and M-14 × N48-1 at stress moisture level. NC-3 × N48-1 showed significant heterosis for all the traits with variable direction at both moisture levels except SER, similarly A50-2 × WFTMS performed in the same way except negative and significant heterotic effects for LA and SER at moisture stress level and non-significant and positive heterosis at normal moisture level. M-14 × WFTMS showed positive and significant heterosis for 100 GW and GYPP and negative and significant heterosis for LA, SF, SS at both moisture levels and for LT at normal moisture level.

Crosses M-14 × T-7, A50-2 × T-7, A50-2 × B-34 and NC-3 × T-7 showed positive and significant heterotic effects at normal and stress moisture levels. Heterosis is the result of accumulation of dominant or partially dominant alleles. Heterosis helps breeders to develop a product with hidden genetic potential and can be exploited for the achievement of good yield (Weerasinghe *et al*., 2004). Bhatnagar *et al*. (2004) reported the classification of maize germplasm in to heterotic group, which may help in exploitation of heterosis in maize. The overall picture of the study reflected that almost the same crosses with positive and significant heterosis in case of 100GW and GYPP have negative and significant heterosis for SS and SF.

This study reflected a relation between SS, SF and GYPP under stress condition. The results regarding relationship between stomatal characteristics and plant water status are not consistent, that may be due to influence of related stomatal characteristics rather than SF and SS. Thus, stomatal characteristics are affecting water status of plants as a complex, and every component of this complex should be studied in relation to other components and with other factors, which influence water status of plants. In the present study it is concluded that both GCA and SCA effects had variable magnitude and direction. Among lines M-14, A50-2, WFTMS and N48-1 can be potentially used in hybridization program. Crosses A50-2 × WFTMS and M-14 × WFTMS are with out-standing heterotic values and stomatal size and stomatal frequency along with other stomatal traits are good reflector of drought tolerance.

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