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GENETIC VARIABILITY AND HETEROSIS FOR YIELD AND YIELD CONTRIBUTING TRAITS IN COWPEA (*Vigna unguiculata* (L) Walp)

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Abstract
Four Cowpea genotypes were crossed using half diallel mating design. The parents and F1's generated from the crosses were evaluated in the Teaching and Research Farm of Joseph Sarwuan Tarka University, Makurdi. The objective of the study was to determine the general and specific combining ability and heterosis for some quantitative traits in cowpea. Highly significant GCA was observed for most of the characters except plant height, peduncle per plant, pod per plant, seed per pod, pod weight per plot, seed yield per plant and grain yield (kg/ha^{-1}). Similarly, significant SCA was observed for most of the characters except for plant height, peduncle per plant, pod length, branches per plant and seed per pod. The best combiners were IT89KD-288, UAM09 1055-6 and UAM10 2021-1 for most of the studied traits, indicating that these genotypes could be considered as good combiners for improving these traits. Based on the SCA effects, cross between IT89KD-288 × UAM10 2021-1 was found to be the most promising combiners in most of the yield and yield contributing traits. Also, the crosses between UAM10 2021-1 × UAM09 1055-6 and UAM09 1051-1 × UAM09 1055-6 exhibited earliness in days to maturity.

Keywords: Cowpea, Genetic, Heterosis, Variability, Combining ability, Diallel mating

Introduction
Cowpea (*Vigna unguiculata* (L) Walp) is one of the ancient grain legumes valued for its nutritional value, especially high protein content (25%), flavor and short cooking time (Ogbonnaya *et al*., 2003). The crop plays a considerable role in the nutritional balance and economy of the rural population in West Africa sub-region (Krasova-Wade *et al*., 2006). West African sub-region is responsible for about 80% of the world cowpea production, with the principal producers being Nigeria and Niger (Ogbonnaya *et al*., 2003). Despite the increasing importance of cowpea in the diet of many Nigerians, yield per hectare remains low. Although yields of 2500 kg/ha are achievable, several constraints have kept farmers' yields constantly low at levels between 350 and 700 kg/ha, (Aremu, 2005).

One of the challenges with yield improvement is to determine if the percentage of variability of yield and its components is heritable. Heritability of a character is important for the cowpea breeder because it provides him an idea of the extent of genetic control for the expression of a particular character. It is usually necessary to evaluate various traits contributing to the overall yield of the genotype in crossbred populations prior to making any decision regarding parental combinations. Pod and seed traits are examples of such yield components in cowpea. Yield per hectare is the product of population density, number of pods per plant, number of seeds per pod and mean seed weight. Hence, seed yield is a complex trait that includes various components and finally results in a highly plastic yield structure (Amiri-Oghan *et al*., 2009; Diepenbrock, 2000).

The present investigation was therefore undertaken to estimate the genetic variation and heterosis for yield and yield components in cowpea (*Vigna unguiculata* (L) Walp) with the aim of developing a strategy for improving yield and yield traits, using diallel mating design.

Materials and Methods The experiment was conducted at the Teaching and Research Farm of the Federal University of Agriculture Makurdi, Benue state of Nigeria between Latitude $7^{0}.41^{//}$ N and Longitude $8^{0}.39^{//}$ E and at the elevation of 97m above sea level with an average of 1150mm of rainfall.

Experimental Materials
The materials used for this experiment consisted of four cowpea genotypes - UAM09 1055-6, UAM10 2021-1, UAM09 1051 and IT89KD-288. The crosses were carried out at the screen house located at the Teaching and Research Farm of the University of Agriculture Makurdi. Six (6) F_1's were generated (IT89KD-288 X UAM09 1051-1, IT89KD-288 X UAM10 2021-1, IT89KD-288 X UAM09 1055-6, UAMO9 1051-1 X UAM10 2021-1, UAM09 1051-1 X UAM09 1055-6, UAM10 2021-1 X UAM09 1055-6) in a partial diallel design.

Experimental layout and cultural practices
The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Treatments (Parent and F_1's) were assigned to a single row of 2m length with inter and intra row spacing of 0.75m and 0.25m, respectively. Seeds were planted on ridges constructed and all cultural practices for cowpea production was carried out. The following data were measured; Plant height (cm), branches per plant, Days to 1st flowering, Days to 50 % flowering, Days to maturity, Number of Pods per plant, Number of peduncles per plant, Number of pods per peduncle, Pod length, Number of seeds per pod, Pod weight per plot, 100-seed weight (g), Seed yield per plant (g) and plot yield (kg)/ha.

Statistical Analysis
All data collected were subjected to Analysis of variance. General and Specific combining ability were determined according to Griffing (1956) Model-I (Fixed effect), Method-2 (Parents and one set of F_1's).
Better parent Heterosis was calculated as the deviation of F_1 from the better parent (**Fonseca and Patterson**, **1968)** and expressed on per cent basis by the following formula

Better parent Heterosis (%)
$$=\frac{\overline{F_1}-\overline{BP}}{\overline{BP}} \times 100$$
Where,
$\overline{F_1}$= mean performance of F_1
$\overline{BP}$= mean performance of the better parent of the respective cross

Mid Parent Heterosis
Mid-parent heterosis was calculated as the deviation of F_1 from the Mid-parent (**Meredith and Bridge**, **1972)** and expressed on per cent basis by the following formula

Mid-parent Heterosis (%)
$$=\frac{\overline{F_1}-\overline{MP}}{\overline{MP}} \times 100$$
Where,
F_1= mean performance of F_1
MP = mean performance of the Mid-parent of the respective cross

Result
Analysis of variance for combining ability of Cowpea crosses is presented in Table 1. Highly significant GCA was observed for all the characters except plant height at 6 weeks after planting, pod per plant, seed per pod, pod weight per plot, seed yield per plant and grain yield (kg/ha^{-1}). Highly significant SCA was observed for all the characters except for plant height at 6 weeks after planting, pod length, branches per plant.

The estimates of General Combining Ability (GCA) effect of four Cowpea parents are presented in Table 2. The GCA effect were significantly different across the studied traits. Genotype IT89KD-288 showed and UAM09 1055-6 were highly significant for days to fifty percent flowering and days to ninety five percent maturity while UAM09 1051-1 showed highly significant GCA for days to fifty percent flowering, days to ninety five percent maturity, pods per peduncle, 100 seed weight and UAM09 1055-6 showed highly significant GCA for days to first flowering, days to fifty percent flowering, days to ninety five percent maturity, number of branches per plant and 100 seed weight. GCA effect for grain yield was significantly different only for UAM09 1055-6 with 92.38 while in the other genotypes the GCA effects were negative**.**

The estimates of Specific Combining Ability (SCA) effect of four Cowpea parents were significant for almost all the traits studied. Grain yield was significant in crosses IT89KD-288 x UAM10 2021-1 (263.87), IT89KD-288 x UAM09 1055-6 (342.24), UAM09 1051-1 x UAM09 1055-6 (-192.56) and UAM10-2021-1 x UAM09 1055-6 (340.53).

Heterosis was measured as percentage increase or decrease over mid parent (relative heterosis) and better parent (heterobeltiosis). The estimation of heterosis over mid parent and better parent for different characters are presented in Table 3. Result on days to first flowering revealed that all crosses exhibited a negative heterosis as compare to their respective mid-parents while highly significant heterosis were observed for the following crosses UAM10 2021-1 × UAM09 1055-6 (-12.98). Similarly, days to 50% flowering exhibited a negative heterosis for all crosses while the IT89KD-288 × UAM10 2021-1 (-16.31) had the least value, result on days to 95% maturity indicated that all crosses except UAM09 1051-1 × UAM09 1055-6 (1.06) exhibited negative and significant heterosis over their respective mid-parents, meanwhile the cross IT89KD-288 × UAM10 2021-1 had the highest value (-5.61). Similarly, all crosses had high significant and negative values over their better parent, meanwhile the cross IT89KD-288 × UAM09 1055-6 had the highest value (-12.56).

Pods per peduncle showed that all crosses had more pods than their respective better-parent with a positive value ranging from 1.66 (UAM10 2021-1 × UAM09 1055-6) to 22.67 (IT89KD-288 × UAM10 2021-1), similarly, results for better parent heterosis indicated that aside IT89KD-288 × UAM09 1051-1 (-3.2) and IT89KD-288 × UAM09 1055-6 (-1.1) the other crosses had positive values ranging from 1.1 (UAM10 2021-1 × UAM09 1055-6) to 7.53 (UAM09 1051-1 × UAM10 2021-1). Result on pod length indicated that all crosses except UAM09 1051-1 × UAM09 1055-6 (-2.00) were positively and longer than their respective better parents with values ranging from 5.26 (UAM09 1051-1 × UAM10 2021-1) to 12.24 (IT89KD-288 × UAM10 2021-1). The estimation of heterosis over mid parent and better parent for grain yield and other traits are presented in Table 4. Pods per plant indicated that all crosses had high and significant values over their respective mid parents ranging from 33.33 (UAM09 1051-1 × UAM09 1055-6) to 103.87 (IT89KD-288 × UAM10 2021-1) similar trend was observed for their respective better parent values ranging from 30.43 (UAM09 1051-1 × UAM09 1055-6) to 100.00 (IT89KD-288 × UAM10 2021-1).

All crosses were significant except UAM09 1051-1 × UAM10 2021-1 for 100 seed weight, with a range of 9.68 to 28.57 value for mid parents heterosis while better parents heterosis ranged between 0 – 21.15. The cross IT89KD-288 × UAM09 1055-6 recorded the highest value for both mid and better parent heterosis. Result on pod weight per plot (UAM10 2021-1 × UAM09 1055-6) recorded the highest mid parent heterosis value of 74.47 while the highest better parent value was 73.68 for IT89KD-288 × UAM10 2021-1 cross. Grain yield showed that the cross between IT89KD-288 × UAM10 2021-1 recording 89.79 and 87.34 highest values for mid and better parents respectively.

Discussion

A general trend of the genetic control of the characters can be ascertained from the estimates of components of GCA and SCA mean squares. In diallel analysis, the GCA is a function of additive genetic effects, but may partially include some dominance effects when gene frequencies are not equal to one half and/or parents included in the analysis of estimate variances. On the other hand, SCA is the function of non-additive genetic effects which include dominance and epistatic effects. In the present study, both GCA and SCA variances were significant for most of the characters except for plant height, peduncle per plant, pods per plant, seeds per pod, pod weight per plot, seed yield per plant and grain yield kg/ha^{-1}. SCA variances were highly significant for days to first flower, days to 50 percent flowering, days to 95 percent maturity, pod per peduncle, pods per plant, 100 seed weight, pod weight per plot, seed yield per plant and grain yield kg/ha^{-1}. This suggested that both additive and non-additive variances were important in the expression of these traits. Significance of both the variances has also been reported by Valarmathi *et al*. (2007), Kwaye *et al*. (2008), Kadam *et al*. (2013), Chudhari *et al*. (2013) and Meena *et al*. (2010). The magnitude of the SCA variance was higher than GCA variance, indicating preponderance of non-additive genes in the control of all the characters studied. Similar results have been reported by Valarmathi *et al*. (2007), (Kwaye *et al*. 2008), Meena *et al*. (2010), Chudhari *et al*. (2013) and Kadam *et al*. (2013) in cowpea for most of these characters.

General combining ability effects were estimated for parents and specific combining ability effects were estimated for hybrids. In the present study, it was observed that none of the parents was good general combiner for all the traits. These results agree with the findings of Patil and Navale (2005), Kwaye *et al*. (2008), Meena *et al*. (2010), Patel and Gupta (2010) Chudhari *et al*. (2013) and Kadam *et al*. (2013) in cowpea. The result of the general combining ability effects of the parents indicated that one of the parent UAM09 1055-6 was a good general combiner for grain yield and other quantitative traits like days to first flower, days to 50 percent flowering, days to 95 percent maturity, peduncle per plant, branches per plant, seed per pod and 100 seed weight hence, it can be considered as the good combining parent as it depicted the good combining ability for seven characters of the twelve characters studied, there by indicating that this parent had the ability to produce higher yield and also higher pods per plant and boldness in the seeds by imparting desirable genes in the progeny on crossing with diverse lines. These findings are in agreement with the findings of Patil and Navale (2005), Kwaye *et al*. (2008) and Meena *et al*., (2010) who also reported general combiner for seed yield. A close relationship between parents, performance and their general combining ability is important in the choice of parents for crossing programme. In the present study, the best general combiners based on GCA and best parents based on performance were different, suggesting for 100 seed weight. The high GCA effects are related to additive gene effects and additive x additive interaction effect (Griffing, 1956) which represents the fixable component of genetic variation. Keeping this in view and considering overall performance of the GCA effects, parents UAM09 1055-6 and UAM10 2021-1 should be used in an intensive breeding programme to exploit the additive and non-additive components of variation of the yield contributing characters. Population involving these lines in multiple crossing programmes may be developed for isolating high yielding genotypes. Furthermore, the parent IT89KD-288 showed high either positive or negative GCA effects for days to 50 percent flowering, days to maturity, pod per peduncle and pod length, parent UAM09 1051-1 showed high positive GCA effects

for pod per peduncle. These parents may be used in component breeding programmes.
For Specific combining ability effects of the hybrids, the cross IT89KD-288 x UAM09 1055-6 was found to be the best combiner for grain yield. The other specific good combiners were UAM10 2021-1 x UAM09 1055-6 and IT89KD-288 x UAM10 2021-1. Further it was observed that this combination also had the higher order SCA effects for days to first flower, days to 50% flowering, pods per plant, pod weight per plot and seed yield per plant. This indicated that though the parents had also good combining ability, they had the ability to produce good specific combination. Therefore, selection should be based on SCA effects of the combination.

Magnitude of Heterosis for Yield and Yield Components in Cowpea

The application of heterosis in breeding is considered to be an outstanding application of principles of genetics to agriculture. Existence of a significant amount of dominance variance is essential for undertaking heterosis breeding programme. The dominance effects are associated with heterozygosity. Therefore, dominance effects are expected to be the maximum in cross pollinated crops and minimum in self-pollinated crops (Katariya, 2014). However, information about heterosis for the identification of potential crosses can offer the maximum chances of obtaining favourable results. Heterosis indicates some degree of genetic diversity between parents hence, with increased genetic diversity; high levels of heterosis would be expected. The heterotic response over mid as well as better parents could be informative to identify true heterotic cross combinations. The amount of heterosis in this study varied among the crosses for characters evaluated. The significant mid- or better- parent heterosis for the cross IT89KD-288 × UAM09 1055-6 and UAM09 1051-1 × UAM10 2021-1 respectively for pods per plant indicates usefulness of these hybrid population, this result corroborates with the finding of Bennet-Laryey and Ofori (1999) who also reported significant high- or better- parent heterosis for pods per plant and seeds per pod. The crosses IT89KD-288 × UAM10 2021-1 and IT89KD-288 × UAM09 1055-6 had longer pods over their mid- and better parent, this result agrees with the findings of Pethe *et al*. (2017) and Patil and Gosavi (2007) who reported desirable Mid-Parent and Better Parent. The number of 100-seed weight might result in increasing weight of pod which resulted in higher pod yield, the following crosses IT89KD-288 × UAM09 1051-1, IT89KD-288 × UAM10 2021-1, IT89KD-288 × UAM09 1055-6, UAM09 1051-1 × UAM09 1055-6, UAM10 2021-1 × UAM09 1055-6 showed significant and positive heterosis over their mid parent this results agrees with the findings of Shashibhushan and Chaudhari (2000) and Patil *et al.* (2005) who also reported positive and significant heterosis for crosses in Cowpea.

Negative value of heterosis for days to flowering and days to 50% flowering is a very desirable attribute since earliness is an important objective in a Cowpea breeding programme. Result obtained from the study showed the following cross IT89KD-288 × UAM09 1051-1 had the least negative value over mid and better parent for days to first flowering while the cross UAM09 1051-1 × UAM09 1055-6 had the least value for days to 50% flowering over mid and better parent, these are in harmony with the findings of Rashwan (2010) and Abd-Elkader (2006) who reported a negative value of -4.45 for days to flowering. The cross UAM10 2021-1 × UAM09 1055-6 and UAM09 1051-1 × UAM09 1055-6 exhibited significant negative heterosis in desired direction over mid and better parent respectively, with regards to days to 95% maturity, these results are similar to the findings of Patel *et al.* (2009) and Karpe (2002) who reported significant negative for GC-0206 x GC-0108 (-11.71 %) for days to maturity. The cross IT89KD-288 × UAM10 2021-1 was significantly higher than both mid and better parent with respect to yield. Similar result was obtained by Wankhade *et al.* (2018) who reported that the cross GC-3 x Wali-4 recorded highest magnitude of heterosis (79.18%).

Conclusion

The parents, IT89KD-288, UAM09 1055-6 and UAM10 2021-1 were good general combiners for seed yield. The crosses IT89KD-288 × UAM10 2021-1, UAM10 2021-1 × UAM09 1055-6 and UAM09 1051-1 × UAM09 1055-6 showed the higher order SCA effect for grain yield and involved poor x average, poor x poor and average x good combining parents. The crosses IT89KD-288 × UAM10 2021-1 was found to be the most promising combinations in most of the yield and yield contributing traits. Also, the crosses UAM10 2021-1 × UAM09 1055-6 and UAM09 1051-1 × UAM09 1055-6 exhibited earliness in days to maturity. These crosses could be exploited in further plant breeding programmes by adopting appropriate breeding techniques in order to evolve high yielding varieties or identification of transgressive segregants from the advanced generation.

Table 1: Mean Square Estimate from Analysis of Variance for Combining Ability

SOV	DF	PHT6	DFF	D50F	D95M	PPP	PDL	BrPP	PDPP	100SDWT	PDWT	SDWT/P	GY (kg/ha)
GCA	3	30.11	33.65**	39.78**	38.10**	0.24**	1.71*	1.73**	4.62	8.67**	0.01	42.90	23901.3
SCA	5	77.39	7.47**	12.66**	2.69**	0.06**	0.89	0.32	136.51**	3.55**	0.07**	454.28**	101570.77**
Error	18	38.87	0.62	1.52	0.39	0.01	0.48	0.15	15.81	0.78	0.01	55.35	15254.68

Key: * and ** significant at $P \leq 0.05$ and $P \leq 0.01$ respectively, PHT6: Plant height at 6 weeks, DFF: Days to first flower, D50%F: Days to 50 percent flowering, D95%M: Days to 95 percent Maturity, , PPP: Number of pod per peduncle, PDL: Pod length, BrPP: Number of Branches per plant, PDPP: Number of Pod per plant, 100SDWT: 100 seed weight, PDWTP: Pod weight per plot, SDWTP: Seed weight per plant and GY: Grain yield kg/ha.

Table 2: General and Specific Combining Ability Effects for Yield and Yield Components in Cowpea

PARENTS	PHT6	DFF	D50F	D95M	PPP	PDL	BrPP	PDPP	100SDWT	PDWT	SDWTP	GY (kg/ha)
GCA												
IT89KD-288	-0.17	0.58	2.17**	1.64**	-0.30**	0.69*	0.25	0.31	-0.33	-0.05	2.00	-40.29
UAM09 1051-1	2.11	-0.14	-0.72	0.25	0.14**	-0.36	0.25	-1.31	0.22	-0.02	-0.17	-11.26
UAM10 2021-1	-3.06	2.64	1.89**	1.75**	0.10**	-0.47	0.31*	0.42	1.50**	-0.01	1.89	-40.82
UAM09 1055-6	1.11	-3.08**	-3.33**	-3.64**	0.07	0.14	-0.81**	0.58	-1.39**	0.08	-3.72	92.38*
CD (0.05)	**4.63**	**0.59**	**0.92**	**0.47**	**0.09**	**0.52**	**0.29**	**2.10**	**0.66**	**0.09**	**5.53**	**91.74**
CD (0.01)	**6.34**	**0.80**	**1.26**	**0.64**	**0.13**	**0.71**	**0.40**	**4.05**	**0.90**	**0.12**	**7.57**	**125.67**
SCA												
IT89KD-288×UAM09 1051-1	-6.41*	0.72	-0.44	-0.72*	0.19**	0.50	0.33	6.83**	0.98*	0.05	9.57*	14.74
IT89KD-288×UAM10 2021-1	14.42**	-3.06**	-4.72**	-2.22**	0.30**	0.94**	-0.06	13.78**	0.70	0.19**	29.18**	263.87**
IT89KD 288×UAM09 1055-6	2.92	-1.00*	-2.83**	-1.50**	0.26**	1.00**	0.39*	6.28**	2.59**	0.26**	9.12*	342.24**
UAMO9-1051-1×UAM10 2021-1	2.14	-2.00**	-2.17**	-0.83**	0.12**	0.33	0.61**	3.06	0.81	0.10	11.68**	48.14
UAM09-1051-1×UAM09 1055-6	8.31**	-0.28	1.06	0.89**	-0.02	-0.61	0.39*	2.56	0.70	-0.20**	1.96	-192.56**
UAM10-2021-1×UAM09 1055-6	-9.19**	-2.72**	-1.56*	0.39	-0.08	0.50	0.33	8.50**	0.76	0.33**	9.90**	340.53**
CD (0.05)	**5.86**	**0.74**	**1.16**	**0.59**	**0.12**	**0.66**	**0.37**	**3.74**	**0.83**	**0.11**	**6.99**	**116.05**
CD (0.01)	**8.03**	**1.02**	**1.59**	**0.81**	**0.16**	**0.90**	**0.50**	**5.12**	**1.14**	**0.15**	**9.58**	**158.97**

Key: * and ** significant at P ≤0.05 and P ≤0.01 respectively, , PHT6: Plant height at 6 weeks, DFF: Days to first flower, D50F: Days to 50 percent flowering, D95M: Days to 95 percent Maturity, PPP: Number of pod per peduncle, PDL: Pod length, BrPP: Number of Branches per plant, PDPP: Number of Pod per plant, 100SDWT: 100 seed weight, PDWTP: Pod weight per plot, SDWTP: Seed weight per plant and GY: Grain yield kg/ha.

Table 3: Mid and Better Parent Heterosis for some traits

	DFF		D50%F		D95M		PPP		PDL		BrPP	
HYBRIDS	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**
IT89KD-288 × UAM09 1051-1	-1.17	-3.79	-5.69	-13.50**	-2.88*	-6.05**	17.65**	-3.20	6.93	3.85	13.51	10.53
IT89KD-288 × UAM10 2021-1	-12.37**	-17.88**	-16.31**	-16.56**	-5.61**	-6.05**	22.67**	2.22	12.24*	5.77	5.26	5.26
IT89KD-288 × UAM09 1055-6	-7.00**	-14.39**	-11.89**	-22.70**	-4.08**	-12.56**	19.21**	-1.10	10.68*	9.62	16.13	-5.26
UAM09 1051-1 × UAM10 2021-1	-9.42**	-17.22**	-9.40**	-16.67**	-2.42*	-5.16**	9.29	7.53	5.26	2.04	18.92*	15.79
UAM09 1051-1 × UAM09 1055-6	-4.24	-9.60**	-0.39	-5.15	1.06	-4.98**	3.26	2.15	-2.00	-3.92	20.00	0.00
UAM10 2021-1 × UAM09 1055-6	-12.98**	-24.50**	-9.47**	-20.37**	-0.51	-8.92**	1.66	1.10	7.22	1.96	16.13	-5.26
S.E.	**0.97**	**1.12**	**1.51**	**1.74**	**0.77**	**0.89**	**0.16**	**0.18**	**0.8563**	**0.989**	**0.48**	**0.55**

Key: S.E: Standard Error, DFF: Days to first flower, D50%F: Days to 50 percent flowering, D95M: Days to 95 percent Maturity, PPP: Number of pod per peduncle, PDL: Pod length, BrPP: Number of Branches per plant, MP: Mid-parent, BP: Better Parent

Table 4: Mid and Better Parent Heterosis for pod per plant, seeds per pod, 100seed weight, pod weight per plot, seed weight per plant and grain yield (kg/ha).

	PDPP		SDPP		100SDWT		PDWT		SDWTP		GY(kg/ha^{-1})	
HYBRIDS	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**
IT89KD-288 × UAM09 1051-1	60.98**	50.00*	-2.78	-2.78	14.55*	8.62	16.67	-3.45	54.67**	43.21*	15.74	-7.26
IT89KD-288 × UAM10 2021-1	103.87**	100.00**	13.43	5.56	11.86*	0.00	73.68**	73.68*	119.19**	115.22**	89.79**	87.34**
IT89KD-288 × UAM09 1055-6	61.90**	47.83*	6.49	0.00	28.57**	21.15**	61.70**	35.71	56.03**	52.78*	75.40**	46.04*
UAMO9 1051-1 × UAM10 2021-1	44.91*	37.50	13.43	5.56	9.68	3.03	29.17	6.90	61.36**	46.91*	20.67	-4.24
UAM09 1051-1 × UAM09 1055-6	33.33	30.43	-1.30	-7.32	13.46*	1.72	-12.28	-13.79	25.49	18.52	-9.86	-14.10
UAM10 2021-1 × UAM09 1055-6	67.25**	55.43**	11.11	-2.44	12.50*	-4.55	74.47**	46.43*	60.29**	54.17*	76.95**	45.81*
S.E.	**4.87**	**5.62**	**0.94**	**1.08**	**1.09**	**1.25**	**0.15**	**0.17**	**9.11**	**10.52**	**151.30**	**174.67**

Key: S.E: Standard Error, PDPP: Number of Pod per plant, SDPP: Number of seeds per pod, 100SDWT: 100 seed weight, PDWT: Pod weight per plot, SDWTP: Seed weight per plant and GY: Grain Yield kg/ha.

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