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## Research Article

### Assessment of frequency distribution for the morphological and yield related traits in $BC_1F_1$ , $BC_2F_1$ and $BC_2F_2$ populations in sweet corn

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#### Abstract

The nature of gene action and the number of genes controlling the traits are the vital criteria for the selection of traits. The present study is to analyze the range of variations within the population and as well as the skewness and kurtosis in backcross and selfed sweet corn populations  $USC1-2-3-1 \times UMI1230\beta^+$  and  $SC1107 \times UMI1230\beta^+$ . In the  $BC_2F_2$  population of  $SC1107 \times UMI1230\beta^+$ , most of the traits showed positive skewness and platykurtic distribution which indicated that complementary gene action played a role and more number of genes is controlling the traits. In  $USC1-2-3-1 \times UMI1230\beta^+$ , single plant yield recorded positive skewness. In some traits such as, the number of tassel branches, cob girth, and leaf breadth showed negative skewness and platykurtic distribution was also observed in both the cross combination which indicated prevalence of duplicate gene action. In order to fix an individual trait and for rapid genetic gain, duplicate gene action is required.

**Keywords:** Sweet corn, Skewness, Kurtosis, Gene action.

#### INTRODUCTION

Sweet corn (*Zea mays* var. *saccharata* (L.)) is widely consumed around the world because of its sweet flavor, tenderness, and ease of digestion (Tracy 1997). The frequency distribution on a scale of measurement is a graphical representation of the number of individuals in each of the category (Gravetter and Wallnau Larry, 2000). The symmetry of the population is measured by the

skewness and it represents gene action (Fisher, 1932). The number of genes controlling a trait and whether the population is left or right tailed is measured by kurtosis (Robson, 1956). The positive and negative skewness is related to the complementary and duplicate gene action. Kurtosis is categorized into platykurtic, leptokurtic, and mesokurtic (Kapur 1980). The present study aims to

study the descriptive statistics and frequency distribution patterns for the backcross ( $BC_1F_1$ ,  $BC_2F_1$ ) and selfed ( $BC_2F_2$ ) population to select useful individuals with high yielding agronomic traits.

## MATERIALS AND METHODS

In order to develop high beta carotene content sweet corn inbred lines, crossing of the inbreds recurrent parents USC1-2-3-1 and SC1107 was made with the donor as UMI1230 $\beta^+$ , resulting on synthesis of two hybrid combinations viz., USC1-2-3-1 $\times$  UMI1230 $\beta^+$  and SC1107 $\times$ UMI1230 $\beta^+$ . The breeding program was initiated by making crosses between the recurrent parents and donor parents during summer, 2018. The  $F_1$  hybrids of the crosses, USC1-2-3-1 $\times$  UMI1230 $\beta^+$  and SC1107 $\times$ UMI1230 $\beta^+$  were raised during summer 2019 and backcrossed with their respective recurrent parents viz., USC1-2-3-1 and SC1107. During Kharif 2019, In order to produce  $BC_2F_1$  population the  $BC_1F_1$  progenies of both the crosses were raised and again backcrossed with their recurrent parents. The  $BC_2F_1$  population was evaluated during summer 2020. The  $BC_2F_1$  population was selfed to generate  $BC_2F_2$  population and evaluated in Kharif 2020.

From the backcrossed ( $BC_1F_1$  and  $BC_2F_1$ ) and selfed ( $BC_2F_2$ ) population, 14 biometrical traits were recorded which includes days to silking (days), days to tasseling (days), plant height (cm), the number of kernel rows per

cob (Nos), ear height (cm), tassel length (cm), the number of kernels per row (Nos), the number of tassel branches (Nos), leaf length (cm), cob length (cm), leaf breadth (cm), cob girth (cm), 100 kernel weight (gms) and Single plant yield (gms). The mean values of the biometrical traits of both backcrossed and selfed populations were used for the calculation of descriptive statistics using the SPSS16.0 software. Skewness and kurtosis deals with higher order statistics and are used for studying the nature of gene action. Skewness helps to identify the deviations in the population from the central tendency. When skewness is positive it describes complementary gene action, whereas negative skewness describes duplicate gene action. Kurtosis deals with the peak of the population and also amount of genes governing the traits. Positive kurtosis indicates less number of genes with the presence of gene action whereas negative kurtosis indicates a large number of genes with the absence of gene action (Poorni *et al.*, 1977).

## RESULTS AND DISCUSSION

Frequency distribution for 14 biometrical traits was observed in USC1-2-3-1 $\times$  UMI1230 $\beta^+$  (Tables 1, 2 and Fig. 1). The skewness and kurtosis were calculated and recorded in Table 5. The traits plant height, leaf length and cob length showed wide variation. In the  $BC_1F_1$  generation, the plant height ranged from 185cm to 195cm with a mean value of 189.60 cm, while, the days to tasseling (54 days to 57 days) and days to silking (56

**Table 1. Estimation of range, mean, standard deviation and variance in  $BC_1F_1$  and  $BC_2F_1$  population of USC1-2-3-1  $\times$  UMI1230 $\beta^+$**

Traits	Progeny (Mean)	$BC_1F_1$		Standard deviation	Variance	Traits	Progeny (Mean)	$BC_2F_1$		Standard deviation	Variance
		Range						Range			
		Min	Max					Min	Max		
DT	55.55	54	57	0.72	0.52	DT	56.04	55	58	0.84	0.70
DS	57.55	56	59	0.72	0.52	DS	58.15	56	60	0.64	0.41
PH	189.60	185	195	4.04	16.34	PH	152.32	151	156	1.06	1.14
EH	94.64	92	97	1.98	3.95	EH	64.64	61	66	1.15	1.33
TL	37.45	35	40	1.64	2.71	TL	24.42	21	25	1.09	1.20
NTB	15.04	14	16	0.80	0.64	NTB	13.80	12	16	1.60	2.58
LL	85.36	81	90	2.77	7.67	LL	71.48	70	76	2.06	4.26
LB	10.78	9	12	0.81	0.67	LB	7.44	4	8	1.22	1.50
CL	16.97	16	18	0.54	0.30	CL	12.96	10	16	1.05	1.12
CG	14.08	13	15	0.53	0.28	CG	10.78	9	11	0.57	0.33
NKRC	15.99	15	18	1.09	1.20	NKRC	11.78	9	12	0.67	0.46
NKR	31.02	30	32	1.13	1.29	NKR	21.72	13	25	1.92	3.71
100KW	26.98	26	28	0.86	0.73	100KW	21.68	17	28	2.21	4.89
SPY	87.09	85	88	0.70	0.49	SPY	73.74	70	75	0.96	0.94

Note - Days to tasseling (DT); Days to Silking (DS); Plant height in cm (PH); Ear height in cm (EH); Tassel length in cm (TL); Number of tassel branches (NTB); Leaf length in cm (LL); Leaf Breadth in cm (LB); Cob length in cm (CL); Cob girth in cm (CG); Number of kernel rows per cob (NKRC); Number of kernels per row (NKC); 100 Kernel weight in g(100KW); Single plant yield in g (SPY).

**Table 2. Estimation of range, mean, standard deviation and variance in BC<sub>2</sub>F<sub>2</sub> population of USC1-2-3-1 × UMI1230β<sup>+</sup>**

Traits	Progeny (Mean)	BC <sub>2</sub> F <sub>2</sub>		Standard deviation	Variance
		Range			
		Min	Max		
DT	57.61	56	60	1.18	1.39
DS	59.58	57	62	1.20	1.45
PH	149.91	140	160	6.49	42.19
EH	66.55	55	80	5.84	34.21
TL	24.67	20	28	2.00	4.03
NTB	10.45	08	13	1.46	2.13
LL	68.00	60	75	3.70	13.73
LB	7.16	06	09	0.85	0.73
CL	13.76	11	18	1.22	1.48
CG	10.21	8	13	1.39	1.93
NKRC	10.99	9	14	1.80	3.26
NKR	21.20	18	24	2.06	4.25
100KW	17.59	16	20	3.49	12.15
SPY	72.01	70	74	0.96	0.94

Note - Days to tasseling (DT); Days to Silking (DS); Plant height in cm (PH); Ear height in cm (EH); Tassel length in cm (TL); Number of tassel branches (NTB); Leaf length in cm (LL); Leaf Breadth in cm (LB); Cob length in cm (CL); Cob girth in cm (CG); Number of kernel rows per cob (NKRC); Number of kernels per row (NKC); 100 Kernel weight in g (100KW); Single plant yield in g (SPY).

days to 59 days) showed a narrow range of variation with an average of 55.55 days and 57.55 days, respectively. The leaf length showed wide range of variation from 81cm to 90 cm having a mean of 85.36 cm. Positive skewness and platykurtic distribution were observed for plant height and leaf length indicating that the genes are governed by complementary gene action. Tamil (2012) and Suresh (2014) have also reported leptokurtic distribution and negative skewness for cob length which indicated that the trait is controlled by less number of genes. In BC<sub>2</sub>F<sub>1</sub> generation, a wide range of variation was observed for plant height, cob length and the number of kernels per row and a narrow range of variation was observed for days to tasseling and days to silking. Plant height ranged from 151 to 156 cm with a mean of 152.32 cm. It exhibited positive skewness with leptokurtic distribution, suggesting that the trait is controlled by less number of genes (Chandana *et al.*, 2018). The cob length ranged from 10 to 16 cm with a mean value of 12.96 cm. The days to tasseling and days to silking ranged from 55 to 58 days and 56 to 60 days with a mean value of 56.04 and 58.15 days respectively. Leaf length exhibited complementary gene action since skewness was positive with platykurtic distribution. In BC<sub>2</sub>F<sub>2</sub> generation, wide variation was observed for plant height, tassel length and leaf length. The plant height ranged from 140 to 160 cm with a mean of 149.91 cm and leaf length ranged from 60 to 75cm with an average of 68 cm. The cob length and single plant yield were observed to have positive skewness and platykurtic distribution,

which showed complementary gene action. The days to tasseling ranged from 56 to 60 days with a mean value of 57.61. The days to silking ranged from 57 days to 62 days with a mean value of 59.58. Single plant yield ranged from 70 to 75g with a mean value of 72.01 g.

Similarly, frequency distribution for 14 biometrical traits was observed for SC1107 × UMI1230β<sup>+</sup> in their backcrossed (BC<sub>1</sub>F<sub>1</sub>, BC<sub>2</sub>F<sub>1</sub>) and selfed (BC<sub>2</sub>F<sub>2</sub>) population (Table 3, 4 and Fig. 2). The skewness and kurtosis were calculated and recorded in Table 5. In BC<sub>1</sub>F<sub>1</sub> generation, plant height, ear height, tassel length, leaf length and single plant yield exhibited a wide range of variation. The plant height ranged from 185 to 201cm with an average of 190.04. The leaf length ranged from 81 to 89cm having an average of 85.15. The Single plant yield ranged from 86 to 93g with an average of 87.91. Positive skewness and leptokurtic distribution was noticed for plant height and single plant yield indicating the role of complementary gene action. The number of kernel rows per cob exhibited negative skewness and leptokurtic distribution suggesting the role of duplicate gene action. In BC<sub>2</sub>F<sub>1</sub> generation, plant height and single plant yield displayed a wide range of variation. The plant height ranged from 131 to 149cm with an average of 146.15. Single plant yield ranged from 70 to 74g with an average of 73.38. Traits such as days to tasseling and days to silking showed a narrow range of variation, ranging from 54 to 57 days with a mean of 55.62 and 56 to 59 days with a mean of 57.47

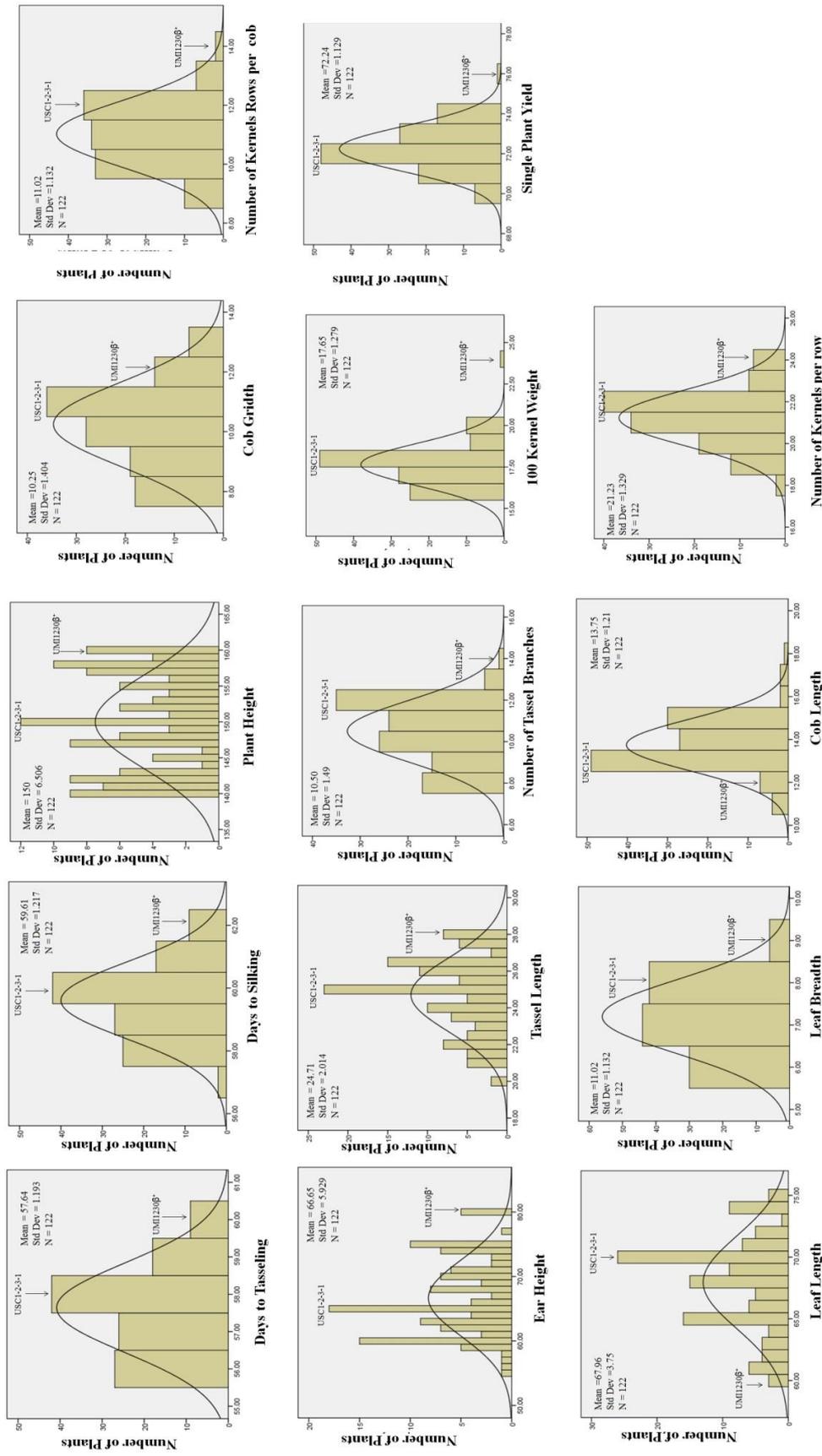


Fig. 1. Frequency distribution for the morphological traits in BC<sub>2</sub>F<sub>2</sub> population of USC1-2-3-1 × UMI1230β

**Table 3. Estimation of range, mean, standard deviation and variance in BC<sub>1</sub>F<sub>1</sub> and BC<sub>2</sub>F<sub>1</sub> population of SC1107 × UMI1230β<sup>+</sup>**

Traits	BC <sub>1</sub> F <sub>1</sub>					BC <sub>2</sub> F <sub>1</sub>					
	Progeny (Mean)	Range		Standard deviation	Variance	Progeny (Mean)	Range		Standard deviation	Variance	
		Min	Max				Min	Max			
DT	55.55	54	57	0.71	0.50	DT	55.62	54	57	0.70	0.49
DS	57.56	56	59	0.72	0.52	DS	57.47	56	59	0.71	0.50
PH	190.04	185	201	4.30	18.50	PH	146.15	131	149	3.28	10.80
EH	95.61	92	119	4.47	20.04	EH	61.48	59	63	1.45	2.13
TL	39.22	34	45	1.31	1.71	TL	28.01	27	29	0.87	0.77
NTB	15.12	14	18	0.85	0.72	NTB	14.11	12	16	1.53	2.36
LL	85.15	81	89	1.06	1.13	LL	66.55	65	68	1.46	2.14
LB	11.04	9	13	0.79	0.62	LB	8.77	8	13	1.46	2.13
CL	17.03	16	19	0.67	0.44	CL	12.31	12	14	0.65	0.43
CG	14.02	13	16	0.83	0.69	CG	10.95	10	12	0.88	0.77
NKRC	16.54	15	18	1.10	1.21	NKRC	13.36	12	15	1.30	1.69
NKR	30.77	29	34	1.48	2.19	NKR	21.80	19	24	1.78	3.16
100KW	27.20	26	28	0.86	0.74	100KW	20.16	19	24	1.43	2.06
SPY	87.91	86	93	1.24	1.56	SPY	73.38	70	74	1.28	1.66

Note - Days to tasseling (DT); Days to Silking (DS); Plant height in cm (PH); Ear height in cm (EH); Tassel length in cm (TL); Number of tassel branches (NTB); Leaf length in cm (LL); Leaf Breadth in cm (LB); Cob length in cm (CL); Cob girth in cm (CG); Number of kernel rows per cob (NKRC); Number of kernels per row (NKC); 100 Kernel weight in g (100KW); Single plant yield in g (SPY).

**Table 4. Estimation of range, mean, standard deviation and variance in BC<sub>2</sub>F<sub>2</sub> population of SC1107 × UMI1230β<sup>+</sup>**

Traits	BC <sub>2</sub> F <sub>2</sub>				
	Progeny (Mean)	Range		Standard deviation	Variance
		Min	Max		
DT	56.35	54	60	1.28	2.20
DS	57.61	55	62	3.16	10.01
PH	145.89	141	160	2.98	8.93
EH	59.9	57	80	1.44	2.65
TL	23.8	21	28	1.64	2.71
NTB	10.6	10	14	1.89	3.57
LL	63.69	60	68	1.02	1.04
LB	5.98	4	9	0.98	0.97
CL	10.01	8	12	1.16	1.34
CG	9.39	7	12	1.12	1.27
NKRC	10.08	8	12	1.49	2.23
NKR	19.55	17	24	1.20	1.46
100KW	17.3	15	20	2.33	3.76
SPY	68.54	61	76	2.12	3.54

Note - Days to tasseling (DT); Days to Silking (DS); Plant height in cm (PH); Ear height in cm (EH); Tassel length in cm (TL); Number of tassel branches (NTB); Leaf length in cm (LL); Leaf Breadth in cm (LB); Cob length in cm (CL); Cob girth in cm (CG); Number of kernel rows per cob (NKRC); Number of kernels per row (NKC); 100 Kernel weight in g (100KW); Single plant yield in g (SPY).

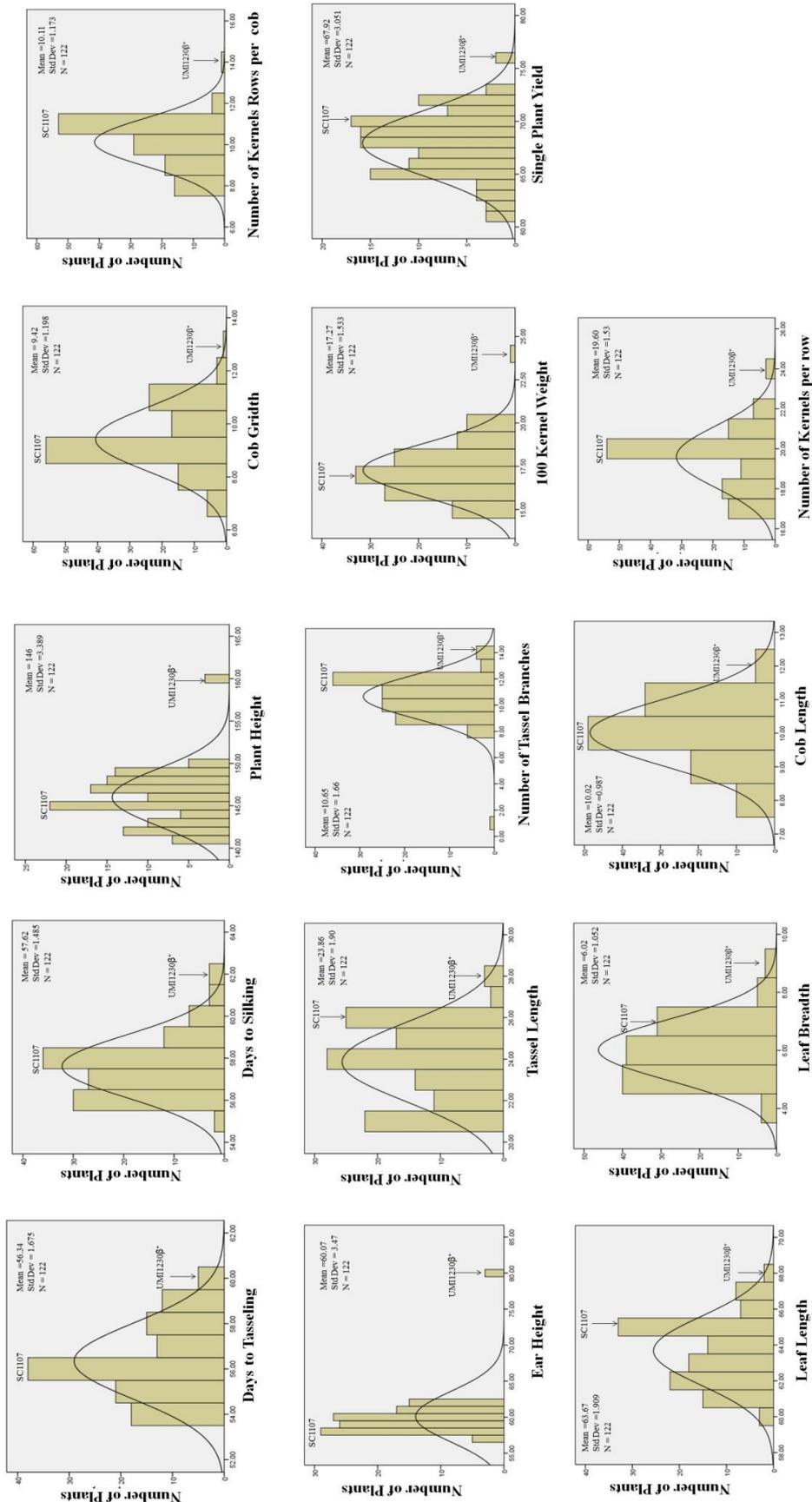


Fig. 2. Frequency distribution for the morphological traits in BC<sub>2</sub>F<sub>2</sub> population of SC1107×UMI1230β\*

**Table 5. Estimation of Skewness and Kurtosis in BC<sub>1</sub>F<sub>1</sub>, BC<sub>2</sub>F<sub>1</sub> and BC<sub>2</sub>F<sub>2</sub> population of USC1-2-3-1× UMI1230β<sup>+</sup> and SC1107× UMI1230β<sup>+</sup>**

Traits	USC1-2-3-1×UMI1230β <sup>+</sup>						SC1107×UMI1230β <sup>+</sup>					
	BC <sub>1</sub> F <sub>1</sub>		BC <sub>2</sub> F <sub>1</sub>		BC <sub>2</sub> F <sub>2</sub>		BC <sub>1</sub> F <sub>1</sub>		BC <sub>2</sub> F <sub>1</sub>		BC <sub>2</sub> F <sub>2</sub>	
	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis
DT	0.28	-0.32	-1.29	-0.35	0.19	-0.75	0.22	-0.28	-0.01	-0.21	0.53	-0.20
DS	0.28	-0.32	-2.00	6.10	0.12	-0.60	0.24	-0.33	0.50	-0.13	0.85	0.69
PH	0.14	-1.45	2.62	6.66	-0.03	-1.30	0.23	-1.03	-1.68	4.20	1.25	4.86
EH	-0.25	-1.40	-2.05	4.40	0.39	-0.66	3.07	11.76	-0.50	-1.29	5.14	33.21
TL	0.03	-1.11	-1.97	3.33	-0.33	-0.65	2.63	13.88	-0.03	-1.72	-0.08	-0.96
NTB	-0.09	1.44	-0.03	-1.70	-0.29	-1.03	0.24	-0.20	-0.30	-1.37	-1.60	8.44
LL	0.07	-1.09	1.14	-0.03	-0.22	-0.53	0.63	7.71	-0.08	-1.98	0.12	-0.80
LB	0.31	-1.22	-2.12	3.53	0.06	-0.91	0.28	0.12	1.60	1.02	0.46	0.01
CL	-0.17	-1.26	0.08	4.86	0.40	0.95	0.57	0.66	1.86	1.94	-0.30	-0.30
CG	0.09	-1.23	-2.69	6.36	-0.01	-0.73	1.01	0.74	0.09	-1.73	0.23	0.32
NKRC	0.17	-1.29	-3.45	12.47	0.05	-0.56	-0.16	-1.29	0.29	-1.67	0.10	-0.38
NKR	0.10	-1.40	-3.97	19.52	-0.10	-0.10	0.38	-0.63	-0.52	-0.93	-0.59	-0.78
100KW	0.03	-1.65	0.51	2.75	0.34	-0.35	0.41	-1.53	0.59	-1.36	0.02	0.18
SPY	-0.03	-1.38	-3.06	10.13	0.07	0.42	1.00	2.42	-2.10	2.88	0.16	-0.49

Note - Days to tasseling (DT); Days to Silking (DS); Plant height in cm (PH); Ear height in cm (EH); Tassel length in cm (TL); Number of tassel branches (NTB); Leaf length in cm (LL); Leaf Breadth in cm (LB); Cob length in cm (CL); Cob girth in cm (CG); Number of kernel rows per cob (NKRC); Number of kernels per row (NKC); 100 Kernel weight in g (100KW); Single plant yield in g (SPY).

respectively. The traits *viz.*, plant height, tassel length and leaf length were noticed with negative skewness and platykurtic distribution, which indicates complementary gene action. Cob length and cob girth were governed by complementary gene action. In BC<sub>2</sub>F<sub>2</sub> generation, plant height, tassel length and single plant yield showed a wide range of variations. The plant height ranged from 141 to 160cm with a mean value of 145.89 and single plant yield ranged from 61 to 76g with a mean value of 68.54. The days to tasseling ranged from 54 to 60 days with a mean value of 56.35 and the days to silking ranged from 55 to 62 days with an average of 57.61. From the population, plant height and single plant yield were observed to exhibit positive skewness and platykurtic distribution which indicates complementary gene action whereas, tassel length and cob length exhibited negative skewness and leptokurtic distribution, which indicates duplicate gene action. The results are similar to Chandana *et al.* (2018) and Neelima *et al.* (2020).

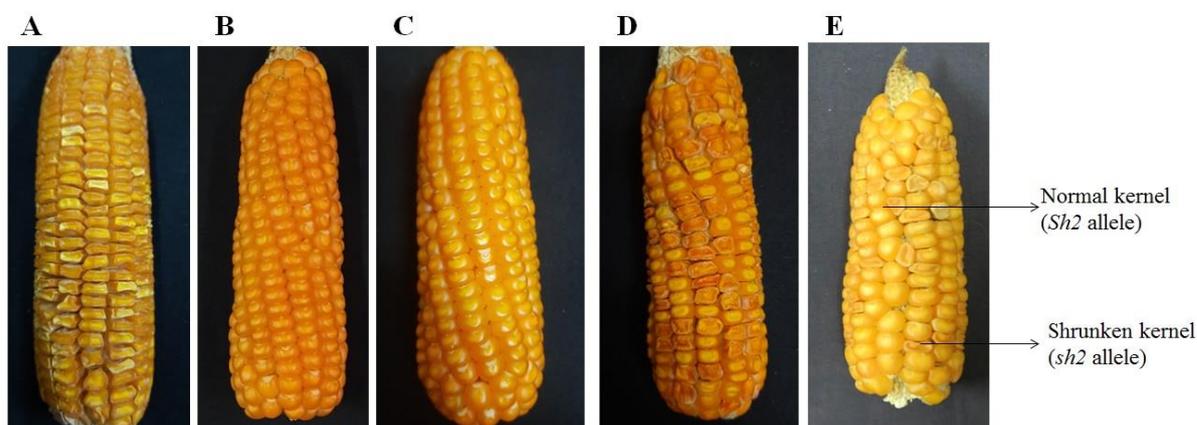
Among the backcrossed and selfed population, various traits like plant height and tassel length showed a wide range of variation whereas, traits like days to tasseling and days to silking showed a narrow range of variation. Among the population, plant height showed positive skewness and platykurtic distribution which suggested the role of complementary gene action. Early generation selections can be practiced in traits governed by

complementary and duplicate gene action while selection could be postponed to later generations for traits with duplicate gene action.

Since plant height, cob length and single plant yield are governed by complementary gene action, the progenies could be selected and forwarded to further generations based on these traits. However for the clear selection of traits, two to three backcrosses are needed. In case of kernel morphology, it could be distinguished as recessive shrunken and dominant normal maize kernel possessing the two genes *sh2* and *Sh2*. These two kernel morphologies helps in the speedy selection of progenies. In the F<sub>1</sub> generation, the kernel morphology was flint due to the law of dominance, but while backcrossing with sweet corn the resulting cob containing 1:1 ratio of *sh2* and *Sh2* allele genotypically and phenotypically were observed. In BC<sub>1</sub>F<sub>2</sub> generation, the kernel morphology was observed to segregate as per the mendelian ratio of 1:2:1 both genotypically and phenotypically (**Fig. 3**).

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**Fig. 3. Kernel morphology of parents and backcross population– A – Sweet corn inbred line with *sh2* allele; B – Normal corn inbred line with *Sh2* allele; C-  $F_1$  Cob with normal kernel (*Sh2* allele); D-  $BC_1F_1$  cob having shrunken kernel (*sh2* allele) and normal kernel (*Sh2* allele) in 1:1 ratio; E- $BC_1F_2$  cob with 1:2:1 ratio.**

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