

Bi-parental population for kernel row number: Source for novel genetic variability for yield and yield component traits in field corn (*Zea mays* L.)

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Abstract Field corn (*Zea mays* L.) is a vital source of calories for humans, and its demand for food, feed, and fuel is increasing with the global population. To meet these demands, breeders aim to enhance grain yield through genetic improvement. One approach to achieve this is by selecting desirable genotypes in early generations, reducing the need for intense selection in later generations. The utilization of F_2 populations for capturing the maximum genetic variability is a promising strategy to expedite the development of improved field corn cultivars. Two F_2 populations were generated by crossing a low Kernel Row Number (KRN) parent with two high KRN parents. The populations were evaluated for various yield-related traits, including KRN, kernel number per row, cob length, cob girth, test weight, plant height, cob height, days to 50% flowering, and grain yield. Significant genetic variability was observed for grain yield, plant height, and cob height in both populations, indicating its potential for genetic improvement. Kernel number per row, cob girth, cob length, days to 50% flowering and KRN exhibited lower genetic variance, suggesting the influence of phenotypic plasticity and the presence of both negative and positive alleles. The heritability estimates were high (>60%) for most traits, indicating the predominant role of genetic factors in their expression. Positive correlations were

found between KRN and several yield-related traits, such as plant height, cob height, cob girth, and grain yield. These findings highlight the importance of KRN in determining grain yield potential and provide insights into the genetic architecture of the trait.

Keywords: Field corn · Kernel row number (KRN) · F_2 population · Correlation · Yield

Introduction

Field corn (*Zea mays* L.) is one of the most important sources of calories for humans. The demand for corn-derived food, feed, and fuel is increasing as the world's population is expanding. Breeders are trying to increase grain output through genetic improvement of field corn germplasm in order to meet these demands. To accomplish this goal, breeders should have the potential of selecting a desirable genotype in the early generations, which avoids intense selection until the later generations. As the global population continues to expand rapidly, the critical challenges of ensuring food security and maintaining agricultural productivity become increasingly prominent (Hallauer and Miranda, 1988). To tackle these challenges, plant breeders have been continuously striving to develop high-yielding field corn varieties with better agronomic traits and enhanced stress tolerance (Duvick, 2001). Among the various plant breeding techniques, the utilization of segregating populations and the exploration of variability for the trait of interest is a promising approach to expedite the development of improved cultivars. Grain yield of field corn is quantitative in nature and polygenically regulated, therefore simultaneous enhancement of all yield components and effective yield

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improvement is essential. Planning of effective breeding program to create high-yielding inbred and hybrids requires generation of considerable genetic variability followed by utilization of correlated yield and yield components traits strategically.

Heritability on the other hand indicates the phenotypic variation due to genetic causes and provides the knowledge on possibility of transmission of trait to next generation. Based on the heritability information, strategies of selection procedures, predicting selection gain and evaluating the relative value of genetic effects are decided. field corn yield is affected by the effective ear number, kernel number per ear, and kernel weight. Kernels per row and kernel row number (KRN) are subsets of kernel number per ear (Brown *et al.*, 2011). The most essential attribute that contributes to productivity is KRN, which is positively associated with yield (Dhillon and Singh, 1977). Genetic enhancement of KRN trait, a vital yield component trait that directly impacts the productivity of field corn, is one of the major objectives in the field corn breeding (Mukri *et al.*, 2023). The extent of heterosis obtained between the diverse parental lines majorly depends on the *per se* performance of the parental lines as well as the genetic control of complimenting traits that yield heterosis. Once the right combination of traits is found in desirable inbred lines, the success achieved in hybrid breeding will be high. The recombinant lines obtained from the cross of two contrasting pure-lines will be one of the target populations for breeder to search for new genetic combinations of traits. Based on the inheritance, number of genes controlling traits as well as linkage among the gene, the creation of novel traits is possible in bi-parental recombinants.

KRN refers to the number of rows of kernels on a cob, and it directly influences the kernels per ear and finally the grain yield (Liu *et al.*, 2016). However, the ear parameters like ear girth and ear length play an important role by holding more KRN and kernels per row, respectively. Development of such inbred lines having high KRN, ear girth and ear length may be time-consuming through forward breeding approaches but in conventional breeding, breeders can search for desirable gene combinations by screening the segregants for trait-based selection. The present study aims to explore the genetic variability for grain yield and associated traits and selection of tailor-made progenies to enhance the total grain per plant in field corn hybrid breeding program.

Materials and methods

Plant materials

The study was conducted in the field corn experimental farm, ICAR-IARI New Delhi (77° 12'E longitude, 28° 08'N latitude). In this investigation, two bi-parental F_2 populations derived from two contrast KRN parents, AI 505 (low KRN) $\times$ AI 541 (high KRN): Population I and AI 505 (low KRN) $\times$ AI 542 (high KRN): Population II, were grown during *kharif*, 2020. Progenies were evaluated for KRN and other yield-related traits like plant height (cm), cob height (cm), days for 50% flowering, kernel number per row, cob length (cm), cob girth (mm), test weight (g), and grain yield (g/plant).

Estimation of variances, heritability and correlation analysis

The variances were calculated using parental and F_2 data. The environmental variance was calculated using the formula, $VE = (VF_1 + VP_1 + VP_2)/3$, where VF_1 was the variance in the F_1 population, and VP_1 and VP_2 were variances of P_1 and P_2 population, respectively (Wright, 1952). As F_2 is heterozygous and heterogeneous the expected variation is due to $V_G + V_E$, hence the phenotypic variance is equal to the variance of F_2 population, *i.e.*, $V_P = VF_2$. V_G is calculated by the equation $V_G = V_P - V_E$. The broad sense heritability for KRN and other yield-related traits were estimated using the formula $h^2 = (VF_2 - VF_1)/VF_2$ (Burton, 1951). Pearson's correlation analysis was used to understand the association of KRN with other traits.

Results

To generate segregants with desirable trait combinations, the parental lines selected should differ in target traits which means they should be diverse. The parental lines used for generating population 1 differed significantly ($P < 0.05$) for most of the yield component traits. These included plant height (-103), cob height (-182), days for 50 % flowering (-20.8), KRN (-33.9), number of kernels per row (6.7), cob length (18.61), test weight (-0.09), grain yield (-5.07), except for the cob girth (-0.4) for which the value was non-significant as determined by t-test (Table 1).

Table 1. Descriptive statistics, genetic variability, and heritability of yield-related traits of population I

Parameter		T-test	Mean	Range	Variance	Standard deviation	V _G	V _E	V _P	<i>h</i> ² (bs)
Plant height (cm)	P ₁	-54.38	107.28	107-108	0.17	0.41	166.3	0.21	166.51	99.8
	P ₂		118.2	117.5-119	0.23	0.48				
	F ₁		154.5	154-155	0.22	0.41				
	F ₂		135.71	100-170	166.51	12.9				
Ear height (cm)	P ₁	-52.07	56.1	56-56.3	0.011	0.1	57.63	0.091	57.72	99.8
	P ₂		61.28	61-61.3	0.08	0.48				
	F ₁		64.45	64-65	0.17	0.42				
	F ₂		58.86	41-80	57.7	7.59				
Daysfor 50% flowering	P ₁	4.33	50.6	50-51	0.27	0.52	4.99	0.24	5.23	95.47
	P ₂		49.6	49-50	0.27	0.29				
	F ₁		52.8	52-53	0.18	0.42				
	F ₂		53.39	50-59	5.23	2.28				
KRN	P ₁	-10.58	12	10-12	0.88	0.94	1.02	0.83	1.85	85.47
	P ₂		16	14-16	0.88	0.94				
	F ₁		13.6	12-14	0.711	0.84				
	F ₂		12.9	10-16	1.85	1.36				
Kernel number per row	P ₁	-5.66	23.5	23-25	0.5	0.7	28.154	0.62	28.76	97.86
	P ₂		25.2	24-26	0.4	0.63				
	F ₁		37.5	36-38	0.94	0.97				
	F ₂		29.6	16-49	28.78	5.36				
Cob length (cm)	P ₁	-10.25	12.49	12-12.69	0.036	0.18	6.83	0.2	7.03	97.18
	P ₂		14.1	14-14.5	0.21	0.45				
	F ₁		19.8	18.5-20	0.34	0.58				
	F ₂		14.9	8-22	7.05	2.65				
Cob girth (cm)	P ₁	-6.3	3.17	3.1-3.2	0.0024	0.04	42.39	0.006	42.4	99.6
	P ₂		3.42	3.25-3.57	0.011	0.1				
	F ₁		4.48	4.4-4.5	0.004	0.06				
	F ₂		2.23	0.18-3.79	0.44	0.67				
Grain yield (g)	P ₁	-23.85	40.2	36-48	32.4	5.69	10.94	12.98	23.92	45.7
	P ₂		53.6	53-54	4.93	2.21				
	F ₁		131.85	130.5-133.5	1.61	1.27				
	F ₂		4.89	11.3-41	23.93	4.89				

Genetic variability and heritability of the traits

In population I, the high genetic variance was recorded for plant height (166.3) followed by cob height (57.63), cob girth (42.39), kernels per row (28.15), cob length (6.83), days to 50% flowering (4.99) and KRN (1.02). Yield component traits like cob girth (0.006), cob height (0.091), plant height (0.21), days to 50% of flowering (0.24), cob length (0.2) have lower environmental variance (V_E), and the grain yield (12.98), kernels per row (0.62),

KRN (0.83) has higher environmental variance (V_E). Phenotypic variance (V_P) was higher for plant height (166.51) followed by cob height (57.72), cob girth (42.4), kernels per row (28.97), grain yield (23.92), cob length (7.03), days to 50% flowering (5.23) and KRN (1.85) (Table 1 and Figure 1).

In population II, the high genetic variance was observed for grain yield (503.14) followed by plant height (306.03), cob height (120.48), kernels per row (28.12), cob girth (23.5), cob length (5.96), days to 50% flowering

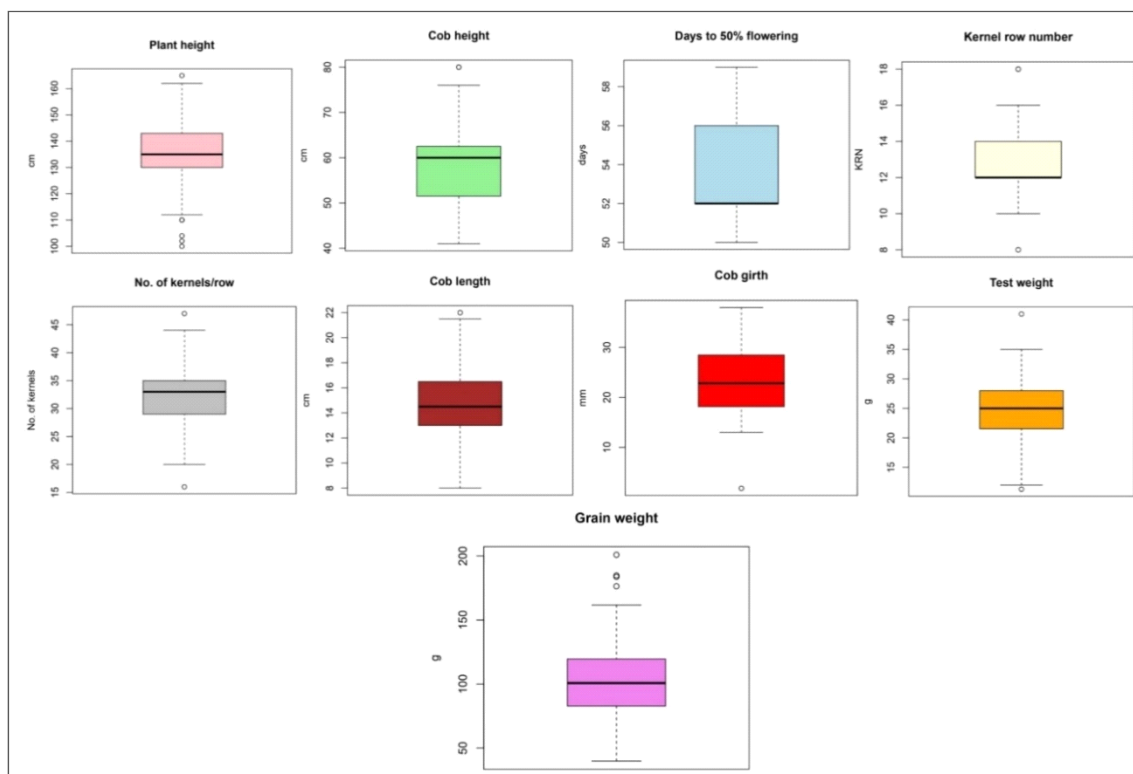


Figure 1. Genetic variation observed in the population I for yield and yield component traits

(5.08) and KRN (3.58). Among all the yield components, cob girth (0.005), cob height (0.012), plant height (0.22), days to 50% of flowering (0.24), cob length (0.13) have lower environmental variance (V_E), and the grain yield (0.96), kernels per row (0.85), KRN (0.61) had relatively higher environmental variance (V_E). Phenotypic variance (V_P) was higher for grain yield (504.1), followed by plant height (306.3), cob height (120.5), kernels per row (28.97), cob girth (24.85), cob length (6.09), days to 50% flowering (5.32) and KRN (4.18) (Table 2 and Figure 2).

In population I, plant height (99.8), cob height (99.8), days for 50% flowering (95.47), KRN (85.47), kernel number per row 97.86, cob length (97.18), cob girth (99.6) recorded high heritability (>60%), whereas grain yield (45.7) has low heritability. Similarly, in population II high estimates of heritability (>60%) were observed for plant height (99.93), cob height (99.99), days to 50% flowering (95.54), KRN (85.47), kernels per row (97.06), cob length (97.83) cob girth (99.8) and grain yield (99.8).

Correlation analysis

In population, I, KRN (0.28), test weight (0.71), cob length (0.56) number of kernels per row (0.62), and plant height (0.28) showed a significantly positive correlation

with grain yield. While, cob height (0.15), cob girth (0.09), and days to 50% flowering (0.05) showed non-significant positive correlations with grain yield.

In population II, KRN showed a significant positive correlation (0.40) with grain yield. Similarly, number of kernels per row (0.74), and test weight (0.60) also showed a significant positive correlation with grain yield.

In population II, KRN showed a significant positive correlation (0.40) with grain yield (g). Similarly, the number of kernels per row (0.74), and test weight (0.60) also showed a significant positive correlation with grain yield (g). Similarly, cob length (0.20), cob height (0.19), and plant height (0.29) also showed a positive correlation with grain yield (g) and showed a positive non-significant correlation with days for 50% flowering (0.08) (Figure 3).

Discussion

This study found high genetic and phenotypic variance for grain yield, plant height, and cob height in both populations, suggesting these traits are under genetic control and can be used to improve field corn yields (Kumar *et al.*, 2014); (Nzuve *et al.*, 2014), and (Jilo *et al.*, 2018). The low genetic and phenotypic variance was seen in kernel number per row, cob girth, cob length, days

Table 2. Descriptive statistics, genetic variability, and heritability of yield-related traits of population II

Parameter		T-test	Mean	Range	Variance	Standard deviation	V _G	V _E	V _P	<i>h</i> ² (bs)
Plant height (cm)	P ₁	-103	107.28	107-108	0.17	107.28	306.03	0.22	306.3	99.93
	P ₂		127.4	127-128	0.211	0.46				
	F ₁		173.5	173-174	0.23	0.53				
	F ₂		145.35	110-190	308.1	17.5				
Cob height (cm)	P ₁	-182	56.1	56-56.1	0.112	56.1	120.48	0.012	120.5	99.99
	P ₂		66.36	66.20-66.50	0.02	0.14				
	F ₁		80.04	80.00-80.10	0.0049	0.53				
	F ₂		70.62	50-100	120.7	10.98				
Daysfor 50% flowering	P ₁	-20.8	50.6	50-51	0.26	0.52	5.08	0.24	5.32	95.54
	P ₂		55.4	55-56	0.26	0.52				
	F ₁		55.8	55-56	0.177	0.42				
	F ₂		55.07	50-59	5.29	2.31				
KRN	P ₁	-33.9	12	10-12	0.88	0.84	3.58	0.61	4.18	85.47
	P ₂		21.6	20-22	1.06	0.84				
	F ₁		17.4	16-18	0.93	0.63				
	F ₂		14.79	12-24	3.66	2.05				
Kernel number per row	P ₁	6.7	23.5	23-25	0.5	0.71	28.12	0.85	28.97	97.06
	P ₂		21.1	20-22	0.77	0.88				
	F ₁		37.8	36-40	1.29	1.14				
	F ₂		29.57	18-45	28.78	5.38				
Cob length (cm)	P ₁	18.61	12.49	12.4-12.69	0.035	0.37	5.96	0.13	6.09	97.83
	P ₂		10.05	9.5-11	0.1361	0.37				
	F ₁		17.65	17-18	0.225	0.47				
	F ₂		13.18	6.5-25	6.11	2.47				
Cob girth (cm)	P ₁	-0.4	3.177	3.11-3.22	0.0024	0.05	24.85	0.005	23.5	99.8
	P ₂		3.19	3.1-3.3	0.0077	0.09				
	F ₁		4.38	4.3-4.4	0.004	0.06				
	F ₂		2.8	2.02-4.02	0.24	0.49				
Grain yield (g)	P ₁	-5.07	36.4	36-37	32.4	0.52	503.14	0.96	504.1	99.8
	P ₂		49.5	48-51	4.1	1.08				
	F ₁		132.9	132-135	261.79	1.2				
	F ₂		85.82	29.92-122.88	505.73	22.45				

for 50% flowering, and KRN, which may be due to phenotypic plasticity and the presence of both negative and positive alleles (Manju *et al.*, 2002), (Shakoor *et al.*, 2007) and (Jilo *et al.*, 2018). The genotypic and phenotypic variance values differed slightly for many component traits, indicating less influence of environmental factors on gene expression. However, grain yield, kernel number per row, and KRN had higher environmental variance, suggesting higher influence of growing environment. This suggests higher chances of success in

selection (Yusuf *et al.*, 2010) and (Jilo *et al.*, 2018). In this study, it was found that plant height, cob height, days for 50% of flowering, KRN, kernel number per row, cob length, cob girth, and grain yield had high heritability (Sibov *et al.*, 2003); (Lu *et al.*, 2011); (Al-Tabbal and Al-Fraihat, 2012) and (Nzuve *et al.*, 2014). Hence, conventional breeding procedures for mentioned traits would improve field corn yields. Taking clues from the above, 10 genotypes each in two populations were selected for future maize breeding programs. Genotypes, 172 and 181 had

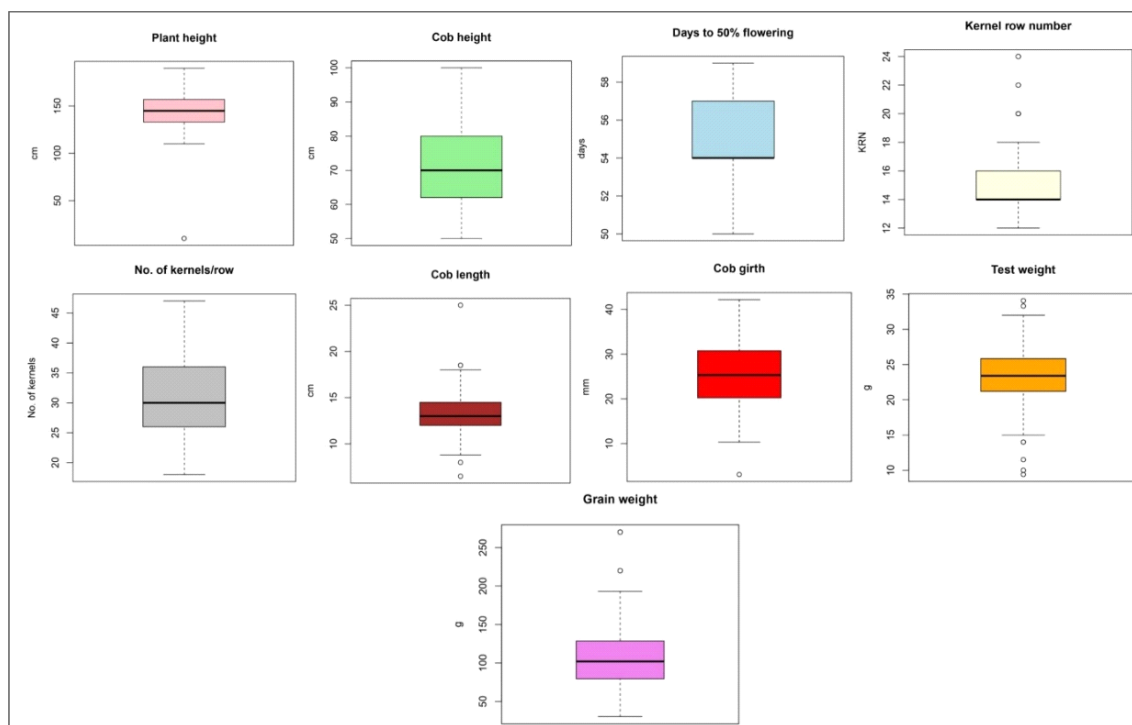


Figure 2. Genetic variation observed in the population II for yield and yield component traits

Table 3. Promising genotypes selected from two bi-parental populations for yield and yield components traits

S.No.	Population I							Population II						
	Genotypes No.	KRN	CL (cm)	CG (mm)	KPR	TW (g)	GY (g/cob)	Genotypes No.	KRN	CL (cm)	CG (mm)	KPR	TW (g)	GY (g/cob)
1	172	18	13.00	35.09	24	25.00	108.00	187	24	11.50	39.35	32	25.60	182.37
2	181	18	18.00	32.52	36	23.50	152.28	083	22	17.00	30.75	40	25.00	220.00
3	019	16	8.50	31.26	16	24.00	61.44	059	20	16.50	23.07	45	30.00	270.00
4	166	16	14.00	26.46	26	20.70	86.11	036	20	15.50	29.14	45	20.80	187.20
5	179	16	12.00	22.72	26	17.00	70.72	005	20	9.00	18.70	27	19.30	104.22
6	192	16	18.30	28.84	35	25.00	140.00	003	18	13.40	31.00	35	17.00	60.00
7	193	16	14.00	36.09	32	15.60	79.87	021	18	12.00	24.50	32	22.00	126.72
8	203	16	14.00	20.97	35	20.00	112.00	053	18	13.20	19.00	35	22.50	141.75
9	001	14	13.00	16.27	35	20.00	98.00	054	18	11.50	30.50	30	29.50	159.30
10	002	14	16.50	27.8	33	27.20	125.66	056	18	12.40	27.10	28	25.20	127.01

KRN: Kernel Row Number, CL: Cob Length, CG: Cob Girth, KPR: Kernels Per Row, TW: Test Weight, GY: Grain Yield

high KRN (18) which also had high grain yield (108 g/cob and 152 g/cob respectively) in population I. Similarly, in population II, genotypes, 187, 083, 059, 036, and 005 had KRN of 20 and above and they realized more than 100 g grain yield per plant (Table 3.).-KRN had a significant positive correlation with plant height, cob height, cob girth, and grain yield (Figure 3 and 4). This may be due to the following reason, as the cob girth increases there is enough space to accommodate a greater number of kernel rows and hence the total number of

kernels per cob which in turn increases the grain yield (Lu *et al.*, 2011) and (Wang *et al.*, 2019). The total grain yield of a plant increases with the increased KRN provided the con length, kernels per row, and test weight are unaffected (Simmons *et al.*, 2020). It is evident from the present investigation that an increase in KRN might increase final grain yield in maize. The selected genotypes can be taken forward for developing inbred lines with desirable yield component traits in general and high KRN lines in particular.

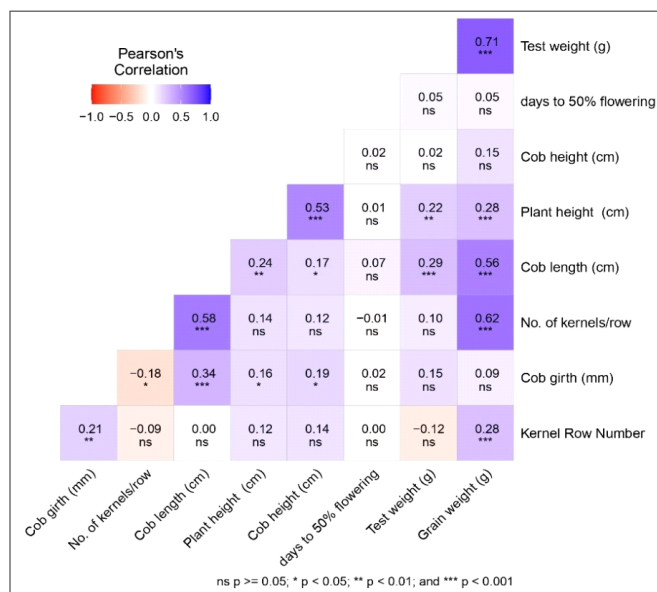


Figure 3. Correlation among nine yield component traits in population I

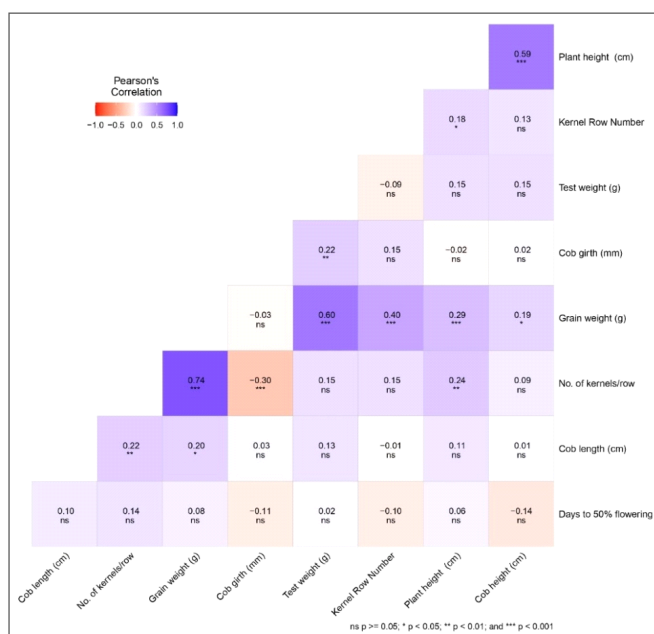


Figure 4. Correlation among nine yield component traits in Population II

Conclusion

The parental lines involved in generating both populations differed significantly for all yield component characters. F_1 had the highest mean for plant height, cob height, number of kernels per row, cob length, test weight, and grain yield. This indicates that these traits are under the control of additive genes, allowing effective selection in early generations and elite genotypes to be isolated from

these populations. Correlation studies revealed that kernel row number had a significant positive correlation with plant height, cob height, cob girth, and grain yield. Grain yield had a positive association with plant height, cob height, kernel row number, number of kernels per row, cob length, and test weight. Specific traits like cob girth, kernels per row, and KRN were found to be the most yield-determinative traits thus simultaneous selection for these traits may lead to yield improvement.

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