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Analysis of Broadsense heritability for agronomical traits of Maiz population (*Zea mays*)

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Abstract

The present study was laid out during *Rabi*, 2012 at Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India with an objective to assess the inheritance of agronomic traits from parent to their off spring of maize back cross (BC₂F₁) populations. For this purpose, five agronomic traits *viz.*, Cob length, Cob diameter, Cob weight, Yield per plant and 100 grain weight were taken among the five backcross populations *viz.*, UMI 79/936 –BC₂F₁ progeny -2, UMI 79/936 –BC₂F₁ progeny -3, UMI 79/936 –BC₂F₁ progeny -7, UMI 79/936 –BC₂F₁ progeny -23 and UMI 79/936 –BC₂F₁ progeny -29 (each progeny had 75 to 100 plants) which was developed by crossing the UMI 79 and UMI 936; and subsequent back cross with UMI 79. Heritability is a measure of the degree (0 to 100%) to which offspring resemble their parents for a specific trait. Result of this study showed that high amount of heritability was observed in most of the progenies which indicating that the variation observed in trait is governed by additive gene action. The backcross progenies *viz.*, BC₂F₁ Progeny -7 (62.57%), UMI 79/936 –BC₂F₁ Progeny -23 (72.67%) and UMI 79/936 –BC₂F₁ Progeny -29 having additive gene interaction for agronomic traits is the immense source and serve as the parent to develop hybrid in maize.

Keywords: Maize, inheritance, offspring, additive gene action and back cross population

Introduction

Maize is one of the world's third leading cereal crops after rice and wheat but ranks first with respect to its production and productivity. It plays a major role as food, feed and as a source of diverse industrially important products. It is mostly grown under wide range of climatic conditions, especially in warmer areas of the temperate region and areas of humid sub-tropical climate. In India, about 28% of maize produced is used for food purposes, about 11% as livestock feed, 48% as poultry feed, 12% in the wet milling industry. The demand for maize is increasing by 2025, maize will be the crop of greatest production globally and by 2050 the demand for maize in the developing world will double.

Heritability is a measure of the degree (0 to 100%) to which offspring resemble their parents for a specific trait. It measures the strength of the relationship between performance (phenotype) and breeding value (genotype) of an individual. Heritability is one important component of the equation used to predict genetic progress from selection to improve a trait. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. Knowledge of heritability and genetic advance of the character indicate the scope for the improvement through selection. With this background, the present study was undertaken to analysis the broad sense heritability to know the genetic component of the variation observed in the agronomic traits of (BC₂F₁) maize population.

Materials and Methods

The present experiment was laid out during *Rabi*, 2012 at Department of Millets, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India. Five backcross populations (BC₂F₁) *viz.*, UMI 79/936 –BC₂F₁ progeny -2, UMI 79/936 –BC₂F₁ Progeny -3, UMI 79/936 –BC₂F₁ Progeny -7, UMI 79/936 –BC₂F₁ Progeny -23 and UMI 79/936 –BC₂F₁ Progeny -29 (each Progeny had 75 to 100 plants) which was developed by crossing the UMI 79 and UMI 936; and subsequent back cross with UMI 79 were selected for this present experiment. In the selected back cross population the data on five agronomic traits *viz.*, Cob length, Cob diameter, Cob weight, Yield per plant and 100 grain weight were recorded.

The estimates of variability such as phenotypic and genotypic coefficient of variation (PVC and GCV) were calculated by adopting the formula suggested by (Burton 1952) [5]. Heritability

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in broad sense was estimated by according to Lush (1950)^[9] and the genetic advance was calculated following Burton (1952)^[5] and Johnson *et al.*(1955)^[7, 8]. The data on the mean,

co-efficient of variation, heritability and genetic advance as per cent of mean for five BC₂F₁ populations are furnished in Table 1 to Table 6.

Table 1: Mean Performance of Parents for five agronomic traits (UMI79 and UMI 936)

S.no	Agronomic Traits	Grand Mean	
		Parent 1-UMI 79	Parent 2-UMI 796
1	Cob length	14.30	12.38
2	Cob diameter	12.80	10.56
3	Cob weight (g)	56.82	33.94
4	Yield per plant (g)	41.68	22.36
5	100 Grain weight (g)	20.10	15.92

Table 2: Genetic parameters observed in Cob Length (cm) of BC₂F₁ Populations in Maize

S.no	Progeny details	Grand Mean BC ₂ F ₁	Range		Variability and Heritability Parameters						
			Minimum value	Maximum value	Vp	Vg	PCV	GCV	h ²	GA	GA (as percentage on mean)
1	UMI 79/936 – BC ₂ F ₁ Progeny -2	12.15	8.22	14.45	5.72	3.11	20.65	15.22	51.65	2.26	16.42
2	UMI 79/936 – BC ₂ F ₁ Progeny -3	13.30	9.30	17.60	7.27	4.84	21.36	16.93	62.25	4.16	26.69
3	UMI 79/936 – BC ₂ F ₁ Progeny -7	14.30	10.30	18.60	8.27	5.84	22.36	17.93	72.74	5.16	27.69
4	UMI 79/936 – BC ₂ F ₁ Progeny -23	12.41	9.21	15.22	2.45	1.98	15.46	12.67	61.89	2.96	20.23
5	UMI 79/936 – BC ₂ F ₁ Progeny -29	17.35	10.4	18.6	7.03	4.59	20.15	15.04	53.62	4.38	21.3

Table 3: Genetic parameters observed in Cob Diameter (cm) of BC₂F₁ Populations in Maize

S.no	Progeny details	Grand Mean BC ₂ F ₁	Range		Variability and Heritability Parameters						
			Minimum value	Maximum value	Vp	Vg	PCV	GCV	h ²	GA	GA (as percentage on mean)
1	UMI 79/936 – BC ₂ F ₁ Progeny -2	10.97	8.42	13.00	4.31	2.30	19.82	14.32	55.12	2.35	15.95
2	UMI 79/936 – BC ₂ F ₁ Progeny -3	12.17	8.50	15.60	4.97	3.39	18.84	14.84	61.19	3.47	23.13
3	UMI 79/936 – BC ₂ F ₁ Progeny -7	13.17	9.50	16.60	5.97	4.39	19.84	15.84	75.47	4.47	24.13
4	UMI 79/936 – BC ₂ F ₁ Progeny -23	10.32	7.92	14.36	2.98	1.34	17.49	14.64	63.42	2.05	22.54
5	UMI 79/936 – BC ₂ F ₁ Progeny -29	15.50	9.70	16.70	6.72	5.14	21.74	18.10	68.49	4.98	29.04

Table 4: Genetic parameters observed in Cob weight (g) of BC₂F₁ Populations in Maize

S.no	Progeny details	Grand Mean BC ₂ F ₁	Range		Variability and Heritability Parameters						
			Minimum value	Maximum value	Vp	Vg	PCV	GCV	h ²	GA	GA (as percentage on mean)
1	UMI 79/936 – BC ₂ F ₁ Progeny -2	32.88	18.12	61.13	155.60	54.12	40.00	23.53	35.23	8.23	25.72
2	UMI 79/936 – BC ₂ F ₁ Progeny -3	44.69	19.00	87.40	288.28	187.24	39.80	32.24	69.43	17.56	38.90
3	UMI 79/936 – BC ₂ F ₁ Progeny -7	45.69	20.00	88.40	289.28	188.24	40.80	33.24	72.83	18.56	39.90
4	UMI 79/936 – BC ₂ F ₁ Progeny -23	30.21	19.45	62.45	157.68	57.43	43.65	24.43	37.87	9.64	27.75
5	UMI 79/936 – BC ₂ F ₁ Progeny -29	60.50	12.20	54.00	269.05	168.01	42.46	33.90	70.16	22.93	53.81

Table 5: Genetic parameters observed in Seed yield per plant (g) of BC₂F₁ Populations of Maize

S.no	Progeny details	Grand Mean BC ₂ F ₁	Range		Variability and Heritability Parameters						
			Minimum value	Maximum value	Vp	Vg	PCV	GCV	h ²	GA	GA (as percentage on mean)
1	UMI 79/936 – BC ₂ F ₁ Progeny -2	22.15	11.23	48.32	147.28	63.25	58.24	38.21	43.78	8.68	36.45
2	UMI 79/936 – BC ₂ F ₁ Progeny -3	32.35	11.20	61.00	159.58	74.88	41.17	28.42	47.59	13.09	39.55
3	UMI 79/936 – BC ₂ F ₁ Progeny -7	33.35	12.20	62.00	160.58	75.88	42.17	29.42	62.57	14.09	40.55
4	UMI 79/936 – BC ₂ F ₁ Progeny -23	13.12	11.43	18.22	8.62	5.87	20.43	18.58	72.67	4.84	28.45
5	UMI 79/936 – BC ₂ F ₁ Progeny -29	62.25	12.20	54.00	200.31	115.61	48.85	37.46	61.26	18.62	57.29

Table 6: Genetic parameters observed in 100 grain weight (g) of BC₂F₁ Populations of Maize

S.no	Progeny details	Grand Mean BC ₂ F ₁	Range		Variability and Heritability Parameters						
			Minimum value	Maximum value	Vp	Vg	PCV	GCV	h ²	GA	GA (as percentage on mean)
1	UMI 79/936 – BC ₂ F ₁ Progeny -2	20.23	15.92	13.94	13.75	21.35	7.64	4.64	20.91	14.35	48.74
2	UMI 79/936 – BC ₂ F ₁ Progeny -3	17.52	11.10	24.46	18.68	15.19	26.46	23.81	81.24	6.36	33.43
3	UMI 79/936 – BC ₂ F ₁ Progeny -7	18.52	12.10	25.46	19.68	16.19	27.46	24.81	84.24	7.36	34.43
4	UMI 79/936 – BC ₂ F ₁ Progeny -23	21.52	16.24	26.84	9.87	6.98	16.65	14.43	82.67	5.89	25.31
5	UMI 79/936 – BC ₂ F ₁ Progeny -29	23.20	12.20	26.21	20.63	17.14	28.98	26.32	83.25	9.22	47.15

Results and Discussion

The result of the present investigation on back crosses population revealed most of the progenies recorded moderate to high amount of heritability with genetic advance. The back cross progenies viz., BC₂F₁ Progeny -3 (62.25), UMI 79/936 – BC₂F₁ Progeny -7 (72.74) and UMI 79/936 – BC₂F₁ Progeny -23 (61.89) were observed high amount of heritability and genetic advance for the trait of cob length. Analysis on cob diameter showed high amount of heritability in the following progenies viz., BC₂F₁ Progeny -3 (61.19%), UMI 79/936 – BC₂F₁ Progeny -7 (75.47%), UMI 79/936 – BC₂F₁ Progeny -23 (63.42%) and UMI 79/936 – BC₂F₁ Progeny -29 (68.49%). The back cross population viz., BC₂F₁ Progeny -3 (69.43%), UMI 79/936 – BC₂F₁ Progeny -7 (72.83%) and UMI 79/936 – BC₂F₁ Progeny -29 (70.16%) showed high amount of heritability and genetic advance for cob weight. Regarding the seed yield per plant progenies viz., BC₂F₁ Progeny -7 (62.57%), UMI 79/936 – BC₂F₁ Progeny -23 (72.67%) and UMI 79/936 – BC₂F₁ Progeny -29 (61.26%) has recorded high amount of heritability. Hence, the analysis revealed that the trait is governed by additive gene action where high heritability observed. Genetic advance explains the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. Similar results was found by Vashishta *et al.* (2013)^[14] and by Bekele and Rao (2014)^[4] for Cob weight and seed yield per plant.

To conclude present study, high amount of broad sense heritability and genetic advance were recorded for the agronomic trait such as cob length, cob diameter, cob weight, seed yield per plant and 100 grain weight which indicates the presence of additive gene action in the traits and variation is occurred due to the occurrence of additive gene interaction among the traits. The backcross progenies viz., BC₂F₁ Progeny -7 (62.57%), UMI 79/936 – BC₂F₁ Progeny -23 (72.67%) and UMI 79/936 – BC₂F₁ Progeny -29 having additive gene interaction for agronomic traits is the immense source and serve as the parent to develop hybrid in maize.

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