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Determining genetic variability of traits in backcross populations of sweet corn (*Zea mays* L. var. *Saccharata*)

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ABSTRACT

To understand the nature of the traits in breeding programme, knowledge on heritability, genetic advance and genetic variability are inevitable. The paramount aim of the present study was to estimate the heritability, genetic advance and genetic variability of the backcross and selfed population of sweet corn and β -carotene rich inbred combinations viz., USC1-2-3-1 \times UMI1230 β^+ and SC1107 \times UMI1230 β^+ in order to identify the plants with superior trait combinations. The study involved the recording of fourteen biometrical traits in both the cross combinations which revealed that in backcross and selfed populations, the phenotypic coefficient of variation (PCV) was found to be greater than the genotypic coefficient of variation (GCV) indicating the probable influence of environment in the expression of the traits evaluated. High heritability was recorded for the important trait single plant yield in both the cross combinations of BC₂F₂ generation. Further, high heritability and high genetic advance as percent of mean was noticed for the traits like plant height, cob length, leaf length and single plant yield under both the cross combinations of BC₂F₂ generation indicates the governance of additive genes in expression of these traits. Hence, selection for these traits would be effective in developing a genotype with improved yield.

KEYWORDS: Maize, Genetic advance, Heritability, Genetic variability.

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INTRODUCTION

Sweet corn (*Zea mays* L. var. *Saccharata*) is one among the specialty corns, which has gained high market demand as it is invariably preferred by all age categories of the world population. Sweet corn ranks sixth among fresh vegetables for per capita consumption. Sweet corn is consumed as immature kernels, consisting mainly of endosperm and ovary wall (immature pericarp) (Mehta *et al.*, 2021). Compared to maize, sweet corn is consumed as raw, boiled and processed food i.e., Kernels, soups, salads, etc. Sweet corn quality is determined by flavor, aroma, and texture of the endosperm and tenderness of the pericarp. *shrunk2* (*sh2*), *sugary1* (*su1*), and *sugar enhancer1* (*se1*) are the genes that distinguish sweet corn from other type of corns. Besides this, genes affecting ear and kernel appearance are also important.

In order to portray the heritable differences among the biometrical traits, genetic variability has to be considered. Based on the genetic variability, the design of the breeding program is designed. For improving a particular quantitative trait of a population, magnitude of the genetic variability is a prerequisite (Dhanwani *et al.*, 2013). By measuring the phenotypic coefficient of variation and genotypic coefficient of variation, the amount of variation in the population can be estimated. Prediction of accumulated genetic variability is due to heritable character or not is difficult. From one generation to another, the transmissibility of a character can be easily understood by studying the heritability of the character. The high heritability of the trait is decided by the additive gene action. The genetic gain due to additive gene action is defined by the genetic advance (Najeeb *et al.*, 2009). In order to make the selection

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to be valid, combining the high heritability and high genetic advance is all the more important. Narrow sense heritability is very limited which includes both additive and epistatic effects but the broad sense heritability is combined with high genetic advance proved a better estimate of a character (Ramanujam & Thirumalachar, 1967). Gaining more knowledge on these parameters would help the crop breeders to form a strong basis for an effective breeding program.

MATERIALS AND METHODS

The experiment is carried out in Department of Agronomy, Directorate of Crop Management, Tamil Nadu Agricultural University, Coimbatore. In the breeding program was constituted with two sweet corn inbred lines *viz.*, USC1-2-3-1 and SC1107 which were used as the recurrent parent and a high beta carotene line UMI1230 β^+ which was used as the donor parent. Hybridization between these parents was carried out to develop the high beta carotene sweet corn cross combinations. Two independent crosses, USC1-2-3-1 \times UMI1230 β^+ and SC1107 \times UMI1230 β^+ were made during *Kharif* 2018 and backcrossed with their respective recurrent parents during *Summer* 2019. The resultant backcross populations (BC₁F₁) were evaluated during *Kharif* 2019 and further backcrossed with their recurrent parents in order to produce the BC₂F₁ population. The BC₂F₁ progenies were evaluated in *Summer* 2020 and selfing was carried out to produce BC₂F₂ population. The BC₂F₂ populations were evaluated during the *Kharif* 2020 season.

Fourteen biometrical traits were recorded in all the populations evaluated based on the guidelines by DUS of PPV&FRA (Anon, 2017) *viz.*, Days to tasseling (DT) in days, Days to Silking (DS) in days, Plant height (PH) in cm, Ear height (EH) in cm, Tassel length (TL) in cm, Number of tassel branches (NTB) in nos; Leaf length (LL) in cm, Leaf Breadth (LB) in cm, Cob length (CL) in cm, Cob girth (CG) in cm, Number of kernel rows per cob (NKRC) in nos, Number of kernels per row (NKR) in nos, 100 Kernel weight (KW) in gms and Single plant yield (SPY) in gms. Among the traits studied, days to tasseling, days to silking, plant height, ear height, tassel length, number of tassel branches, leaf length, leaf breadth were recorded before harvesting of cobs while cob length, cob girth, number of kernel rows per cob, number of kernels per row, 100 Kernel weight and single plant yield were recorded after the harvest of the cobs.

As per the method formulated by Burton (1952), phenotypic coefficient of variation, genotypic coefficient of variation was calculated. The range of phenotypic coefficient of variation, genotypic coefficient of variation were represented as low (<10%), moderate (10-20%) and high (>20%) as suggested by Sivasubramanian and Madhavamenon (1973). The method described by Lush (1940) was adopted to estimate the heritability of different traits studied. The range of the heritability was adopted from Robinson *et al.*, 1945 which included low (<30%), moderate (30-60%) and high (>60%). The genetic advance and genetic advance as the percent of mean was calculated by following the method given by Johnson *et al.*,

(1955), which ranged from low (<10%), moderate (10-20%) and high (>20%). In the present study, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean were analyzed for the backcrossed (BC₁F₁, BC₂F₁) and selfed (BC₂F₂) populations along with their parents. In general, the range of variation will be estimated especially in segregating populations for a maize breeding program. Through the estimation of heritability, the traits which are controlled by heritable or non-heritable factors is undoubtedly understood besides knowing that whether the heritability is due to additive gene action or non-additive gene action (Falcon & Mackey, 1996). Therefore, combining the heritability and genetic advance will provide precise knowledge on the genetic gain through additive gene action (Bello *et al.*, 2012).

RESULTS AND DISCUSSION

For the heritability and genetic advance as percent of mean arrived for the cross USC1-2-3-1 \times UMI1230 β^+ in respect of fourteen yield traits evaluated are furnished in Table 1, 2 and 3. In BC₁F₁ generation, highest mean value was recorded in plant height (189.60 cm), followed by ear height (94.64) and single plant yield (87.09) whereas the lowest mean value was recorded

Table 1: Estimation of variability in BC₁F₁ population of USC1-2-3-1 \times UMI1230 β^+ and SC1107 \times UMI1230 β^+

Cross	Traits	Parent (Mean)	Progeny (Mean)	Range		h ²	GAM (%)
				Min	Max		
USC1-2-3-1 \times UMI1230 β^+	DT	58.00	55.55	54.00	57.00	75.00	1.57
	DS	60.00	57.55	56.00	59.00	78.00	2.78
	PH	150.80	189.60	185.00	195.00	69.67	1.89
	EH	64.90	94.64	92.00	97.00	76.93	5.86
	TL	21.28	37.45	35.00	40.00	83.61	7.01
	NTB	12.00	15.04	14.00	16.00	82.99	6.04
	LL	70.45	85.36	81.00	90.00	71.32	2.15
	LB	8.50	10.78	9.00	12.00	67.39	7.93
	CL	13.00	16.97	16.00	18.00	78.13	6.31
	CG	11.40	14.08	13.00	15.00	81.01	1.40
	NKRC	12.10	15.99	15.00	18.00	79.56	1.69
	NKR	22.50	31.02	30.00	32.00	84.23	8.65
	100KW	22.50	26.98	26.00	28.00	74.24	3.67
	SPY	74.85	87.09	85.00	88.00	78.91	4.05
SC1107 \times UMI1230 β^+	DT	56.00	55.55	54.00	57.00	81.23	1.43
	DS	58.00	57.56	56.00	59.00	77.68	2.65
	PH	145.00	190.04	185.00	201.00	63.92	5.71
	EH	60.00	95.61	92.00	119.00	82.48	9.22
	TL	26.00	39.22	34.00	45.00	62.81	8.39
	NTB	12.00	15.12	14.00	18.00	73.53	3.60
	LL	65.00	85.15	81.00	89.00	66.14	5.41
	LB	7.00	11.04	9.00	13.00	79.42	11.26
	CL	10.00	17.03	16.00	19.00	82.44	2.86
	CG	9.00	14.02	13.00	16.00	80.31	6.19
	NKRC	10.00	16.54	15.00	18.00	61.72	6.32
	NKR	20.00	30.77	29.00	34.00	84.40	7.31
	100KW	17.00	27.20	26.00	28.00	71.21	10.11
	SPY	70.00	87.91	86.00	93.00	70.62	4.33

DT – Days to tasseling; DS – Days to Silking; PH – Plant height; EH – Ear height; TL – Tassel length; NTB – Number of tassel branches; LL – Leaf length; LB – Leaf Breadth; CL – Cob length; CG – Cob girth; NKRC – Number of kernel rows per cob; NKR – Number of kernels per row; KW – 100 Kernel weight; SPY – Single plant yield.
h² – Heritability; GAM – Genetic Advance as per of Mean.

Table 2: Estimation of variability in BC₂F₁ population of USC1-2-3-1×UMI1230β⁺ and SC1107×UMI1230β⁺

Cross	Traits	Parent (Mean)	Progeny (Mean)	Range		h ²	GAM (%)
				Min	Max		
USC1-2-3-1 ×UMI1230β ⁺	DT	58.00	56.04	55.00	56.00	78.33	2.93
	DS	60.00	58.15	56.00	59.00	73.21	2.55
	PH	150.80	152.32	151.00	156.00	63.81	3.31
	EH	64.90	64.64	61.00	66.00	77.23	23.57
	TL	25.01	24.42	21.00	25.00	87.04	16.72
	NTB	12.00	13.80	12.00	16.00	82.29	6.20
	LL	70.45	71.48	70.00	76.00	64.60	5.31
	LB	8.50	7.44	4.00	8.00	87.07	4.82
	CL	13.00	12.96	10.00	16.00	84.62	12.73
	CG	11.40	10.78	9.00	11.00	72.09	6.01
	NKRC	12.10	11.78	9.00	12.00	87.11	2.60
	NKR	22.50	21.72	13.00	25.00	85.03	6.61
	100KW	22.50	21.68	17.00	28.00	86.33	2.33
	SPY	74.85	73.74	70.00	75.00	70.04	28.14
SC1107 ×UMI1230β ⁺	DT	56.00	55.62	54.00	57.00	75.29	3.67
	DS	58.00	57.47	56.00	59.00	73.91	2.64
	PH	145.00	146.15	131.00	149.00	81.43	1.93
	EH	60.00	61.48	59.00	63.00	76.34	1.20
	TL	26.00	28.01	27.00	29.00	74.82	3.04
	NTB	12.00	14.11	12.00	16.00	81.90	6.80
	LL	65.00	66.55	65.00	68.00	72.77	5.42
	LB	7.00	8.77	8.00	13.00	70.15	2.97
	CL	10.00	12.31	12.00	14.00	79.44	11.32
	CG	9.00	10.95	10.00	12.00	83.77	10.17
	NKRC	10.00	13.36	12.00	15.00	76.57	7.21
	NKR	20.00	21.80	19.00	24.00	88.08	2.23
	100KW	17.00	20.16	19.00	24.00	72.07	5.46
	SPY	70.00	73.38	70.00	74.00	89.71	12.32

DT – Days to tasseling; DS – Days to Silking; PH – Plant height;
 EH – Ear height; TL – Tassel length; NTB – Number of tassel branches;
 LL – Leaf length; LB – Leaf Breadth; CL – Cob length; CG – Cob girth;
 NKRC – Number of kernel rows per cob; NKR – Number of kernels per
 row; KW – 100 Kernel weight; SPY – Single plant yield.
 h² – Heritability; GAM – Genetic Advance as per of Mean.

in leaf breadth (10.78). Phenotypic coefficient of variation and genotypic coefficient of variation values have revealed a range from 1.37% to 6.32% and 1.13% to 5.79%. All the traits showed higher heritability ranging from 69.67% in plant height to 84.23% in number of kernels per row. Highest genetic advance as percent of mean was recorded in number of kernels per row (8.65%) followed by leaf breadth (7.93%) and the lowest genetic advance as percent of mean was noticed in cob girth (1.40%). In BC₂F₁ population, highest mean value was recorded in plant height (152.32) followed by single plant yield (73.74) and the lowest mean were registered in leaf breadth (7.44). High phenotypic coefficient of variation and genotypic coefficient of variation recorded among all the traits which ranged from the 0.94% to 15.42% and 0.62% to 14.85% respectively. Higher heritability was displayed by almost all the traits studied which ranged from single plant yield (70.04%) to number of kernel rows per cob (87.11%). Highest genetic advance as percent of mean was displayed by single plant yield (28.14%) followed by ear height (23.57%) and tassel length (16.72%). Highest heritability and genetic advance as percent of mean was recorded in single plant yield (70.74% and 28.14%), ear height (77.23% and 23.57%) which indicates the predominance of additive gene action in governance of these traits. In BC₂F₂ population, the mean value ranged from 7.17 (leaf breadth) to 149.81 (plant

Table 3: Estimation of variability in BC₂F₂ population of USC1-2-3-1×UMI1230β⁺ and SC1107×UMI1230β⁺

Cross	Traits	Parent (Mean)	Progeny (Mean)	Range		h ²	GAM (%)
				Min	Max		
USC1-2-3-1 ×UMI1230β ⁺	DT	58.00	57.61	56.00	60.00	73.64	2.99
	DS	60.00	59.81	57.00	62.00	80.63	3.43
	PH	150.00	149.81	140.00	160.00	73.64	3.08
	EH	65.00	66.55	55.00	18.00	82.25	10.56
	TL	25.00	24.67	20.00	28.00	76.83	12.54
	NTB	12.00	10.45	8.00	13.00	71.87	16.43
	LL	70.00	68.00	60.00	75.00	82.43	21.59
	LB	8.00	7.17	6.00	9.00	76.45	17.89
	CL	13.00	13.76	11.00	18.00	84.13	13.89
	CG	11.00	10.21	8.00	13.00	79.02	15.73
	NKRC	12.00	10.99	9.00	14.00	86.41	25.89
	NKR	22.00	21.2	18.00	24.00	72.91	15.52
	100KW	18.00	17.59	16.00	20.00	73.91	6.21
	SPY	72.00	72.01	70.00	74.00	87.33	15.82
SC1107 ×UMI1230β ⁺	DT	56.00	56.35	54.00	60.00	71.44	3.22
	DS	58.00	57.61	55.00	62.00	74.53	4.71
	PH	145.00	145.89	141.00	160.00	87.89	2.93
	EH	60.00	59.9	57.00	80.00	76.43	24.56
	TL	26.00	23.8	21.00	28.00	81.79	26.43
	NTB	12.00	10.6	10.00	14.00	75.12	15.69
	LL	65.00	63.69	60.00	68.00	71.25	11.43
	LB	7.00	5.98	4.00	9.00	77.03	22.57
	CL	10.00	10.01	8.00	12.00	88.25	14.51
	CG	9.00	9.39	7.00	12.00	74.20	21.39
	NKRC	10.00	10.08	8.00	12.00	70.37	23.76
	NKR	20.00	19.55	17.00	24.00	72.77	26.11
	100KW	17	17.3	15	20	86.96	31.13
	SPY	70	68.54	61	76	87.13	21.19

DT – Days to tasseling; DS – Days to Silking; PH – Plant height;
 EH – Ear height; TL – Tassel length; NTB – Number of tassel branches;
 LL – Leaf length; LB – Leaf Breadth; CL – Cob length; CG – Cob girth;
 NKRC – Number of kernel rows per cob; NKR – Number of kernels per
 row; KW – 100 Kernel weight; SPY – Single plant yield.
 h² – Heritability; GAM – Genetic Advance as per of Mean.

height). Phenotypic coefficient of variation and genotypic coefficient of variation ranged from 1.89% to 18.41% and 1.34% to 16.52% respectively (Figure 1).

Similarly, the heritability and genetic advance as percent of mean was arrived for the backcrossed (BC₁F₁, BC₂F₁) and selfed (BC₂F₂) populations of SC1107×UMI1230β⁺ (Table 1, 2 and 3). In BC₁F₁ population, the highest mean value is noticed in plant height (190.04) followed by ear height (95.61) and single plant yield (87.91). Phenotypic coefficient of variation and genotypic coefficient of variation ranged from 1.05% to 8.42% and 0.84% to 7.31% respectively. High heritability was observed for all the traits which ranged from number of kernel rows per cob (61.72%) to number of kernels per row (84.40%). It was closely followed by number of number of kernels per row (83.50%), ear height (82.48%) and cob length (82.44%). With regard to genetic advance as percent of mean, traits like leaf breadth (11.26%) and 100 Kernel weight (10.11%) recorded highest level. In BC₂F₁ population, highest mean was observed in plant height (146.15) followed by single plant yield (73.38) and the lowest mean was recorded in the leaf breadth (8.77). PCV and GCV ranged from 0.81% (leaf length) to 8.54% (tassel branches) and 0.77% (leaf length) to 7.11% (number of kernel rows) respectively. High level of heritability was recorded in

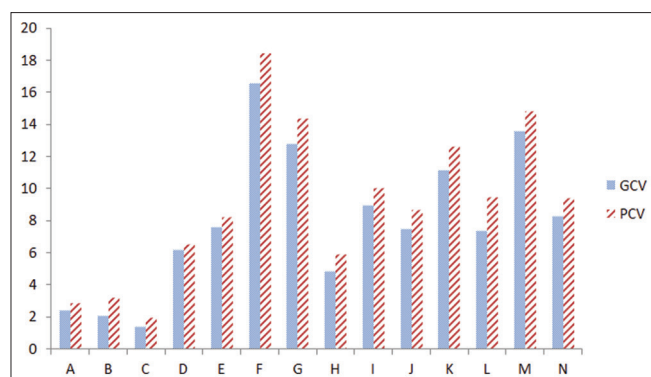


Figure 1: Phenotypic and Genotypic Coefficient of variation in BC₂F₂ of USC1-2-3-1xUMI1230β+ GCV – Genotypic Coefficient of Variation, PCV – Phenotypic Coefficient of Variation. A – Days to tasseling; B – Days to Silking; C – Plant height; D – Ear height; E – Tassel length; F – Number of tassel branches; G – Leaf length; H – Leaf Breadth; I – Cob length; J – Cob girth; K – Number of kernel rows per cob; L – Number of kernels per row; M – 100 Kernel weight; N – Single plant yield

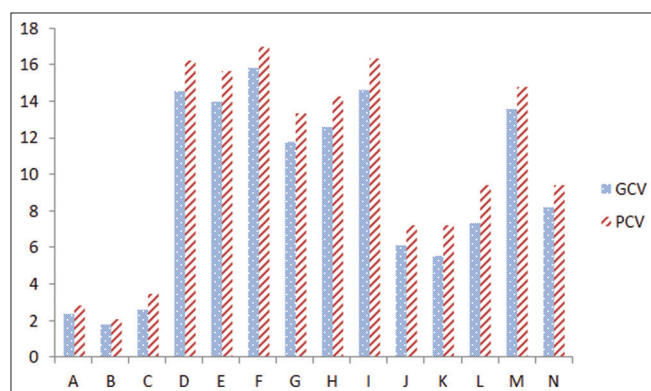


Figure 2: Phenotypic and Genotypic Coefficient of variation in BC₂F₂ of SC1107xUMI1230β+ GCV – Genotypic Coefficient of Variation, PCV – Phenotypic Coefficient of Variation. A – Days to tasseling; B – Days to Silking; C – Plant height; D – Ear height; E – Tassel length; F – Number of tassel branches; G – Leaf length; H – Leaf Breadth; I – Cob length; J – Cob girth; K – Number of kernel rows per cob; L – Number of kernels per row; M – 100 Kernel weight; N – Single plant yield

single plant yield (89.71%) followed by number of kernels per row (88.08%) and the lowest heritability was recorded in the 100 kernel weight (72.07%). The cob traits, cob length (11.32%), cob girth (10.17%) and single plant yield (12.32%) recorded high level of genetic advance as percent of mean. Heritability and genetic advance as percent of mean value was noticed to be higher in cob length (79.44% and 11.32%), cob girth (83.77% and 10.17%) and single plant yield (89.71% and 12.32%).

In BC₂F₂ population, the highest mean value was recorded in plant height (145.89) followed by single plant yield (68.54) and lowest mean was displayed by leaf breadth (5.98). Phenotypic coefficient of variation ranged from 1.79% (Plant height) to 15.79% (Number of tassel branches) and genotypic coefficient of variation ranged from 2.09% (Days to silking) to 16.98% (Cob length) (Figure 2). Although, the level of heritability recorded was high for the most of the traits studied, it was highest for single plant yield (87.13%) and lowest for leaf length (71.25%).

With regard to genetic advance as percent of mean, the 100 kernel weight (31.13%) recorded the highest value followed by the tassel length (26.43%). The heritability and genetic advance as percent of mean was recorded to be the highest in tassel length (81.79% and 26.43%) followed by 100 kernel weight (86.96% and 31.13%) and single plant yield (87.13% and 21.19%) which indicates governance of additive genes in expression of these traits.

Generally, the phenotypic coefficient of variation is greater than the genotypic coefficient of variation due the influence of the environment. The G×E interaction also plays a vital role in the performance of the trait. Higher heritability and genetic advance as percent of mean noticed for the traits such as plant height, leaf length and single plant yield indicates that these traits are controlled by the additive gene action and selection for these traits would be effective in these segregating populations to develop the genetically improved genotypes with the enhanced yield.

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