Genetic Variability and Correlation among Yield and Yield Contributing Traits in Sweet Corn

B. Suhaisini, R. Ravikesavan* and A.Yuvaraja
Department of Millets, Tamil Nadu Agricultural University, Coimbatore

A total of 50 hybrids was generated by Line x Tester mating design using ten lines and five testers of sweet corn. These hybrids along with parents and checks were evaluated at TNAU, Coimbatore during *Kharif*-2015. Genotypes were significantly different for all the traits under study. Green cob yield was found to have positive significant correlation with number of kernel rows per cob, plant height, green cob weight, total chlorophyll content, cob length, cob breadth, 100 seed weight, number of kernels per row indicating that indirect selection for yield through these traits will be effective. Green cob yield had no significant correlation with total sugar content of kernels indicating the scope of developing high yielding hybrids with high sugar content. Traits *viz.,* tassel branching, green cob weight, number of kernels per row, green cob yield, 100 seed weight, reducing sugar, non reducing sugar, photosynthetic efficiency, stomatal conductance and total chlorophyll content recorded high genetic advance as per cent of mean coupled with high heritability thus providing maximum opportunity for improvement and genetic gain through selection of these traits.

Key words: Sweet corn, Line x Tester, Genetic variability, Correlation.

Sweet corn (*Zea mays* L. *saccharata*) which is bred through recessive gene mutation of field corn also known as sugar corn, is one of the most popular vegetable in countries like USA and Canada. Sweet corn is introduced to India from United States. Due to its sweet taste and tenderness, cultivation of sweet corn is the first choice of the farmers nowadays for green fodder and green cobs.

Genetic progress depends on the existence of genetic variability (Allard 2000). The magnitude of genetic variability for different traits and the extent of heritability of desirable traits play a vital role in deciding the success of any crop improvement programme. The estimates of variability for yield and yield contributing characters and their heritable components are more important in any crop-breeding programme. Heritability estimates play a role in deciding the selection intensity, while genetic advance is helpful in predicting the gain under selection.

Association studies reveal the degree and direction of association between two or more variables. Knowledge of the strength and type of association is an important prerequisite for the formulation of breeding procedures (Breese and Haywards, 1972). A knowledge of the association between yield and its component traits helps in improving the efficiency of selection.

Therefore, keeping in view the significance of variability and association studies in breeding programme, present investigation was undertaken in sweet corn.

*Corresponding author email: chithuragul@gmail.com

Materials and Methods

Fifteen elite sweet corn inbreds were raised at Department of Millets, Tamil Nadu Agricultural University, Coimbatore during Summer, 2015. All the 15 inbreds were crossed in Line x Tester (10 lines and 5 testers) fashion to obtain 50 cross combinations. Evaluation of single cross hybrids, parents and checks (Sugar-75 and Madhuri) was done in *Kharif* 2015 at Millet Breeding Station, Tamil Nadu Agricultural University, Coimbatore under RBD with three replications. Biometrical observations were recorded on five tagged randomly selected plants in each replication for each genotype and the data recorded on these plants was used to arrive at the replication mean. The replication wise mean values were subjected to statistical analysis. The traits *viz.*, days to 50% tasseling, days to silking, days to 50% silking, tassel length, tassel branches, plant height, cob placement height, green cob weight, cob length, cob breadth, number of kernel rows per cob, number of kernels per rows, green cob yield and hundred seed weight were recorded. The quality of sweet corn was ascertained by conducting biochemical tests. The immature kernels was collected at milky stage and stored at -20^{0}C and this was used as the sample for estimation of quality traits. Total sugars were estimated using Anthrone method (Yemm and Willis, 1954), reducing sugar by Nelson Somogyi method (Somogyi 1952), non-reducing sugar by subtracting reducing sugar from total sugar. Physiological parameters viz., photosynthetic efficiency, stomatal conductance, transpiration rate and total chlorophyll content were recorded in parents and hybrids using PPS and SPAD meter at flowering stage of the crop.

The data generated was analysed for arriving at meaningful interpretations.

Results and Discussion

The estimates of $\sigma^2 g$, $\sigma^2 p$, genotypic (GCV) and phenotypic coefficients of variation (PCV), heritability and genetic advance as percent of mean (GAM) for different characters have been presented in Table 1.

In general, for all the traits studied, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). The phenotypic coefficient of variation ranged from 5.42 (days to 50% tasseling) to 69.65 per cent (reducing sugars). The genotypic coefficient of variation ranged from 3.87 (Days to 50% tasseling) to 47.59 per cent (Reducing sugars). In the present study, though the phenotypic variances were greater than the genotypic variance for most of the traits, the differences between phenotypic and genotypic variance were minimum indicating the less influence of environmental factors (Sumathi *et al.,* 2010).

Heritability and Genetic Advance

High heritability was observed for trais *viz.,* photosynthetic efficiency (97.35 per cent), total sugars (97.29 per cent), non reducing sugars (97.28 per cent), plant height (95.25 per cent), dry cob weight (93.2 per cent), green cob weight (93 per cent), cob placement height (91.73 per cent), green cob yield (86.76 per cent), stomatal conductance (78.16). Similar results of high heritability was obtained by Bharathi (2014), Kumar (2014) for 50% tasseling, 50% silking, plant height, ear height, ear girth, number of kernel rows per cob,100 seed weight and grain yield per plant.

The estimates of genetic advance as percent of mean (GAM) ranged from 5.61 to 83.21 per cent. High estimate of genetic advance as percent of mean (GAM) was noticed for reducing sugars (83.21 per cent), stomatal conductance (72.34 per cent), photosynthetic efficiency (64.14 per cent), non reducing sugars (51.06 per cent), total sugars (49.11 per cent), green cob weight (45.05 per cent), green cob yield (41.55 per cent), tassel branching (29.01 per cent), hundred seed weight (27.77 per cent) and number of kernels per row (27.34 percent). The results obtained are in accordance with the results of Azam *et al.*(2014) for yield/plant and ear height; Bharathi (2014) for cob yield, hundred grain weight, cob length, number of kernel rows per cob , number of kernels per row, tassel length, number of tassel branches and cob girth.

Table 1. Variability parameters for biometrical, quality and physiological traits in sweet corn

Characters	GV	PV	EV	GCV	PCV	Heritability	GA(%) of mean
Days to 50% tasseling	3.38	6.63	3.25	3.87	5.42	50.99	5.69
Days to 50% silking	5.23	8.77	3.54	4.46	5.77	59.66	7.09
Plant height(cm)	275.51	289.25	13.74	8.80	9.02	95.25	17.70
Tassel length(cm)	5.43	10.77	5.34	6.81	9.59	50.42	9.96
Tassel branching	11.94	18.17	6.23	17.37	21.43	65.72	29.01
Green cob weight(g)	1595.48	1715.62	120.14	22.68	23.52	93.00	45.05
Cob length(cm)	1.64	3.91	2.27	7.16	11.07	41.87	9.55
Cob breadth(cm)	1.09	2.43	1.34	7.41	11.05	44.99	10.24
Number of kernel rows per cob	2.97	4.68	1.71	11.90	14.93	63.49	19.53
Number of kernels per row	29.04	38.65	9.61	15.31	17.66	75.15	27.34
Green cob yield(t\ha)	5.93	6.83	0.90	21.65	23.25	86.76	41.55
100 seed weight	2.53	3.34	0.81	15.49	17.80	75.73	27.77
Total sugars	13.75	14.13	0.38	24.17	24.50	97.29	49.11
Reducing sugars	0.07	0.15	0.08	47.59	69.65	46.67	83.21
Non reducing sugars	13.80	14.19	0.38	25.13	25.48	97.28	51.06
Photosynthetic efficiency	193.21	198.47	5.27	31.56	31.98	97.35	64.14
Stomatal conductance	18.99	19.07	0.08	39.72	44.93	78.16	72.34
Total chlorophyll content	36.54	55.14	18.59	11.74	14.41	66.29	19.68

Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance (Johnson *et al.*, 1955).Traits viz., days to 50% tasseling, days to silking, days to 50% silking, tassel length and cob length recorded low heritability with low genetic advance, Similar results of low heritability coupled with low genetic advance were reported by Singh and Singh (2011) for days to maturity. Characters *viz.,* tassel branching, green cob weight, number of kernels per row, green cob yield, 100 seed weight, reducing sugar, non reducing sugar, photosynthetic efficiency, stomatal conductance and total chlorophyll content recorded high genetic advance as per cent of mean coupled with high heritability.

Table 2. Genotypic correlation coefficient values for different traits

	DFT	DFS	PH	TL	TB	GW	CL	CB	KC	KR	HW	TS	RS	NRS	PE	SC	CHL	YLD
DFT	1	0.947**	-0.184	0.003	-0.315*	-0.277*	-0.392**	-0.501**	-0.23	-0.64**	-0.486**	-0.133	0.145	-0.145	-0.019	0.067	-0.571**	-0.199
DFS		1	-0.215	0.101	-0.182	-0.298*	-0.505	-0.541	-0.309*	-0.651**	-0.492**	-0.208	0.112	-0.216	-0.042	0.012	-0.472**	-0.253*
PH			1	0.594**	0.086	0.541**	0.608**	0.563**	0.525**	0.388**	0.476**	-0.142	-0.278*	-0.119	-0.024	0.114	0.554**	0.511**
TL				1	0.495**	0.381**	0.387**	0.391**	0.097	0.117	0.315*	-0.19	0.08	-0.196	0.191	0.177	0.213	0.213
TB					1	0.122	0.489**	0.368**	0.071	0.473**	0.239*	0.13	0.004	0.13	-0.016	0.016	0.124	-0.002
GW						1	0.905**	0.984**	0.759**	0.558**	0.423**	-0.08	-0.128	-0.069	0.1	0.215	0.462**	0.491**
CL							1	0.926**	0.7**	0.864**	0.541**	0.017	-0.18	0.032	0.121	0.046	0.491**	0.418**
CB								1	0.756**	0.798**	0.511**	0.055	-0.238*	0.075	0.18	0.261*	0.493**	0.387**
KC									1	0.57**	0.247*	-0.059	-0.303**	-0.034	-0.08	0.137	0.417**	0.529**
KR										1	0.387**	0.1	-0.246*	0.12	-0.005	-0.016	0.467**	0.253**
HW											1	0.07	-0.174	0.084	-0.001	0.088	0.629**	0.333**
TS												1	0.015	0.997**	0.068	0.089	0.039	-0.066
RS													1	-0.068**	0.081	-0.029	-0.281*	-0.117
NRS														1	0.061	0.091	0.062	-0.056
PE															1	0.761**	0.013	-0.17
SC																1	0.068	-0.159
CHL																	1	0.448**
YLD																		1

DFT- Days to 50% tasseling, **DFS**-Days to 50% silking,, **PH**- plant height, **TL**-Tassel length, **TB-** Tassel branches, **GW**-Green cob weight, **CL**- Cob length, **CB**- Cob breadth**, KC**- number of kernel rows per cob, number of kernels per rows, **HW**-100 seed weight, **TS**- Total sugars, **RS**- Reducing sugars, **NRS**- Non reducing sugars**, PE**-photosynthetic efficiency**, SC**- Stomatal conductance, **CHL**-Total chlorophyll content, **YLD**- Green cob yield

Hence, exercising selection on these traits can give maximum opportunity for improvement and genetic gain as expected. Similar findings were reported by Alake *et al.* (2008) for grain yield and kernel row per cob.

Association of characters

The genotypic correlation coefficient estimated between yield and its components including quality traits and physiological parameters and inter-correlation among the different yield attributes are furnished in Table 2.

Days to 50% silking (-0.253) recorded significant negative association with yield indicating that selection for early 50% silking will also be desirable to increase grain yield by decreasing anthesis silking interval (ASI) in sweet corn apart from yield contributing traits. Hybrids with high yield and early duration will be advantageous. Similar results are reported by Umakanth *et al.*(2000) and Nigussie and Zelleke (2001) for days to 50% silking. Plant height (0.511), green cob weight (0.491), cob length (0.418) and cob breadth (0.387) registered significant positive association with yield in this study too as indicated by *Kashiani et al. (2010) for green cob weight.* Number of kernel rows per cob (0.529) and number of kernels per cob (0.253) and *100 seed weight (0.333)* had significant positive association with green cob yield and as earlier obtained by Thanga Hemavathy *et al.* (2008), *Nemati et al. (2009) and Beiragi et al. (2011).* Total chlorophyll content (0.448) registered significant positive association with yield. Similar result of positive correlation of chlorophyll content and yield was observed by Gekas *et al.*,(2013).

Hence, in breeding programmes, these traits can be used as selection indices in order to identify good inbreds for use in breeding programmes. There was no significant association existed between yield and total sugar content in kernels indicating the scope of development of high yielding hybrids with high sugar content. Ashish *et al.* (2010) in his studies also found the same relationship between yield and sugar content.

References

Alake, C.O., D.K. Ojo, O.A. Oduwaye and M.A. Adekoya. 2008. Genetic variability and correlation studies in yield and yield related characters of tropical maize (*Zea mays* L.). *ASSET Series A.,* **8(1):** 14-27.

Allard R.W.,2000 . Principles of plant breeding 2nd Ed.John Wiley & Sons, New York. 254p.

Ashish Khanduri, B. M. Prasanna, Firoz Hossain and P. C. Lakhera, 2010. "Genetic analyses and association studies of yield components and kernel sugar concentration in sweet corn". *Indian J. Agric. Sci.,* **70(3):** 257-263.

Azam, M.G., U. Sarker and Banik,2014. Genetic variability of yield and its contributing characters on CIMMYT maize inbreds under drought stress. *Bangladesh Journal of Agricultural Research.,* **39(3):** 419-426.

Beiragi, M., M. Ebrahimi, K. Mostafavi, M.Golbashy and S.Khorasani.2011. A study of morphological basis of corn (Zea mays L.) yield under drought stess condition using correlation and path coefficient analysis. *J.Cereals Oilseeds.,* **2(2):** 32-37.

Bharathi P.2014. Exploitation of heterosis in maize (*Zea mays* L.) under water limiting environment. *M.Sc.,(Ag) Thesis*, Tamil Nadu Agricultural University, Coimbatore, India. p:104

Breese, E.L. and Haywards, M.O. (1972). The genetic basis of present breeding methods in forage crops. *Euphytica.,* **21**: 324-336.

Gekas, F., Pankou, C., Mylonas, I., Ninou, E., Sinapidou, E., Lithourgidis, A., Papathanasiou, F., Petrevska, J.K., Papadopoulou, F., Zouliamis, P. and Tsaprounis, G., 2013. The Use of Chlorophyll Meter Readings for the Selection of Maize Inbred Lines under Drought Stress. Int.J.Biomol.Agric.Food.Biotechnol.Eng., 7(8): 815-819.

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

Kashiani, P., G. Saleh, J.M. Panandam, N.A.P. Abdullah, and A. Selamat, 2012. Demarcation of informative chromosomes in tropical sweet corn inbred lines using microsatellite DNA markers. *Genet. Mol. Bio.,* **35(3)** :614-621.

Kumar, G.P., N.Reddy, S.S. Kumar,. and V. Rao, , 2014. Genetic variability and genetic advance studies in newly development maize genotype (Zea mays L.). *Inter. J. Pur. Appli. Bio. Sci.,* **2(1)** :272-275.

Nemati , A., M. Sedghi, R.S. Sharif and M.N. Seiedi.2009. Investigation of correlation between traits and path analyais of corn(Zea mays L.) grain yield at the climate of Ardabil region (Northwest Iran). *Not. Bot. Hort. Agrobot.,* **37(1):**194-198.

Nigussie, M. and H. Zelleke.2001. Heterosis and combining ability in diallel among eight elite maize populations. *African Crop Sci. J.,* **9(3):**1-3.

Singh, S.B and A.K. Singh, 2011. Heterotic expression and combining ability analysis for yield and yield components over environments in yellow maize (*Zea mays* L.). *Progressive Agriculture.,* **11 (2):** 409-419.

Somogyi. 1952. A new reagent for the determination of sugar. *J. Biol. Chem.,* 195 : 19-23.

Sumathi, P., S. Madineni and P. Veerabadhiran. 2010. Genetic variability for different biometrical traits in pearl millet genotypes [*Pennisetum glaucum* (L.) R. Br.]. *Electron J. Plant Breed* **(4):** 437-440.

Thanga Hemavathy, A., K. Balaji, S.M. Ibrahim, G. Anand and Deepa Sankar. 2008. Genetic variability and correlation studies in maize(Zea mays L.). *Agric. Sci. Digest.,* **28(2)**: 112-114.

Umakanth, A.V., E. Satyanarayana and M.N. Kumar.2000. Correlation and heritability studies in Ashwini maize composite. *Ann.Agric. Res.,* 21 : 328-330.

Yemm E. W., A. J Willis. 1954. The estimation of carbohydrates in plant extract by anthrone. Biochemistry, 508-514.