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Research Note

Estimates of genetic variability among the backcross populations involving UMI1200 and UMI1230 maize inbreds

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Abstract
A knowledge of genetic variability parameters, heritability and genetic advance of the traits is essential in a breeding programme to select and advance a right individual from a population. The aim of this study was to estimate the genetic variability among the backcross (BC_1F_1, BC_2F_1) and selfed (BC_2F_2) population derived from two independent crosses of maize inbreds (UMI 1200 × VQL1 and UMI 1230 × VQL1) and select the efficient individual. Fourteen morphological traits were used to estimate the genetic variability components. The populations exhibited high PCV than the corresponding GCV for all the traits. Yield and its attributes like cob length and girth, number of kernel rows/ cob, number of kernels/ row and 100 grain weight revealed high heritability with high genetic advance as percent of mean in BC_2F_2 generations of both the crosses. Hence these traits indicated the presence of additive gene action and selection would be effective.

Key words
Maize Inbred, backcross and selfed population, Genetic Variability, Heritability, Genetic Advance.

Maize (*Zea mays* L.), being third most important cereal crop in world serves as food source, feed for cattle and poultry, raw material for industrial purpose. In India maize is cultivated over an area of 8.69 million .ha and production has reached 21.80MT. (Anonymous, 2016 in AICRIP on maize). Information on magnitude of the genetic variation governing the characters is the most important for effective selection and genetic improvement of crop species. The extent of variability present in a character can be known through phenotypic and genotypic coefficient of variation. Estimation of genetic variability alone does not give a clear suggestion of the possible improvement that can be achieved through selection and it should be used in combination with heritability and genetic advance (Singh *et al*, 2011). Genetic advance describes the amount of gain acquired in a character when a selection pressure is imposed. The traits with high heritability and high genetic advance indicate that they are governed by additive gene action and selection of such traits would be more suitable for crop improvement. Several researches have reported high heritability and high genetic advance for yield and its contributes in maize (Bello *et al.*, 2012; Jilo *et al.*, 2018; Sharma *et al*., 2015). High heritability and high genetic advance for plant height, kernel rows per ears, 1000 kernel weight, ear height, and grain yield per hectare was reported by Atnafu and Rao (2014). Maruthi and Rani (2015) also revealed high genetic advance as per cent of mean and high heritability for ear height, plant height, number of kernels per ears, ear length and diameter and 1000-grain weight. Therefore, the present study was aimed to assess the nature of genetic variability, heritability, genetic advance and genetic advance as percent of mean among the backcross and selfed population in maize.

The experimental material consisted of inbred lines UMI 1200 and UMI 1230 (parents of prevalent hybrid CO 6) from Tamil Nadu Agricultural University, Coimbatore and a Quality Protein Maize (QPM) donar VQL 1 from VPKAS, Almora. The maize inbreds UMI 1200 and UMI1230 were used as recurrent parent and VQL1 was used as donor parent. Crosses were made among UMI 1200 × VQL1 and UMI 1230 × VQL1 during *kharif* 2015 at Agricultural Research Station (ARS), TNAU, Vaigai Dam. The F_1s were raised during *rabi* 2016 and the selected F_1s were backcrossed with its respective recurrent parent to develop BC_1F_1. During, *kharif* 2016, BC_1F_1 plants were raised and evaluated, the selected BC_1F_1s were backcrossed with its respective recurrent parent to develop BC_2F_1. The BC_2F_1 population was raised during *rabi* 2017 and the selected plants were selfed to generate BC_2F_2 and assessment of this BC_2F_2 was done during *kharif* 2017 at ARS, Bhavanisagar. All the recommended agronomic practices including plant protection measures were followed to raise the crop.

Observations were taken for 14 morphological, yield and yield related traits, categorized and presented chronologically, regarding the plant stage that were taken.. Traits taken include, days to tasseling (days), days to silking (days), plant height (cm), ear height (cm), tassel length (cm), number of tassel branches (Nos.), leaf length (cm), leaf breadth (cm), cob length (cm), cob girth (cm), number of kernel rows per cob (Nos.), number of kernels per row (Nos.), 100 grain weight (g) and single plant yield (g).

The observed traits were used to estimate phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2 in broad sense), genetic advance (GA) and genetic advance as percent of mean (GAM) in BC_1F_1, BC_2F_1 and BC_2F_2 populations along with the parents. The average variance observed in the parent UMI 1200 and UMI 1230 were considered as environmental variance. The genotypic variance of each trait was estimated by subtracting the estimated environmental variance from the phenotypic variance (Lush, 1940). The PCV and GCV were estimated by following the methods of Burton (1952) and its range was categorised as low (<10%); moderate (10-20%) and high (>20%) as suggested by Sivasubramanian and Madhavamenon (1973). Broad sense heritability was calculated by using the formula proposed by Lush (1940) and classified into low (<30%); moderate (30-60%) and high (>60%) as proposed by Robinson et al. (1949). Genetic advance and genetic advance as percent of mean were assessed according to the methods of Johnson *et al.,* 1955 and classified into low (<10%); moderate (10-20%) and high (>20%).

Successful crop improvement in a breeding programme is influenced by both magnitude of genetic variability for the different characters and the extent to which the desirable trait is heritable (Hussain *et al,* 2011; and Bello *et al,* 2012). Heritability provides information about degree of particular phenotypic character passed on to successive generation (Falconer and Mackay, 1996). Genetic advance shows how much gain is obtained by a character under selection pressure (Bello *et al*, 2012). The traits with high heritability and high genetic advance will be suitable for selection. In the present experiment, mean performance of the recurrent parents, BC_1F_1, BC_2F_1 and BC_2F_2 populations, range, GCV, PCV, heritability (h^2), genetic advance (GA) and genetic advance as percent of mean (GAM) for crosses UMI 1200 × VQL1 and UMI 1230 × VQL1 were studied and presented in Table 1 and 2.

In general, the PCV was greater than GCV for all the traits in all generations which indicates the influence of environmental factor. In BC_1F_1 the traits cob girth (10.97, 12.51) and number of kernels per row (11.88, 12.75) recorded moderate GCV and PCV while the traits 100 grain weight (10.44) and single plant yield (10.16) exhibited moderate PCV. All the other traits recorded low GCV and PCV values (Table 1). Similarly in BC_2F_1 population none of the trait expressed high GCV and PCV (Table 1). Moderate GCV and PCV was recorded for cob length (11.59, 12.59) High heritability was observed for all the traits ranging from 62.58% in leaf breadth to 90.51% in plant height among BC_1F_1 population and from 70.20% in number of tassel branches to 91.46% among BC_2F_1 population. High GAM was observed in number of kernels per row (22.81%) in BC_1F_1 and cob length (22.71%) in BC_2F_1 population respectively. All the other traits exhibited low to moderate GAM. These results may be due to low variation among the individuals in the BC_1F_1 and BC_2F_1 populations respectively. However in BC_2F_2 population high variability was recorded. High GCV and PCV was registered by the traits tassel length (21.11%, 21.53%), number of tassel branches (26.59, 27.93), 100 grain weight (22.42, 23.02) and single plant yield (22.68, 22.84) respectively (Table 1). Similar results were revealed by Alake *et al*, 2008; Bello *et al*, 2012; Nzuve *et al*, 2014 and for 100 grain weigh yield per plant. The traits leaf length (19.80, 21.00) and leaf breadth (18.57, 20.65) expressed moderate GVC and high PCV. Low GCV and PCV was recorded for days to tasseling (5.03, 5.30) and silking (4.98, 5.07) (Table 1). All the traits registered high heritability. Highest heritability was observed for single plant yield (98.65%) followed plant height (96.80%), cob length (96.62%), days to silking (96.44%), ear height (95.72%), number of kernels per row (95.24%), 100 grain weight (94.91%). The other traits exhibited more than 80% heritability. The earlier results of, Rafiq *et al.* 2010 who reported high heritability for different yield controlling traits in maize supports the present study. However the traits that exhibits high heritability may not necessarily express high genetic advance. Hence, high heritability accompanied with high genetic advance would of great value in selection process (Nadarajan *et al.* 2016). In the present study lowest GAM was found in days to tasseling (9.83%) and moderate GAM was observed in days to silking (10.07%). Highest GAM was observed in number of tassel branches (52.14%) followed by single plant yield (46.41%), 100 grain weight (45.00%), number of kernel rows per cob and tassel length (42.64%), leaf length (38.45%), leaf breadth (34.39%), ear height (34.23%), cob girth (32.98%), number of kernels per row (30.62%), cob length (28.64%) and plant height (22.27%). From these result it is understood that these traits with high heritability and GAM were governed by additive gene action and thus selection would be achieved with greater value. These results were comparable with findings of Hefny (2011) who revealed high heritability and genetic advance for 100 grain weight and yield per plant. GAM was low in days to tasseling and silking. It also had low GCV, PCV and GA. It shows that these would be governed by non-additive gene action and variation found in them is due to environmental effect and direct selection for such trait is not advisable. Anshuman *et al.* (2014), Sesay *et al.* (2016) and Vashistha *et al.* (2013) also recorded low genetic variability for days to 50% flowering and silking in maize

In all the three generations (BC_1F_1, BC_2F_1 and BC_2F_2), the PCV was comparatively higher than GCV. In BC_1F_1 population, none of the characters expressed high GCV or PCV. Moderate GCV and PCV was detected in number of tassel branches (10.12, 11.75), 100 grain weight (10.10, 10.60) and single plant yield (11.14, 11.55). Heritability for all the traits was found to be high with maximum of 93.02% (single plant yield) and minimum of 65.92% (days to silking) heritability percent. However high GAM was perceived by single plant yield (22.13%) alone (Table 2). Correspondingly in BC_2F_1 moderate GCV and PCV was noted in number of tassel branches (11.81, 13.33), and single plant yield (12.96, 13.24). Though all the characters were found to have high heritability percentage, high heritability along with GAM was observed in single plant yield (95.81% and 26.14% respectively). In BC_2F_2 population, moderate GCV and PCV was witnessed for all the traits except days to tasseling (3.02, 3.34) and silking (2.71, 2.95) and plant height (9.59, 9.78). Moderate to high GCV and PCV for these traits was conveyed by Alake *et al.* (2008). Heritability estimates was high for all the traits under study (Table 2). The heritability percent ranged from 97.59 % (single plant yield) to 81.66% (days to tasseling).

High heritability for yield and its attributes in maize was reported by Hefny (2011);); Sharma *et al*. (2015); Rafiq *et al.* 2010. Highest GAM was revealed by single plant yield (40.07%), followed by tassel length (36.15%), ear height (34.90%), leaf breadth (34.81), cob length (33.50%), number of tassel branches (33.21%), number of kernel rows / cob (29.72%), cob girth (28.22), 100 grain weight (26.51%), leaf length (25.78%) and number of kernels / row (22.27%). Plant height recorded moderate GAM of 19.39%. Hefny (2011); and Sharma *et al*. (2015) also reported high heritability and genetic advance as percent of mean for grain yield. Days to tasseling and silking had a low GAM of 5.63% and 5.13% respectively. Anshuman *et al.* (2014); Sesay *et al.* (2106) and Vashistha *et al.* (2013) also recorded low genetic variability for days to 50% flowering and silking in maize

The traits studied in this investigation showed varied levels of variability, heritability and genetic advance as percent of mean in both the crosses. Broad sense heritability provides the information on additive portion of the total phenotypic variance. The superiority of additive gene effects controlling a trait usually resulted from high heritability combined with high genetic advance, whereas the traits governed by non-additive gene actions could give high heritability with low genetic advance. In the present study, in backcross population (BC_1F_1 and BC_2F_1) most of the characters resulted with high heritability but low to moderate GCV, PCV, GA and GAM for both the crosses. This might be due to the low variation within the backcross population. However in BC_2F_2 population single plant yield and yield attributing characters were found to have high to moderate GCV and PCV. High heritability along with high genetic advance as percent of mean was detected for single plant yield, 100 grain weight, plant height, ear height, number of kernels/ row, number of kernel rows/ cob, cob length and cob girth. Hence selection response for these characters would be effective. Days to tasseling and silking exhibited high heritability and low GA and GAM. These traits would be governed by non-additive gene action and selection for these traits would be ineffective.

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Table 1. Variability estimates of BC_1F_1, BC_2F_1 and BC_2F_2 population in cross UMI 1200 × VQL 1

Generation	Trait	UMI1200 (mean)	Mean	Range		GCV	PCV	h^2	GA	GAM
				Min	Max					
BC_1F_1	DT	59.50	57.51	56.00	60.00	1.86	2.11	77.35	1.93	3.36
	DS	61.50	60.54	58.00	63.00	1.97	2.19	81.02	2.21	3.65
	PH	150.78	198.91	190.90	216.70	1.77	2.12	90.51	6.10	3.06
	EH	62.63	91.53	87.30	95.50	1.51	1.86	86.09	2.32	2.54
	TL	31.78	50.82	45.90	57.30	3.39	3.95	73.52	3.04	5.99
	NTB	11.75	14.79	13.00	17.00	4.64	6.07	68.96	1.08	7.33
	LL	53.25	72.36	63.40	79.30	3.89	4.41	77.92	5.12	7.08
	LB	7.025	8.07	7.20	9.10	4.60	5.82	62.58	0.61	7.50
	CL	13.28	20.55	17.00	25.80	8.92	9.58	86.68	3.51	17.10
	CG	13.35	15.02	12.10	19.60	10.97	12.51	76.89	2.98	19.82
	NKR/C	13.28	15.47	14.00	18.00	7.22	9.06	63.56	1.83	11.86
	NK/R	26.75	32.40	25.00	40.00	11.88	12.75	86.82	7.39	22.81
	100GW	26.70	32.07	25.80	39.80	9.29	10.44	79.25	5.47	17.05
	SPY	87.35	159.68	126.05	184.80	9.60	10.16	89.30	29.85	18.69
BC_2F_1	DT	59.50	59.50	57.00	63.00	2.13	2.34	82.80	2.37	3.99
	DS	61.50	62.09	58.00	67.00	2.39	2.57	86.90	2.86	4.60
	PH	153.30	170.67	158.50	187.00	2.56	2.82	82.05	8.14	4.77
	EH	60.88	83.62	76.70	90.10	3.31	3.61	84.08	5.23	6.25
	TL	31.80	42.55	37.10	46.50	4.73	5.32	78.82	3.68	8.64
	NTB	12.25	13.18	11.00	16.00	5.82	6.95	70.20	1.32	10.05
	LL	52.93	61.24	55.60	68.50	4.98	5.45	83.40	5.73	9.36
	LB	6.50	7.40	6.00	8.70	6.97	8.03	75.44	0.92	12.47
	CL	13.58	16.30	12.80	21.90	11.59	12.19	90.48	3.70	22.71
	CG	12.50	15.96	13.50	18.30	7.39	8.10	83.25	2.22	13.89
	NKR/C	13.53	14.98	14.00	18.00	5.89	6.81	74.79	1.57	10.49
	NK/R	26.75	30.84	25.00	37.00	9.36	9.86	90.09	5.64	18.30
	100GW	26.20	29.09	23.30	35.90	9.47	10.14	87.22	5.30	18.23
	SPY	88.38	133.20	111.30	149.90	7.39	7.73	91.46	19.40	14.56
BC_2F_2	DT	59.75	57.56	51.00	64.00	5.03	5.30	90.14	5.66	9.83
	DS	61.50	60.32	53.00	67.00	4.98	5.07	96.44	6.07	10.07
	PH	154.43	166.04	123.00	200.50	10.99	11.17	96.80	36.98	22.27
	EH	62.68	72.44	44.00	94.20	16.99	17.36	95.72	24.80	34.23
	TL	31.93	33.88	16.70	47.20	21.11	21.53	96.15	14.45	42.64
	NTB	11.25	11.20	4.00	18.00	26.59	27.93	90.62	5.84	52.14
	LL	53.53	53.93	29.10	75.80	19.80	21.00	88.86	20.74	38.45
	LB	7.175	7.07	4.20	10.20	18.57	20.65	80.83	2.43	34.39
	CL	14.30	17.72	11.40	22.70	14.14	14.39	96.62	5.08	28.64
	CG	12.70	13.36	8.90	18.40	17.20	18.48	86.64	4.40	32.98
	NKR/C	13.00	13.89	8.00	20.00	22.12	23.63	87.61	5.92	42.64
	NK/R	26.75	36.94	21.00	47.00	15.23	15.61	95.24	11.31	30.62
	100GW	27.00	28.99	16.00	43.20	22.42	23.02	94.91	13.05	45.00
	SPY	91.33	143.56	84.67	199.87	22.68	22.84	98.65	66.63	46.41

Note: GCV- Genotypic Coefficient of Variation ; PCV – Phenotypic Coefficient of Variation ; h^2 – Heritability ; GA – Genetic Advance ; GAM – Genetic Advance as Percent of Mean ; 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 ; NKR/C – Number of Kernel Rows /Cob ; NK/R - Number of Kernels /row ; 100GW – 100 Grain Weight ; SPY – Single Plant Yield.

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Table 2. Variability estimates of BC_1F_1, BC_2F_1 and BC_2F_2 population in cross UMI 1230 × VQL 1

Generation	Trait	UMI1230 (mean)	Mean	Range Min	Range Max	GCV	PCV	h^2	GA	GAM
BC_1F_1	DT	58.20	53.67	52.00	58.00	2.17	2.67	66.01	1.95	3.64
	DS	60.20	56.41	53.00	60.00	2.06	2.54	65.92	1.95	3.45
	PH	137.94	186.22	171.00	206.30	4.43	4.96	79.71	15.16	8.14
	EH	47.84	91.48	84.60	98.40	4.02	4.59	76.43	6.62	7.23
	TL	28.98	44.00	38.40	49.50	6.04	7.41	66.36	4.46	10.13
	NTB	10.80	14.03	11.00	17.00	10.12	11.75	74.23	2.52	17.97
	LL	52.28	69.14	59.40	75.60	4.20	4.92	72.98	5.11	7.39
	LB	8.64	10.09	9.00	11.70	6.77	8.05	70.72	1.18	11.72
	CL	12.72	16.03	11.40	19.40	8.08	9.20	77.14	2.34	14.62
	CG	11.88	12.76	9.40	14.50	6.25	7.37	72.03	1.39	10.93
	NKR/C	11.22	16.14	14.00	18.00	7.86	9.02	75.84	2.27	14.09
	NK/R	25.00	31.80	26.00	39.00	9.71	10.21	90.51	6.05	19.03
	100GW	24.23	31.44	26.40	38.40	10.10	10.60	90.79	6.23	19.82
	SPY	76.73	159.70	136.00	195.20	11.14	11.55	93.02	35.35	22.13
BC_2F_1	DT	58.60	58.61	56.00	60.00	1.77	2.00	78.13	1.88	3.22
	DS	60.60	61.25	58.00	63.00	1.80	2.01	80.22	2.04	3.32
	PH	138.76	173.81	163.60	185.90	3.42	3.55	93.16	11.83	6.81
	EH	48.04	80.31	75.40	86.00	3.38	3.60	88.46	5.26	6.55
	TL	27.78	28.22	22.90	35.40	7.87	8.65	82.75	4.16	14.74
	NTB	11.10	10.71	8.00	15.00	11.81	13.33	78.41	2.31	21.54
	LL	52.22	56.39	50.70	67.10	5.18	5.97	75.22	5.22	9.25
	LB	8.70	10.61	8.40	12.50	8.83	9.60	84.57	1.77	16.73
	CL	12.96	13.67	10.00	16.90	8.76	9.62	83.05	2.25	16.45
	CG	12.10	11.00	8.40	12.80	6.80	7.21	88.88	1.45	13.21
	NKR/C	11.76	14.33	12.00	16.00	9.88	10.43	89.57	2.76	19.25
	NK/R	24.00	28.30	23.00	34.00	9.92	10.23	94.04	5.61	19.82
	100GW	24.20	28.13	22.60	33.20	8.94	9.25	93.42	5.01	17.79
	SPY	73.88	113.47	95.20	157.10	12.96	13.24	95.81	29.66	26.14
BC_2F_2	DT	58.80	58.42	55.00	62.00	3.02	3.34	81.66	3.29	5.63
	DS	61.00	61.02	58.00	65.00	2.71	2.95	84.52	3.13	5.13
	PH	139.37	176.72	135.70	210.90	9.59	9.78	96.29	34.27	19.39
	EH	48.20	75.51	47.60	96.70	17.34	17.74	95.51	26.35	34.90
	TL	28.25	39.77	26.20	50.60	17.93	18.31	95.82	14.38	36.15
	NTB	10.60	10.54	7.00	15.00	17.31	18.58	86.78	3.50	33.21
	LL	54.15	65.39	49.50	80.60	13.76	15.14	82.66	16.86	25.78
	LB	8.475	9.18	5.00	12.40	17.76	18.66	90.59	3.19	34.81
	CL	12.57	15.91	10.00	21.00	16.76	17.27	94.14	5.33	33.50
	CG	11.75	13.36	10.10	17.50	14.13	14.58	93.94	3.77	28.22
	NKR/C	11.77	14.12	10.00	18.00	14.76	15.10	95.55	4.20	29.72
	NK/R	24.00	30.44	22.00	36.00	11.12	11.44	94.50	6.78	22.27
	100GW	23.95	25.69	17.00	37.20	13.09	13.33	96.56	6.81	26.51
	SPY	73.50	111.92	67.20	176.20	19.69	19.93	97.59	44.84	40.07

Note: GCV- Genotypic Coefficient of Variation ; PCV – Phenotypic Coefficient of Variation ; h^2 – Heritability ; GA – Genetic Advance ; GAM – Genetic Advance as Percent of Mean ; 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 ; NKR/C – Number of Kernel Rows /Cob ; NK/R - Number of Kernels /row ; 100GW – 100 Grain Weight ; SPY – Single Plant Yield.