Electronic Journal of Plant Breeding, 6(2): 500-505 (June 2015)
ISSN 0975-928X

Research Note

Genetic variability and correlation among yield and quality traits in sweet corn

M C Dagla[1*], R N Gadag[2], O P Sharma[3] And Narendra Kumar[1]
[1]Division of Genetics, Indian Agricultural Research Institute, New Delhi-110 012
[2] Directorate of Maize Research, New Delhi-110 012
[3]Directorate of Groundnut Research, Junagadh–362 001 Gujarat
Email: manu9322gen@gmail.com

(Received:12 Aug 2014; Accepted:13 May 2015)

Abstract
The 45 hybrids generated by half diallel mating design using ten inbred lines of sweet corn were evaluated at IARI, New Delhi during *kharif*-2008. There were significant differences with respect to all the studied yield and biochemical attributes. High genotypic and phenotypic variance were recorded by plant height, cob placement height, grain rows cob^{-1}, hundred grains weight, grain yield and starch content. The difference between genotypic coefficient of variation and phenotypic coefficient of variation was less for all the traits, indicating that improvement is possible through phenotypic selection. High heritability coupled with high genetic advance for cobs plant^{-1}, reducing, non-reducing and total sugars and oil contents, suggests that selection may be effective for these traits. The yield attributing traits showed the high heritability, but low genetic advance indicating non-additive gene action. High genotypic positive correlation was observed between flowering and maturity days, indicates that selection for earliness can be done on the basis of these traits simultaneously. Cob length and grains row^{-1} showed the positive correlation. There was no strong correlation between yield attributes and biochemical parameters. There was positive correlation between; non-reducing sugar - total sugars, non-reducing sugar - oil content and total sugars - oil content which indicates that sugar content and oil content both can be increased simultaneously by the selection programme.

Keywords
Sweet corn, genetic variability, correlation, yield, quality

Maize occupies an important place in the world agriculture, being grown in more than 150 countries, including USA, China, Brazil, Mexico, France and India. It is the third most important cereal crop in India after rice and wheat with an area of 72 m ha and production of 216 mt with an average productivity of 3000kg hectare^{-1} (FAOSTAT, 2011). Sweet corn possesses additional and characteristic features, and due to this it's global spread, increasing demand and premium price make them attractive options for the farmers in many countries including India. Due to limited research initiatives till now, cultivars with high productivity in sweet corn is very less. Green ears of starchy field corns are also consumed in various forms while sweet corn is more suited for such usage.

This will provide the basis for the development of the next generation of specialty corn and of new products to meet future needs. In this article information is presented on the genetic variation, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) for yield attributing traits as well as biochemical traits and their associations. Heritability estimates aid in deciding selection intensity, whereas genetic advance predicts the genetic gain likely to be achieved in the generation of selection.
Yield, a dependent character is the resultant effect of a number of quantitative characters. The study of association between pairs of these attributes provides basis for further selection. It is very useful to plant breeder for faster assessment of high yielding genotypes in selection programme. The correlation reflects the extent of association between a particular character and seed yield. The efficiency of selection depends on the identification of genetic variability from the phenotypic expression. Therefore, keeping in view the significance of these parameters, which are really important for assessment of variability in hybrid populations for development of superior inbred lines the present investigation was undertaken in sweet corn.

The ten diverse sweet corn inbred lines were used as parents. The crosses were made in all possible combinations excluding the reciprocals at Agricultural Research Station, Amberpet, Hyderabad during *Rabi* 2007-08. Their 45 hybrids and parents were evaluated at Delhi during *kharif*-2008 in randomized block design (RBD) with three replications, and each replication was put in two tiers. Each entry per replication had three rows of 5m length; with row to row and plant to plant spacing were 75 cm and 20 cm, respectively. Recommended agronomic package of practices was followed for raising the good crop. The experimental plot was kept free from weeds by manual weeding twice.

The total sugars, protein content, starch content, and oil content were recorded with the help of near infra-red spectroscopy. Reducing sugar was analysed by Nelson Somogeyi method (Sadasivam and Manickam, 2008) and non-reducing sugar was obtained through subtracting the reducing sugar from the total sugar.

Analysis of variance for the design of the experiment was carried out to know the significant differences among the hybrids which were based on the method suggested by Panse and Sukhatme (1967). The phenotypic and genotypic components of variance were estimated as explained by Johnson *et al*. (1955). Coefficient of variation (CV) was calculated by the formula suggested by Burton (1952) for both the phenotypic and genotypic coefficients of variation. Heritability (broad sense) [h^2(b)] was calculated by using the formula proposed by Allard (1960). Expected genetic advance was calculated using the methodology suggested by Allard (1960) at 5 per cent selection intensity using the constant 'k' as 2.06.

The analysis of covariance for all the possible pairs of the characters under investigation was carried out using the procedure described by Panse and Sukhatme (1967). The genotypic (r_g) and phenotypic (r_p) correlation coefficients were calculated as under by adopting the procedure expounded by Miller *et al*. (1958). The significance of correlation was tested according to method of Fisher and Yates (1943).

The phenotypic range of variation is not a precise criterion of judging the amount of genetic variation present in the population. The genetic parameters like genotypic coefficient of variation, heritability and genetic advance (Table-1) are important to study the extent of genetic variability more precisely since breeding potential of genotypes depends on the amount of genetic variability which is a prerequisite for response to selection. The phenotypic variance was partitioned into its genotypic and environmental components to know the genetic variability present for each trait and the magnitude of trait. It was observed that for all the traits, genotypic component of variation was higher than environmental component indicating phenotypic variability was a variable measure of genetic variability. Hence, selection would be effective for these traits. High estimates of genotypic and phenotypic variance were observed for plant height, cob placement height, grains row^{-1}, grain yield and starch content. The moderate GCV and PCV were observed for cob placement height, cob length, cobs plant^{-1}, grain rows cob^{-1}, grains row^{-1}, hundred grains weight, reducing sugar, non-reducing sugar, total sugars and oil contents. The low GCV and PCV were observed for days to tasseling, days to silking, days to maturity, plant height, cob width, grain yield plant^{-1}, and starch and protein contents. In the present study, the difference between PCV and GCV was least for all the traits suggesting improvement by phenotypic selection is possible.

It is not possible to determine the amount of variability which is heritable, with the help of genotypic coefficient of variation alone. GCV together with heritability estimates would give a better idea about the amount of genetic advance to be expected from selection. In crop improvement, only the genetic component of variation is important since only that component is transmitted to the next generation. Heritability indicated the effectiveness with which selection of genotypes would be based on phenotypic performance. Shift in gene frequency towards superior side under selection pressure is termed as genetic advance and is generally expressed as a percentage of mean (genetic gain). Johnson *et al.* (1955) found that it is more useful to estimate heritability value together with genetic advance in predicting the ultimate choice of the best genotypes by selection. However, high genetic gain along with high heritability showed most effective condition for selection. All the traits showed high heritability except cob width which has moderate heritability. Thus results indicated the substantial contribution of additive genetic variance in the expression of these traits and could be improved through individual plant selection.

High heritability coupled with high genetic advance was observed for cobs plant^{-1}, reducing sugar, non-reducing sugar, total sugars, and oil contents, which suggests that most likely heritability was due to additive gene effects and selection may be effective. High heritability coupled with low genetic advance was observed for days to tasseling, silking and maturity, plant height, cob placement height, cob length and width, grain rows cob^{-1}, grains row^{-1}, hundred grains weight, grain yield and starch, and protein contents. This indicated that traits are governed by non-additive gene action. The high heritability is being exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding.

Some traits showed high genotypic and phenotypic variance like plant height, cob placement height, grain rows cob^{-1}, hundred grains weight, grain yield plant^{-1} and starch content. The difference between GCV and PCV was less for all the traits suggesting that improvement is possible through phenotypic selection. High heritability coupled with high genetic advance for cobs per plant, reducing, non-reducing and total sugar and oil content, suggests that there is a higher additive gene effects and selection may be effective. The other yield attributing traits showed the high heritability, but low genetic advance, indicating non-additive gene action.

Yield is a complex trait determined by a number of attributes which, in turn, are generally controlled and influenced by environment. The results of the present study, which revealed comparatively higher degree of genotypic correlation coefficient than their phenotypic counterpart, in most of the traits, indicated that though there was a high degree of association between two traits at genotypic level, their phenotypic association was lessened due to the influence of environment. In few traits, however, the phenotypic correlations were slightly higher than their genotypic counterpart which implied that the non-genetic causes inflated the value of genotypic correlation because of the influence of the environmental factors (Table-2).

Grain yield plant^{-1} was found to be highly significant and positively correlated with plant height, cob placement height, cob length and cob width, grain rows cob^{-1} and grains row^{-1} indicating that these traits are mainly influencing the yield positively in the sweet corn. Thus, selection practices for the improvement in one trait will automatically result in the improvement in the other, even through direct selection for improvement has not been made for complex yield characters. Grain yield plant^{-1} also showed the negative correlation with days to tasseling, days to silking, days to maturity, which might be useful for the selection of short duration with high yielding genotypes. The similar results were obtained by Singhel *et al.* (2006), Saidaiah *et al*. (2008) and Vaghela *et al*. (2009).

The days to silking was also negatively correlated with cob width followed by grain yield, grain rows cob^{-1} and grains row^{-1} which is desirable association because we need the high yielding genotypes with short duration. Days to maturity showed the medium positive association with oil content, which suggested that increasing in the days to maturity, also increased the oil content in grains. Cob length was highly positively associated with grains row^{-1}, and both traits are also positively correlated with yield, hence the synchronized direct selection can be done on the basis of these traits. The analogous findings were observed by Tiwari and Varma (1999), Umakantha and Khan (2001), Venugopal *et al*. (2003) and El-shouny *et al.* (2005).

The biochemical traits have no significant correlation directly to grain yield, but with yield attributing traits correlation was observed. Reducing sugar content was positively correlated with days to tasseling, days to silking, days to maturity, cob width and negatively correlated with hundred grains weight. The reducing sugar content is contributing towards the some yield components. The non-reducing sugar content and total sugar content have the positive association with days to tasseling, days to silking and days to maturity. The non-reducing sugar and total sugar was negatively associated with plant height, cob placement height, cob length, rows cob^{-1} and grains row^{-1}. Hundred grains weight, showed negative association with non-reducing sugar but positive association with total sugar which was desirable for the sweet corn improvement. The starch content showed the positive association with plant height, cob placement height and hundred grains weight. So whether, the increasing the sugar content or starch content both will increase the hundred grains weight.

The protein content and oil content both showed the positive association with days to tasseling, days to silking and days to maturity and negative association with plant height, cob placement height, cob length and hundred grains weight. The similar findings were obtained by Yue *et al.* (2007), Zhang *et al.* (2007) and Ramezani *et al.* (2009). Among the biochemical traits reducing sugar content has the positive association with non-reducing sugar, total sugars, protein and oil contents, but negative association with starch content. Non-reducing sugar content has the positive correlation with total sugars, protein and oil contents but negative with starch content. The starch content has the very high negative association with protein, oil and sugar content. The medium positive association was found between the protein and oil content. The negative strong correlations were observed between starch content-protein content and starch content-oil content. This indicates that the protein, oil and sugar can be increased simultaneously by decreasing the starch content.

It can be concluded that the difference between GCV and PCV was less for all the traits suggesting that improvement is possible through phenotypic selection. High heritability coupled with high genetic advance for cobs plant^{-1}, reducing, non-reducing and total sugar and oil contents, advocates that there is a higher additive gene effects and selection may be effective. The yield attributing traits showed the high heritability, but low genetic advance, indicating non-additive gene action. On the basis of strong correlation among studied parameters, the biochemical components may be increased without much affecting the yield and its components. Yield can be enhanced through increasing the yield component traits. Most of the traits studied in this experiment were either significantly positive correlated or independent. The present finding exhibits substantial opportunities to the breeders for improvement of these traits in maize cultivars and also suggests further exploration of a new source of elite breeding stocks containing a high level of these nutritionally important compounds. Finally, these findings may also help in bio-fortification of maize.

High genotypic positive correlation was observed between days to tasselling-days to silking, days to tasseling- days to maturity and days to silking-days to maturity. In these traits the positive correlation indicates that selection for earliness can be done by using the basis of these traits simultaneously. Grain yield showed the positive correlation with plant height, cob placement height, cob length, cob width, grain rows cob^{-1}, and grains row^{-1}. So, the yield attributing traits can be used for selection programme and yield can be enhanced through increasing the yield component traits.

References

Allard, R.W. 1960. Principles of Plant Breeding. J Wiley and Sons. Inc. New York and London.

Burton, G.W. 1952. Quantitative inheritance in grasses. Proceedings of Internal. Grassland Cong. **1**: 227-283.

El Shouny, K. A., El Bagoury, O. H., Ibrahim, K. I. M. and Al Ahmad, S. A. 2005. Correlation and path coefficient

analysis in four yellow maize crosses under two planting dates. *Arab Universities J. Agr. Sc.,* **13(2):** 327-339.

Fisher, R. A., and F. Yates. 1943. Statistical tables for biological, agricultural and medical research, 2nd ed. Oliver and Boyd Ltd., London. 98 p.

Johnson, H. W., Robinson, H. F. and Comstock, R. F. 1955. Estimates of genetic and environmental variability in soybean. *Agron. J.,* **47**: 314-318.

Miller, P. A., Williams, J. C., Robinson, H. F. and Comstock, R. E. 1958. Estimates of genotypic and environmental variances and covariances in upland cotton and their implication in selection. *Agron J.* **50**: 126-131.

Panse, V. G. and Sukhatme, P. V. 1978. Statistical Methods for Agricultural Workers. 3rd ed., ICAR, New Delhi. p347.

Ramezani, M., Rahimi, M. and Samezadeh, L. H. 2009. Relationship between yield and other agronomic traits in maize lines and hybrids. *Agricultural Science Tabriz.* **19(1):** 146-157.

Saidaiah, P., Satyanarayana, E. and Kumar, S. S. 2008. Association and path coefficient analysis in maize (*Zea mays* L.). *Agric. Sci. Digest*, **28(2):** 79-83.

Singhal, N., Verma, S. S., Baskheti, D. C. and Kumar, A. 2006. Heritability, genetic advance, correlation and path coefficient estimation in high quality protein maize (*Zea mays* L.). *Asian J. Bio Sci*., **1(2):** 54 56.

Tiwari, V. K. and Verma, S. S. 1999. Correlation and path coefficient analysis in baby corn (*Zea mays* L.). *Agr. Sci. Digest,* **19(4)**: 230-234.

Umakanth, A. V. and Khan, H. A. 2001. Correlation and path analysis of grain yield and yield components in maize (*Zea mays* L.). *J. Res. ANGRAU.,* **29(2/3):** 87-90.

Vaghela, P. K., Patel, D. B., Parmar, D. J. and Macwana, S. S. 2009. Correlation and path coefficient analysis in baby corn (*Zea mays* L.). *Res. Crops.,* **10(1):** 135-137.

Venugopal, M., Ansari, N. A. and Rajanikanth, T. 2003. Correlation and path analysis in maize (*Zea mays* L.). *Crop Res.,* **25(3):** 525-529.

Yue, S. J., Wang, X. M., Zeng, M. H. and Cai, W. H. 2007. Correlation and path analysis on yield traits of F1 generation of super sweet maize. *J. Maize Sci.* **15(1):** 41-43 and 58.

Zhang, L., Dong, S. T., Liu, C. H., Wang, K. J., Zhang, J. W., Liu, P. 2007. Correlation analysis on maize test weight, yield and quality. *Scientia Agricultura Sinica.* **40(2):** 405-411.

Sadasivam S, Manickam A, 2008. Biochemical Methods. New Age International (P) Limited, Publishers, New Delhi. p4.

Table 1. Genetic parameters of variation for yield and quality attributes in sweet corn hybrids

Characters	Mean ±S.Em	Range	Coefficient of variance		Heritability (%)	Genetic Advance	Genetic Gain (%)
			Genotypic	Phenotypic			
Days to tasseling (No.)	49 ±0.91	45-53	2.97	4.40	45.57	2.00	2.92
Days to silking (No.)	52 ±0.99	48-56	2.76	4.30	41.22	1.91	2.64
Days to maturity (No.)	81 ±1.08	78-86	1.55	2.78	31.06	1.45	1.48
Plant height (cm)	141 ±5.11	104-177	9.30	11.22	68.73	22.43	3.35
Cob placement height (cm)	67 ±3.3	51-85	11.80	14.58	65.48	13.12	5.43
Cob length (cm)	14 ±0.72	10-17	10.07	13.31	57.32	2.25	10.47
Cob diameter (cm)	3.3 ±0.16	2.6-3.6	5.21	9.71	28.76	0.19	13.21
Cobs plant^{-1}(No.)	2 ±0.09	1-3	27.24	28.05	94.32	1.22	49.32
Grain rows cob^{-1} (No.)	13 ±0.55	8-16	11.58	13.68	71.70	2.66	12.39
Grains row^{-1} (No.)	27 ±1.66	17-34	13.46	17.28	60.66	5.74	9.01
100-grains weight (g)	13 ±0.75	9-19	12.94	16.23	63.59	2.81	12.69
Grain yield plant^{-1} (g)	67 ±2.75	44-75	8.92	11.40	61.19	9.63	4.63
Reducing sugar content (%)	3 ±0.16	1-4	28.71	30.53	88.41	1.48	45.75
Non-reducing sugar content (%)	8 ±0.49	4-14	26.73	28.66	87.01	4.26	24.89
Total sugars content (%)	11 ±0.47	5-17	24.28	25.42	91.28	5.23	20.90
Starch content (%)	53 ±1.25	39-67	9.41	10.26	84.17	9.46	5.78
Protein content (%)	17 ±0.55	13-20	8.83	10.48	70.97	2.59	9.52
Oil content (%)	10 ±0.44	6-12	14.13	15.91	78.81	2.67	15.80

Table 2. Genotypic and phenotypic (above and below diagonal) correlation coefficients for yield and quality traits in sweet corn hybrids

Traits	**DT**	**DS**	**DM**	**PH**	**CPH**	**CL**	**CW**	**NCP**	**GRC**	**NGR**	**HGW**	**GYP**	**RSC**	**NRSC**	**TSC**	**SC**	**PC**	**OC**
DT	-	0.904**	0.752**	-0.333**	-0.395**	-0.246**	-0.764**	0.318**	-0.553**	-0.351**	-0.117	-0.577**	0.313**	0.375**	0.399**	-0.4**	0.43**	0.439**
DS	0.594**	-	0.695**	-0.404**	-0.313**	-0.15	-0.583**	0.252**	-0.513**	-0.188*	0.127	-0.427**	0.183*	0.356**	0.342**	-0.248**	0.281**	0.381**
DM	0.655**	0.462**	-	-0.027	-0.127	-0.36**	-0.466**	0.16*	-0.472**	-0.131	-0.097	-0.237**	0.393**	0.422**	0.458**	-0.435**	0.394**	0.533**
PH	-0.196*	-0.208**	-0.117	-	0.671**	0.434**	0.391**	-0.098	0.345**	0.423**	0.392**	0.354**	-0.152	-0.322**	-0.307**	0.299**	-0.421**	-0.308**
CPH	-0.249**	-0.203**	-0.101	0.511**	-	0.29**	0.24**	-0.164*	0.19*	0.367**	0.266**	0.44**	-0.107	-0.286**	-0.267**	0.273**	-0.38**	-0.247**
CL	-0.089	-0.106	-0.144	0.338**	0.257**	-	0.215**	0.004	0.403**	0.869**	-0.292**	0.173*	-0.051	-0.304**	-0.281**	0.139	-0.16*	-0.214**
CW	-0.22**	-0.19*	-0.092	0.202**	0.057	0.206**	-	-0.168*	0.595**	0.095	-0.185*	0.424**	-0.131	0.131	0.074	-0.011	0.031	-0.042
NCP	0.197*	0.146	0.087	-0.046	-0.117	0.013	-0.069	-	-0.223**	-0.086	-0.026	-0.42**	0.159*	0.09	0.121	-0.099	0.213**	0.086
GRC	-0.312**	-0.331**	-0.262**	0.314**	0.187*	0.413**	0.335**	-0.181*	-	0.434**	-0.32**	0.09	0.12	-0.231**	-0.156*	0.093	-0.161*	-0.065
NGR	-0.054	-0.073	-0.005	0.358**	0.281**	0.623**	0.108	-0.049	0.365**	-	-0.297**	0.187*	0.147	-0.248**	-0.17*	0.187*	-0.158*	-0.125
HGW	-0.015	0.003	0.001	0.338**	0.164*	-0.061	0.043	-0.007	-0.141	-0.146	-	0.109	-0.197*	-0.329**	0.323**	0.333**	-0.372**	-0.351**
GYP	-0.352**	-0.338**	-0.165*	0.237**	0.26**	0.207**	0.162*	-0.317**	0.213**	0.102	0.148	-	-0.116	-0.05	-0.075	-0.021	-0.015	-0.071
RS	0.175*	0.123	0.211**	-0.116	-0.065	-0.065	-0.098	0.146	0.076	0.114	-0.171*	-0.129	-	0.457**	0.676**	-0.432**	0.417**	0.687**
NRS	0.293**	0.188*	0.201**	-0.209**	-0.212**	-0.191*	0.082	0.079	-0.18*	-0.144	-0.211**	-0.013	0.365**	-	0.969**	-0.662**	0.638**	0.809**
TS	0.307**	0.195*	0.248**	-0.217**	-0.2*	-0.185*	0.038	0.109	-0.135	-0.097	-0.232**	-0.052	0.608**	0.951**	-	-0.677**	0.653**	0.876**
SC	-0.205**	-0.147	-0.148	0.193*	0.168*	0.08	-0.004	-0.112	0.045	0.112	0.283**	-0.041	-0.373**	-0.566**	-0.591**	-	-0.916**	-0.831**
PC	0.222**	0.171*	0.173*	-0.231**	-0.212**	-0.046	-0.021	0.2*	-0.104	-0.077	-0.177*	0.007	0.342**	0.498**	0.519**	-0.726**	-	0.71**
OC	0.354**	0.296**	0.307**	-0.228**	-0.151	-0.136	0.006	0.057	-0.135	-0.101	-0.238**	-0.089	0.594**	0.699**	0.77**	-0.643**	0.538**	-

*, **Significant at 0.05 and 0.01 levels, respectively

DT-days to tasseling, DS- days to silking, DM- days to maturity, PH- plant height, CPH- cob placement height, CL-cob length, CW- cob width, NCP-number of cobs plant^{-1}, GRC- grain rows cob^{-1}, NGR-number of grains row^{-1}, HGW- hundred grains weight, GYP- grain yield plant^{-1}, RSC- reducing sugar content, NRSC- non-reducing sugar content, TSC- total sugar content, SC- starch content, PC-protein content, OC- oil content