Crop improvement through conventional and non-conventional breeding approaches for grain yield and quality traits in *Zea mays*

Fawad Ali[1], Naila Kanwal[1], Muhammad Ahsan[1], Qurban Ali[1,2] and Nabeel Khan Niazi[3,4]

[1.] Department of Plant Breeding and Genetics, University of Agriculture Faisalabad Pakistan
[2.] Centre of Excellence in Molecular Biology, University of the Punjab, Lahore Pakistan
[3.] Institute of Soil and Environmental Sciences, University of Agriculture Faisalabad Pakistan
[4.] Adjunct Research Fellow, Sothern Cross University Australia
Corresponding Author: fawadniazi_a@yahoo.com, saim1692@gmail.com

Abstract: *Zea mays* is an important cash crop grown for food and feed throughout the world. The growth, yield and quality of corn grain and fodder are highly affected by various biotic and abiotic factors that caused reduction in output. The crop yield and quality may be improved through conventional breeding by selecting genotypes on the basis of genetic variability. Various statistical analysis and designs like randomized complete design, randomized complete block design, factor factorial analysis, combining ability analysis, heterosis, heterobeltiosis, additive, dominance and gene interactions helped plant breeders to identified best inbred lines, synthetic varieties and hybrids. The traits that are under polygenic control may be improved through quantitative genetics and quantitative plant breeding approaches. The non-conventional or advanced molecular plant breeding now a day helping in improving the potential of crop plant by inducing gene (s) of interest in crop plants. Biotechnology also helped to develop biotic and abiotic resistant crop genotypes. In present review, the role of conventional and non-conventional breeding has been explained for better understanding of breeders to work with conventional and molecular plant breeding.

Introduction

Maize (*Zea mays* L.) is a widely grown cereal crop and first most important in ranking among all cultivated cereals (Ali *et al.,* 2014). Maize flour and its oil are the cheapest source of energy but Pakistan is still deficient in its production. Local production of edible oil does not fulfill our demand not more than 30 %. Maize is the major contributor of edible oil world-wide. Availability of total edible oil during 2010-11 was 1.7 million tones, while the local production was 696 thousand tones which fulfill 25 % of total requirement and the remaining 75% demand was met through import from the other world. Maize accounts for 4.8% of total cropped area and play important role in agricultural output which is 3.5%. Maize is grown on an area of area of 939 thousand hectares with total production of 3341 thousand tons with an average yield of 2892 kg ha^{-1}. Maize in Pakistan is cultivated on 939 thousand hectares; whereas, the local seed production is 1512.4 thousand tones and 4614.2 thousand tons is imported. Oil production is 0.31 thousand tones which is very much deficient. It is a rich source of edible oil that contains high oil contents (40-45%). From health point of view it is considered as good quality oil because it has high mono and polyunsaturated fatty acids viz., oleic and linoleic acids that comprises 90% of total fatty acids (Rai, 2002). Maize has many uses. Its grain is a rich source of starch, vitamins, proteins and minerals. One hundred gram of fresh grain contains 361 calories of energy, 9.4 g protein; 4.3g fat, 74.4g carbohydrate, 1.8g fibre; 1.3g ash, 10.6 per cent water, 140mg vitamins, 9mg calcium, 290mg, phosphorus and 2.5mg iron (Premlatha *et al.,* 2011; Ali *et al.,* 2014ab).In maize oil the presence of soluble vitamins viz., A, D, E and K makes the premium quality of its oil that is good for heart patient (Evertt *et al*. 1987). Maize is used for the manufacturing of vegetable ghee, corn flour, pasta and margarine. It is also being used as poultry and animal feed. When maize seed is integrated into soil it recovers the soil fertility because, it is a good source of calcium, nitrogen and potassium (Robert *et al*. 1993). Maize is highly cross pollinated crop and is ideally suited for heterosis exploitation. In maize, heterosis breeding developed successfully after the detection of cytoplasmic male sterility source (Leclercq, 1969) and fertility restoration (Kinman, 1970) that provided the required vigor to commercial hybrid seed production. Most of the hybrids have been released for commercial cultivation by public and private sectors. The North Carolina Design II is an efficient breeding method to assess the large number of inbreds. It provides us male and female

variances that how much they can contribute to develop good hybrids. It provides the information on the relative importance of general and specific combining ability effects to understand the genetic basis of important plant characters viz., plant height, stem diameter, leaf area, seed weight, grain yield and oil contents etc. The general combining ability (GCA) of males and females means the average value of its performance in hybrids when crossed with each other. The specific combining ability (SCA) means the performance of individual hybrids (Fick and Miller, 1997).

Water stress on corn and role of Biotechnology

Water scarcity, salinity, water logging, high and low temperature extremes and diseases attack in the field are mainly faced by the maize plants which experiences biotic and abiotic stresses during the different time of growing season (Trester and Bacic, 2005, Araus *et al*., 2002). Continuous improvement and development of crops by increasing tolerance to abiotic stresses specifically is very much important for world food security (Denby and Gehring, 2005). Water availability (100 %, 75 %, or 60% of daily transpiration) by growing maize on three levels during a period of silking and at two plant densities (6 and 10 plants per meter square) no nutrition limitation was given to produce different levels of resource availability of water (Echarte and Tollenaar, 2006). There are three critical growth stages before silking, at silking and during grain filling. At these stages the water stress causes a significant reduction in yield (Ghooshch, *et al*., 2008). Now the time has come if we want to take a lot of yield and want to make improvement in maize crop so we should use the biotechnology, in maize improvement program to ensure sufficient production (Machuka, 2001; Pingali and Pandy, 2001). Studies reveal that tissue culture work about the recalcitrance of maize lines and mature embryos has been done (Bohorova *et al*., 1995; Hodges *et al*., 1986), and regeneration of maize lines from mature embryos has been successfully completed and in other cereal crops (Akula *et al*., 1999; Green and Phillips, 1974; Ozgen *et al*., 1998; Rueb *et al*., 1994; Wang, 1987; Ward and Jordan, 2001). No plantlets were regenerated to induce the callus from mature embryo of maize (Green *et al*., 1974). Maize plants can be regenerated from mature embryos with a frequency ranging from 19.85 to 32.4% (Huang and Wei 2004). Efficient regeneration system using split mature seeds were used as explants for successful regeneration of maize plant for two hybrid and two inbred temperate maize lines (Al-Abed *et al*., 2006). A Successful regeneration of one inbred and one open pollinated tropical maize line from mature zygotic embryos using split seed technique could be used in tissue culturing (Abebe *et*

al., 2008; Hannan *et al*., 2015). Plant regeneration system was successfully developed from calli initiated from plant anthers (Ting *et al*. 1981), from immature inflorescences (Pareddy and Petolino 1990), from tassels taken as immature (Songstad *et al*. 1992), segments of leaf used for regeneration (Ray and Gosh 1990), parts of plants at seedling stages (Santos *et al*. 1984), shoot tips of plants (O'Connor-Sanchez *et al*. 2002) and meristematic tissues from shoot apices (Zhang *et al*. 2002).

To make a considerable and remarkable molecular breeding could be used to make improvement involving marker assisted selection and genetic transformation (Bruce *et al*., 2001; Frame *et al*., 2000; Machuka, 2001; Zaheer *et al*., 2015). The cereals like wheat, barley and maize are the most suitable explants for in vitro culture and plant regeneration is obtained from immature embryos (Armstrong and Green, 1985; Green and Phillips, 1975; Ray and Ghosh, 1990). The callus formation from maize embryo is mainly dependent upon the genotype used (Fluminhan and Aguiar-Perecin, 1998; Lee and Phillips, 1987). When we compare the maize with other cereals and rice, it is found and remarkably noted that for callus induction and plant regeneration, maize is particularly challenging crop (Rafiq *et al*., 2010; Frame *et al*., 2006; Vega *et al*., 2008; Sidorov and Duncan, 2009), as well as some tropical germplasms (Valdez-Ortiz *et al*., 2007). To obtain a successful generation of transgenic crops the efficiency of tissue culturing is very much important to infuse a tolerance against biotic and abiotic stresses. The successful regeneration of maize has been reported from mature seed excised embryos (Huang and Wei 2004; Al-Abed *et al*., 2006; Butt *et al*., 2015) and shoot meristems (Sairam *et al*., 2003). Regeneration potential is positively correlated with genotype used and composition of the cultivation medium (Rout and Lucas, 1996; Eudes *et al*., 2003).

Tissue culture

Qamar *et al*., (2015) studied that the gene for insect/pest and herbicide resistance can be successfully transferred in callus of corn. Wagdy (2002) used tissue culturing technique on two maize varieties. The successful callus could be grown from immature zygotic embryo. The callus exhibited regeneration ability so he delivered a bar gene in the maize line namely line 1 by using plasmid DNA (pBARGUS) and screenable gus gene. He used the electroporation system using gene gun for gene delivery into the callus. Later on the polymerase chain reaction, southern analysis and northern analysis confirmed that the plants were successfully transformed. Khatun *et al*. (2003) studied that the callus induction from mature seed scutella of rice could be done. They used three different growing

basal media named MS, N and R. The four genotypes L × 297, IR64, V19 and IR64-1-1-4 were checked. Among three different basal media the MS (Murashage and Skoog) was the best for callus initiation (82.50 %) but not best for regeneration. R (regeneration media) media was the best for regeneration of plantlets from the mature seed derived callus. Danson *et al.* (2006) explained the callus induction and regeneration of three maize varieties from immature seed derived embryo. They used the three different basal media N6 (Chu), MS (Murashage and Skoog) and LS (Linsmaier and Skoog) but he found the best N6 media. N6 was the best media. Five different concentrations of N6 salts (10, 30, 50, 70 and 100 %). He found under 50 % salt concentration the callus induction and regeneration was best of immature seed derived embryo of under investigated maize line L1. Furthermore he used the agrobacterium for T-DNA delivery of desired gene into the callus and successfully made the transgenic plants. He confirmed these plants by transient GUS expression. Abebe *et al.* (2008) made experiment of tissue culturing on two maize inbred lines. They made calus from imature zygotic embryo. They used the LS (Linsmaier and Skoog) basal media fortified with B5 vitamins. They found that 62.3 % of type I and 75.6 % of type II callus can be produced by placing the embryo derived from mature seed. They used the different concentrations of 2,4-Dichlorophenoxyaceticacid (0%, 1% and 2%). The most suitable concentration of 2,4-Dichlorophenoxyaceticacid (2,4-D) was 2 % for successful callus. Furthermore they checked the regeneration capacity of callus on the regeneration media and found the positive results.

Huang *et al.* (2004) did experiment on maize regeneration system. They developed the callus from mature seed excised embryo. They used the 2,4-Dichlorophenoxyaceticacid (4mg/l) and silver nitrate (10 md/l) in MS (Murashage and Skoog) basal media for better embryogenesis. The successful callus was developed. For successful regeneration they supplemented MS (Murashage and Skoog) with indole-3-butyric acid and got successful plantlets. They concluded that this efficient regeneration system could be used for genetic transformation of maize. Decima *et al.,* (2010) planned an experiment on twenty two maize lines. They formed the callus by using N6 and MS (Murashage and Skoog) medias. Among the twenty two lines four lines were the best for callus formation moreover these four lines were genetically identical also. They suggested the results that genotype of the plant is very much responsible for successful callus formation and regeneration of plantlets. Krakowsky *et al.* (2007) used tissue culturing for successful callus formation and regeneration. They used quantitative trait loci (QTL) mapping to examine the maize genotypes which is better responsive to callus formation and regeneration. 126 recombinant lines (RILs) were used and observed that Mo17 was the best responsive to type I callus. Total of eleven bins were observed on eight chromosome during quantitative trait loci (QTL) mapping. The candidate genes for the abscisic acid were the most responsible to type I callus formation. However the allelic variability for known candidate genes should be understand more to find out the more genetic basis of maize genotypes responsive to type I callus formation.

Genetic studies based on conventional techniques

Study of the behaviour of qualitative, quantitative and physiological traits in maize are important because many such traits like protein, oil, maturity characters, plant height, leaf length, leaf area, number of leaves per plant, green fodder yield, grain yield per plant, sub-stomata CO_2 absorption, leaf temperature, transpiration rate, photosynthetic rate and yield per hectare are under polygenic control (Ali *et al*., 2014abcd). The literature collected is reviewed here under with respect to, study of F_1 hybrids. Evaluation of lines by hybrid and mean inbred performance, combining ability and gene action, character-wise review, variability, heritability and other genetic parameters and finally all the data was subjected under North Carolina Design II.

Grain Yield

Annapurna *et al.,* (1998) and Venugopal *et al.* (2003) showed that seed yield was positively and significantly correlated with plant height, ear circumference, number of seeds per row, number of seed rows per ear, number of seeds per ear and test weight exercised maximum direct influence on yield. Growing degree days to the reproductive phase had the highest negative direct effect on grain yield. Datu (1998) reported correlations using the date of flowering, plant height and the number of leaves as indirect selection criteria may results in a positive correlated response in earliness, yield potential and superior stalk quality. Khakim *et al.* (1998) noticed that grain yield was positively correlated with plant and ear insertion height, leaf area, ear number, ear length, grain rows per cob, grain per row and per cob, grain weight per cob, ear weight and 1000-grain weight. Srivas and Singh (2004) observed that dry fodder yield per plant, a dependent trait was significantly and positively associated with green fodder yield and its contributing traits such as plant height, days to 50 per cent silking, number of leaves per plant, stem girth, leaf blade length, leaf width and sheath length to increase the grain yield the ultimate goal. Manivannan (1998) and Ahmad *et al.*, (2003) reported that ear circumference, kernels per row,

1000-grain weight, kernels per row and ear length had significant and positive correlation with grain yield. High and positive direct effects were observed for kernel rows and 1000-grain weight. It was suggested that maximum correlation of grain yield was obtained with number of kernels per row followed by leaf area, plant height, tassel length and ear length; path analysis revealed that the number of kernels per row, plant height, ear width, leaf area and 1000-grain weight had positive direct effect on grain yield (Ali *et al*., 2014; Gautam *et al.* 1999 and Kumar *et al.* 1999).

Viola *et al.* (2003) revealed that early silking and harvesting of fresh cobs, greater plant height, cob length, cob weight, cob height and number of cobs per plant and lesser cob girth directly contributed to increase grain yield. Ei-Shouny *et al.* (2005) showed that grain yield per plant correlated positively and significantly with ear diameter, ear length, number of kernels per row, 100-kernel weight, grain rows per ear, ear height, plant height and days to silking. Under normal planting date and with number of kernels per row, ear diameter, 100-kernel weight, ear length, number of rows per ear, ear height and days to silking under late planting date. Singh *et al.* (2003); Ali and Ahsan (2015) and Ali *et al*., (2015) observed that ear leaf area had the highest positive direct effect on green fodder yield per plant at genotypic and phenotypic levels followed by dry matter yield per plant, ear length and days to 50 per cent silking. Maize yield is mainly influenced by ear length, followed by number of kernels per row, ear width, grain rows per ear, growth period and 1000-seed weight. Kernel percentage per ear and number of pointless ears had minimum effect on maize yield (Ali *et al*., 2014ab and Heping *et al*., 2004). Swarnalatha and Shaik (2001) indicated that the plant height, days to 75 per cent silking and maturity, ear length, number of seeds per row and 100-grain weight positively influenced the yield directly and also indirectly through several yield components. Umakanth and Khan (2001) observed that grain yield per plot showed significant and positive correlations with ear circumference, ear length, plant height and 100-seed weight. Path analysis revealed that plant height followed by number of seeds per row, 100-seed weight, ear length and ear circumference showed maximum positive direct genotypic effects as well as indirect contribution through other characters on grain yield. Shelake *et al.* (2005) noticed that grain yield was positively and highly correlated with number of grains per cob, biological yield per plant, harvest index, 100-grain weight, cob length, number of grain rows per cob and cob girth hence grain yield is increased. Wali *et al.* (2006) observed that yield was positively associated with plant height, ear

length, ear circumference, number of kernels per row, fodder yield per plot and 100-grain weight, but was negatively correlated with number of days to 50 per cent silking at the phenotypic and genetic levels. The grain yield per plant was positively associated with plant height, ear length, ear circumference, kernels per row, fodder yield per plot and 100-grain weight at the phenotypic and genetic levels.

Sumathi *et al.* (2005) genotypic correlation studies indicated that ear weight, number of rows per ear, number of kernels/row, and total number of kernels/ ear were positively associated with grain yield. Oil per cent exhibited negatively non-significant correlation with grain yield, whereas it showed positive association with number of rows/ ear only. Path coefficient analysis revealed that number of kernels per row showed high direct effect on grain yield followed by 100 seed weight, number of rows per ear and total number of kernels per plant. Abirami *et al.* (2007) indicated that grain yield showed positive association with oil content and protein content. Path analysis showed that the weight of the cob contributed to the maximum direct effect to grain yield. It implied that selection for weight of the cob will be highly effective for the improvement of grain yield. Harjinder *et al.* (2006) reported significant positive correlations for grain yield with days to 75 per cent husk, plant height, ear height, and number of ears. It was also noticed that grain yield was significantly correlated with plant height, ear diameter, ear length, rare ear length, 100-kernel weight and grain production rate. Grain yield was most highly correlated with ear diameter, followed by 100-kernel weight, plant height, ear length and grain production rate. Bhiote *et al.* (2007) showed dry matter and crude protein yields showed positive and significant correlation with green forage yield and had positive direct influence on their correlation with green forage yield. Sofi and Rather (2007) reported that path analysis indicated that 100-seed weight had greatest direct effect on grain yield, followed by number of kernels per row, number of kernel rows per ear, ear length and ear diameter. Rafiq *et al.,* (2010) reported that genotypic correlation of all the parameters showed significant results. Path analysis revealed the fact that 100-grain weight exhibited a significant effect on grain yield followed by plant height, ear length and ear diameter. Most of the traits exerted positive indirect effects on grain yield. Higher heritability and genetic advance for ear length, plant height, grain yield per plant may be used for selecting higher yielding maize genotypes (Ali *et al*., 2011ab; Mustafa *et al*., 2013; Ahsan et al., 2013; Ali *et al*., 2013ab and Ali *et al*., 2014c). Wannows *et al.,* (2010) explained his studies on five maize hybrids that broad sense heritability, additive gene

action, interrelationship among the traits, genotypic and phenotypic correlation and path coefficient analysis revealed significant differences on grain yield. Plant height, ear height, leaf area index, specific leaf weight and physiological maturity had significant differences on grain yield of plant. The path analysis also showed that ear diameter, leaf area index and physiological maturity had positive direct and indirect effects on grain yield.

Watto *et al*. (2009) indicated that leaf area index, ear diameter and physiological maturity had high positive direct and indirect effect on grain yield. Yousuf and Saleem (2001) found that plant height, number of kernel rows per ear and number of kernels per row were significant for grain yield. Kernel rows per ear and 100 seed weight were used as secondary objective during selection process for better yield (Hefny 2011; Ali et al., 2013c; Ahsan *et al*., 2011). Divergent selection for oil and protein concentration in maize was initiated in 1896 by C.G. Hopkins (Dudley, 2007). This long-term selection process is used as a tool for understanding the genetics of a trait. Recurrent selection, based on the evaluation of oil and protein content of individual ears, was carried out by Hopkins for 48 generations. This selection experiment has been carried out for over 100 generations and continues today with advanced analytical techniques (Illinois, 2009). The Illinois Long-Term Selection Experiment has resulted in populations that span the known extremes for maize kernel protein and oil content and have been valuable in studies of physiological mechanisms controlling protein content of grain (Moose *et al*., 2004). Populations Illinois Low Oil (ILO) and Illinois Low Protein (ILP) have reached their lower limits for these traits and selection has been discontinued due to poor germination rates (Moose *et al*., 2004). After 48 generations of selection, reverse selection was applied to each population to determine if genetic variability in the selected populations had been exhausted (Dudley, 2007). Continued progress has been seen in each of these reverse selection strains, indicating that sufficient genetic variability remained to make genetic gains even after extensive selection (Dudley and Lambert, 2004). Abdulai *et al* (2009) worked on eight nine hybrids and determined that genotype adaptability is very much important to attain better yield. They gave the results that seven out of nine genotypes were more stable in the environment. The genotypic and phenotypic correlation visualized the fact that all parameters had positive correlation with grain yield. Among the five hybrids the Vivek hybrid 5 performed the best and can be used for next two or three generations in future breeding program (Singh *et al*., 1998). Aslam *et al* (2003) found that path coefficient analysis

revealed that leaf venation via the root to shoot ratio had maximum direct effect while net photosynthetic rate exerted the highest negative effect on grain yield.

Quality Parameters

Saleem *et al.,* (2008) studied that oil content, protein content, linolinic acid, lauric acid, linoleic acid, sugar contents, starch and carbohydrate amount had significant effect on grain yield. Path coefficient analysis gave the results that grain starch content and lauric acid had positive effect on grain yield via other traits. Premlatha *et al* (2011) found that grains per row, grain yield per plant, hundred grain weight, rows per cob, number of grains per row and oil content had significant effect on grain yield. They studied that the hybrid UMI 278 × UMI 314 had significant specific combining ability with highest estimates of economic heterosis for protein content and rows per cob but the UMI 334 × UMI 314 had significant positive specific combining ability with highest estimates of economic heterosis for protein content and oil content both with higher grain yield.

Mbuya *et al.,* (2011) found that lysine content, carotenoid content, protein content, oil content had significant result on grain yield. Krishnaveni (1983) obtained fat content from 3.2 to 4.6 per cent in hybrids and hybrid UMI-140 × UMI-134 contained highest amount of oil. Letchworth and Lambert (1998) evaluated the quality traits in maize inbred and hybrids and found that oil concentration was significantly higher in open pollinated kernels than in self-pollinated kernels. Dubey *et al*. (2001) observed that the two parent single cross hybrids exhibited the highest magnitude of economic heterosis among the selected conventional and nonconventional two parent and multi-parents for oil content. Shanthi *et al*. (2002) studied the nature of gene action and combining ability for crop yield, oil and protein contents in maize lines developed through L × T design, which revealed the preponderance of non-additive gene action. Alexander (1999) examined xenia effects on percentage oil in maize grain and on grain yield and reported that oil percentage and caloric content of grain from the high oil pollinator resulted in an overall increase of 75 per cent in oil content without reducing grain yield.

Cao Yong Guo *et al*. (1999) concluded that oil content also increased seed protein and lysine content significantly but reduced yield, 100-grain weight, ear weight, grain weight per ear, plant height and ear circumference. Kumar and Kumar (2000) reported that oil content was high in late maturing and dwarf plant types with low number of seed rows and seeds per ear in addition to lower 100- grain weight. Radochinskaya (2001) used lines with 4 to 10.5 per cent oil content and reported that the best single cross hybrids showed 7 to 11 per cent oil content.

Thompson *et al*. (2002) found that lower grain yield, higher grain moisture content and lower test weight were associated with top cross blends. So, these characters have to be considered while determining top cross high oil content, hybrid production costs, especially if high oil content grain is being produced under contract. Krishnaveni (1983) reported that starch content ranged from 41 to 75 per cent in hybrids and the hybrid UMI-47 × MUI-134 contained the highest amount of starch. Shalygina *et al*. (1990) screened 128 inbred lines of maize for highest starch and sugar content to select best lines to be used in breeding program for increased grain quality and reported V- 239A, B-187 and V-461 as promising lines with higher content of starch and sugar. Mazzoni and Robutti (1990) reported average starch yields for flint (Cargill-157) and dent (Cargill-P17) hybrid as 57.62 and 52.59 per cent, respectively. Alika and Ojomo (1996) demonstrated that additive and non-additive gene actions significantly influenced the variation of starch content and gel spread. Additive gene action was more pronounced, implicating the effectiveness of selection for starch yield through a recurrent selection procedure. Reciprocal effects were equally significant for grain starch content, an indication of the importance of cytoplasmic effects. Pasztor *et al*. (1998) observed that an increase in 1000-kernel weight was accompanied by a rise in the starch and protein content. Wang *et al*. (1998) observed heterosis for starch content was higher than protein content, while heterosis for protein content was negative. Daneswar and Dickinson (1999) obtained the starch content ranged from 64.6 to 72.58 per cent on dry weight basis in G-4646 hybrid. Larissa *et al*. (2004) reported significant kernel composition association in the three starch production genes, sh-1, sh-2 and ht-2, tests for association with either starch pasting characteristics and/or analyze content were significant in sh-1, sh-2 and aa1.

Variability, heritability and other genetic parameters

Phenotypic variability expressed by a genotype or a group of genotypes in any species can be portioned into genotypic and phenotypic components. The genotypic components being the heritable part of the total variability, its magnitude on yield and its component character influences the selecting strategies to be adopted by the breeder. Fisher (1918) partitioned the total genetic variance (i) additive genetic variance, which is the sum of additive genetic variances contributed by individual loci (ii) Dominance variance component which results from intra allelic interaction of genes at segregating loci (iii) epistatic variance results from inter allelic interaction of genes at segregating loci. Lush (1940)

defined heritability in both broad sense and narrow sense. In broad sense, heritability refers to the functioning of the whole genotype as a unit and is used in contrast with the environmental effects. In the narrow sense, heritability largely includes only the average effect of genes transmitted additively from parent to off spring. Warner (1952) has suggested different technique for estimating the degree of heritability in crop plant which is based on parent offspring regression variance component from an analysis of variance and approximation of non-heritable variance from genetically uniform population to estimate the total genetic variance.

Comstock (1955) reported that phenotype associated with a given genotype varies with the environment. This leads to complete inconsistency of genotypic value, a different value of a given genotype relative to every variance of environment major or minor. Hayman (1958) partitioned epistatic variance into additive × additive, additive × dominance and dominance × dominance components for two loci, three loci in or more. Longquist (1964) reported that phenotype of a quantitative character was mainly due to the joint action of genotype and environment. Debnath and Azad Mak (1993) studied that heritability estimates were highest for ear height in all environments after the removal of the interactive effects. Abirami *et al*. (2005) reported that genotypic and phenotypic coefficient of variance was higher for total sugar content, plant yield, weight of the cob, oil content and ear height. Heritability estimates were high for all the characters investigated. High heritability coupled with high genetic advance was observed for number of grains per cob. Sprague and Tatum (1942) formulated the concepts of combining abilities. General combining ability is the average performance of a strain in series of cross combinations, estimated from the performance of F1s from the crosses, whereas specific combining ability is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of average performance of lines involved. Griffing (1956) has shown relationship between various heritable variance components and GCA and SCA variances. Thus, GCA variance is due to additive variance and additive × additive interaction variance. While, SCA variance is due to dominance variance, additive × additive variance, additive × dominance variance and dominance × dominance variance components. Estimates of the variances due to GCA and SCA provide an appropriate diagnosis of the predominant role of additive or non-additive variances of gene action. Gardner (1963) reported that ratio of additive to non-additive gene action is to be considered in order to decide the predominance of the kind of

genetic variation for a given character. If the ratio of additive to non-additive gene action is more than unity indicates the major role of additive variance in controlling the expression of a character, whereas, less unity indicates the importance of non additive variance.

Tandan *et al*. (1970) opined that the combining ability analysis was found to be better than graphical analysis in predicting the prepotency of cultures especially in the later generations, when the expression of dominance effect was reduced. According to Dhillon and Singh (1976), general combining ability was more important than specific combining ability for the inheritance of days to 50 per cent silking, grain moisture, plant height, ear height, ear length, ear circumference and kernel row number but not for grain yield. Martin and Hallauer (1976) studied diallel analysis for ear length, ear circumference, 100-grain weight, number of grain rows and yield and concluded that epistasis was more frequent for all characters except for 100-grain weight. Epistasis was most common for ear circumference and number of grain rows and least common for yield. Bhalla and Khehra (1977) found significant general combining ability for yield per plant, ear length, plant height. The predominance of additive gene effects found for plant height, 100-grain weight, while non-additive effects were important for ear height and grain yield per plant. The predominance of additive gene action found for days to silking and non-additive gene action for grain yield per plant. According to Altinbas and Tosum (1998) GCA and SCA variances for grain yield per plant and other yield components indicated that screening the parental lines and crosses based on combining ability effects for 100-grain weight and ear length should be effective. Dutu (1998) observed that plant height was controlled by additive and non-additive gene actions and cytoplasmic inheritance. The leaves per plant were controlled by additive genes only. Joshi *et al*. (1998) revealed that there was preponderance of non-additive gene action in the expression of yield per plant, protein content and starch content, while for oil content and 100-grain weight there was preponderance of additive gene action. Lou *et al*. (1998) concluded that most plant and ear characters were improved with additive and dominance effects of the female parents. He emphasized that GCA variance was more important for ear length, number or kernel rows per ear, but SCA variance was important for other characters like grain yield per plot, ear circumference, number of kernels per ear row, 100-kernel weight, days to 50 per cent silking, plant height and ear height.

Mikhailov and Chernov (1999) reported that partial dominance of the positive allele is the main type of allelic interaction in the loci controlling kernel row number. Paul and Debnath (1999) obtained significant gca and sca effects for all characters studied viz., days to silking, plant height and ear height. Talleei and Kochaksaraei (1999) observed significant gca effects for plant height, ear height, kernel length and yield per plant. Geetha and Jayaraman (2000) reported that additive and dominance components were significant for plant height, number of kernel rows per cob, number of kernels per row, ear weight, 100-grain weight and grain yield. Gupta and Nagda (2000) observed variances due to variety heterosis and its components were significant for all the characters studied. Ei-Moula *et al*. (2004) indicated that magnitude of delta 2-GCA was greater for days to 50 per cent silking plant and ear height, while detla 2 SCA was greater for number of ears per 100 plant and grain yield. Interaction delta 2 SCA × L was higher than that of the delta 2-SCA × L was higher than that of the delta 2 GCA × L for all traits indicating that the non-additive type of gene action was more affected by environment conditions than the additive type. Malik *et al*. (2004) reported that temperate material gave GCA effects for striking characters contributing towards high grain yield i.e., plant and ear height, leaf area, ears per plant, ear weight kernels per row. Vafias and Ipsilandis (2005) observed that rapid lines developed from combining half sib/S1 evaluation may ensure high and stable crossing performances, based on additive gene action. Stability and uniformity of performance of three way crosses was due to proper breeding incorporated in single cross hybrid and to high stable inbred line performance.

Conclusions

It was concluded from all above studies that the improvement of corn yield and quality is much important to enhance crop yield and productivity. Biotechnology and conventional plant breeding are playing an important role in crop improvement.

References

1. Abdulai, M., P. Y. K. Sallah and O. S. Kantank. 2007. Maize grain yield stability analysis in full season lowland maize in Ghana. Int. J. Agri. Biol. 9: 41-45.
2. Abebe, A., Kassa, T., Degefu, T., & Hassen, E., 2008. Investigation on seroprevalence of bovine brucellosis and related major reproductive health disorders in Ada'a Liben Dairy Cooperative. Eth. Vet. J., 12: 19-31.
3. Abirami, S., Vanniarajan, C., Arumugachamy, S. and Uma, D., 2007, Correlation and path analysis for morphological and biochemical

traits in maize genotypes. Plant Archives, 7: 109-113.

4. Ahmed. M.A., S.E. Sadek, Abd El-Ghany, H.M. 2006. Genetic differences of product energy of four parents inbred lines and five yellow hybrid maize (Zea mays L.) genotypes grown in Egypt. J. Appl. Sci. Res. 2: 153-158.

5. Ahsan, M., A. Farooq, I. Khaliq, Q. Ali, M. Aslam and M. Kashif. 2013. Inheritance of various yield contributing traits in maize (*Zea mays* L.) at low moisture condition. African J. Agri. Res. 8(4): 413-420.

6. Ahsan, M., M. M. Hussain, J. Farooq, I. Khaliq, A. Farooq, Q. Ali and M. Kashif, 2011. Physio-genetic behavior of maize seedlings at water deficit conditions. Cercetari Agronomice in Moldova, 146: 41-49.

7. Akula C, Akula A, Henry R (1999). Improved regeneration efficiency from mature embryos of barley cultivars. Biol. Plant. 42: 505-513.

8. Al-Abed D., S. Redrabhatla, R. Talla and S. Goldman. 2006. Split-seed: a new tool for maize researchers. Planta. 223: 1355-1360.

9. Ali Q & M Ahsan, (2015). Correlation analysis for various grain contributing traits of *Zea mays*. African Journal of Agricultural Research, 10(23), 2350-2354.

10. Ali, Q., M. Ahsan, M.H.N. Tahir and S.M.A. Basra, 2012. Genetic evaluation of maize (*Zea mays* L.) accessions for growth related seedling traits. *IJAVMS,* 6: 164-172.

11. Ali, Q., Ahsan, M., Tahir, M. H. N., & Basra, S. M. A. (2014e). Gene action and Correlation Studies for Various Grain and its Contributing Traits in Maize (Zea mays L). *Bothalia*, *44*(2), 80-91.

12. Ali Q, Ahsan M, Ali F, Aslam M, Khan NH, Munzoor M, Mustafa HSB, Muhammad S. 2013a. Heritability, heterosis and heterobeltiosis studies for morphological traits of maize (Zea mays L.) seedlings. Adv. life sci., 1(1): 52-63.

13. Ali, Q., A. Ali, M. Tariq, M.A. abbas, B. Sarwar, M. Ahmad, M.F. Awaan, S. Ahmad, Z.A. Nazar, F. Akram, A. Shahzad, T.R. Samiullah, I.A. Nasir, and T. Husnain 2014a. Gene Action for Various Grain and Fodder Quality Traits in *Zea Mays*. *Journal of Food and Nutrition Research*, 2(10): 704-717.

14. Ali, Q., Elahi, M., Ahsan, M., Tahir, M. H. N., & Basra, S. M. A. (2011). Genetic evaluation of maize (Zea mays L.) genotypes at seedling stage under moisture stress. *International Journal for Agro Veterinary and Medical Sciences*, *5*(2), 184-193.

15. Ali Q, Ali A, Ahsan M, Ali S, Khan NH, Muhammad S, Abbas HG, Nasir IA, Husnain T.

2014d. Line × Tester analysis for morpho-physiological traits of Zea mays L. seedlings. Adv. life sci., 1(4): 242-253.

16. Ali Q, Ali A, Awan MF, Tariq M, Ali S, Samiullah TR, Azam S, Din S, Ahmad M, Sharif NM, Muhammad S, Khan NH, Ahsan M, Nasir IA and Hussain T. 2014b. Combining ability analysis for various physiological, grain yield and quality traits of *Zea mays* L. Life Sci J 11(8s):540-551.

17. Ali, Q., Ahsan, M., & Ali, F. (2013b). Genetic advance, heritability, correlation, heterosis and heterobeltiosis for morphological traits of maize (Zea mays L).*Albanian Journal of Agricultural Sciences*, *12*(4), 689-698.

18. Ali, Q., Ahsan, M., Mustafa, H. S. B., & Hasan, E. U. (2013c). Studies of genetic variability and correlation among morphological traits of maize (Zea mays L.) at seedling stage. *Albanian Journal of Agricultural Sciences*, *12*(3), 405-410.

19. Ali Q, Ali A, Waseem M, Muzaffar A, Ahmad S, Ali S, Awan MF, Samiullah TR, Nasir IA, and Tayyab H. Correlation analysis for morpho-physiological traits of maize (*Zea mays* L.). Life Sci J 2014c;11(12s):9-13.

20. Ali Q, M Ahsan, SA Qasrani, I Ramzan, SU Malook, A Sher, A Shakoor and MK Mubarik. 2015. Genetic Variability and Correlation Analysis for Various Morpho-Physiological Traits in Maize (*Zea mays* L.) For Green Fodder Yield. American-Eurasian J. Agric. & Environ. Sci., 15 (7): 1298-1303.

21. Ali Q, M Ahsan, NH Khan, M Waseem and F Ali. 2014f. An overview of *Zea mays* for the improvement of yield and quality traits through conventional breeding. *Nat Sci.* 12(8):71-84.

22. Ali, F., Ahsan, M., Saeed, N. A., Ahmed, M., Ali, Q., Kanwal, N., & Niazi, N. K. (2014). Establishment and optimization of callus-to-plant regeneration system using mature and immature embryos of maize (Zea mays). *International Journal of Agriculture and Biology*, *16*(1), 111-117.

23. Alexander, D. E., 1999, Oil content Vs grain yield in corn. Maydica, 44: 111-112.

24. Alok K, Gangashetti A and Dahiya, HG, 1999, Analysis of direct and indirect effects of quantitative traits in diallel crosses of Maize. Annals.

25. Annapurna, D., Khan, K. H. A. and Shaik Mohammad, 1998, Genotypic, phenotype correlations and path coefficient analysis between seed yield and other associated characters in tall genotypes of maize. Crop Res., 16: 205-209.

26. Anonymous. 2008. Agriculture Statistics, FAOSTAT, United Nation Organization.

27. Anonymous. 2011-12. Economic Survey of Pakistan. Govt. of Pakistan, Finance and Economic Affairs Division, Islamabad, Pakistan: pp-21.

28. Araus, J., G. A. Slafer, M. P. Reynolds and C. Toyo. 2002. Plant breeding and drought in C3 cereals, what should we breed for? Ann. Bot., 89: 925-940.

29. Armstrong CL, Green CE. (1985). Establishment and maintenance of friable, embryogenic maize callus and the involvement of L-proline. Planta 164: 207-214.

30. Aslam, M. and M. H. N. Tahir. 2003. Correlation and path coefficient analysis of different morophological traits of maize inbred under water stress conditions. Int. J. Agri. Biol. 5: 446-448.

31. Bao, H., Zhang J., Zhao L., Yu-Yan S. and Dou M., 2004, Path analysis of ear characters in spring inbred maize lines. J. Jilin Agric. Univ., 26: 16-18.

32. Bhalla, S. K. and Khehra, A. S. 1977. Analysis of combining ability in maize at varying plant densities. Crop. Impr. Maydica. 22: 19-26.

33. Bhiote, K. D., Pardeshi, S. R. and Mhaske, B. M., 2007, Correlation and path analysis studies in forage maize. Agric. Sci. Dig., 27: 146-147.

34. Bohorova N. E, Luna B, Briton R. M, Huerta L. D, Hoistington DA (1995). Regeneration potential of tropical, subtropical, mid-altitude, and highland maize inbreds. Maydica 40: 275-281.

35. Bruce, W.B., Gregory O.E. and Thomas C. 2001. Molecular and physiological approaches to maize improvement for drought tolerance. J. of Experim. Botany. 53: 13-25

36. Butt SJ, Varis S, Nasir IA, Sheraz S, Shahid A, Ali Q. Micro Propagation in Advanced Vegetable Production: A Review. (2015). Adv. Life Sci. 2(2). pp: 48-57.

37. Cao Yong Guo, Kong Fanling and Son Ton Ming, 1999, Effects of population improvement for high oil content maize and selection method evaluation. Journal of China Agric. Univ., 4: 83-89.

38. Comstock, R. E., 1955, Theory of quantative genetics. Synthesis, Cold Spring Harbor, Symposia Ceuant. Biol., 20: 93-102 .

39. Comstock, R. E., 1955, Theory of quantative genetics. Synthesis, Cold Spring Harbor, Symposia Ceuant. Biol., 20: 93-102 .

40. Daneswar, M. H. and Dickinson, D. B., 1999, Investigation of phytoglycogen sugar and starch content in sugar and starch corn (*Zea mays* L.). Crop Res., 17: 199-208.

41. Danson, J.W., M. Lagat and M. Mbogori, 2006. Screening tropical maize lines for the production and regeneration of friable and embryogenic type II callus. Afr. J. Biotechnol., 5: 2367–2370.

42. Datu, H. 1998. Phenotypic and genotypic correlations between vegetative period and grain yield and other agronomic trait in early maize. Analete Institului Ceretari pentra Cerela Si Plante Technice Fundule.65: 101-109.

43. Debnath, S. C. and Azad Mak., 1993, Response to environmental changes to components of variation and other genetic matters in maize. Pak. J. Sci. Ind. Res., 36: 6-7.

44. DÉCIMA ONETO, C.A.; GONZÁLEZ, G. and LEWI, D. (2010). Biolistic maize transformation: Improving and simplifying the protocol efficiency. African Journal of Agricultural Research, vol. 5, no. 25, p. 3561-3570.

45. Denby, K. and C. Gehring. 2005. Engineering drought and salinity tolerance in plants: lessons from genome-wide expression profiling in Arabidopsis. Trends in Biotech., 23: 547-552.

46. Dhillon, B. S. and Singh, J. 1976. Diallel analysis of yield and other traits of maize varieties. SABRAO Journal, 8: 147-152.

47. Du J., Grant D., Tian Z., Nelson R.T., Zhu L., Shoemaker R.C., Ma J. (2010a). SoyTEdb: A comprehensive database of transposable elements in the soybean genome. BMC Genomics 11: 113.

48. Dubey, R. B., Joshi, V. N. and Pandiya, N. K., 2001, heterosis and combining ability for quality, yield and maturity traits in conventional and non-conventional hybrids of maize. Ind. J. Genet. Plant Breeding., 61: 353-355.

49. Dudley J., Lambert R. (2004). 100 generations of selection for oil and protein in corn. Plant Breeding Reviews 24:79-110.

50. Dudley J.W. (2007) From Means to QTL: The Illinois Long-Term Selection Experiment as a Case Study in Quantitative Genetics. Crop Sci. 47:S-20-31.

51. Dutu, H., 1998, Phenotypic and genotypic correlations between vegetative period and grain yield and other agronomic trait in early maize. Analete Instutului de Cercetari pentra cereale Si plante Technice Fundulea, 65: 101-109.

52. Echarte, L. and M. Tollenaar. 2006. Kernel set in maize hybrids and their inbred lines exposed to stress. Crop Sci. 46:870–878.

53. Ei-Moula, M. A. A., Barakat, A. A. and Ahmed, A. A. 2004. Combining ability type gene action

for grain yield and other attributes in maize (*Zea mays* L.). Aust. J. Agric. Sci. 35: 129-142.

54. Ei-Shouny, K. A., Ei-Bagowly, O. H., Ibrahim, K. I. M. and Ai-Ahmad, S. A., 2005, Correlation and path analysis in four yellow maize crosses under two planting dates. Arab Univ. J. Agric. Sci., 13: 327-339.

55. Eudes F., Acharya S., Laroche A., Selinger L.B., Cheng K.J. (2003): A novel method to induce direct somatic embryogenesis, secondary embryogenesis and regenera tion of fertile green cereal plants. Plant Cell Tiss. Org. Cult., 73: 147–157.

56. Evertt, N. P., K. E. Robinson and D. Mascarenhas. 1987. Genetic Engineering of Sunflower (*Helianthus annuus* L.). Biotechnology 5(1): 1201-1204.

57. Fick, G. N. and J. F. Miller. 1997. Sunflower breeding. In: sunflower technology and production, edited by E. E. Schneiter. SA, CSSA. Madison, Wisconsin, USA.

58. Fisher, R. A., 1918, The correlation between relatives on the supposition of Mendelian inheritance. Trans. Roy. Society Edin., 52: 399-433.

59. Fluminhan A, Aguiar-Perecin MLR. (1998). Embriogenic response and mitotic instability in callus cultures derived from maize inbred lines differing in heterochromatic knob content of chromosomes. Annals of Botany 82: 569-576.

60. Frame B, Zhang H, Cocciolone S, Sidorenko L, Dietrich C, Pegg S, Zhen S, Schnable P, Wang K (2000) Production of transgenic maize from bombarded Type II callus: effect of gold particle size and callus morphology on transformation efficiency. In Vitro Cell Dev Biol Plant 36: 21–29.

61. Gardner, C. O. 1963. Estimation of genetic parameters in cross-pollinated plants and their implications in plant breeding. Statistical Genetics and Plant Breeding. NASNRS Washington D. C. Publication, 982: 228-234.

62. Gautam, A. S., Mittal, R. K. and Bhandari, J. G., 1999, Correlations and path coefficient analysis in maize (*Zea mays* L.). Ann. Agric. Biotechnol. Res., 4: 169-171.

63. Geetha, K. and Jayaraman, N. 2000. Genetic analysis of yield in maize (*Zea mays* L.) Madras Agric. J. 87: 638-640.

64. Ghooshchi F, Seilsepour M,Jafari P (2008). Effects of water stress on yield and some agronomic traits of maize [SC 301]. American-Eurasian J. Agric. Environ. Sci., 4: 302-305.

65. Green, C. E. and R. L. Phillips. 1974. Plant regeneration from tissue cultures of maize. Crop Science. 15: 417-421.

66. Green, C. E. and R. L. Phillips. 1975. Plant regeneration from tissue cultures of maize. Crop Science. 15: 417-421.

67. Griffing, B. 1956. Concept of general combining ability and specific combining ability in relation to diallel crossing system. Aust. J. Biol. Sci. 9: 463-493.

68. Gupta, S. C. and A. K. Nagda. 2000. Analysis of variety diallel cross for yield and its components in winter maize. Ind. J. Genet. and Plant Breeding. 60: 301-303.

69. Hannan A, Qasim M, Bashir A, Hasan EU. Ali Q, Mustafa HSB. Biotechnology: A tool for the improvement of human life**. *Nat Sci* 2015;13(7):19-33.

70. Harjinder, S., J. S. Chawla and M. S. Grewal. 2006. Correlation and path coefficient analysis on some elite genotypes. Crop Improv. 33: 31-33.

71. Hayman, B.I. 1958. The separation of epistatic from additive and dominance variation in generation means. Heredity. 12: 371-390

72. Hefny, M., 2011. Genetic parameters and path analysis of yield and its components in corn inbred lines (Zea mays L.) at different sowing days. Asian Journal of Crop Science 3(3):106-117.

73. Hodges, T. K., K. K Kamo, C. W. Imbrie and M. R. Becwar. 1986. Genotype specificity of somatic embryogenesis and regeneration in maize. Biotechnology. 4: 219-224.

74. Huang, X. and Z. Wei. 2004. High frequency plant regeneration through callus initiation from mature embryos of maize (Zea Mays L.). Plant Cell Rep. 22: 793-800.

75. Huang, X. and Z. Wei. 2004. High frequency plant regeneration through callus initiation from mature embryos of maize (Zea Mays L.). Plant Cell Rep. 22: 793-800.

76. Illinois U.o. (2009) The Illinois Maize Breeding and Genetics Laboratory, A Tradition of Excellence, Urbana, I. L. maize populations. Crop Sci., 4: 227-228.

77. Joshi, V. N., N. K. Pandiya and R. B. Dubey. 1998. Heterosis and combining ability for quality and yield in early maturing single cross hybrids of maize (*Zea mays* L.). Ind. J. Genet. and Plant Breeding. 58: 519-524.

78. Khakim, A., S. Stoyanova and G. Tsankova, 1998. Establishing the correlation between yield and some morphological reproductive and biochemical characters in maize. Rantenie dini Nauki. 35: 419-422.

79. Khatun, N., Bari, M.A., Islam, R., Huda, S., Siddique, N.A., Rahman, M.H., Mollah, M.U. 2003. Callus induction and regeneration from

nodal segment of potato cultivar Diamant, J. Biol. Sci., 3: 1101 1106.

80. Kinman, M.L. 1970. New development in USDA and state experiment station sunflower breeding programs. Proc. Fourth Int. Sunflower Conference, Memphis 10: 181-183.

81. Krakowsky MD, Lee M, Holland JB (2007) Genotypic correlation and 651 multivariate QTL analyses for cell wall components and resistance to stalk tunneling by the European corn borer in maize. Crop Sci 47 (2):485-488.

82. Krishnaveni, S. 1983. Biochemical constituents of certain promising maize cultures. Madras Agric. J. 70: 139-140.

83. Kumar, N. M. V. and S. Kumar. 2000. Studies on characters association and path coefficient for grain yield and oil content in maize (Zea mays L.). Ann. Agric. Res. 21: 73- 78.

84. Lambert, R. J., D. E. Alexander and Z. J. Han. 1998. A high oil pollinator enhancement of kernel oil and effects on grain yields of maize hybrids. Agron. J. 90: 211- 215.

85. Larissa, M. W., S. R. White, M. Ana, R. Torbert, M. Rocheford and B. Edwards. 2004. Dissection of maize kernel composition and starch production by candidate gene association. Plant Cell. 16: 2719-2733.

86. Leclercq, P. 1969. The sterile male cytoplasmic chezle tournesoil. Annales de I' Ameliorationdes plants. 19: 99-106.

87. Lee, M. and Phillips, R.L. (1987). Genomic rearrangements in maize induced by tissue culture. Genome 29: 122-128.

88. Lonnquist, J. H., 1964. A modification of the ear to row procedures for the improvement of maize (Zea mays L.) Int. J. Breed. Anadohi.8: 90-100.

89. Lou, X. Y., D. Q. Zhang, L. Yu-Zhang and J. Zhao. 1998. A study of the genetic effects of maize ears and related traits. Zhejian Nongye Texue. 1: 21-24.

90. Lush, J. L. 1940. Intersize correlationb regression of offsping on dary as a method of estimating heritability of characters. Prov. Amer. Soc. Ani. Prod. 33: 293-301.

91. Machuka, J. S. 2001. Agricultural Biotechnology for Africa. African scientists and farmers must feed their own people. Plant Physiol. 126: 16-19.

92. Malik, S. I., H. N. Malik, N. M. Minhas and M. Muhammad. 2004. General and specific combining ability studies in maize diallel crosses. Int. J. Agric. and Biol. 6: 856-859.

93. Manivannan, N. 1998. Character association and component analysis in maize. Madras Agric. J. 85: 293-294.

94. Martin, J. H. and A. R. Hallauer. 1976. Relation between heterozygosis and yield for four types of maize inbred lines. Egyptian J. of Genet. pp: 119-135.

95. Mazzoni, M. R. and J. L. Robutti. 1990. Evaluation of a method for predicting industrial yield of maize starch. Maize Abstract, 49: 1487.

96. Mikhailov, H. E. and A. A. Chernov. 1999. Genetic-statistical of kernel row number in maize. Tsitologiya-i-Gnetika. 35: 19-25.

97. O'Connor-Snchez, A., J. L. Cabrera-Ponce, M. Valdez-Melara, P. Tillez-Rodraguez, J. L. Hernendez and L. Herrera-Estrella. .2002. Transgenic maize plants of tropical and subtropical genotypes obtained from calluses containing organogenic and embryogenic-like structures derived from shoot tips. Plant Cell Rep. 21:302–312 of Biology, 15: 173-176.

98. Özgen, M., M. Turet, S. Altmok, C. Sancak. 1998. Efficient callus culture induction and plant regeneration from embryo culture of winter maize (Triticum aestivum L.) genotypes. Plant Cell Rep. 18: 331-335.

99. Pareddy, D. R., J. F. Petolino. 1990. Somatic embryogenesis and plant regeneration from immature inflorescences of several elite inbreds of maize. Plant Sci. 67:211–219

100. Pasztor, K., Z. Gyori and S. Szilagyi. 1998. Changes in the protein, starch, ash, fibre and fat contents of maize parental lines and hybrids. Noventy Texmeles. 47: 271-278.

101. Paul, K. K., and S. C. Debanth. 1999. Combining ability analysis in maize (Zea mays L.). Pakistan J. Scientific and Industrial Res. 42: 141-144.

102. Pingali, P. L., S. Pandy. 2001. Meeting world maize needs: Technological opportunities and priorities for the public sector. In: CIMMYT 1999-2000 World Maize Facts and Trends, Mexico. pp 1-20.

103. Premlatha, M., A. Kalamani and A. Nirmalakumari. 2011. Hetrosis and combining ability for grain yield and quality in maize. Adv. Environ. Biol. 5: 1264-1266.

104. Qamar, Z, Aaliya K, Nasir IA, Farooq AM, Tabassum B, Qurban A, Ali A, Awan MF, Tariq M and Husnain T. An overview of genetic transformation of glyphosate resistant gene in Zea mays. Nat Sci. 2015;13(3): 80-90.

105. Rafiq, M., M. Rafiq, A. Hussain and M. Altaf. 2010. Studies on heritability, correlation and path analysis in maize. J. Agric. Res. 48: 35-38.

106. Rai, M. 2002. Oilseeds in India. Andhra Pradesh Agric. Reg. Res. J. 20: 13-15.

107. Ray DS, Ghosh PD, 1990. Somatic embryogenesis and plant regeneration from

cultured leaf explants of Zea mays. Ann Bot 66: 497-500.

108. Robert, I., C. Harry and B. Kaplan. 1993. Sunflower; an American native. Colombia, USA.

109. Rout, J.R. and W.J. Lucas. 1996. Characterization and manipulation of embryogenic response from *in vitro* cultured immature inflorescences of rice (*Oryza sativa* L.). *Planta*, 198: 127-138.

110. Rueb, S., M. Leneman, R. Schilperoort, L. Hensgens. 1994. Efficient plant regeneration through somatic embryogenesis from callus induced on mature rice embryos (*Oryza sativa* L.). Plant Cell Tissue Organ Cult. 36: 259-264.

111. Sairam RV, Parani M, Franklin G, Lifeng Z, Smith B, MacDougall J, Wilber C, Sheikhi H, Kashikar N, Meeker K, Al-Abed D, Berry K, Vierling R, Goldman SL (2003) Shoot meristem: an ideal explant for Zea mays L. transformation. Genome 46:323–329.

112. Santos, M.A., Torné, J.M., and Blanco, J.L., 1984, Methods of obtaining maize totipotent tissues I. Seedling segment culture, Plant Sci. Lett., 33:309–315.

113. Shalygina, G. H., V. M. Ghikhova and Z. V. Chmeleva. 1990. Grain quality in inbred lines of maize under irrigation in lower volga area. Genetike-i-Seletsii. 124: 14-19.

114. Shanthi, P., E. Satyanarayana and G. J. M. Reddy. 2002. Genetic studies for grain yield and oil improvement in maize. Res. on Crops. 3: 588-591.

115. Shelake, D. V., S. G. Bhave, V. W. Bendale, R. R. Madav and U. B. Pethe. 2005. Genetic factors influencing grain yield in maize. J. Ecobiol. 17: 521-528.

116. Sidorov V, Duncan D (2009). Agrobacterium-mediated maize transformation: immature embryos versus callus. In: Paul Scott M (eds) Methods in Molecular Biology: Transgenic Maize. Humana Press, Totowa, New Jersey, pp 47-58.

117. Singh, D. N. and I. S. Singh. 1998. Line × tester analysis in maize (*Zea mays* L.). J. Res. Agric. Univ. 10: 177-182.

118. Singh, P. K., P. B. Jha and P. Kumar, 2003. Path coefficient for green fodder yield and grain yield in maize (*Zea mays* L.). J. Appl. Biol. 13: 29-32.

119. Sofi, P. A. and A. G. Rather. 2007. Studies on genetic variability, correlation and path analysis in maize (*Zea mays* L.). Maize Genetics Co-operation News lett. 81: 26-27.

120. Songstad DD, Peterson WL, Armstrong CL, 1992. Establishment of friable embryogenic (type II) callus from immature tassels of Zea mays (Poaceae). Am J Bot 79: 761–764.

121. Sprague, G. F. and L. A. Tatum. 1942. General vs specific combining ability in single crosses of quantitative traits in diallel crosses of maize. Ann. Biol. 15: 173-176.

122. Srivas, S. K. and U. P. Singh. 2004. Genetic variability, character association and path analysis of yield and its component traits in forage maize (*Zea mays* L.). Range management and Agroforestry. 25: 149-153.

123. Sumathi, P., A. Nirmalakumari, and K. Mohanraj. 2005. Genetic variability and traits interrelationship studies in industrially utilized oil rich CIMMYT lines of maize *(Zea mays L)*. Madras Agric. J. 92: 612 – 617.

124. Swarnalatha, D. I. and M. Shaik. 2001. Character association and path coefficient analysis of grain yield and components in double crosses of maize. Crop Res. 21: 255-359.

125. Talleei, A. and H. N. K. Kochaksaraei. 1999. Study of combining ability and cytoplasmic effects in maize diallel crosses. Iranian J. Agric. Sci. 30: 761-769.

126. Tandan, J. P., A. N. Joshi and K. B. L. Jain. 1970. Comparison of graphic and combining ability analysis of diallel crosses in wheat. Ind. J. Genet. 30: 91-103.

127. Thompson, P. R., A. B. Geyer, L. D. Lotz, H. J. Siegrist and T. L. Dobbels. 2002. Top cross high oil corn production: Agronomic performance. Agron. J. 94: 290- 299.

128. Ting, Y. C, M. Yu and W. Z. Zheng. 1981. Improved anther culture of maize. Plant Sci. Lett. 23:139–145.

129. Trester, M. and A. Bacic. 2005. Abiotic stress tolerance in grasses, From model plants to crop plants. Plant Physiol. 137: 791-793

130. Umakanth, A. V. and H. A. Khan. 2001. Correlation path analysis of grain yield and yield components in maize (*Zea mays* L.). Hyderabad J. Res. 29: 87-90.

131. Vafias, B. N. and C. G. Ipsilandis. 2005. Combining ability, gene action and yielding performance in maize. Asian J. Plant Sci. 4: 50-55.

132. Valdez-Ortiz A, Medina-Godoy S, Valverde AE, Paredes-Lopez O (2007). A transgenic tropical maize line generated by the direct transformation of the embryo-scutellum by A. tumefaciens. Plant Cell Tissue Organ Cult. 91: 201-214.

133. Vega JM, Yu W, Kennon A, Chen X, Zhang Z (2008) Improvement of Agrobacterium-mediated transformation in Hi-II maize (*Zea*

mays L.) using standard binary vectors. Plant Cell Rep 27: 297–305.

134. Venugopal, M., N. A. Ansari and T. Rajanikanth. 2003. Correlation and path analysis in maize (Zea mays L.).Crop Res., Hisar. 25: 525-529.

135. Viola, G., Ganesh, M., Reddy, S. S. and Kumar, C. V. S. 2003. Studies on correlation an path coefficient analysis of elite baby corn (*Zea mays* L.) lines. Prog. Agric. 3: 22-24.

136. Wagdy, A.S. 2002. Production of herbicide-resistant transgenic maize plants using electroporation of seed-derived embryos. Plant Molec. Biol. Report. 3: 303-304.

137. Wali, M. C., Salimath, P. M., Prashanth, M. and Harlapur, S. I. 2006. Studies on character association as influenced by yield, starch and oil in maize (*Zea mays* L.). Karnataka J. Agric. Sci. 19: 932-935.

138. Wang A. 1987. Callus induction and plant regeneration from maize mature embryos. Plant Cell Rep. 6: 360-362.

139. Wang, Z. H., Wang, Y. B., Wang, Y. P., Zhang, X. and Zhudin, M. 1998. Classification, utilization and improvement of the main germplasm heterosis of maize in China. J. Henan Agric. Sci. 2: 3-6.

140. Wannows, A. A., H. K. Azzam and S. A. Al-Ahmad. 2010. Genetic variance, heritability, correlation and path coefficient analysis in yellow maize crosses. Agric. Biol. J. N. Am. 1: 630-637.

141. Ward K, M. Jordan. 2001. Callus formation and plant regeneration from immature and mature maize embryos of rye (*Secale cereale* L.). In Vitro Cell Dev. Biol. Plant 37: 361-368.

142. Warner, J. N. 1952. A method for estimating heritability. Agron. J. 44: 227-430.

143. Watto, F. M., M. Saleem, M. Ahsan, M. Sajjad and W. Ali. 2009. Genetic analysis for yield potential and quality traits in maize. Am-Euras. J. Agric. Environ. Sci. 6: 723-729.

144. Yousuf, M. and M. Saleem. 2001. Correlation analysis of S1 families of maize for grain yield and its components. Int. J. Agri. Biol. 3: 387-388.

145. Zaheer Y, Fatima A, Mustafa HSB, Hasan EU and Mahmood T. Innovations of Biotechnology to diagnose and Cure Various Human Diseases. *Nat Sci* 2015;13(7):41-61.

146. Zhang S, Carrier W, Lemaux PG, 2002. Transformation of recalcitrant maize elite inbreds using in vitro shoot meristematic cultures induced from germinated seedlings. Plant Cell Rep 21: 263-270.

7/25/2015