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Research Article

Genetic variability, heritability and genetic advance studies in backcross populations of maize (*Zea mays* L.)

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Abstract

Genetic variability, heritability and genetic advance of a character assist in setting up the breeding programmes for the improvement of the particular trait. In the current study high estimates of PCV and GCV were recorded for cob weight and single plant yield among the cross derivatives of UMI 1200 × CE 477. The GCV estimates of single plant yield (23.28 in BC_1F_1, 38.10 in BC_2F_1 and 33.23 in BC_2F_2) was observed in the cross derivatives of UMI 1200 × CE 477. Higher PCV and GCV values were obtained for cob weight and single plant in the other cross UMI 1230 × CE 477 also. The GCV values for single plant yield (39.00 in BC_1F_1, 39.00 in BC_2F_1 and 37.11 in BC_2F_2) were found among the cross derivatives of UMI 1230 × CE 477. The PCV and GCV values suggested sufficient variability and thus offers scope for genetic improvement through selection. Both the characters cob weight and single plant yield exhibited higher heritability associated with high genetic advance and hence direct selection of such characters would be effective in improving the yield.

Key words

Maize, variability, heritability, genetic advance, gene action

Introduction

Maize or corn (*Zea mays* (L.)) is an important cereal crop belonging to the family *Poaceae* cultivated globally. It is a diploid species with chromosome number 2n = 20. It is grown widely for food, fodder, biofuel other and industrial uses. The maize production plays an important role in agriculture dependent world economy as it is a valuable ingredient of agro based industries affecting large proportion of world population. Globally, maize occupies an area of 186.86 million hectares, with a production of 1078.56 million tonnes and productivity of 5.77 tonnes ha^{-1} (USDA, 2018). In India, maize is grown throughout the year in all states of the country for human consumption and animal feed. It is cultivated in an area of 9.63 million hectares, with a production of 25.90 million tonnes and productivity of 2.69 tonnes ha^{-1}(www.indiastat.com). Several million people, particularly in the developing countries from Asia and Africa, derive their protein and calorie requirements from maize. Genetic variability for various agronomic characters is a key component of breeding programmes for broadening the gene pool of crops. The knowledge of nature and magnitude of genotypic and phenotypic variability present in the crop species plays a vital role in formulating a successful breeding programme to evolve superior cultivars (Abdurakhmonov and Abdukarimov (2008) and Dhanwani *et al.*, (2013). The extent of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects. The parameters genotypic and phenotypic coefficients of variation are useful in detecting the amount of variability present for a particular character in a given population. Most of the characters of breeder's interest are complex, polygenic and are the resultant of a number of component characters. Grain yield is also one of such dependent traits which is influenced by many independent characters. Heritability is a measure of phenotypic variance and has predictive function in plant breeding and gives the information on the extent to which the particular character can be transmitted to successive generations. Genetic advance explains the degree of gain obtained in a character under particular selection programme. Traits exhibiting high heritability and genetic advance are controlled by additive. High heritability coupled with high genetic advance as percent of mean estimates offers the most suitable condition for selection and breeding in maize (Patil *et al.*, (2016), Sravanthi *et al.*, (2017), Bisen *et al.*, (2018). Generally, the characters plant height, cob weight, and single plant yield exhibits higher values for PCV, GCV, heritability and genetic advance as percent of mean. Beula *et al.*, (2018) reported higher values for PCV, GCV, heritability and genetic advance as percent of mean for grain yield. Mani and Deshpande., (2016) reported higher values of PCV, GCV, heritability and genetic advance as percent of mean for cob weight. Keeping these foregoing points in view, the present investigation was undertaken with a view to estimate genetic variance, heritability and genetic advance in three backcross populations of two cross combinations of maize. Selection in F_1s, BC_1F_1s, BC_2F_1s and BC_2F_2s based on the PCV, GCV, heritability and Genetic advance as percent of mean gives more efficient outcomes and improves the parental genome recovery to a greater extent.

Materials and Methods

The present scientific investigation was conducted at two locations viz., Agricultural Research Station, Vaigai Dam and Agricultural Research Station, Bhavanisagar. The experimental material comprised of two elite maize inbreds viz., UMI 1200 and UMI 1230 which are the parents of the popular maize hybrid Co 6. UMI 1200 and UMI 1230 were taken as the recurrent parents and the β-carotene rich inbred viz., CE 477 was taken as the donor parent. Parents were raised in ridges of 4m length with a spacing of 60 × 25 cm as inter and intra row spacing. Crosses were made between the two recurrent parents and the donor parent independently. Crosses of two different combinations UMI 1200 × CE 477 and UMI 1230 × CE 477 were made and the F1s were raised in the field. The recurrent parents were used as the female parents and the donor parent was used as the male parent. The F_1s were used as female parents and recurrent parents as pollen parents to develop BC_1F_1 population and the subsequent BC_2F_1 population was also developed in the same manner. The BC_2F_1 population was selfed and BC_2F_2 population was arrived at. The F_1 population was raised during Kharif 2016 at Agricultural Research station, Vaigai Dam. BC_1F_1 population was raised during Rabi 2017, BC_2F_1 during Kharif 2017 and BC_2F_2 population during Kharif 2018 at Agricultural Research station, Bhavnisagar. A population size of not less than 100 was maintained during every season for both the crosses. In the cross combination UMI 1200 × CE 477, the population size of BC_1F_1 was 106, BC_2F_1 was 136 and that of BC_2F_2 was 112. Similarly, the population size of UMI 1230 × CE 477 was 121 for BC_1F_1, 146 for BC_2F_1, and 102 for BC_2F_2.

Observations were recorded in five randomly tagged plants for thirteen biometrical characters. The observations were taken following DUS guidelines of PPV & FRA (Anon, 2007). During crop growth, observations on plant height, days to 50% tasseling, days to 50% silking, leaf length, leaf breadth and tassel length were taken. After harvest, with the harvested cobs, observations on cob length, cob width, number of kernel rows per cob, number of kernels per row, 100 grain weight and single plant yield.

Standard statistical procedure was followed for the analysis of variance, genotypic and phenotypic coefficient of variation (Falconer., 1981), heritability and genetic advance as percent of mean (Johnson et al., 1955).

Results and Discussion

The analysis of variance revealed significant differences among the lines indicating sufficient variability in all the characters in the three different populations BC_1F_1, BC_2F_1 and BC_2F_2. The estimates of variability in the backcross population on the basis of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of mean (GAM) for 13 characters for two crosses (UMI 1200 × CE 477 and UMI 1230 × CE 477) were presented in Table 1. and 2.

The mean values for all the thirteen biometrical characters showed steady decrease in the backcross populations. Marked difference in the mean values between the parents and the progenies were noted for plant height, cob weight and single plant yield. The plant height of the parent UMI 1200 was 157.53 cm, the F_1 and backcross progenies of UMI 1200 × CE 477 recorded plant height of 255.83 cm (F_1), 232.35 cm (BC_1F_1), 212.00 cm (BC_2F_1) and 180.16 cm (BC_2F_2). The other recurrent parent recorded a plant height of 176.21 cm and the progenies of UMI 1230 × CE 477 recorded mean values of 270.96 cm (F_1), 250.22 cm (BC_1F_1), 225.96 cm (BC_2F_1) and 191.64 cm (BC_2F_2). The cob weight of the recurrent parent UMI 1200 was 84.63 g, the F_1 and backcross progenies of UMI 1200 × CE 477 recorded cob weight of 190.67 g (F_1), 170.37 g (BC_1F_1), 150.52 g (BC_2F_1) and 103.63 g (BC_2F_2). UMI 1230 recorded a cob weight of 104.16 g and the progenies of UMI 1230 × CE 477 recorded mean values of 207.03 g (F_1), 182.15 g g (BC_1F_1), 160.87 g (BC_2F_1) and 115.67 g (BC_2F_2).

The recurrent parent of the cross UMI 1200 × CE 477 recorded a single plant yield of 73.90 g and the single plant yield of its subsequent generations were 170.51 g (F_1), 150.19 g (BC_1F_1), 125.93 g (BC_2F_1) and 89.93 g (BC_2F_2). The other population of UMI 1230 × CE 477 recorded mean values of 184.02 g (F_1), 165.96 g (BC_1F_1), 135.29 g (BC_2F_1) and 100.34 g (BC_2F_2) where the parental value is 82.22 g. The mean values of the BC_1F_1 population were lesser than the F_1 population, and the mean performance of BC_2F_1 population was lesser than the BC_1F_1 population. With every additional backcross, the mean values showed a shift towards the parental means which shows the additional parental genome recovery with every backcross. The BC_2F_2 population of both the crosses UMI 1200 × CE 477 and UMI 1230 × CE 477 were almost identical to the respective recurrent parents UMI 1200 and UMI 1230. The recovery of the recurrent parent genome was studied with in BC_2F_2 population of both the crosses UMI 1200 × CE 477 and UMI 1230 × CE 477. The recovery percentage varied widely and ten genotypes having parental higher parental genome recovery were represented in the table 3. and table 4. with their agronomic performance. Three genotypes from each cross were selected based on the parental genome recovery. The genotypes DBT 1-1-1-17-5-5, DBT 1-1-1-17-5-14 and DBT 1-1-1-17-9-6 with the parental genome recovery of 92.28%, 91.61% and 92.26% were selected among the backcross population of UMI 1200 × CE 477. The selected genotypes of the UMI 1230 × CE 477 cross were DBT 2-1-4-7-7-7, DBT 2-1-4-7-1-9 and DBT 2-1-3-12-12-2 with the parental genome recovery of 91.32%, 92.37% and 91.61% respectively. The agronomic performance of the selected lines was given in table 4. and 5.

The backcross populations of both the crosses UMI 1200 × CE 477 and UMI 1230 × CE 477 viz., BC_1F_1, BC_2F_1 and BC_2F_2 exhibited high exhibited higher PCV and GCV values for cob weight and grain yield per plant. The PCV values for cob weight were 27.95 in $BC_1F_{1,}$23.16 in BC_2F_1 and 21.44 in BC_2F_2 and the GCV values were 27.74 in $BC_1F_{1,}$ 22.11in BC_2F_1 and 20.45 in BC_2F_2 among the cross derivatives of UMI 1200 × CE 477. The PCV values for single plant yield were 24.32 in $BC_1F_{1,}$ 38.17 in BC_2F_1 and 33.23 in BC_2F_2 among the cross derivatives of UMI 1200 × CE 477 and the GCV were 23.28 in $BC_1F_{1,}$ 38.10 in BC_2F_1 and 33.23 in $BC_2F_{2.}$ Similarly, higher PCV values were obtained for cob weight (29.24 in $BC_1F_{1,}$ 31.21 in BC_2F_1 and 21.10 in BC_2F_2) and single plant yield of 40.28 in $BC_1F_{1,}$ 41.28 in $BC_2F_1$and 38.87 in BC_2F_2 in the cross derivatives of UMI 1230 × CE 477. Higher GCV values for single plant yield (39.00 in $BC_1F_{1,}$ 39.00 in BC_2F_1 and 37.11 in BC_2F_2) was found among the UMI 1230 × CE 477 population.

Higher GCV values for these characters show that the variation in these two characters was contributed due to genotypic difference. Higher GCV values shows that selection based on the variations in these characters would be effective. Slightly, higher PCV values reveal the limited influence of environment on these characters. All the thirteen characters showed higher PCV values compared to GCV values. Similar results of higher PCV and GCV for grain yield was reported earlier by Beula et al., (2018) and Dar et al., (2018) and similar results for cob weight was reported earlier by Kinfe et al., (2015), Mani and Deshpande et al., (2016) and Bisen et al., (2018).

Moderate to low PCV and GCV values were obtained for the characters cob length and number of kernels per row. Similar results of moderate PCV and GCV for cob length was reported by Sravanthi et al., (2017), Bisen et al., (2018), Sravanthi et al., (2017), Bisen et al., (2018), Beula et al., (2018) and Barman et al., (2018). Moderate estimates of PCV and GCV for number of kernels per row were earlier reported by Barman et al., (2018), Beula et al., 2018 and Dar et al., (2018).

Lower PCV and GCV values were obtained in days to 50% tasseling, days to 50% silking, leaf length, leaf width, tassel length, number of kernel rows per cob and 100 grain weight. Similar results for days to 50% tasseling and days to 50% silking were reported earlier by Beula et al., 2018 and Dar et al., (2018). Also, lower PCV and GCV values for number of kernel rows per cob were reported earlier by Beula et al., (2018), Barman et al., (2018), Bisen et al., (2018) and Dar et al., (2018). Similar results for 100 grain weight were earlier reported by by Kinfe et al., (2015) and Bisen et al., (2018).

High heritability accompanied with high genetic advance as percent as mean was observed for cob weight and grain yield per plant for the crosses UMI 1200 × CE 477 and UMI 1230 × CE 477 in three backcross populations BC_1F_1, BC_2F_1 and BC_2F_2. Cob weight exhibited higher heritability values in UMI 1200 × CE 477 population (99.60 in $BC_1F_{1,}$ 92.10 in $BC_2F_1$and 91.12 in BC_2F_2) and UMI 1230 × CE 477 population (98.10 in $BC_1F_{1,}$ 82.80 in $BC_2F_1$and 96.30 in BC_2F_2). Higher GAM values were observed for cob weight in the UMI 1200 × CE 477 population (57.17 in $BC_1F_{1,}$ 28.10 in BC_2F_1 and 40.30 in BC_2F_2) and UMI 1230 × CE 477 populations (59.10 in $BC_1F_{1,}$ 53.39 in BC_2F_1 and 42.78 in BC_2F_2).The heritability values for single plant yield of the cross derivatives of UMI 1200 × CE 477 were 91.10 in $BC_1F_{1,}$ 98.50 in BC_2F_1 and 97.34 in BC_2F_2 and the GAM values were 46.00 in $BC_1F_{1,}$ 77.65 in BC_2F_1 and 67.69 in BC_2F_2population. High heritability (94.10 in $BC_1F_{1,}$ 89.00 in $BC_2F_1$and 91.08 in BC_2F_2) and high GAM (78.10 in $BC_1F_{1,}$ 76.00 in BC_2F_1and73.09 in BC_2F_2) for single plant yield was observed in the backcross populations of UMI 1230 × CE 477 also. The above results show that these two characters were under additive gene action. This shows the lesser influence of environment on these characters and selection and breeding strategies focussing on these characters gives better results. Higher heritability and genetic advance for cob weight were earlier reported by Mani and Deshpande et al., (2016) and Bisen et al., (2018). Similarly, higher values for heritability and genetic advance for single plant yield was earlier reported by Beula et al., (2018), Bisen et al., (2018) and Barman et al., (2018).

Higher values for heritability and low genetic advance were reported in the characters 50% tasseling, days to 50% silking, leaf width, number of kernel rows per cob and number of kernels per row and 100 grain weight. This indicates the presence of epistatis and dominant gene action. These traits could be exploited through heterosis breeding after the introgression is complete. Similar reports were reported earlier in days to 50% silking and days to 50% silking by Mani and Deshpande et al., (2016) and Dar et al., (2018). Similarly, high heritability accompanied with low genetic advance in number of kernel rows per cob and number of kernels per row was reported by (2016) and Barman et al., (2018).

The current scientific investigation revealed the information on extent of variation, estimates of heritability and expected genetic advance of thirteen different biometrical characters. High estimates of genotypic and phenotypic coefficient of variation were observed for cob weight and grain yield per plant, suggesting sufficient variability existing in these two characters and thus offers scope for genetic improvement through selection in these two characters. The characters cob weight and single plant yield which exhibited higher PCV and GCV, also exhibited higher heritability and genetic advance as percent of mean, suggesting that these two traits are controlled by additive gene action and selection will be efficient with these traits. The characters 50% tasseling, days to 50% silking, leaf length, leaf width, tassel length, cob length, cob width, number of kernel rows per cob, number of kernels per row and 100 grain weight exhibited high to moderate heritability with low genetic advance and these traits were under the control of non-additive type of gene action and its response to selection will be limited.

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Table 1. Variability analysis in BC_1F_1, BC_2F_1 and BC_2F_2 population of UMI 1200 × CE 477 cross combination

CHR	BC_1F_1							BC_2F_1							BC_2F_2						
	P1	**Mean**	**Range**	**PCV %**	**GCV %**	**h^2 %**	**GAM %**	**P1**	**Mean**	**Range**	**PCV %**	**GCV %**	**h^2 %**	**GAM %**	**P1**	**Mean**	**Range**	**PCV %**	**GCV %**	**h^2 %**	**GAM %**
PHT	157.91	232.35	207.40-255.60	5.54	4.12	55.30	1.44	158.41	212.00	191.00-231.40	5.01	4.56	82.70	1.69	159.80	180.16	150.64-218.60	7.73	7.36	90.70	2.14
DTT	60.20	55.44	53.00-58.00	3.00	2.64	77.50	4.80	60.00	55.21	53.00-57.00	2.45	2.13	75.60	3.81	59.60	58.18	56.00-60.00	2.21	2.02	83.90	3.82
DTS	63.20	57.44	55.00-60.00	2.90	2.55	77.50	2.47	62.80	58.21	56.00-60.00	2.32	2.05	78.10	2.20	62.60	61.18	59.00-63.00	2.10	1.93	83.90	2.03
LL	52.50	74.70	69.40-80.40	4.14	3.85	86.60	2.54	52.64	71.66	63.10-79.90	6.25	6.06	93.80	2.85	53.13	58.68	50.30-67.40	6.31	6.01	90.80	3.37
LW	6.13	8.29	7.00-9.50	7.73	7.19	75.00	10.44	6.18	7.58	6.80-8.50	5.78	5.23	81.70	9.62	6.18	6.50	5.80-7.00	4.43	4.00	81.80	9.08
TL	28.73	40.36	36.70-43.90	4.75	4.01	71.40	3.69	28.88	36.51	34.30-38.90	3.17	2.45	59.70	2.89	29.29	32.30	25.40-37.70	9.76	9.67	98.00	4.15
CL	12.21	17.09	13.90-20.90	11.54	10.89	89.00	8.68	12.41	16.28	14.00-19.80	8.31	7.86	89.40	7.51	12.49	14.06	11.30-16.40	9.67	9.24	91.40	8.45
CW	3.19	4.04	3.60-4.50	7.48	4.95	43.80	10.96	3.13	3.67	3.40-4.00	3.67	3.15	73.90	10.98	3.17	3.36	3.00-3.70	5.05	4.81	90.50	13.22
CWT	82.53	170.37	151.90-189.50	27.95	27.74	99.60	57.17	84.34	150.52	127.49-172.65	23.16	22.11	92.10	28.10	84.548	103.63	80.64-124.18	21.44	20.45	91.12	40.30
KRC	13.5	18.39	16.00-21.00	7.80	5.74	54.10	5.98	12.6	16.18	14.00-19.00	7.53	6.81	82.00	7.50	12.40	14.58	11.00-17.00	11.54	10.99	90.60	9.20
KR	21.80	33.41	30.00-37.00	11.97	10.69	73.00	4.79	22.10	31.19	14.00-19.00	12.82	11.89	85.90	6.95	22.10	27.51	21.00-32.00	9.88	9.51	92.60	5.96
100 GW	18.37	33.41	30.04-37.41	5.57	4.68	70.66	4.37	20.06	31.36	27.02-35.46	6.88	6.50	89.30	4.93	20.743	24.30	18.47-31.92	12.51	12.18	94.80	6.69
SPY	69.101	150.19	131.13-169.50	24.32	23.28	91.10	46.00	71.47	125.93	106.77-143.60	38.17	38.10	98.50	77.65	73.06	89.93	70.35-108.83	33.67	33.23	97.34	67.69

Where, CHR- Character, PHT – Plant height (cm), DTT – Days to 50% tasseling, DTS – Days to 50% silking, LL – Leaf length (cm), LW – Leaf width (cm), TL – Tassel length (cm), CL – Cob length (cm), CW – Cob width (cm), CWT – Cob weight (g), KRC – Number of kernel rows per cob, KR – Number of kernels per row, 100 GW – 100 grain weight (g) and SPY – Single plant yield (g).

Table 2 Variability analysis in BC$_1$F$_1$, BC$_2$F$_1$ and BC$_2$F$_2$ population of UMI 1230 × CE 477 cross combination

CHR	BC$_1$F$_1$							BC$_2$F$_1$							BC$_2$F$_2$						
	P1	Mean	Range	PCV %	GCV %	h^2 %	GAM %	P1	Mean	Range	PCV %	GCV %	h^2 %	GAM %	P1	Mean	Range	PCV %	GCV %	h^2 %	GAM %
PHT	172.82	250.22	232.00-266.40	3.71	2.49	44.90	0.97	178.34	225.96	207.30-250.40	4.94	4.48	82.30	1.63	175.80	191.64	170.56-215.20	5.51	5.21	89.60	1.78
DTT	58.30	53.45	51.00-56.00	2.82	2.52	80.00	2.40	58.00	53.68	51.00-56.00	2.92	2.64	81.90	4.92	58.90	56.71	54.00-59.00	2.48	2.26	83.60	4.27
DTS	61.30	56.45	54.00-59.00	2.67	2.39	80.00	2.40	61.00	56.68	54.00-59.00	2.76	2.50	81.90	2.43	61.90	58.71	56.00-61.00	2.39	2.19	83.60	2.21
LL	62.45	77.56	66.90-89.60	7.61	3.97	92.40	3.13	62.45	73.93	67.40-80.60	4.33	3.73	74.00	2.64	62.13	62.63	60.70-65.30	1.71	1.56	83.20	1.81
LW	7.55	9.51	8.60-10.30	5.01	18.22	24.2	3.38	7.31	8.72	8.00-9.50	4.40	3.81	75.10	7.77	7.33	7.58	7.10-8.20	3.74	3.47	86.10	7.61
TL	33.41	42.11	37.60-46.60	5.42	4.95	83.40	3.94	33.89	39.89	35.60-42.80	4.59	4.13	80.60	3.74	32.55	34.96	30.40-38.40	5.24	4.86	86.10	4.19
CL	13.13	19.83	15.90-23.60	10.52	7.31	82.60	8.00	13.86	18.4	16.20-20.80	6.75	6.03	79.80	6.67	13.85	16.5	13.00-19.00	6.92	6.38	84.90	7.06
CW	3.31	4.22	4.00-4.40	2.25	5.83	38.80	5.17	3.37	4.17	4.00-4.40	2.81	2.56	83.20	8.97	3.38	3.49	3.10-3.80	4.42	4.26	93.00	10.92
CWT	101.56	182.15	161.00-203.90	29.24	28.89	98.10	59.10	101.56	160.87	133.90-192.00	31.21	28.41	82.80	53.39	102.511	115.67	100.54-129.76	21.10	21.49	96.30	42.78
KRC	13.70	20.87	18.00-24.00	7.20	6.70	50.2	5.10	13.70	18.93	17.00-21.00	4.82	4.09	72.00	5.45	13.8	15.75	12.00-18.00	10.42	10.07	93.40	7.93
KR	27.30	35.22	32.00-39.00	11.36	9.84	54.30	3.67	27.80	33.97	31.00-37.00	4.36	3.69	71.60	3.80	28.4	29.62	27.00-33.00	5.71	5.20	82.90	4.82
100 GW	21.93	35.72	28.34-43.44	10.10	9.80	94.10	5.07	22.43	31.67	26.13-37.23	8.17	7.72	89.50	5.33	23.64	26.51	20.07-32.55	10.98	9.95	82.20	7.08
SPY	79.105	165.96	149.94-182.06	40.28	39.00	94.10	78.10	81.97	135.29	112.17-160.80	41.28	39.00	89.00	76.00	83.72	100.34	85.51-115.67	38.87	37.11	91.08	73.09

Where, CHR- Character, PHT – Plant height (cm), DTT – Days to 50% tasseling, DTS – Days to 50% silking, LL – Leaf length (cm), LW – Leaf width (cm), TL – Tassel length (cm), CL – Cob length (cm), CW – Cob width (cm), CWT – Cob weight (g), KRC – Number of kernel rows per cob, KR – Number of kernels per row, 100 GW – 100 grain weight (g) and SPY – Single plant yield (g).

Table 3. Agronomic performance and recovery of recurrent parent genome of selected BC_2F_2 genotypes of the cross UMI 1200 × CE 477

Genotype	PHT	DTT	DTS	LL	LW	TL	CL	CW	CWT	KRC	KR	100 GW	SPY	Recovery of recurrent parent genome (%)
DBT 1-1-1-17-5-5	170.47	59.00	62.00	59.90	6.10	37.70	15.40	3.20	91.23	11.00	24.00	24.31	79.31	92.28
DBT 1-1-1-17-5-14	173.14	60.00	63.00	54.30	6.60	32.50	12.90	3.60	92.67	16.00	23.00	26.04	78.32	91.61
DBT-1-9-18-11-5-8	185.74	60.00	63.00	59.10	6.90	30.80	14.60	3.10	99.54	17.00	30.00	28.81	82.34	89.91
DBT 1-13-6-3-5-10	172.40	57.00	60.00	60.10	6.40	32.50	14.40	3.20	100.34	17.00	30.00	22.73	87.94	84.35
DBT 1-13-6-3-6-16	175.90	58.00	61.00	57.70	6.90	34.20	14.70	3.20	99.61	12.00	24.00	25.13	87.21	84.24
DBT 1-1-1-17-9-6	171.32	59.00	62.00	58.50	6.10	36.80	14.10	3.50	91.31	13.00	31.00	20.63	78.91	92.26
DBT 1-14-2-17-2-1	179.30	60.00	63.00	60.90	6.20	36.30	15.10	3.60	95.41	17.00	30.00	23.21	83.01	87.11
DBT 1-14-2-17-5-16	178.00	56.00	59.00	55.30	6.50	31.50	13.60	3.50	95.32	17.00	30.00	23.93	82.92	87.45
DBT 1-14-2-17-6-4	179.40	60.00	63.00	57.30	6.30	32.50	13.80	3.40	100.63	11.00	30.00	23.03	88.23	82.65
DBT 1-18-7-4-1-17	177.80	59.00	62.00	61.50	6.40	36.10	14.90	3.60	98.64	17.00	29.00	26.41	86.24	84.67

PHT – Plant height (cm), DTT – Days to tasseling, DTS – Days to silking, LL – Leaf length (cm), LW – Leaf width (cm), TL – Tassel length (cm), CL – Cob length (cm), CW – Cob width (cm), CWT – Cob weight (g), KRC – Number of kernel rows per cob, KR – Number of kernels per row, 100 GW – 100 grain weight (g) and SPY – Single plant yield (g).

Table 4. Agronomic performance and recovery of recurrent parent genome of selected BC_2F_2 genotypes of the cross UMI 1230 × CE 477

Genotype	PHT	DTT	DTS	LL	LW	TL	CL	CW	CWT	KRC	KR	100 GW	SPY	Recovery of recurrent parent genome (%)
DBT 2-1-4-7-7-7	189.3	56.00	58.00	63.70	7.20	36.60	14.30	3.60	111.62	14.00	28.00	32.55	91.64	91.32
DBT 2-2-3-9-6-11	192.4	57.00	59.00	63.00	7.30	34.20	14.60	3.60	112.31	15.00	30.00	28.34	90.14	91.11
DBT 2-4-11-9-3-7	195.2	57.00	59.00	62.30	7.40	34.80	15.30	3.40	117.64	12.00	28.00	31.57	95.31	86.79
DBT 2-1-4-7-1-9	187.3	59.00	61.00	63.50	7.50	36.00	15.50	3.60	110.34	13.00	30.00	29.02	91.00	92.37
DBT 2-13-2-1-2-9	189.6	58.00	60.00	62.80	7.20	35.70	14.90	3.40	113.06	15.00	29.00	31.01	95.72	89.17
DBT 2-13-10-20-2-10	201.3	56.00	58.00	64.80	7.30	36.70	14.30	3.40	115.34	14.00	30.00	28.97	98.00	85.31
DBT 2-17-12-14-6-14	192.3	59.00	61.00	63.90	7.40	37.90	14.80	3.60	119.47	16.00	28.00	31.07	96.21	86.38
DBT 2-1-3-12-12-2	188.5	59.00	61.00	63.80	7.30	35.50	15.10	3.60	112.31	14.00	30.00	26.86	90.74	91.61
DBT 2-37-20-17-6-4	192.3	58.00	60.00	64.60	7.40	36.10	15.80	3.60	115.47	14.00	29.00	30.09	98.13	86.92
DBT 2-39-17-5-1-19	201.4	60.00	62.00	64.70	7.30	37.30	16.00	3.70	112.64	17.00	30.00	27.54	95.30	87.24

PHT – Plant height (cm), DTT – Days to tasseling, DTS – Days to silking, LL – Leaf length (cm), LW – Leaf width (cm), TL – Tassel length (cm), CL – Cob length (cm), CW – Cob width (cm), CWT – Cob weight (g), KRC – Number of kernel rows per cob, KR – Number of kernels per row, 100 GW – 100 grain weight (g) and SPY – Single plant yield (g).