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Research Article

Assessment of genetic variability, heritability and genetic advance in backcross population of BC_1F_1, BC_2F_1 and BC_2F_2 in maize

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Abstract
Genetic variability, heritability and genetic advance are the important factors which provides the knowledge about the nature of traits in breeding programme. The aim of this study is to estimate the genetic variability, heritability, and genetic advance in the backcross population of UMI1200β^+ × HKI163 and UMI1230β^+ × HKI163 to identify the individuals in the population with superior agronomic traits. Fourteen biometrical traits were analysed and thus revealed that all the backcross (BC_1F_1, BC_2F_1) and selfed (BC_2F_2) generations, phenotypic coeffiecient of variation is higher than the genotypic coefficient of variation. Highest heritability combined with genetic advance as percent of mean was observed in BC_2F_2 generation for 100 kernel weight (UMI1200β^+ × HKI163) and single plant yield (UMI1230β^+ × HKI163). Hence, the genetic gain of the individuals in the population are controlled by additive gene action.

Keyword
Maize, genetic variability, heritability, genetic advance, marker assisted backcross breeding.

Introduction

Maize improvement programmes aims at improving the yield and yield attributing traits by studying of magnitude of variability, heritability and genetic advance of the individuals in the population. To portray the heritable differences within a population, genetic variability plays an important role based on which the design of the breeding programme is created. In order to improve a population for a quantitative trait, the nature and magnitude of the genetic variability is a prerequisite (Dhanwani *et al.*, 2013). The amount of variation that is present in a population is estimated by measuring the Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). Hence, to predict whether the accumulated genetic variability is due to a heritable character or a non heritable character is difficult to predict. The transmissibility of a character from one generation to the other can be easily understood by studying the heritability of the character and is required for selecting the desired trait for the crop improvement programme. The high heritability of a character is decided by the additive gene action and hence is difficult to identify the characters having high heritability. The genetic advance helps to define the degree of genetic gain due to the additive gene action (Najeeb *et al.*, 2009). High heritability along with high genetic advance forms the basis of selection. The narrow sense heritability is very limited as it includes both additive and epistatic effects whereas the broad sense heritability coupled with high genetic advance proved to be a better estimate of a character (Ramanujam and Thirumalachar, 1967). A sound knowledge of these parameters forms the basis for an effective breeding programme. The present study aimed at assessing the mean, range, Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance mean for the yield and yield contributing traits in maize.

Materials and Methods

The high β-carotene inbreds *viz.*, UMI1200β^+ and UMI1230β^+ were used as a recurrent parents and HKI163 as a donor parent. Two independent crosses were made to generate F_1's in Kharif 2016 and backcrossed to its recurrent parent to produce BC_1F_1 during Rabi 2016. Another round of backcross was made using the BC_1F_1 progenies during Kharif 2017 to produce BC_2F_1 and the BC_2F_1 progenies were selfed to develop BC_2F_2 population which was evaluated during Rabi 2017.

Fourteen agronomical traits were recorded in ten randomly selected plants based on the guidelines by DUS of PPV & FRA (Anon, 2017). The characters *viz.,* days to tasseling (DT), days to silking (DS), plant height (PH), ear height (EH), tassel length (TL), number of tassel branches (NTB), leaf length (LL), leaf breadth (LB) were recorded before the harvest and cob length (CL), cob girth (CG), number of kernel rows per cob (NKRC), number of kernels per row (NKPR), cob weight (CW) and single plant yield (SPY) and 100 grain weight (100GW) were recorded after the harvest. These traits were used to analyze the Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), heritability (h^2 in the broad sence), genetic advance (GA), and genetic advance as percent of mean for the two backcrossed (BC_1F_1 and BC_2F_1) and one selfed (BC_2F_2) generations along with their recurrent parents.

The genetic variability can be estimated by subtracting the variability caused due to the environment from the phenotypic variation (Lush, 1940). The Phenotypic Coefficient of Variation and the Genotypic Coefficient of Variation were calculated based on the method formulated by Burton (1952) and the range used to portray the variation was low (<10%), moderate (10-20%). High (>20%) suggested by Sivasubramanian and madhavamenon (1973). For estimating the heritability of a character the method given by Lush (1940) was used that takes into account the broad sense heritability and followed the range that included low (<30%) moderate (30-60%) and high (>60%) as suggested by Robinson *et al.,* 1945. The genetic advance and the genetic advance as the percent of mean was calculated by the method formulated by Johnson *et al.*, 1955 and the ranges were as low (<10%) moderate (10-20%) and high (>20%). The present study aimed at the estimation of the mean performance range, PCV, GCV, h^2, GA, GA as percent of mean for the backcrossed generations (BC_1F_1 and BC_2F_1) and the selfed (BC_2F_2) generations along with their parents.

Results and Discussion

Estimation of the magnitude of variation in segregating population is the prerequisite for many of the maize breeding programme. In this contest, estimate of heritability provides knowledge about whether the characters are controlled by heritable or non heritable factor (Falconer and Mackay, 1996). It is tedious to identify the heritability estimate, which is due to additive gene action or non additive gene action. Hence, estimation of genetic advance combined with heritability provides the knowledge about the genetic gain through additive gene action (Bello *et al.,* 2012).

Heritability and genetic advance as percent of mean for fourteen yield attributing traits was studied for UMI1200β^+ × HKI163 in BC_1F_1, BC_2F_1 and BC_2F_2 generations (Table 1,2 and 3). In BC_1F_1 highest mean value was recorded in plant height (196.99) followed by single plant yield (161.57) and lowest mean value was recorded in number of kernel rows per cob (14.92). The phenotypic coefficient of variation is greater than the genotypic coefficient of variation which showed the influence of environment. For all the fourteen traits studied low PCV and GCV was recorded which ranged from 1.15% to 6.71% and 1.00% to 5.08%. Higher heritability was recorded in all the traits ranging from 68.17% in cob length to 95.41% cob girth except for number of kernel rows per cob showed moderate heritability (57.37%). Low genetic advance as percent of mean was recorded in all the traits which indicate lesser variation in the individuals of the population. In $BC_2F_{1,}$plant height (161.32) followed by single plant yield (95.60) showed highest mean value among the traits which ranged from 14.39 to 161.32. All the traits showed higher phenotypic coefficient of variation ranging from (0.83% to 16.65%) comparing to the genotypic coefficient of variation ranging from (0.77% to 15.54%). Highest heritability was recorded in all the traits ranged from 64.60% in 100 kernel weight to 87.11% in single plant yield. Highest genetic advance as percent of mean was recorded in 29.88% in single plant yield followed by 23.04% in tassel length, 19.31% in number of kernel rows per cob and 17.24% in number of tassel branches which showed additive gene action is predominant in the genetic gain of the individuals in the population. Highest heritability and genetic advance as percent of mean was recorded in single plant yield (87.11% and 29.88%), number of tassel branches (83.62% and 17.24%), and tassel length (82.87% and 23.04%) and number of kernel rows per cob (82.29% and 19.31%). This indicated that the additive gene action is predominant in the genetic gain of the individuals in the population. In $BC_2F_{2,}$ the mean value of the progenies ranged from 7.20 in leaf breadth to 155.04 in plant height. The phenotypic coefficient of variation ranged from 1.39% to18.59% performed higher than the genotypic coefficient of variation which ranges from 1.18% to 16.53 % (Figure 1). Highest heritability was noticed in all the traits ranging from 71.84% in number of kernel rows per cob and 87.40% in single plant yield. Highest genetic advance as percent of mean was recorded and ranges from 10.99% in ear height and 30.26% in number of tassel branches. High heritability percentage coupled with genetic advance as percent of mean is recorded in single plant yield (87.40% and 15.97%), 100 kernel weight (86.01% and 25.89%), number of kernels per row (84.31% and 13.89%), ear height (82.35% and 10.99%). Number of tassel branches (79.02% and 30.26%), cob girth (76.82% and 15.39%) and cob length (76.17% and 17.89%) indicates that the genetic gain is advanced by the additive gene. The results are in accordance with Nadarajan *et al.*, (2016).

Similarly the heritability and genetic advance as percent of mean for fourteen yield attributing traits was studied for UMI1200β$^+$ × HKI163 in BC_1F_1, BC_2F_1 and BC_2F_2 generations (Table 1,2 and 3). In BC_1F_1 population higher mean value was recorded in plant height (139.11) followed by single plant yield (76.98) and the phenotypic coefficient of variation is greater than the genotypic variation due to the influence of environment.PCV and GCV ranges from 1.01% to 7.16% and 0.83% to 6.27%. Highest heritability was recorded in all the traits ranging from 67.82% in days to tasseling to 87.32% in 100 kernel weight. The genetic advance as percent mean showed more performance in leaf length (11.26%), followed by 100 kernel weight (10.69%) and leaf breadth (10.32%). Highest heritability and genetic advance as percent of mean was observed in 100 kernel weight (87.32% and 10.69%), leaf length (76.65% and 11.26%) and leaf breadth (74.38% and 10.32%) which in turn reflects the more genetic gain with additive gene action. Similarly in the BC_2F_1 population highest mean value was noticed on plant height (161.32) followed by single plant yield (95.60) and the lowest mean value were recorded in 6.99 in leaf breadth. Phenotypic coefficient of variation ranged from 0.81% in leaf length to 9.51% in number of tassel branches higher than the genotypic coefficient of variation ranging between 0.69% in leaf length to 8.75% in number of tassel branches. Heritability percentage was higher in all the traits studied which ranges from 71.07% in number of kernels per row to 90.35% in cob length. The highest genetic advance as percent of mean was noticed for number of tassel branches (16.60%) and single plant yield (11.37%). Both the heritability and genetic advance as percent of mean was higher in single plant yield (89.07% and 11.37%) and number of tassel branches (84.77% and 16.60%) which indicated the additive gene action involved in the genetic gain of the population. In BC_2F_2 the highest mean was recorded in plant height (146.53) followed by single plant yield (95.81). Phenotypic coefficient of variation was higher than the genotypic coefficient of variation shown in Figure 2. Heritability percentage was observed from 71.44% in days to tasseling to 88.25% in 100 kernel weight. Genetic advance as percent of mean was observed from 2.42% in days to silking to 31.15% in 100 kernel weight. Highest heritability and genetic advance as percent of mean was reported in 100 kernel weight (88.25% and 31.15%), single plant yield (87.03% and 11.15%), number of kernel rows (86.94% and 21.39%), number of tassel branches (86.09% and 29.77%), cob length (85.79% and 16.83%), ear height (84.29% and 24.34%), tassel length (83.76% and 26.60%), leaf breadth (77.51% and 22.58%), leaf length (77.41% and 21.86%) and cob girth (74.20% and 11.22%). This indicates the additive gene action engaged in the genetic gain of the individuals in the population.

Among the biometrical traits studied single plant yield shows highest heritability and genetic advance as percent of mean in BC_2F_1 (87.11% and 29.88%) and BC_2F_2 (87.40% and 15.97%) of UMI1200β$^+$ × HKI163 backcross population. The cross UMI1230β$^+$ × HKI163 for the trait 100 kernel weight showed highest heritability combined with genetic advance as percent of mean in the BC_1F_1 (87.32% and 10.69) and BC_2F_2 (88.25% and 31.15). This indicates that the genetic gain of the individuals was controlled by the additive gene action.

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Table 1. Estimation of variability in BC_1F_1 of UMI1200β^+×HKI163 and UMI1230β^+×HKI163

Cross	Traits	Parent (Mean)	Progeny (Mean)	Range		h^2	GAM
				Min	Max		
UMI1200β^+×HKI163	DT	58.00	55.97	55.00	57.00	75.97	1.80
	DS	60.00	58.67	57.00	60.00	70.81	2.17
	PH	160.11	196.99	191.00	202.00	69.02	1.84
	EH	75.00	82.99	78.00	88.00	79.55	4.89
	TL	29.98	54.27	50.00	59.50	70.00	7.44
	NTB	11.00	15.74	14.50	16.60	75.62	6.04
	LL	55.38	65.70	65.00	68.00	77.43	1.98
	LB	6.80	8.30	8.10	8.50	84.44	2.15
	CL	10.52	15.73	10.70	17.00	68.17	6.27
	CG	12.88	15.68	15.00	16.90	95.41	5.19
	NKRC	12.00	14.93	14.00	16.00	57.37	7.93
	NKR	25.00	31.97	30.00	33.00	79.07	4.82
	100KW	25.57	32.08	28.60	33.90	84.76	6.31
	SPY	90.67	161.57	155.00	169.50	84.70	4.00
UMI1230β^+×HKI163	DT	58.10	55.38	55.00	57.00	67.82	1.40
	DS	60.92	52.40	52.00	54.00	74.95	1.69
	PH	139.11	184.29	170.00	207.00	79.09	8.24
	EH	47.72	73.02	70.00	75.00	87.19	3.60
	TL	27.53	43.01	40.00	44.00	71.55	4.33
	NTB	11.42	14.89	14.00	18.00	73.48	8.73
	LL	48.79	87.31	80.00	105.00	76.65	11.26
	LB	9.70	10.29	9.10	11.50	74.38	10.32
	CL	12.84	14.31	14.00	14.80	85.38	2.86
	CG	12.10	15.18	14.00	15.99	73.97	5.18
	NKRC	11.54	14.81	14.00	16.00	78.38	6.91
	NKR	24.00	33.47	31.00	37.00	74.76	6.44
	100KW	24.20	31.38	28.10	34.90	87.32	10.69
	SPY	76.98	142.62	133.70	149.70	81.39	4.99

Note: GCV- Genotypic Coefficient of Variation; PCV- Phenotypic Coefficient of Variation; h2- Heritability; GAM- Genetic Advance as per 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; NKRC- Number of kernel rows per cob; NKR- Number of kernel rows; KW- Kernel weight; SPY- Single plant yield

Table 2. Estimation of variability in BC_2F_1 of UMI1200β^+×HKI163 and UMI1230β^+×HKI163

Cross	Traits	Parent (Mean)	Mean	Range		h^2	GAM
				Min	Max		
UMI1200β^+×HKI163	DT	58	58.69	56.00	60.00	79.46	2.66
	DS	61	61.39	60.00	63.00	80.66	2.55
	PH	160.1	161.32	160.00	166.50	86.33	1.47
	EH	75	76.84	75.00	79.00	78.61	3.19
	TL	30	33.80	30.00	77.00	82.87	23.04
	NTB	11	12.34	9.00	14.00	83.62	17.24
	LL	55	55.14	54.00	59.00	72.09	2.55
	LB	6.8	6.99	6.70	7.80	85.03	6.20
	CL	10	16.45	10.00	14.00	84.63	6.61
	CG	14.88	16.47	14.00	15.90	75.95	5.99
	NKRC	12	14.39	12.00	16.00	82.29	19.31
	NKR	25	25.76	25.00	29.00	87.07	6.01
	100KW	25.56	25.48	25.00	26.60	64.60	2.60
	SPY	90.666	95.60	90.00	105.00	87.11	29.88
UMI1230β^+×HKI163	DT	60	58.97	58.00	60.00	75.41	2.15
	DS	62	61.51	60.00	63.00	73.14	1.93
	PH	152	152.28	150.00	157.00	71.07	1.31
	EH	51	51.83	51.00	55.00	87.48	3.52
	TL	28.4	28.44	28.00	29.50	76.57	2.64
	NTB	11	12.05	11.00	15.00	84.77	16.60
	LL	55	55.43	55.00	56.00	72.30	1.20
	LB	7.5	7.61	7.40	7.80	81.60	2.97
	CL	13	13.33	13.00	14.30	90.35	3.67
	CG	11	11.18	11.00	11.50	72.49	1.92
	NKRC	12	12.38	12.00	13.00	83.77	6.80
	NKR	25	25.52	25.00	26.50	71.07	3.04
	100KW	25	25.85	25.00	27.90	88.08	5.46
	SPY	84	87.80	83.00	100.00	89.07	11.37

Note: GCV- Genotypic Coefficient of Variation; PCV- Phenotypic Coefficient of Variation; h2- Heritability; GAM- Genetic Advance as per 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; NKRC- Number of kernel rows per cob; NKR- Number of kernel rows; KW- Kernel weight; SPY- Single plant yield

Table 3. Estimation of variability in BC_2F_2 of UMI1200β^+×HKI163 and UMI1230β^+×HKI163

Cross	Traits	Parent (Mean)	Mean	Range		h^2	GAM
				Min	Max		
UMI1200β^+×HKI163	DT	58.06	58.90	56.00	60.00	73.87	2.99
	DS	60.53	61.50	58.00	63.00	81.74	3.76
	PH	161.04	155.04	157.00	166.00	72.60	2.08
	EH	69.21	62.87	57.00	76.00	82.25	10.99
	TL	27.34	31.86	20.00	35.40	73.28	13.33
	NTB	11.74	11.00	7.00	17.00	79.02	30.26
	LL	55.08	53.53	32.90	74.20	73.41	20.13
	LB	6.45	7.20	5.50	7.20	77.20	8.43
	CL	11.46	14.08	8.40	15.10	76.17	17.89
	CG	12.53	11.90	10.00	15.90	76.82	15.39
	NKRC	12.20	12.75	8.00	16.00	71.84	21.88
	NKR	25.78	21.00	22.30	29.50	84.31	13.89
	100KW	23.85	27.00	15.00	33.00	86.01	25.89
	SPY	81.22	82.00	66.00	95.00	87.40	15.97
UMI1230β^+×HKI163	DT	57.63	59.75	56.00	62.00	71.44	3.43
	DS	60.80	62.67	60.00	64.00	77.71	2.42
	PH	142.10	146.53	135.50	157.50	74.68	4.94
	EH	48.20	51.06	35.40	69.60	84.29	24.34
	TL	28.83	31.79	23.25	46.00	83.76	26.60
	NTB	10.95	12.45	8.00	16.00	86.09	29.77
	LL	54.12	54.78	41.20	73.40	77.41	21.86
	LB	8.48	7.83	5.10	10.80	77.51	22.58
	CL	13.63	14.80	11.40	17.00	85.79	16.83
	CG	12.60	13.41	11.30	16.73	74.20	11.22
	NKRC	13.58	12.32	12.00	14.00	80.47	9.96
	NKR	23.50	24.30	18.00	30.00	86.94	21.39
	100KW	23.39	28.68	18.60	38.50	88.25	31.15
	SPY	81.43	95.81	83.30	111.50	87.03	11.15

Note: GCV- Genotypic Coefficient of Variation; PCV- Phenotypic Coefficient of Variation; h2- Heritability; GAM- Genetic Advance as per 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; NKRC- Number of kernel rows per cob; NKR- Number of kernel rows; KW- Kernel weight; SPY- Single plant yield

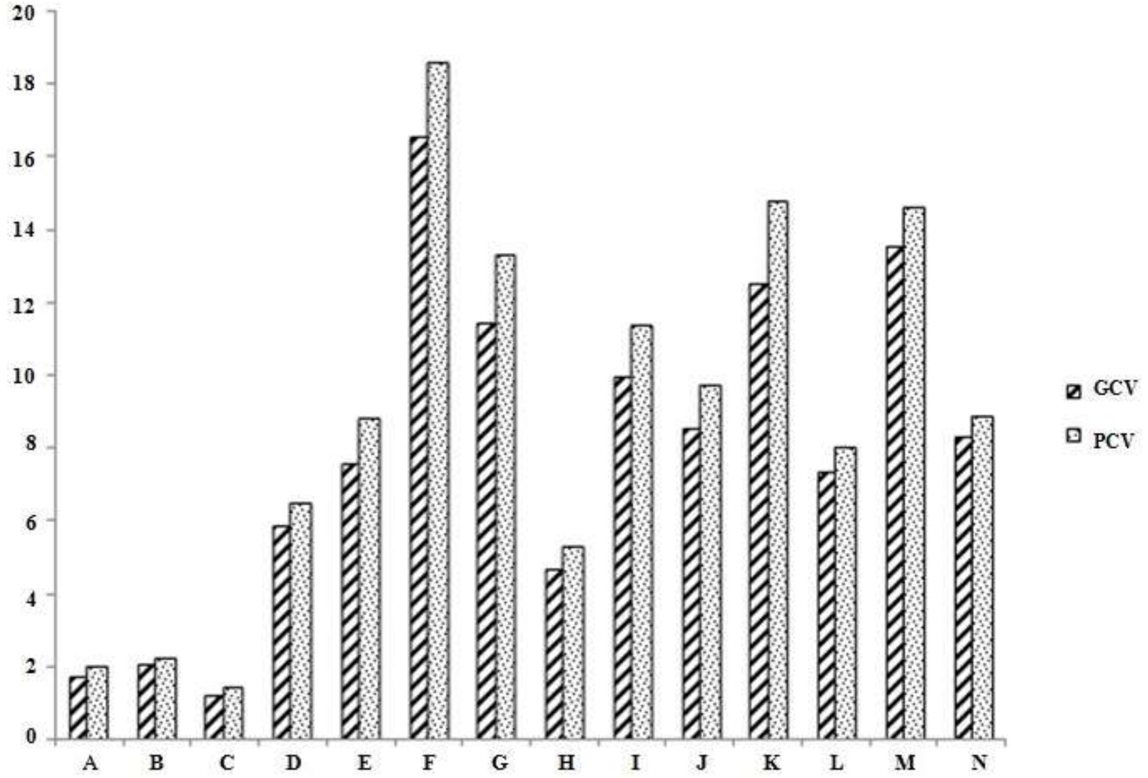

Figure 1. Phenotypic and Genotypic coefficient of variation in BC_2F_2 of UMI1200β^{+}×HKI163.
Note: GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, A- Days to tasseling, B- Days to silking, C- Plant height, D- Ear height, E- Tassel length, F- Number of tassel branches, 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

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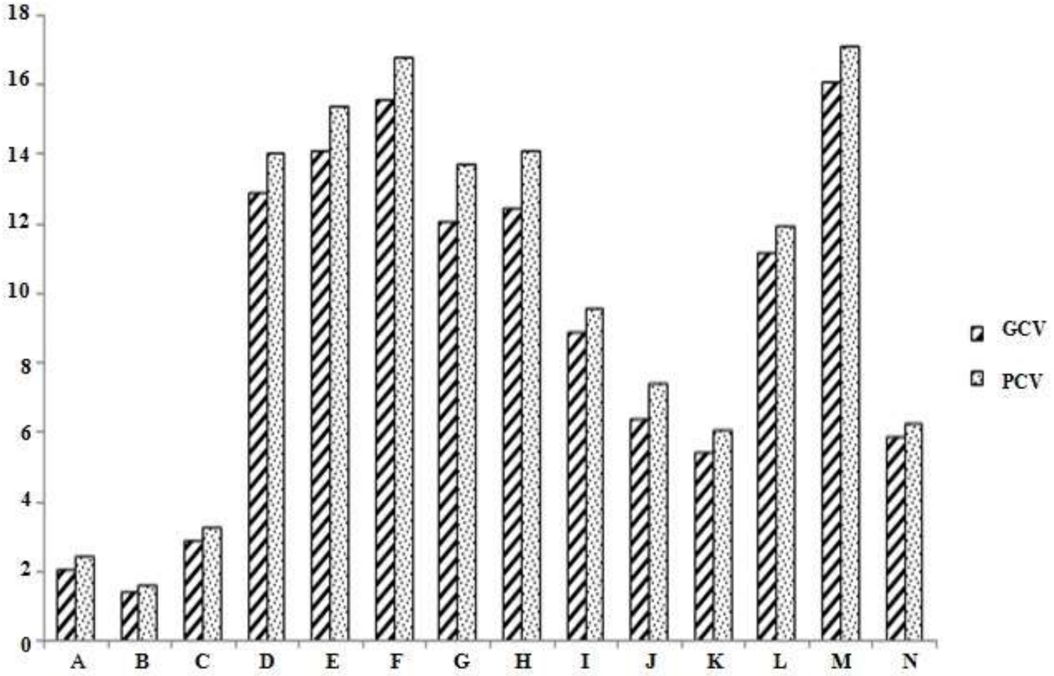

Figure 2. Phenotypic and Genotypic coefficient of variation in BC_2F_2 of UMI1230β^+×HKI163.
Note: GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, A- Days to tasseling, B- Days to silking, C- Plant height, D- Ear height, E- Tassel length, F- Number of tassel branches, 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

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