

## ASSOCIATION ANALYSIS IN DIFFERENT GENERATIONS OF MAIZE

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(Received : 29 April 2020; Accepted : 12 May 2020)

### SUMMARY

The experiment was conducted to develop and evaluate six single cross hybrids and their  $F_2$  populations developed from crossing and selfing between five inbred lines of maize at experimental area of CCS Haryana Agricultural University Regional Research Station, Uchani, Karnal during both the growing seasons of 2014-16 to estimate correlation analysis for the generations viz., parents ( $P_1$  and  $P_2$ ),  $F_1$ ,  $F_2$  and back crosses ( $BC_1$  and  $BC_2$ ) in six crosses for 15 quantitative traits. Correlation is an important in estimating the relative importance of various characters on grain yield. From the association analysis it was found that grain yield per plant showed significant positive correlation with days to 50% tasselling, days to 50% silking, days to maturity, plant height, ear height, cob length, cob diameter, number of grains per cob, 100 grain weight, shelling percentage and lysine content whereas it was found significant negative with protein and starch content. Protein content had significant negative correlation with tryptophan content and tryptophan is significantly positively correlated with lysine content. It was imperative that plant height having strong positive correlation with grain yield was found promising in all the six crosses studied, thus considered as important selection criteria in improving hybrid maize for high grain yield, fodder yield and quality on the basis of association among other characters also. All the six crosses and specially their selected  $F_2$  plants are of great importance for population development programme for the development of inbreds and hybrids from the  $F_2$  population by crossing promising genotypes on the basis of per se performance.

**Key words :** Association analysis, correlation, yield, quality, maize

Maize (*Zea mays* L.) occupies an important position in world economy and trade as a food, feed, biofuel and an industrial grain crop. It is commonly used in animal feed as an energy source for its high starch content (Sharma *et al.*, 2015). There is a tremendous pressure of livestock on available total feed and fodder, as land available for fodder production has been decreasing. In this situation maize is the solution provider. It has occupied an important position in the food stocks of the country producing suitable quality forage for a given situation requires knowing the factors that affect forage quality, then exercising management accordingly (Sharma *et al.*, 2016). Breeding for high yield and improved quality is one of the major objectives to increase productivity in maize. However, yield is a complex quantitative character generally having low heritability and is influenced by many components or contributing traits both in positive and negative directions. Association between traits is important to deal with any crop breeding program as genetic change in a given trait may change positively or negatively other trait simultaneously. In addition, in most breeding programs

the strategy is based on selection for several traits simultaneously and, therefore, knowledge on the genetic association between traits is inevitably useful for the establishment of selection criteria. Therefore, the correlation studies were made to assess the genetic relationships among different yield components and quality characters at genotypic level, through association analysis for enhancing the usefulness of selection for grain yield improvement along with other quality characters in maize. Correlations among grain yield and its components were studied in five maize populations which need to be improved for grain yield with the aim of choosing an efficient breeding strategy.

The experimental material consisted of five inbred lines, out of which 3 inbred lines (HKI 209, HKI 1332, HKI 325-17AN) were crossed to 2 inbred lines (HKI 1128, HKI 163) to generate six crosses viz., HKI 209 x HKI 1128, HKI 209 x HKI 163, HKI 1332 x HKI 1128, HKI 1332 x HKI 163, HKI 325-17AN x HKI 1128 and HKI 325-17AN x HKI 163 during the growing season of *kharif* 2014. Part of seeds from each of the six parental inbred lines and their resultant  $F_1$  hybrids were planted in the field during *rabi* 2014-15

to produce F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations. F<sub>2</sub> generation of each cross was produced by selfing the F<sub>1</sub> plants. Thus, the genetic material for field evaluation was finally comprised of six generations *i.e.* parents (P<sub>1</sub> and P<sub>2</sub>), F<sub>1</sub>, F<sub>2</sub> and back crosses (BC<sub>1</sub> and BC<sub>2</sub>) of six crosses. Above mentioned generations were developed over two growing seasons (*Kharif* 2014 and *Rabi* 2014-2015) for each cross by using manual pollination procedures for crossing and selfing. All the plants generated from the above crossed and selfed combinations were grown in a single row of 5 meter length and the distance between rows and plants was kept at 60cm and 20 cm respectively during *Kharif* 2015 along with standard checks. All recommended agronomic practices were adopted to raise a good crop. The best plants in each generations *i.e.* 25-40 cobs in F<sub>2</sub> and 5 cobs for each of BC<sub>1</sub> and BC<sub>2</sub> were selected from each cross, over the standard checks and the data on 15 quantitative traits were recorded. The nature and extent of association between different traits were studied by computing correlation coefficient (r) between pairs of traits. Genotypic coefficient of correlation between two characters was determined by using the variance and covariance components as suggested by Al-Jibouri *et al.* (1958).

**Correlation coefficient analysis**

Among the yield and its attributing traits in crosses 1 to 6 respectively, grain yield per plant exhibited positive and significant association with days to 50% tasselling, days to 50% silking, days to maturity, plant height, ear height, cob length, and cob diameter, number of grains per cob, 100 grain weight and shelling percentage in all the crosses studied which

indicate that by increasing these attributes, could invariably increase grain yield (Table 1). Similar findings were reported by Dar *et al.* (2015). Exceptionally it was found that grain yield per plant had positive but non-significant association with characters *viz.*, 50 % tasselling in cross 3, days to 50 % silking in cross 3, cob diameter in cross 4, 100 grain weight in cross 4 and shelling % in cross 1.

The correlation coefficients in pooled generations also demonstrate similar results for grain yield per plant as it was having positive significant association with 50 % tasselling, days to 50% silking, days to maturity, plant height, ear height, cob length, and cob diameter, number of grains per cob, 100 grain weight and shelling percentage (Table 2). The results are in agreement with earlier findings of Madhav *et al.*, (2019) who also reported similar correlations among different characters in six generations derived individually from two maize populations. Among yield and quality traits, grain yield per plant established significant negative association with protein content and oil content in five crosses (cross 1, cross 2, cross 3, cross 5 and cross 6 for protein content and for oil content cross 1, cross 2, cross 3, cross 4 and cross 5). However exceptions are cross 4 and cross 6 which were found positively correlated for protein and oil content respectively but found non-significant. Sreckov *et al.* (2011) studied the correlation between grain yield and oil content in two testcross populations of maize and found that the relationship was negative with the first population, while in the second population grain yield was positively associated with kernel oil content. The results were in agreement with Aliu *et al.*, (2012), where grain yield per plant had significant and negative correlation with protein

TABLE 1  
Correlation coefficients for various characters over different generations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>) of all the crosses with grain yield per plant

Characters	50% T	50% S	Mat	PH	EH	CL	CD	NGPC	100GW	Shelling (%)	Protein	Tryp	Oil	Starch
<b>Grain yield per plant</b>														
Cross 1	0.43*	0.43*	0.45*	0.83**	0.80**	0.77**	0.68**	0.95**	0.75**	0.03	-0.49*	0.66**	-0.58**	0.42**
Cross 2	0.34*	0.38*	0.42*	0.51**	0.42*	0.58**	0.55**	0.86**	0.64**	0.32*	-0.79*	-0.56**	-0.49**	0.11
Cross 3	0.11	0.17	0.32*	0.65**	0.53**	0.46**	0.58**	0.96**	0.61**	0.31*	-0.89**	0.34*	-0.58**	0.65**
Cross 4	0.60**	0.58**	0.41**	0.59**	0.48**	0.54**	0.26	0.32*	0.19	0.29*	0.26	-0.13	-0.29*	-0.24
Cross 5	0.60**	0.58**	0.41**	0.59**	0.48**	0.54**	0.26	0.32*	0.19	0.29*	0.26	-0.13	-0.29*	-0.24
Cross 6	0.38**	0.34*	0.40**	0.80**	0.61**	0.51**	0.65**	0.81**	0.52**	0.40**	-0.43**	-0.62**	0.22	0.13

Where, DT = Days 50% tasselling, DS = Days to 50% silking, DM = Days to maturity, PH = Plant height (cm), EH = Ear height (cm), CL = Cob length (cm), CD = Cob diameter (cm), NGPC = Number of grains / cob, 100 GW = 100 grain weight (g), GYPP = Grain yield per plant (g), Shelling % = Shelling percentage, PC = Protein content (%), TRP = Tryptophan content (%), OC = Oil content (%), SC = Starch content (%).

content and oil content. But, contradictory with findings of Muhammad Saleem *et al.* (2008) who found that oil content is positively and significantly correlated with grain yield. Similar association was found in pooled generations with both protein content and oil content which was defended by Deif *et al.* (2012), who observed significant negative correlation between protein and oil content.

In all the individual crosses and pooled generations of these six crosses starch content was positively associated with grain yield per plant for cross 1, 2, 3 and 5 except in cross 4 where it exhibited negative but non-significant and in cross 6 it was found positive but non-significant. The results are in conformity with previous findings of Madhav *et al.*, (2019) who reported existence of different levels of correlated responses in the different generations. Aliu *et al.* (2012) and Mahesh *et al.* (2013) observed positive correlation between grain yield and starch content. Increasing grain yield is directly correlated with starch. This is due to the fact that the highest proportion of maize grain occupied by endosperm, whereas small proportion occupied by embryo. As size of the endosperm increases starch also increases, while oil content decreases because oil mainly present in germ or embryo. Yield and starch are positively correlated. As yield increases size of endosperm increases in turn increases the starch content. With

tryptophan content, grain yield per plant established significant positive association in cross 1, cross 3, cross 5 and for pooled generations also but had significant negative correlation in cross 2 and 6 while in cross 4 tryptophan content had negative but non-significant association (Table 2).

The result provides a measure of association between the characters and reveals the character that might be useful as an index for selection. In all the six crosses studied as well as in pooled generation's analysis of these crosses, protein content established significant negative association with tryptophan content. Similarly, days to 50 % tasselling exhibited significant positive association with days to 50 % silking and days to maturity and with plant height the similar association was also reported. Therefore, it could be concluded that positive significant correlations between grain yield and other yield contributing characters indicated the possibility of achieving higher yield in terms of both grain yield and biomass. Also the positive correlations among cross specific quality characters indicated that more than one quality character can be improved simultaneously. This study concluded that grain yield per plant showed significant positive correlation with days to 50 % tasselling, days to 50 % silking, days to maturity, plant height, ear height, cob length, cob diameter, number of grains per cob, 100 grain weight, shelling

TABLE 2

Pooled Correlation coefficients for various characters over different generations (P1, P2, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>) of all the 6 crosses

	50% T	50% S	Mat	PH	EH	CL	CD	NGPC	100GW	Shelling %	Protein	Tryp	Oil	Starch
50% T														
50% S	0.92**													
Mat	0.80**	0.76**												
PH	0.42**	0.41**	0.50**											
EH	0.31*	0.26	0.30*	0.73**										
CL	0.28*	0.32*	0.22	0.79**	0.56**									
CD	0.16	0.06	0.11	0.52**	0.45**	0.37**								
NGPC	0.15	0.07	0.33*	0.58**	0.53**	0.61**	0.52**							
100G	0.15	-0.10	0.20	0.47**	0.44**	0.61**	0.49**	0.57**						
Shelling %	-0.02	-0.06	0.13	0.27*	0.20	0.24	0.21	0.27*	0.43**					
Protein	-0.15	-0.13	-0.07	-0.04	-0.05	0.06	0.03	-0.02	-0.13	0.00				
Tryp	-0.17	-0.13	-0.18	0.26	0.19	0.30*	0.23	0.25	0.25	0.13	-0.58**			
Oil	-0.18	-0.20	-0.20	0.10	0.12	0.14	0.11	-0.01	0.21	0.16	-0.01	0.07		
Starch	-0.12	-0.08	-0.11	0.36*	0.29*	0.39**	0.19	0.40**	0.10	0.18	-0.06	0.17	-0.10	
GYPP	0.31*	0.28*	0.32*	0.67**	0.55**	0.59**	0.53**	0.77**	0.61**	0.38**	-0.49**	0.05	-0.34*	0.25

Where, DT = Days 50% tasselling, DS = Days to 50% silking, DM = Days to maturity, PH = Plant height (cm), EH = Ear height (cm), CL = Cob length (cm), CD = Cob diameter (cm), NGPC = Number of grains / cob, 100 GW = 100 grain weight (g), GYPP = Grain yield per plant (g), Shelling % = Shelling percentage, PC = Protein content (%), TRP = Tryptophan content (%), OC = Oil content (%), SC = Starch content (%).

percentage, lysine content whereas it was found significant negative with protein and starch content. Protein content had significant negative correlation with tryptophan content and tryptophan is significantly positively correlated with lysine content.

The existence of different levels of correlated responses in the different generations (*i.e.* heterogeneity in correlation coefficient) suggested that during the breeding procedure, the selection for and against any trait would require the detailed study of the correlated response of the parents in different generations of maize. The selection for these characters could be considered as important selection criteria in improving hybrid maize for high grain yield and fodder yield and quality, as plant height is considered as important character for fodder yield. Thus it could be concluded that all the six crosses and specially their selected F<sub>2</sub> plants are of great importance for population development programme for the development of in bred and hybrids from the F<sub>2</sub> population by crossing promising genotypes on the basis of per se performance. These findings would be of great help to the breeders for improving the inbreds of maize, which can further be used in synthesizing the high yielding single cross hybrids and three way cross hybrids for quality fodder.

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