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RESEARCH ARTICLE

Unraveling the influence of kernel row number and cob-related traits on the expression of heterosis in field corn (*Zea mays* L.)

Ganapati Mukri*, Jayant S. Bhat[1], Chandu Singh, R.N. Gadag, Shilpa, K.V. Gowtham and Digvender Pal

Abstract

Kernel row number (KRN) is an important agronomic trait of the female inflorescence and it is a significant breeding target. In the investigation, a set of 280 inbred lines derived from multiple disease-resistant pools was characterized for KRN and other cob-related traits. Out of 280 inbred lines, 45 lines differing for KRN were selected and evaluated at two locations and three environments. The inbred lines showed significant variation in yield and yield contributing traits at both locations and all the environments considered for evaluation. The KRN and other traits showed a high phenotypic coefficient of variation (ranged 6.47–24.39), genotypic coefficient of variation (ranged 6.47–24.39), and heritability (ranged 71.5–99.6), which were consistent across environments, suggesting the stability of performance of inbred lines and the possibility of genetic gain through selection for these traits. Further, the contrast inbred lines for the KRN trait were identified, which ranged from 10-12 rows (AI 504, AI 505, AI 515, AI 516, AI 518, and AI 519 low KRN) to 18-24 rows (AI 545, AI 536, AI 537, AI 542, AI 543, and AI 544 high KRN). These selected lines (six lines each) were crossed in a diallel fashion and generated 144 F_1 combinations. Hybrids so obtained showed significant variation for KRN and other yield component traits, coupled with significant general combining ability (GCA) and specific combining ability (SCA**)** variances and effects. The ratio of GCA/SCA variance and effect suggested that all the traits, including KRN, are governed by additive gene action. The combinations having low × low KRN have not expressed any significant heterosis, but the cross involving low × high KRN, and high ×high KRN showed significant heterosis for grain yield of hybrids *viz.,* AH-4271, AH-4152, AH-4139, AH-4072, and AH-4039. Hence, the parental lines of these selected hybrids have the potential to improve the productivity of field corn and are also sources for future heterosis breeding programs.

Keywords: Field corn, kernel row number, diallel mating, combining ability, KRN contribution.

Introduction

The demand for maize has steadily increased in recent decades and is expected to rise further as consumption of maize is estimated to double by 2050 (Alexandratos and Bruinsma 2012). Yield is a complex trait, controlled by polygenes and influenced by component traits. Hence, the genetic dissection of traits correlated with yield would contribute to the understanding of the complex biological pathway of yield formation and yield improvement (Ribaut et al. 1997; Wen and Zhu 2005). The yield attributes like kernel row number (KRN), kernel weight, kernel per row, and cob length have significant correlations with yield and always have higher heritability than grain yield (Austin and Lee 1996; Messmer et al. 2009).

The heterosis phenomenon is well-established and most exploited in maize to improve productivity. However, the extent of heterosis varies with the genetic distance of parents, the nature of traits under investigation, and the prevailing environment (Fujimoto et al. 2018). Therefore, the exploitation of heterosis requires a systematic selection of parental lines followed by the choice of parents who produce high heterotic effects, when crossed, due to superior combining ability (Singh et al. 2019). Additionally, hybrid breeding requires complementary pools of parental lines with a proven genetic base for the development of

Division of Genetics, ICAR- Indian Agricultural Research Institute, New Delhi 110 012, India

[1]ICAR- Indian Agricultural Research Institute, Regional Research Centre, Dharwad 658 005, Karnataka, India

***Corresponding Author:** Ganapathi Mukri, Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India, E-Mail: ganapati4121@gmail.com

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hybrids with superior performance (Xiao et al. 2021).

Precision followed in the selection of inbred parents is much more important to attaining high genetic gain through heterosis breeding (Labroo et al. 2021). Hence, it is very much required to understand the major yield contributing traits, which are specifically related to the parental line performance and hybrid performance *vis-a-vis* their role in the realization of maximum heterosis in field corn. The present investigation focused on understanding the role of the KRN and other yield attributes and their possible utilization in heterosis breeding to enhance the productivity of field corn.

Materials and methods

Selection of inbred lines

The development of diverse inbred lines is the fundamental requirement of heterosis breeding. The material (inbred lines) selected for the present study was derived from the broad-based Multiple Disease Resistant (MDR) pools through the pedigree method. A total of 280 early to medium-maturing fixed lines were chosen as working germplasm during the year 2015 and are being maintained at ICAR-IARI, New Delhi. These inbred lines were screened for different target traits, as per the requirements of the field corn breeding program at the center, during the rainy season of 2016. These inbred lines were characterized for KRN, yield, and yield contributing traits, and 80 inbred lines were evaluated further in an augmented design, for the above traits with special emphasis on KRN, during the post-rainy season of 2016-17. From these, 45 promising inbred lines varying for KRN and yield attributing traits were selected and further evaluated in randomized block design with three replications across two locations and three environments (E1, E2 and E3) during 2017 (E1) and 2017-18 (E2) at ICAR-IARI, New Delhi, and 2017-18 (E3) at IARI- Regional Research Centre (RRC) Dharwad, Karnataka, respectively (Fig. 1).

From the above evaluation, inbred lines with contrasting KRN phenotypes were selected. Among these, six inbred lines were low KRN (12-14 KRN) and six were of high KRN (18 and above KRN) types. These selected 12 inbred lines were crossed in a full diallel fashion (12x12) at IARI-New Delhi during the post-rainy season of 2018-19.

Hybrid development using the diallel method

The full diallel mating design (with reciprocal) was used to generate 144 F_1 hybrids from selected 12 inbred lines. The generated 144 F_1 combinations were evaluated for their KRN and yield and yield component traits using a resolvable block design (Alpha Lattice) with 12 blocks and two replications at IARI-New Delhi during the rainy season of 2019. The sequence of line selection, hybrid development, and their evaluation is depicted in the flow chart presented (Fig. 2).

Field experiment and data collection

Inbred lines, as well as hybrids, were grown in two-row plots each of three meters in length with a spacing of 75×20 cm so that 30 plants were maintained in the 4.5 m^2 net sown area. All the recommended crop management practices were followed to raise a healthy crop across locations and environments.

Trait measurement

The KRN, yield, and other yield attributing traits such as cob length (CL), cob girth (CG), kernels per row (KPR), test weight (TW), kernel thickness (KT), kernel length (KL) and grain yield were recorded on the randomly selected five plants of each replication. The KRN, CL, CG, and KPR were recorded using the standard method of measurement and counting, respectively. A randomly selected 100 kernels was weighed to record test weight (g) and randomly selected 10 kernels

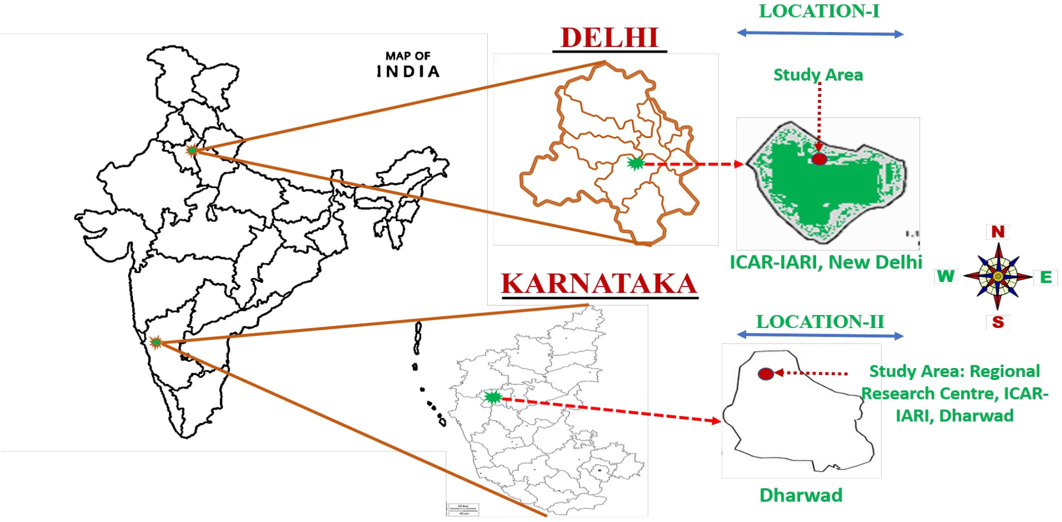


Fig. 1. Depiction of study location

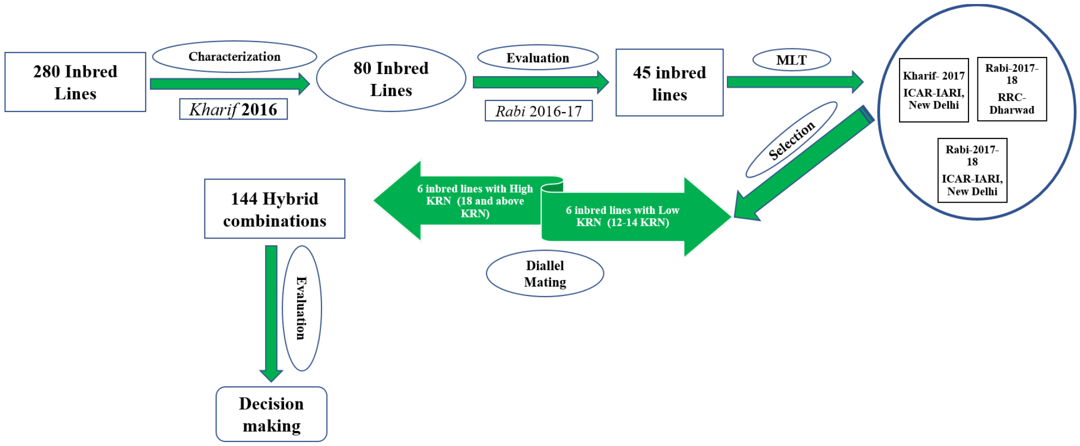


Fig. 2. Schematic diagram illustrating breeding pipeline of selecting parental lines and development of hybrids

from a given inbred line was measured for KT (mm) and KL (mm), using a Vernier caliper. The grain yield per hectare (tha^{-1}) was estimated using the grain yield recorded on the total cob weight of the two-row plot from each genotype using the following formula.

$$\text{Grain yield at 15\% moisture (t ha}^{-1}\text{)} = \frac{\text{Plot cob yield (kg)} \times \text{MF} \times \text{SF} \times 1000}{\text{plot area (m}^{2}\text{)} \times 85}$$

Where, MF = Moisture factor = (1-moisture content in decimals)/100 and SF = Shelling factor in decimals

Statistical analysis

The data obtained on yield and yield component traits were analyzed through SAS 9.3 v (http://stat.iasri.res.in/2013) and the TNAUSTAT-Statistical package (Manivannan 2014). Genotypic (GCV) and phenotypic (PCV) coefficients of variation were computed (Singh and Chaudhary 2004). Heritability estimates were categorized (Singh 2001) as low (< 40%), medium (40–59%), moderately high (60–79%), and very high (> 80%). The combining ability parameters, *viz.*, *GCA* and *SCA* variance and effects, were computed (Sprague and Tatum 1942; Griffing 1956).

Results and discussion

Parental lines Evaluation and Selection

The success of any crop improvement program depends upon the genetic variability and heritability of the target traits in the genetic resources available to the breeder (Ogunniyan and Olakojo 2015). Adequate genetic variability provides the breeder with ample options for the selection of desirable plant types/inbreds with target traits, which in turn provides for the development of high-yielding hybrids (Ogunniyan et al.2001). In the present investigation, a set of 280 fixed inbred line panels was evaluated for kernel row number (KRN) and other yield-attributing traits. Out of 280 lines, 80 lines showed wider variation for the studied traits. Further, 80 lines were again characterized for traits, and out of 80 lines, 45 inbred lines were distinct and these lines were evaluated across two locations and three environments to understand the genetic variability for KRN along with other yield component traits (Fig. 2).

Analysis of variance of inbred lines

Highly significant mean sum of squares due to genotype for KRN, yield, and other yield components *viz.*, cob length (CL), cob girth (CG), kernel per row (KPR), test weight (TW), kernel length (KL), kernel thickness (KT) and grain yield across locations and environments were observed (Table 1). Bhat et al. (2024) also reported a highly significant variation due to genotypes, crosses, parents, lines, and parents vs crosses for a number of traits, including the number of kernel rows per cob and other yield contributing trait under rainy and post-rainy seasons. The mean CL recorded 12.48 cm in E1, 12.88 cm in E2, and 12.16 in E3, which ranged from 7.20 to 20.60 cm across the locations. The CG ranged from 2.70 to 5.05 cm with a mean of 3.59 cm in E1, 3.58 cm in E2, and 3.22 in E3. The mean KRN observed was 15.24 in E1, 15.47 in E2, and 15.90 in E3, with a range of 10.00 to 24.00 across the locations and environments. The mean KPR observed was 21.76, 22.18, and 22.68 in E1, E2, and E3, respectively, with a wide range of 13.37 to 31.85. The TW ranged from 14.90 to 30.90 g across locations and environments, with a mean value of 21.89, 21.57, and 21.37 E1, E2, and E3, respectively. The KL varies from 7.60 to 9.85 mm across the tested location within environment, with a mean value of 8.94, 8.96, and 9.06 mm, and E1, E2, and E3, respectively. KT recorded a mean value of 6.82 mm at E1, 6.98 at E2 and 6.89 at E3, which varied from 4.45 to 8.25 mm across the environments. The grain yield recorded was 2.74, 2.70, and 3.15 tha^{-1} in E1, E2, and E3, respectively, with the mean value recorded for grain yield being 1.22 to 3.15 tha^{-1} (Table 2).

Coefficient of variation of traits among inbred lines

The phenotypic coefficient of variation (PCV) for CL was 22.8, 21.34, and 20.47 at E1, E2, and E3, respectively, whereas the genotypic coefficient of variation (GCV) for CL was

Table 1. **ANOVA of inbred lines for KRN and associated traits at different environments**

Environments	Source	DF	Mean Sum of Square (MSS)							
			CL	CG	KRN	KPR	TW	KL	KT	YLD
E1	Rep.	1	0.01	0.01	0.03	3.84	0.04	0.05	0.02	0.10
	Trt.	44	15.93**	0.56**	18.62**	42.86**	29.92**	0.744**	1.05**	0.90**
E2	Rep.	1	0.29	0.00	0.34	2.92	1.05	0.01	0.01	0.01
	Trt.	44	15.08**	0.57**	22.27**	38.75**	21.71**	1.14**	1.44*	0.85*
E3	Rep.	1	0.70	0.07	0.01	9.09	3.52	0.34	0.13	0.11
	Trt.	44	12.26**	0.47**	24.60**	41.03**	23.77**	0.83**	0.87*	0.54*

*Significance at 5% level of probability; **Significance at 1% level of probability; Rep= Replication; Trt= Treatment, E1= *Kharif* 2017, IARI, E2= *Rabi* 2017-18 IARI, E3: *Rabi* 2017-18, RRC Dharwad, CL = Cob Length, CG = Cob girth, KRN=Kernel Row Number, KPR= Kernels per Row, TW = Test Weight-100 seed weight, KL = Kernel Length, KT = Kernel Thickness and YLD = Yield (Grain Yield).

Table 2. **Genetic variability and heritability of KRN and other yield-related traits of inbred lines**

Trait (s)	Mean			Range	PCV			GCV			h^2(BS)		
	E1	E2	E3		E1	E2	E3	E1	E2	E3	E1	E2	E3
CL(cm)	12.48	12.88	12.16	7.20-20.60	22.80	21.34	20.47	22.43	21.28	20.27	96.70	99.50	98.00
CG(cm)	3.59	3.58	3.22	2.70-5.05	15.01	15.28	15.21	14.46	14.52	15.03	92.80	90.30	97.60
KRN	15.24	15.47	15.90	10.00-24.00	20.06	21.59	22.45	19.99	21.55	21.66	99.40	99.60	93.00
KPR	21.76	22.18	22.68	13.37-31.85	21.55	20.04	20.84	21.00	19.64	19.06	94.90	96.00	83.60
TW	21.89	21.57	21.37	14.90-30.90	18.21	15.89	16.96	17.12	14.63	15.26	88.40	84.90	81.00
KL(mm)	8.94	8.96	9.06	7.60-9.85	7.16	8.58	7.58	6.47	8.29	6.61	81.71	93.20	75.80
KT(mm)	6.82	6.98	6.89	4.45-8.25	11.48	12.29	10.07	9.71	12.06	9.11	71.50	96.40	81.80
YLD(t/ha)	2.74	2.70	3.15	1.22-3.83	24.57	24.62	16.88	24.39	23.61	15.91	98.51	92.00	88.90

E1 = *Kharif* 2017, IARI, E^2= *Rabi* 2017-18, IARI, E3= *Rabi* 2017-18, RRC Dharwad, PCV= phenotypic coefficient of variation, GCV= genotypic coefficient of variation, h^2(BS)= heritability broad sense, CL = Cob Length, CG = Cob girth, KRN=Kernel Row Number, KPR = Kernels per Row, TW = Test Weight-100 seed weight, KL = Kernel Length, KT = Kernel Thickness and YLD = Yield (Grain Yield)

22.43, 21.28, and 20.27 in E1, E2, and E3, respectively. For the CG, PCV was observed at 15.0, 15.28, 15.21% and GCV was 14.46, 14.52, and 15.03% across all environments. The PCV of 20.0, 21.59, and 22.45%, as well as the GCV of 19.99, 21.55, and 21.66%, were recorded by KRN across E1, E2, and E3, respectively. For the trait KPR, the PCV recorded was 21.50%, 20.04%, and 20.84%, while GCV was 21.00, 19.64, and 19.06% in E1, E2, and E3, respectively. The PCV recorded by KL was 7.16, 8.58, and 7.58%, whereas GCV was 6.47, 8.29, and 6.61% in E1, E2, and E3, respectively. The PCV of 11.40, 12.29, and 10.07%, as well as the GCV of 9.71, 12.06, and 9.11%, respectively, across the environment were recorded by KT. The TW recorded PCV of 18.2, 15.89, 16.96% and GCV of 17.12, 14.63, 15.26%, respectively in E1, E2, and E3. The grain yield exhibited PCV of 24.50, 24.62, 16.88%, and GCV of 24.39, 23.61, and 15.91%, respectively, across the environments (Table 2).

Heritability of traits among inbred lines

The heritability (broad sense) was estimated for all the traits under investigation. The CL and CG recorded heritability of 99.70, 99.50, 98 and 92.80, 90.30, and 97.60 percent, respectively, for E1, E2, and E3. KRN and KPR recorded 99.40, 99.60, 93.00, and 94.90, 96.00, and 83.60 percent heritability, respectively, across environments. Similarly, TW and grain yield showed 88.40, 84.90, 81.00 and 98.51, 92.00, and 88.90 percent heritability across environments (Table 2).

This implied that the selected 45 lines have substantial genetic variability and hence the selection is effective for these traits. Further, strategy and criteria of selection can be devised after analyzing other genetic parameters and the selected lines can be utilized for the development of heterotic maize hybrids (Abe and Adelegan 2019). Similarly, PCV and GCV were high (>20%) for CL, KRN, KPR, and grain yield across environments, TW recorded moderate (10–20%) and KL and KT recorded low estimates (<10%) of PCV and GCV, respectively, across environments (Sivasubramanian and Menon 1973). The PCV values were slightly higher than GCV, and the difference between these two coefficients for all the traits were narrow, indicating very little experimental error and environmental effects of the studied traits. Higher GCV and heritability (bs) indicated the existence of substantial genetic variation for CL, KRN, KPR, and grain yield. Further, it suggested that the selection of individual

Table 3. Yield and yield component traits of selected high and low KRN inbred lines

S.No	Inbred lines	KRN	CL	CG	KPR	TW	KL	KT	YLD t/ha
High KRN									
1	AI 536	18.00	9.81	4.10	19.00	23.28	9.72	7.32	3.54
2	AI 537	20.00	11.62	4.23	21.00	20.25	9.11	6.40	3.55
3	AI 542	20.00	11.21	4.31	20.00	28.13	9.73	7.61	3.56
4	AI 543	20.00	12.23	4.92	21.00	26.15	9.85	8.02	3.60
5	AI 544	20.00	14.75	4.35	27.00	25.00	9.67	7.73	3.61
6	AI 545	24.00	14.92	3.47	29.00	18.39	9.15	6.75	3.70
Low KRN									
1	AI 504	12.00	10.90	2.57	17.00	20.27	7.82	6.33	1.36
2	AI 505	12.00	11.58	3.12	19.00	23.08	8.53	7.23	2.00
3	AI 515	14.00	12.69	3.22	24.00	18.35	9.07	5.98	2.48
4	AI 516	14.00	13.03	3.15	21.00	21.70	9.15	7.08	2.63
5	AI 518	14.00	10.55	2.68	20.00	18.40	7.97	6.32	2.60
6	AI 519	14.00	10.38	3.57	20.00	22.57	9.65	7.87	2.73

KRN=Kernel Row Number, CL=Cob Length, CG=Cob girth, KPR=Kernels per Row, TW= Test Weight-100 seed weight, KL=Kernel Length, KT= Kernel Thickness and YLD=Yield (Grain Yield)

lines will be effective for the genetic enhancement of traits and heterosis breeding (Jilo et al. 2018). This suggested the accuracy of experimentation, estimates, and stability of performance across different locations and environments, implying that augmentation of productivity in maize is possible through the selection of potential inbred lines and heterosis breeding from the pool of inbreds studied (Yu et al. 2020)

Selection of inbred lines with contrasting KRN phenotypes

These 45 inbred lines showed wider variation in the studied traits, which ranged from 10-12 rows (AI 504) to 18–24 rows (AI 545). From the KRN data, six high KRN lines (≥18 rows) and six low KRN lines (≤14 rows) were identified (Table 3 and Fig. 3). The six inbred lines, AI 536, AI 537, AI 542, AI 543, AI 544, and AI 545, were selected for high KRN phenotype; AI 504, AI 505, AI 515, AI 516, AI 518, and AI 519 were selected for low KRN (12-14 rows). Among the selected six high KRN lines, grain yield ranged from 3.54 to 3.70 tha^{-1}, the TW varied from 18.39 to 28. 13 g, the CL and CG of high KRN genotypes ranged from 9.81 to14.92 cm and 3.47 to 4.92 cm, respectively. The range for KPR was 19.00 to 29.00, whereas KL varied between 9.11 and 9.83 mm and KL showed 6.40 to 8.02 mm. Among the six selected low KRN inbred lines, grain yield ranged from 1.36 to 2.73 tha^{-1}. For CL and CG, among low KRN genotypes, the lowest values were recorded by AI 519 (10.38 cm) and AI 504 (2.57 cm), respectively, while the highest values were for AI 516 (13.03 cm) and AI 519 (3.57 cm), respectively. The KPR and TW ranged from 17.00 to 24.00 and 18.35 to 23.08 g, respectively. The range for KL was 7.82 to 9.15 mm, whereas the KT ranged from 5.98 to 7.87 mm. Further, the contrast inbred lines for the KRN trait were selected (six lines each high and low KRN, respectively) and crossed in a 12 x 12 full diallel fashion, generating 144 F$_1$ combinations.

The General Combining Ability (GCA) variance and effects of KRN and other yield-associated traits

The generated 144 F$_1$ hybrids revealed a highly significant mean sum of squares due to *GCA*, *SCA*, and reciprocal effects for all the traits except for KRN (Table 4). KRN trait, AI 536, AI 537, AI 542, AI 504, and AI 515 showed significantly positive *GCA* effects of 0.41, 0.56, 0.51, 0.68, and 0.41, respectively, whereas AI 544, AI 545, AI 16 and AI 519 recorded negative and significant *GCA* effects. AI 516, AI 518, and AI 519 (0.99, 0.91, and 0.58, respectively) showed positive and significant *GCA* effects while AI 543 and AI 545 had significant negative *GCA* effects for CL traits. Similarly, for the CG, AI 537, AI 542, and AI 518 showed significantly positive *GCA* effects of 0.24, 0.15, and 0.14, respectively. None of the inbred lines recorded a significantly positive *GCA* effect for KPR, but on the contrary, AI 518 recorded a significant negative *GCA* effect (-1.16). AI 542, AI 518, and AI 519 showed significant positive *GCA* effects of 2.54, 1.53, and 2.95, respectively, while seven inbreds showed negative significant negative *GCA* effects for TW. For grain yield, AI 542 and AI 519 had significant positive *GCA* effects (0.93 and 0.25, respectively), whereas AI 544, AI 505, and AI 515 had significantly negative *GCA* effects (Table 5).

Table 4. ANOVA for combining ability of 12 ×12 diallel mating of inbred lines

Sources	DF	CL	CG	KRN	KPR	TW	YLD
gca effect	11	7.38**	0.35**	6.89	6.41*	60.76**	4.53**
sca effect	66	4.32**	0.14**	3.85	14.68**	12.72**	1.32**
Reciprocal effect	66	4.55**	0.19**	4.87	12.18**	15.57**	2.76**
Error	143	1.39	0.03	0.33	3.24	2.47	0.39

GCA=general combining ability, SCA=specific combining ability, DF=Degree of freedom, CL=Cob Length, CG=Cob girth, KRN=kernel row number, KPR=Kernels per Row, TW=Test Weight-100 seed weight and YLD=Yield (Grain Yield)

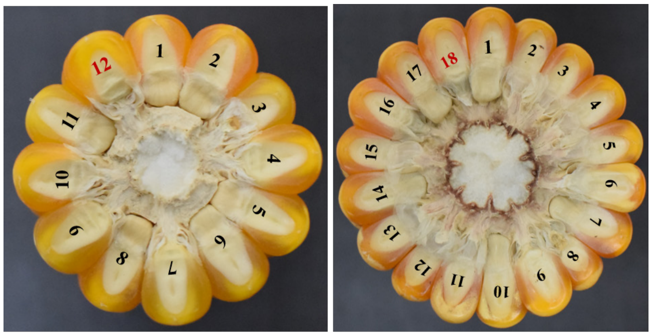
Table 5. The general combining ability (GCA) effects of 12 inbred lines

Inbred lines	Yield and yield contributing traits					
	CL	CG	KRN	KPR	TW	YLD
AI 536	-0.26	-0.05	0.41**	0.10	-0.92**	-0.11
AI 537	-0.04	0.24**	0.56**	0.43	0.59	0.58
AI 542	0.14	0.15**	0.51**	0.23	2.54**	0.93**
AI 543	-0.74**	0.01	0.14	-0.09	-1.55**	-0.17
AI 544	-0.25	-0.16**	-0.96**	0.47	-1.55**	-0.71**
AI 545	-0.51*	0.01	-0.33**	-0.02	-0.61*	-0.19
AI 504	-0.44	-0.06*	0.68**	0.34	-1.24**	-0.01
AI 505	-0.28	-0.05	-0.37	-0.54	-0.76*	-0.36**
AI 515	-0.12	-0.13**	0.41**	-0.57	-1.33**	-0.25*
AI 516	0.99**	-0.09**	-0.60**	0.56	0.34	-0.14
AI 518	0.91**	0.14**	0.02	-1.16**	1.53**	0.19
AI 519	0.58*	0.01	-0.48**	0.25	2.95**	0.25*

CL = Cob Length, CG = Cob girth, KRN=kernel row number, KPR=Kernels per Row, TW = Test Weight-100 seed weight and YLD = Yield (Grain Yield)

The Specific Combining Ability (SCA) variance and effects of KRN and other yield-associated traits

A set of 66 straight crosses was analyzed for *SCA* effects; among them, 16 and 19 crosses showed positive and negative, respectively, significant *SCA* effects for the KRN trait and other yield-associated traits. The 08 and 16 crosses showed positive and negative *SCA* effects, respectively, for the KRN trait. 10 and 08 cross positive and negative, respectively, *SCA* effect for the CL trait. Further, 13 crosses each had a positive as well as a negative *SCA* effect for the CG trait. The hybrids AI 542 × AI 544, AI 542 × AI 545, AI 542 × AI 543, AI 536 × AI 542 and AI 504 × AI 542 were the top five hybrid combinations for the KRN trait. For TW and grain yield, 10 and 08 crosses respectively recorded a positive significant *SCA* effect, whereas 11 and 05 crosses respectively recorded negative significant *SCA* effects for both traits. The rest of the cross combinations recorded either non-significant positive or negative *SCA* effects (Table 6.).



Low Kernel Row Number (AI 504) High Kernel Row Number (AI 545)

Fig. 3. Contrasting inbred lines for KRN trait

The combining ability effects and variance parameters would help the breeder select the best-performing hybrids followed by parents for heterosis breeding (Bello et al. 2012 and Malvar et al.2001). In the present study, the mean sum of squares due to *GCA* effects and *SCA* effects were highly significant for all the traits. KRN implies the role of both additive and dominant gene action in controlling these traits. However, grain yield is a complex trait and is a function of its component traits (Zhang 2016; Singh et al. 2019). This means that a line having significantly positive *GCA* effects for grain yield as well as for traits like KRN, TW, CG, *etc.*, would produce heterotic hybrid combinations.

Table 6. *The specific combining ability (SCA) effects of 66 straight crosses*

S.No	Hybrid	CL	CG	KRN	KPR	TW	YLD
1	AI 504 X AI 505	2.40**	-0.03	-0.38	6.22**	2.55*	1.65**
2	AI 504 X AI 515	-0.68	0.15	1.07	-1.88	-1.41	0.13
3	AI 504 X AI 516	1.84	-0.13	-1.76**	1.74	3.28**	0.53
4	AI 504 X AI 518	1.83*	0.10	-1.26**	2.08	1.92	0.24
5	AI 504 X AI 519	-0.17	0.31**	0.12	1.52	1.51	1.24**
6	AI 504 X AI 536	1.29	0.17	-0.69	0.41	3.71**	0.81*
7	AI 504 X AI 537	-0.54	0.01	0.65	-1.00	-0.93	-0.68
8	AI 504 X AI 542	-0.55	0.18	2.26**	2.97*	-1.88	0.77
9	AI 504 X AI 543	-0.14	0.08	1.18**	1.69	-1.73	-0.17
10	AI 504 X AI 544	-0.32	-0.17	-0.13	-1.38	-3.25**	-1.03*
11	AI 504 X AI 545	2.28**	0.15	0.25	2.95*	0.25	1.05**
12	AI 505 X AI 515	-0.03	-0.25*	-1.18**	0.44	0.90	-0.14
13	AI 505 X AI 516	1.60*	-0.09	-1.51**	0.31	1.19	0.21
14	AI 505 X AI 518	-0.77	0.02	-0.51	-1.94	-0.43	-0.21
15	AI 505 X AI 519	2.05**	-0.04	-0.94*	0.04	1.35	-0.41
16	AI 505 X AI 536	-1.37	-0.08	0.34	-0.57	-3.34**	-0.77
17	AI 505 X AI 537	-0.94	0.63**	1.89**	-2.68*	4.12**	1.22**
18	AI 505 X AI 542	-0.18	-0.01	3.11**	-0.90	-1.62	-0.10
19	AI 505 X AI 543	-1.27	0.17	0.92*	-1.69	-0.47	-0.31
20	AI 505 X AI 544	-2.23**	0.33**	0.50	-4.47**	-0.96	-0.69
21	AI 505 X AI 545	-0.33	-0.39**	-0.59	-0.23	-1.89	-1.12**
22	AI 515 X AI 516	-0.23	0.27**	0.63	-2.23	1.89	0.87*
23	AI 515 X AI 518	0.54	-0.05	-1.26**	4.10**	-2.11*	0.36
24	AI 515 X AI 519	-2.36**	0.33**	1.50**	-4.05**	-1.39	-0.05
25	AI 515 X AI 536	1.23	0.04	0.19	2.47*	-0.19	0.37
26	AI 515 X AI 537	-0.16	-0.15	-0.65	-0.48	-2.17*	-0.39
27	AI 515 X AI 542	0.48	-0.24*	-1.23**	0.69	1.55	-0.62
28	AI 515 X AI 543	0.97	-0.45**	-2.32**	1.90	-1.92	-1.17**
29	AI 515 X AI 544	1.60*	-0.09	-0.14	-0.52	1.58	-0.22
30	AI 515 X AI 545	0.13	0.01	-0.24	-0.83	2.07*	0.40
31	AI 516 X AI 518	-0.24	-0.11	2.00**	-0.22	-3.49**	-0.29
32	AI 516 X AI 519	-2.36**	0.08	0.08	-4.23**	0.21	-1.05**
33	AI 516 X AI 536	-0.47	0.28**	2.46**	-0.50	-1.57	0.34
34	AI 516 X AI 537	-0.16	0.15	1.91**	1.18	-1.13	0.23
35	AI 516 X AI 542	1.14	-0.01	-0.16	4.26**	1.81	0.63
36	AI 516 X AI 543	-0.53	-0.02	-0.94*	2.02	1.26	0.62
37	AI 516 X AI 544	-0.98	0.24*	0.43	0.94	-1.69	0.08
38	AI 516 X AI 545	-2.22**	-0.02	0.62	-2.50*	-2.93**	-0.72
39	AI 518 X AI 519	0.62	0.05	0.08	3.15**	2.88**	0.95*
40	AI 518 X AI 536	-1.01	-0.29**	-1.63**	-3.30**	-0.08	-0.88*
41	AI 518 X AI 537	1.13	-0.34**	-1.08**	-3.22**	2.46*	-0.35
42	AI 518 X AI 542	0.49	0.03	0.83*	0.40	-1.31	-0.20
43	AI 518 X AI 543	-0.13	-0.31**	-1.15**	1.56	-0.21	-0.12
44	AI 518 X AI 544	-1.95*	0.29**	1.07**	-0.95	1.41	0.19
45	AI 518 X AI 545	-0.11	0.33**	0.52	-0.76	-1.41	-0.55
46	AI 519 X AI 536	2.18**	-0.30**	-0.95*	4.02**	1.65	0.25
47	AI 519 X AI 537	0.82	0.03	-0.70	-0.48	1.32	-0.04

Contd.....

48	AI 519 X AI 542	-1.62*	-0.29**	-1.69**	-3.35**	-5.05**	-2.11**
49	AI 519 X AI 543	1.46	-0.23*	-0.17	1.70	-1.82	0.17
50	AI 519 X AI 544	0.41	-0.01	0.30	1.72	1.13	0.27
51	AI 519 X AI 545	0.29	-0.24*	0.80*	0.96	-3.18**	-0.35
52	AI 536 X AI 537	-0.37	-0.21*	-0.82*	-1.09	0.77	-0.58
53	AI 536 X AI 542	1.16	0.35**	0.49	0.481	0.87	0.65
54	AI 536 X AI 543	-1.88*	0.15	1.21**	-2.30*	-1.64	-0.31
55	AI 536 X AI 544	-0.99	-0.13	-0.31	-1.08	2.85**	-0.13
56	AI 536 X AI 545	-0.88	0.01	0.38	-0.29	-3.57**	-0.62
57	AI 537 X AI 542	1.56*	-0.20	-2.15**	1.16	6.04**	0.41
58	AI 537 X AI 543	1.12	-0.26*	-1.73**	3.03**	-1.87	-0.66
59	AI 537 X AI 544	-1.41	-0.05	0.43	1.05	-2.09*	0.64
60	AI 537 X AI 545	0.12	0.40**	1.63**	2.29	-1.90	0.80*
61	AI 542 X AI 543	-0.67	0.42**	1.97**	-2.98*	0.42	0.41
62	AI 542 X AI 544	0.89	-0.09	-1.34**	-0.21	2.45*	0.12
63	AI 542 X AI 545	-1.87*	0.17	0.45	-0.82	-1.38	-0.17
64	AI 543 X AI 544	2.44**	0.40**	2.37**	-1.30	-3.64**	0.46
65	AI 543 X AI 545	0.73	-0.08	-0.83*	-0.36	4.91**	0.19
66	AI 544 X AI 545	1.63*	-0.18	-1.65**	3.75**	1.30	0.57

CL = Cob Length, CG = Cob girth, KRN=kernel row number, KPR=Kernels per Row, TW = Test Weight-100 seed weight and YLD=Yield (Grain Yield)

Table 7. ANOVA yield and yield component traits of hybrids

Source	DF	Mean Sum of Square (MSS)						
		CL	CG	KRN	KPR	NC	TW	YLD
Replication	1	2.11	0.02	0.01	0.39	6.12	2.19	0.01
Block	11	4.58	0.04	0.66	6.50	25.40	76.50	4.12
Hybrid	132	8.82**	0.27**	7.78**	23.26**	28.44**	13.64	4.89**
Error	132	2.64	0.05	0.66	6.48	13.98	15.58	0.97
Corrected total	287	-	-	-	-	-	-	-

DF = degree of freedom, Cob Length (CL), Cob Girth (CG), Kernel Row Number (KRN), Kernels per row (KPR), Number of cobs (NC), Test weight (TW), and Grain Yield (YLD)

Line AI 542 recorded significantly positive *GCA* effects for KRN, CG, TW, and grain yield. This type of inbred is useful in the effective exploitation of *GCA* effects in breeding high-yielding maize hybrids (Chiuta and Mutengwa 2020; Reddy et al. 2013). Concurrently, this line can be used as a donor for the genetic enhancement of KRN in maize (Yu et al. 2020). The lines with high *GCA* effects for KRN, viz., AI 545, AI 544, etc., can be used in a multiple crossing program to develop opposite heterotic pools and for isolating desirable lines with increased KRN in maize, which are expected to cross well with the members of the opposite group (Reddy et al. 2013). In our study, the role of both additive and dominance components is involved for all traits, as evidenced by the highly significant mean sum of squares due to *GCA* and *SCA* effects. However, GCA variance was higher than SCA variance for all the traits except KPR, indicating the predominant role of additive gene action in controlling these traits. Therefore,

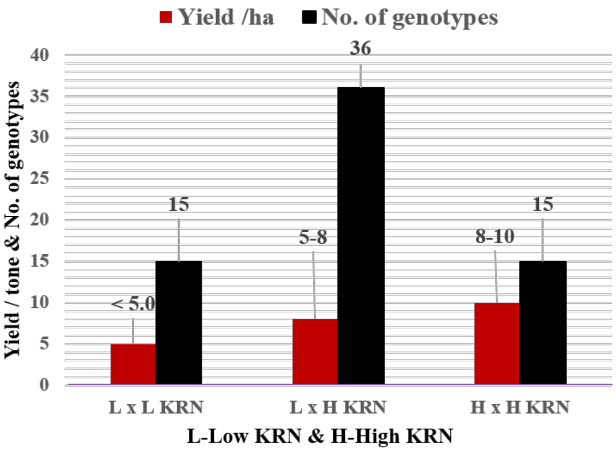


Fig. 4. Influence of parental lines KRN on the grain yield of hybrid

improvement in KRN is possible individually by inbred improvement program as well as by heterosis breeding (Dehghanpour and Ehdaie, 2013; Pswarayi and Vivek, 2008) and thereby grain yields (Sibiya et al., 2013).

Among the 66 straight cross hybrids, 07 recorded significantly positive *SCA* effects for grain yield, of which five recorded desirables for multiple component traits that finally led to a high-yielding genotype. For instance, AI 505 x AI 537 for CG, KRN, TW, and yield, and AI 504 x AI 505 for CL, KPR, TW, and yield. This might be due to the formation of superior gene recombination for these multiple traits in the hybrid. The best-specific combiners having the highest magnitude of significant *SCA* effects in a favorable direction, with higher *per se,* may be exploited in heterosis breeding and the advanced stage of testing (Reddy et al. 2013).

Analysis of variance and per se performance of hybrids

The mean sum of squares due to hybrids for all the traits were highly significant, while the mean sum of squares due to replication and block was non-significant (Table 7). Some of the high-yielding hybrids worth mentioning are AI 536 × AI 537, AI 536 × AI 542, AI 536 × AI 543, AI 536 × AI 544, AI 536 × AI 545, AI 537 × AI 542, AI 537 × AI 543, AI 537 × AI 544, AI 537 × AI 545, AI 542 × AI 543, AI 542 × AI 544, AI 542 × AI 545, AI 543 × AI 544, AI 543 × AI 545, and AI 544 × AI 545. To understand the contribution of the KRN of parental inbred lines to the KRN of hybrids, we analyzed the mean grain yield of hybrids *vis a vis* KRN of parental lines. It was observed that the low x low KRN (12–14) combinations realized lower grain yield (5 t/ha). When the KRN of one of the parents is increased (low KRN x high KRN), the yield levels of hybrids also increase to 5 to 8 tha^{-1}. Interestingly, the yield of hybrids (AH-4271, AH-4152, AH-4139, AH-4072, and AH-4039) increased substantially when both the parents were high, *i.e.*, high x high KRN (8–10.30 tha^{-1}) (Fig. 4). Hence, the increased grain yield can be achieved possibly by selecting not only high KRN pollen donors but also by choosing a high KRN seed parent. These encouraging results suggested carrying out further necessary dissection of the genetics of the KRN trait, which in turn will provide the genetic basis for systematic improvement and incorporation of the trait into a hybrid breeding program to enhance the productivity of field corn.

Authors' contribution

Conceptualization of research (GM); Designing of the experiments (SB, GM, RNG); Contribution of experimental materials (GM, RNG); Execution of field/lab experiments and data collection (DP, KVG, S); Analysis of data and interpretation (GM, RNG, JSB); Preparation of the manuscript (GM, RNG, JSB).

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