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RESEARCH ARTICLE

Heterotic grouping of Indian baby corn lines based on combining ability

Pardeep Kumar, Ningthai Longmei, B. S. Jat, Mukesh Choudhary, K. R. Yathish, Bharat Bhushan, Meenakshi Goyal[1] and Sujay Rakshit*

Abstract

The present study involved estimating the combining ability effects and heterotic grouping to increase the efficacy of parental selection for successful hybrid development. A total of 52 F_1 hybrids were generated by Line × Tester mating design by crossing 26 diverse maize inbred lines with two testers, namely, HKI 323 and HKI 1105. The 26 baby corn inbred lines were classified into a different heterotic group based on the specific combining ability (SCA) effects and heterotic groups specific and general combining ability (HSGCA). The SCA effects and HSGCA of baby corn yield without husk (BCY) classified the inbred lines into five and four groups, respectively. This is the first study of heterotic's grouping for baby corn germplasm considering BCY based on SCA and HSGCA methods. The information generated through heterotic grouping may be used to derive new inbred lines and develop different heterotic combinations for further utilization in breeding programs.

Keywords: Baby corn, GCA, Heterotic grouping, HSGCA, SCA

Introduction

Maize (*Zea mays* L.) is considered a special crop due to its wide adaptability, food, feed use, and as raw materials for industrial processing to generate products like starch, alcoholic beverages, oil, textiles, pharmaceuticals, cosmetics, etc. In the present era of climate variability, maize cultivation may ease the burden of farmers in African and South-Asian countries. It can play an important role in crop diversification in improving household food security, providing diet diversity, and improving their income, particularly of smallholder farmers in the agricultural sector (Mango et al. 2018). Baby corn is a special type of maize, which is a whole unfertilized immature cob harvested at the silk emergence stage (silk length of about 1–3 cm) or as the dehusked tender ear of the female inflorescence maize plant (Kapoor 2002). Baby corn is highly nutritive and its nutritional quality is comparable to some of the popular seasonal vegetables (Kumar et al. 2020). It is one of the richest sources of phosphorus besides protein, vitamins and iron (Sapna et al. 2020). It has a huge demand in the international market because of its nutritive value and organoleptic properties, which helps the maize growing countries earn foreign exchange. Besides being consumed as fresh, it is also used to prepare many diverse food products like pizza, pakora, soup and after the harvest, plant parts, *viz.*, stem with leaves and husk serves as excellent green fodder for livestock. Hence, baby corn can help boost the income of farmers in peri-urban areas as farmers can take four to five crops in a year, which helps generate more employment throughout the year.

Heterotic grouping of the available germplasm in any breeding program is crucial to developing high-yielding hybrids (Fan et al. 2008). Further, evaluating a large number of parental lines and their all possible cross combinations will be impractical without knowing heterotic grouping (Mahato et al. 2021). Hence, it saves time and labor to evaluate undesirable hybrids. The systematic classification

ICAR-Indian Institute of Maize Research, PAU Campus, Ludhiana 141 004, Punjab, India

[1]Punjab Agricultural University, Ludhiana 141 004, Punjab, India

***Corresponding Author:** Sujay Rakshit, ICAR-Indian Institute of Maize Research, PAU Campus, Ludhiana 141 004, Punjab, India, E-Mail: s.rakshit@icar.gov.in

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of inbreds into heterotic groups for exploitation of heterosis in maize was achieved by (Melchinger and Gumber 1998). Further, Melchinger and Gumber (1998) defined a heterotic group, as a group of related or unrelated genotypes from the same or different populations, which display similar combining ability (CA) and heterotic response when crossed with genotypes from other genetically distinct germplasm groups. In general heterotic grouping was done by considering the specific combining ability (SCA) effect of grain yield as proposed by (Vasal et al. 1992)-an inbred line that possessed negative SCA with any one of a heterotic tester was grouped with that tester with which it revealed negative effects.

Fan et al. (2008) proposed the heterotic groups specific and general combining ability (HSGCA) method for considering both general combining ability (GCA) and SCA to classify the lines into the clearcut heterotic group. Then the HSGCA method was used by several researchers and found that it is more efficient than the SCA method and even markers-based. The earlier studies on the comparison of SCA and HSGCA methods of analysis have indicated that the HSGCA method has been most efficient based on the breeding efficiency as compared to SCA (Fan et al. 2009; Akinwale et al. 2014; Badu-Apraku et al. 2015; Mahato et al. 2021). Therefore, the present study was carried out to compare both the methods to classify the baby corn lines into heterotic groups and to identify the best method with more breeding efficiency.

Materials and methods

The present study was conducted using 26 inbred lines derived from different source populations (Table 2). A total of 52 F_1 crosses were generated during *spring* season of 2019 by crossing 26 inbred lines with two testers, HKI 323 and HKI 1105 in the Line × Tester mating design. The hybrids were evaluated along with two baby corn hybrids, namely, HM 4 and G 5417 as checks in randomized block design in *kharif* 2020 at the experimental farm, ICAR-Indian Institute of Maize Research, Ludhiana, Punjab, India. The HM 4 is one of the public sector leading hybrid due to the opposite heterotic's nature of its parents. Therefore its parents are used for heterotic grouping of baby corn lines. The experimental unit consists of two rows of three-meter length plots with 50 cm spacing in between rows and 15 cm plant to plant spacing. All other management practices such as fertilizer application, intercultural operations and harvesting, were performed as per the recommended package of practice (Bamboriya et al. 2020). The observations for days to silking (DS), baby corn yield with husk (BCYH) q/ha, baby corn yield (BCY) q/ha and fodder yield (FY) q/ha traits were recorded on plot basis, whereas baby corn diameter (BCD) and baby corn length (BCL) were recorded in cm on five randomly selected baby corn. The data was analyzed using the Line × Tester function of agricolae package in R software to estimate the GCA and SCA effects as described by (Kempthorne 1957).

Heterotic grouping of baby lines was subjected based on the SCA and HSGCA methods after considering baby corn yield. The heterotic grouping based on SCA effect was carried out as suggested by Vasal et al. (1992) an inbred line showed negative SCA after crossing with one of the testers, which indicates that tester and lines belong to the same heterotic group and HSGCA based as suggested by Fan et al. (2008), Fan et al. (2009), Annor et al. (2019) and Mahato et al. (2021). Further, 26 baby corn inbred lines were allocated to different heterotic groups based on the Euclidean distance generated from Ward's minimum variance cluster analysis of SCA and HSGCA using stats and factoextra function in R package. Subsequently, breeding efficiency was calculated to determine the best heterotic grouping method among the SCA and HSGCA as described by Fan et al. (2009) and Badu-Apraku et al. (2016). To compare the breeding efficiencies of the two heterotic grouping methods, the 52 hybrids were arranged into three groups: highest yielder, moderate yielder, and lowest yielders. Later on, these were divided into inter-group and within-group hybrids for calculating the breeding efficiency.

Results

Analysis of variance

Analysis of variance of Line × Tester for yield and other characters are presented in Table 1. The results showed that genotypes (lines, crosses, testers and interaction of Line × Tester) exhibited significant differences among themselves for all the traits studied except BCL, indicating adequate variability in the materials for making valid experimentation and inferences. The mean sum of squares due to lines was higher and more significant than testers for the traits, *viz.*, DS, BCYH, BCY and FY, indicating that the selected lines were diverse for the traits.

Estimation GCA and SCA effects

The GCA effects of 26 inbred lines are presented in supplementary Table 1. The baby corn inbred lines, *viz.*, L_4, L_5, L_6, L_7, L_{13}, L_{16}, L_{18} and L_{20} exhibited positive significant GCA effects for BCYH. The lines L_5, L_{15}, L_{16}, L_{20} and L_{21} found significant GCA effects for BCY while L5 and T1 were positively significant for BCD. Similarly, L_3, L_4, L_6, L_7, L_8, L_{16}, L_{18}, L_{20}, L_{21} and L_{22} showed positive and significant GCA effects on fodder yield. The estimated GCA effects indicated that L5, L16 and L20 were showed significant and positive GCA effects for most of the traits. Likewise, GCA effects of lines and the SCA effects of 52 cross combinations are given in Supplementary Table S1. The cross $L_{15} \times T_1$ showed a negative & significant SCA effect DS indicated for short duration compared to other crosses. The crosses found promising with significant positive SCA effects were $L_8 \times T_2$, $L_{12} \times T_1$, $L_{14} \times$

Table 1. Mean square (ANOVA) of 52 test crosses and two standard checks for baby corn yield and other traits

Source of variation	d.f.	DS	BCYH	BCY	BCD	BCL	FY
Replicates	2	3.704**	160.772**	24.807**	0.091**	0.020	81174.164**
Treatments	53	1.718*	361.824**	28.527**	0.019*	1.341	18391.855**
Crosses	51	1.771*	344.319**	29.215**	0.020**	1.354	18698.865**
Line	25	2.824**	443.827**	41.348**	0.019*	1.653	28724.630**
Tester	1	0.779	261.715**	26.674**	0.121**	1.087	3628.622
L × T	25	0.759	248.116**	17.184**	0.016*	1.065	9275.909**
Checks	1	0.250	1416.393**	14.707**	0.010	0.005	20083.138**
Error	53	0.666	42.757	4.089	0.011	1.286	2400.824
CD (5 %)		1.616	12.947	4.004	0.204	2.245	97.016
CD (1%)		2.146	17.197	5.318	0.271	2.982	128.865
CV (%)		1.65	19.87	24.46	9.33	12.79	19.91

* = 0.05 % significant, ** = 0.01 % significant, d.f. = Degree of freedom, DS = Days to silking, BCYH = Baby corn yield (husk), BCY = Baby corn yield (without husk), BCD = Baby corn diameter, BCL = Baby corn length and FY = Fodder yield.

T$_1$, L$_{21}$ × T$_1$ and L$_{23}$ × T$_1$ for (BCYH), L$_8$ × T$_2$, L$_{12}$ × T$_1$ for (BCY), L$_3$ × T$_2$, L$_{12}$ × T$_1$ and L$_{14}$ × T$_1$ for (FY). Further, no cross combinations were found significant SCA effects for BCD and BCL traits.

Heterotic grouping of baby corn inbreds

A total of 26 inbred lines along with two testers, HKI 323 (denoted as B group) and HKI 1105 (denoted as A group) were used for heterotic grouping based on BCY parameter (Table 2). The BCY is an important trait in baby corn cultivation; hence the same was selected for heterotic grouping. Out of 26 inbred lines, 12 lines revealed negative SCA effects with HKI 323 and grouped under heterotic group B, while the other 14 inbred lines were grouped under A, which showed negative SCA effects with HKI 1105. A total of five groups were formed based on the dendrogram analysis using SCA effects as described in Table 3 and Fig 1 b. The clusters 1, 2 and 4 consisted of 1, 7 and 4 inbred lines, respectively and belong to the B group while clusters 3 and 5 contained 7 genotypes in each which belonged to the A group. In the case of the HSGCA method, a total of 26 genotypes were classified into four groups among these 4, 7, 7 and 8 inbred lines belonging to clusters 1, 2, 3 and 4, respectively (Table 3 and Fig. 1a). Further, the HSGCA method clearly defined the inbred lines into four clusters; cluster 1 mostly consisted of the genotypes that were not classified into any group and designated as an unidentified group (Un) except 4 and 21, which fell under cluster 4. The inbred lines showed positive HSGCA with both the testers and were defined as an unidentified group. Further, cluster 2 consisted of the genotypes which belong to the B group (showed negative HSGCA with the tester B) while cluster 4 with genotypes of the A group (showed negative HSGCA with the tester A). On the other hand, cluster number 3 had those genotypes that showed negative HSGCA with both the tester, then based on the highest negative value allotted to the respective group as described by Fan et al. (2009). Hence cluster 3 consisted of the mixture of genotypes of

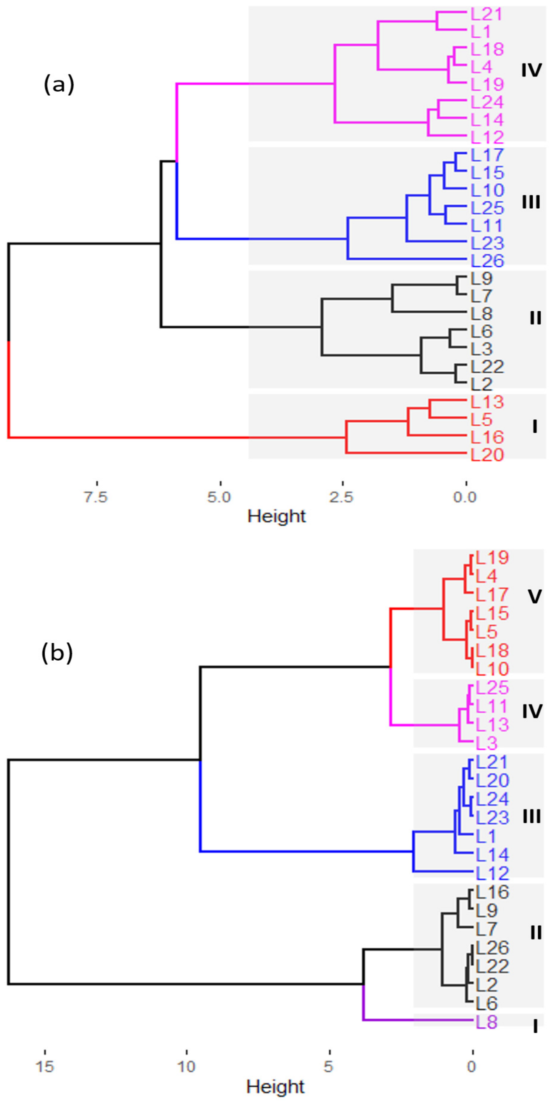

Fig. 1. Dendrograms of 26 baby corn inbred lines constructed from (a) HSGCA and (b) SCA methods using Ward's minimum variance cluster analysis using Euclidean based distance

Table 2. Heterotic grouping of inbred lines based on the positive SCA effects for baby corn yield

Lines	GCA	Pedigree	SCA		Heterotic Groups (SCA)	Heterotic Groups (HSGCA)
			HKI 323 (B group)	HKI 1105 (A group)		
L_1	1.46	(VH-53/Farm seed baby corn)-82-4⊗	1.71	-1.71	A	A
L_2	-1.55	(G-5417/ MLSP-177600)-68-4⊗	-1.81	1.81	B	B
L_3	-0.72	Omaxe hybrid-13-5⊗	-0.94	0.94	B	B
L_4	0.31	(Omaxe baby corn/Omaxe sweet corn)-72-4⊗	0.09	-0.09	A	Un
L_5	4.84	(VH-45/VQPM-1)-64-4⊗	0.83	-0.83	A	Un
L_6	-0.07	(G-5414/0450C1)-94-4⊗	-1.49	1.49	B	B
L_7	1.53	(VH-53/CMVL baby corn-1)-5-4⊗	-2.72	2.72	B	B
L_8	1.74	(CMVL baby corn-2/CMVL baby corn-1)-14⊗	-5.34*	5.34*	B	B
L_9	1.54	(VH-53/CMVL baby corn-2)-150-4⊗	-2.04	2.04	B	B
L_{10}	-2.02	Omaxe hybrid-13-5⊗	0.69	-0.69	A	A
L_{11}	-2.01	(G-5414/MLSP1770483)-32-4⊗	-0.57	0.57	B	B
L_{12}	-0.99	F1 hybrid baby corn-105-5⊗	4.16	-4.16	A	A
L_{13}	3.25	(G-5414/MLSP-1770057)-77-4⊗	-0.31	0.31	B	Un
L_{14}	-0.42	Omaxe hybrid-76-5⊗	2.76	-2.76	A	A
L_{15}	-3.12	(Omaxe baby corn/Omaxe sweet corn)-72-4⊗	0.93	-0.93	A	A
L_{16}	5.04	(ATS baby corn hybrid)-1-4⊗	-2.21	2.21	B	Un
L_{17}	-2.91	(Omaxe baby corn/Omaxe sweet corn)-86-4⊗	0.42	-0.42	A	A
L_{18}	0.51	(Soil me baby corn/IMR-33)-105-4⊗	0.69	-0.69	A	A
L_{19}	-0.39	Vivek hybrid-21-100-4⊗	0.16	-0.16	A	A
L_{20}	8.54	F1 hybrid baby corn-105-5⊗	2.39	-2.39	A	Un
L_{21}	2.93	(Omaxe baby corn/Omaxe sweet corn)-63-4⊗	2.25	-2.25	A	Un
L_{22}	-2.06	(Omaxe baby corn/Omaxe sweet corn)-48-4⊗	-1.67	1.67	B	B
L_{23}	-4.09	(Omaxe baby corn/Omaxe sweet corn)-51-4⊗	2.03	-2.03	A	A
L_{24}	-1.71	(VH-53/CMVL baby corn-1)-5-4⊗	2.10	-2.10	A	A
L_{25}	-3.05	(HQPM-1/HM-1)-146-4⊗	-0.44	0.44	B	B
L_{26}	-6.59	(Omaxe baby corn/Omaxe sweet corn)-90-4⊗	-1.67	1.67	B	B

*= 0.05 % significant, **= 0.01 % significant, Un= Unidentified group

Table 3. Summary of the heterotic groups of 26 baby corn inbred lines identified by different heterotic grouping methods

Methods	Groups (Clusters)				
	1	2	3	4	5
SCA	L 8	L 6, L 2, L 22, L 26, L 7, L 9, L 16	L 12, L 14, L 1, L 23, L 24, L 20, L 21	L 3, L 13, L 11, L 25	L 10, L 18, L 5, L 15, L 17, L 4, L 19
HSGCA	L 20, L 16, L 5, L 13	L 2, L 22, L 3, L 6, L 8, L 7, L 9	L 26, L 23, L 11, L 25, L 10, L 15, L 17	L 12, L 14, L 24, L 19, L 4, L 18, L 1, 21	---

both groups A & B. The dendrogram constructed using both SCA and HSGCA methods showed different cluster patterns but the distribution of genotypes was perfect.

Comparison of efficiencies for heterotic grouping methods

The calculated breeding efficiency for heterotic grouping methods, SCA and HSGCA is presented in Table 4. The total 52 cross combinations lined up into higher-yielding to lower-yielding in ascending order. Further, based on the BCY the crosses were divided into three groups: higher-yielding, moderate yielding, and lowest yielding. After that, these were classified into inter-group and within-group hybrids to calculate the breeding efficiency. The SCA method identified 12 hybrids as high-yielding, 18 as medium yielding and 6 as low-yielders While the HSGCA method identified 7 hybrids as high-yielding, 7 as medium and 6 were identified as low-yielding hybrids. The HSGCA method recorded the highest

Table 4. Breeding efficiencies (%) of heterotic grouping methods in classifying lines into heterotic groups as compared using standard procedure.

Yield group	Cross type	SCA	HSGCA
1	Intergroup	12	7
1	Within group	4	0
2	Intergroup	18	7
2	Within group	9	7
3	Intergroup	6	6
3	Within group	13	13
Breeding efficiency (%)		41.66	50.0

breeding efficiency (50.0 %) compared to SCA method (41.66 %). Based on these results, the HSGCA method was more efficient at identifying superior hybrids in intergroup crosses relative to SCA method.

Discussion

Baby corn is a normal type of maize grown for its young, fresh, finger-like green ears, harvested at the time of silk emergence and before pollination and currently known as specialty corn. Despite the multiple uses of baby corn, knowledge on breeding strategies to be followed for improvement in baby corn is negligible (Chauhan and Mohan 2010). The present study revealed a significant difference for mean squares due to genotypes, crosses and lines for BCYH, BCY, BCD, FY, indicating sufficient diversity presented for these traits, which proved the predominant role of dominance and non-additive effects for the genetic control of all the traits. Therefore, both additive and non-additive effects govern the target traits in the study.

Combining ability analysis plays a vital role in selecting suitable parents and the nature and magnitude of gene effects controlling quantitative traits (Basbag et al. 2007). The genotypes that are superior in terms of GCA and SCA for different traits could be used to develop more heterotic populations for developing high-yielding hybrids (Akinwale et al. 2014). In the present study, both positive and negative GCA effects were observed for all the traits. Other researchers also reported both positive and negative GCA effects for grain yield in maize. The higher positive significant GCA effects were found in the lines, *viz.*, L_{20}, L_{16} and L_6 (BCYH), L_5, L_{16} and L_{20} (BCY), L_5 (BCD), L_4, L_7, and L_3 (FY). Rodrigues and da Silva (2002) also observed the significant positive GCA for the number of baby corn per plant, baby corn length, baby corn weight and baby corn yield per plot. The inbreds with significant and positive GCA effects for various traits indicated that these inbreds possess favorable alleles for grain yield and contributing traits to their progenies (Bad-Apraku et al. 2015). A total of nine crosses out of 52, *viz.*, $L_{15} \times T_1$ (DS); $L_8 \times T_2$, $L_{12} \times T_1$ and $L_{23} \times T_1$ (BCYH); $L_{12} \times T_2$ and $L_8 \times T_2$ (BCY); $L_3 \times T_2$, $L_{14} \times T_1$ and $L_{12} \times T_1$ (FY) showed promising performance for the traits in parenthesis. Hence, superior hybrid combinations with at least one parental line which has the most favorable effects of general combining ability are required.

The availability of efficient testers who can classify the inbred lines into different heterotic groups in an effective way to develop high-yielding hybrids and synthetic varieties (Annor et al. 2019). The testers used in the present study could be utilized for the cost-effective classification of baby corn inbred lines into heterotic groups based to assess the combining ability to identify the promising hybrid combinations for baby corn yield. The total 26 baby corn inbred lines used under this study were classified into the heterotic group by SCA and HSGCA methods, considering the baby corn yield. Different researchers used these methods to classify the inbred lines of maize into heterotic groups (Bapu-Adraku et al. 2015, Annor et al. 2020 and Mahato et al. 2021). Further, the highest breeding efficiency was also observed in the present study for the HSGCA heterotic grouping method compared to the SCA-based heterotic grouping method, which indicated that the HSGCA method was more effective for classifying the baby corn inbred lines into heterotic groups for baby corn yield. It was confirmed from the above results that the HSGCA method is more reliable to classify the inbred lines into the heterotic group for developing high-yielding baby corn hybrids. Therefore, crossing lines from opposite HSGCA heterotic groups leads to more productive hybrids. The findings of the present study that the HSGCA method is more efficient than SCA is agreed with different researchers in maize (Fan et el. 2009, Akinwale et al. 2014, Badu-Apraku et al. 2015, Annor et al. 2019, Oyetunde et al. 2020 and Mahato et al. 2021)

HSGCA was found more efficient to classify the baby corn inbred lines into heterotic groups. Further, maximum heterosis could be exploited by using the inbred lines with positive and significant GCA effects and using the lines from opposite heterotic groups based on the HSGCA method. In the future, the above heterotic grouping methods might be matched with molecular markers for comparing their efficiency.

Authors' contribution

Conceptualization of research (PK, SR); Designing of the experiments (PK, BSJ); Contribution of experimental materials (PK, MC); Execution of field/lab experiments and data collection (PK, BSJ and YKR); Analysis of data and interpretation (PK, SR, MC); Preparation of the manuscript (PK, NL, MG, BB, SR, YKR).

Supplementary materials

Supplementary Table S1 having combining ability analysis data is presented.

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Supplementary Table S1. General and specific combining ability (GCA & SCA) effects of 26 inbreds and 52 crosses for different traits

	DS			BCYH			BCY			BCD			BCL			FY		
		SCA			SCA			SCA			SCA			SCA			SCA	
Lines	GCA	T 1	T 2	GCA	T 1	T 2	GCA	T 1	T 2	GCA	T 1	T 2	GCA	T 1	T 2	GCA	T 1	T 2
L_1	-0.61	0.09	-0.09	3.41	8.50	-8.50	1.46	1.71	-1.71	-0.04	-.011	0.11	-0.30	0.12	-0.12	7.72	6.95	-6.95
L_2	-0.61	0.09	-0.09	-3.21	-4.65	4.65	-1.55	-1.81	1.81	-0.03	0.06	-0.06	-0.13	-0.60	0.60	-16.78	-46.41	46.41
L_3	-0.61	0.09	-0.09	-5.46	-0.14	0.14	-0.72	-0.94	0.94	0.01	-0.02	0.02	0.75	-0.79	0.79	91.44**	-147.22**	147.22**
L_4	-0.61	0.09	-0.09	7.94*	-3.87	3.87	0.31	0.09	-0.09	-0.02	-0.02	0.02	1.10	0.24	-0.24	102.3**	-50.14	50.14
L_5	0.39	-0.91	0.91	6.94*	1.90	-1.90	4.84	0.83	-0.83	0.14**	0.06	-0.06	-0.36	-0.42	0.42	-15.74	-17.30	17.30
L_6	-0.61	0.09	-0.09	11.52*	-7.22	7.22	-0.07	-1.49	1.49	-0.10	0.09	-0.09	-0.85	0.00	-0.00	95.43**	-7.86	7.86
L_7	-0.11	0.59	-0.59	8.65*	-8.19	8.19	1.53	-2.72	2.72	-0.03	-0.05	0.05	0.51	-0.01	0.01	121.92**	17.02	-17.02
L_8	-0.61	0.09	-0.09	4.16	-16.38**	16.38**	1.74	-5.34*	5.34*	-0.07	-0.05	0.05	0.55	0.20	-0.20	58.77*	-9.21	9.21
L_9	-0.61	0.09	-0.09	-0.73	-6.87	6.87	1.54	-2.04	2.04	0.08	-0.06	0.06	-0.07	-0.03	0.03	-8.33	-34.73	34.73
L_{10}	-0.61	0.09	-0.09	0.56	2.31	-2.31	-2.02	0.69	-0.69	0.09	-0.06	0.06	-0.68	-0.20	0.20	-41.37	41.74	-41.74
L_{11}	-0.61	0.09	-0.09	-10.20**	-4.80	4.80	-2.01	-0.57	0.57	0.02	0.10	-0.10	0.03	0.01	-0.01	-115.73**	25.91	-25.91
L_{12}	-0.11	0.59	-0.59	-2.86	17.33**	-17.33**	-0.99	4.16	-4.16	-0.01	0.03	-0.03	-0.29	-0.05	0.05	6.57	73.22*	-73.22*
L_{13}	-0.61	0.09	-0.09	7.56*	-4.35	4.35	3.25	-0.31	0.31	-0.02	0.04	-0.04	-0.07	-0.04	0.04	31.35	14.59	-14.59
L_{14}	0.14	-0.66	0.66	-0.79	12.40**	-12.40**	-0.42	2.76	-2.76	-0.09	0.09	-0.09	0.14	-0.50	0.50	-53.57*	103.71**	-103.71
L_{15}	0.64	-1.16*	1.16*	-15.24	0.18	-0.18	-3.12	0.93	-0.93	-0.06	0.09	-0.09	0.21	-0.24	0.24	-149.15**	18.79	-18.79
L_{16}	-0.61	0.09	-0.09	20.62**	-8.32	8.32	5.04	-2.21	2.21	-0.06	-0.04	0.04	-0.02	-0.28	0.28	83.90**	-40.76	40.76
L_{17}	-0.61	0.09	-0.09	-10.07**	-0.86	0.86	-2.91	0.42	-0.42	0.05	0.03	-0.03	-1.94**	1.46	-1.46	-115.67**	-14.06	-14.06
L_{18}	0.64	0.34	-0.34	8.52*	4.65	-4.65	0.51	0.69	-0.69	-0.05	0.06	-0.06	0.24	-0.01	0.01	78.02**	-4.30	4.30
L_{19}	-0.36	0.34	-0.34	-2.44	3.58	-3.58	-0.39	0.16	-0.16	0.08	-0.02	0.02	0.83	-0.76	0.76	23.59	17.90	-17.90
L_{20}	-0.11	-0.41	0.41	21.05**	0.58	-0.58	8.54	2.39	-2.39	0.07	0.04	-0.04	0.30	0.28	-0.28	58.78*	-9.53	9.53
L_{21}	0.14	-0.16	0.16	6.51	10.27*	-10.27*	2.93	2.25	-2.25	0.06	-0.07	0.07	0.20	0.23	-0.23	55.70*	7.94	-7.94
L_{22}	1.89**	0.09	-0.09	-3.61	-6.32	6.32	-2.06	-1.67	1.67	0.08	-0.01	0.01	0.47	0.21	-0.21	64.77	4.60	-4.60
L_{23}	1.64**	-0.66	0.66	-12.63**	12.70**	-12.70**	-4.09	2.03	-2.03	-0.05	-0.08	0.08	-0.01	1.18	-1.18	-142.53**	1.86	-1.86
L_{24}	-0.11	0.09	-0.09	-10.65**	6.31	-6.31	-1.71	2.10	-2.10	0.06	0.02	-0.02	0.47	-0.58	0.58	-61.71*	36.43	-36.43
L_{25}	0.14	0.34	-0.34	-5.54	-1.82	1.82	-3.05	-0.44	0.44	-0.14**	-0.10	0.10	-0.04	0.59	-0.59	11.90	63.37	-63.37
L_{26}	2.39**	0.59	-0.59	-23.99**	-6.90	6.90	-6.59	-1.67	1.67	0.04	-0.03	0.03	-1.16*	0.02	-0.02	-171.31**	-52.82	52.82

T 1=HKI 323, T 2=HKI 1105, DS = Days to silking, BCYH = Baby corn yield (husk), BCY = Baby corn yield (without husk), BCD = Baby corn diameter, BCL = Baby corn length and FY = Fodder yield.