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RESEARCH ARTICLE

Gene action and pattern of inheritance for quantitative characters of peppers (*Capsicum spp*)

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Abstract

Gene action of yield and yield contributing traits of peppers (*Capsicum spp*) was studied in half diallel mating design involving seven (7) parental genotypes to generate twenty one (21) single cross hybrids during 2022 (April-July) planting season at the Department of Crop Science teaching and research farm University of Uyo, Uyo. Parents and the F_1's were planted during August-December, 2022 to produce F_2's and some F_1 plants were back cross to their respective parents to produce their backcrosses (BCP_1 and BCP_2). The F_2 and backcrosses were evaluated during April-July, 2023 planting season. The data obtained were subjected to generational mean analysis to determine the type of genes action involves in yield and yield contributing traits of pepper. Heritability in broad and narrow sense were estimated. The result showed that, all types of gene action i.e. additive, dominance and interaction components were found to play a major role in the inheritance of yield and yield contributing traits of pepper. High broad sense heritability (>70%) and narrow sense heritability (>50%) for fruit yield per hectare was obtained in all the hybrids with few exceptions. Dominance gene effect was found to be positive and higher in magnitude in all the hybrids for number of fruits per plant, fruit weight per plant and fruit yield per hectare when compared with other genes action indicating hybridization (heterosis breeding) as the best breeding method to improve the productivity of pepper.

Keywords: Gene action, pepper, diallel, heritability, yield

Introduction

Pepper (*Capsicum sp*) is an economically important crop belonging to the family *Solanaceae* which is an indispensable group of vegetables. It originated from South and Central America while the major centre of diversity is Brazil. Pepper is an essential ingredient in global food industries, adding flavour, pungency, colour, taste, vitamins A and C and antioxidants such as carotenoids, ascorbic acid, flavanoids, and polyphenols. Antioxidant compounds present in the different colours (green, yellow, orange, and red) of peppers give them an antioxidative potential which helps protect the body from oxidative damage induced by free radicals when consumed (Nadeem *et al.*, 2011). The gene actions among traits are the basis for initiating the effective breeding programme.

Inheritance analysis of qualitative and quantitative character can show the number of genes controlling certain characters, gene actions, and other genetic information thus making selection more effective and efficient (Arif *et al.,* 2011; Yunandra *et al.,* 2018; Chibesa *et al.,* 2019). According to Derera and Musimwa (2015), generation mean analysis is a tool that can be used to investigate genetic effects in models other than the additive-dominant model. The linear components; additive (a), dominance (d), additive x additive (aa), additive x dominance (ad), and dominance x dominance (dd) can be compared to provide explanations for additive and dominant gene actions for the planning of plant breeding programmes with high efficiency. Therefore, study of inheritance of plant characters become important in maximizing uses of genetic potential in effective breeding programmes.

Hence, the objectives of this study were to generate information on genetic architecture and inheritance of yield and yield component characters of pepper.

Materials and methods

The experiment was conducted at the Crop Science Department teaching and research farm, University of Uyo, Akwa Ibom State. Uyo is located within the humid tropical rainforest zone of southeastern Nigeria. It has coordinates of latitudes $4^0 30^1$N and $5^0 27^1$N, and longitudes $7^0 50^1$E and $8^0 25^1$E and altitude 38.1m above sea level. There are two distinct seasons in Uyo: the wet, rainy season and the dry season. According to Umoh *et al.,* (2013), Uyo has average annual rainfall of 2530.8 mm, relative humidity of 80.83% and temperature of 26^0C-28^0C. The research was carried out from March, 2022 to December, 2023. Seven parental genotypes of pepper (A=Piquante yellow, B=Scotch bonnet, C=Antillais, D=Big sun, E=Tatse, F=Ntuen okpo used as a checked and G=Efia), selected from the germplasm were crossed in half diallel mating design to generate twenty one (21) single crosses during 2022 (April-July) planting season. Seeds of parents and the F_1's were planted during August-December, 2022 to produce F_2's and were cross back to their respective parents to generate their backcrosses (BCP). The parents, F_1, F_2, BCP_1 and BCP_2 of each cross were evaluated in a randomized complete block design (RCBD) with three replicates during April-July, 2023. Planting was done at a spacing of 50 × 50 cm and inorganic compound fertilizer, N.P.K (15:15:15) was applied at the rate of 250 kg per hectare at three weeks after transplanting. Weeding was done manually on the field as when due. Data were collected on the following parameters: number fruits per plant, fruit weight per plant (g), and fruit yield per hectare (tonnes). The estimates of the various gene effects of yield and yield component traits were obtained using generational mean data from the parents, F_1's, F_2's and backcrosses (BCP_1's and BCP_2's) according to the relationship given by Hayman (1958) model as explained by Singh and Chaudhary (1985). Test of significant was done based on the relationship as describe by Gamble (1962).

t value of effect = (gene effect) / √(variance of gene effect)

The variance estimate method was used to estimate the genetic variances of the quantitative traits as described by Acquaah (2007). The estimates of heritability in broad and narrow sense was done as described by Acquaah (2007). The variance of the parental lines, F_1, F_2, BC_1, BC_2 population were used to determine the additive variance, dominance variance, genotypic variance, phenotypic variance environmental variance and heritability. Genetic advance (GA) and the genetic advance as percentage of the mean (GAM) was calculated as described by Johnson et al. (1955).

Results and discussion

Additive gene effect showed that 13 hybrids exhibited significant positive effect number of fruits per plant, 15 hybrids for fruit weight per plant and 5 hybrids for fruit yield per hectare. Dominant gene effect was positive and significant in all the hybrids for number of fruits per plant, fruit weight per plant and fruit yield per hectare. Additive x additive gene effect was found to be positive and significant in 19 hybrids number of fruits per plant, 7 hybrids for weight of fruit per plant and there was no hybrid that exhibited positive and significant additive x additive gene effect for fruit yield per hectare. Additive x dominant gene effect showed that 5 hybrids exhibited significant positive effect for number of fruits per plant, 13 hybrids for fruit weight per plant and 1 hybrid for fruit yield per hectare. Dominant x dominant gene effect shows that no hybrid exhibited positive and significant effect for number of fruits per plant and fruit yield per hectare while 12 hybrids showed a significant positive dominant x dominant gene effect for fruit weight per plant (Table 1, 2 and 3). Gene action plays a significant role in selecting the breeding strategy used to create cultivar types such as hybrid, pure line, synthetic, etc (Akpan *et al.,* 2017). For number of fruits per plant, fruit weight per plant, and fruit yield per hectare, the dominant and dominant x dominant gene action demonstrated a high magnitude of positive effect in the majority of the hybrids. This suggests that these attributes are primarily governed by dominant and dominant x dominant gene action and could be utilized through heterosis breeding. Earlier Navhale et al. (2014) who observed high magnitude of positive dominant and dominant x dominant gene action for number of dry fruits per plant, number of green fruits per plant, green fruit yield per plant and dry fruit yield per plant in pepper, Yunandra et al. (2018) who observed high magnitude of positive dominant and dominant x dominant gene effect for fruit weight and yield, Nascimento et al. (2019) who observed high magnitude of positive dominant gene effect for fruit yield per plant and fruit weight. The highest broad and narrow sense heritability of 77.02% and 69.47% respectively, were observed in the hybrid C♀×F♂ for number of fruits per plant, 86.23% and 75.76% respectively, was obtained in A♀×G♂ hybrid for fruit weight per plant while the hybrid C♀×D♂ had the highest broad sense heritability of 87.69% and the hybrid A♀×C♂ (68.82%) gave the highest narrow sense heritability for fruit yield per hectare. The least broad sense heritability was obtained in D♀×F♂ (65.91%) and the least narrow sense heritability was found in B♀×G♂ hybrid (50.80%) for number of fruits per plant, the least broad and narrow sense heritability of 68.83% and 43.83% respectively was observed in A♀×E♂ hybrid for fruit weight per plant while D♀×G♂ hybrid (78.13%) and E♀×F♂ hybrid (48.64%) gave the least broad and narrow sense heritability for fruit yield per hectare. Partial dominance was observed in all the hybrids for number of fruits per plant, fruit weight per plant and fruit yield per hectare. The highest GAM was obtained in the hybrid E♀×G♂ (29.69%) for number of fruits per plant, the hybrid E♀×F♂ (4.35%) for fruit weight per plant and the hybrid D♀×E♂ (100.27%) for fruit yield per hectare while the least was observed in A♀×C♂ hybrid (14.25%) for number of fruits per plant, A♀×B♂ hybrid (2.36%) for fruit weight per plant and C♀×G♂ hybrid (68.90%) for fruit yield per hectare (Table 4, 6 and 6). Heritability gives an indication of the degree of genetic control over a trait's expression and the accuracy with which a phenotype predicts a trait's breeding value. These traits are highly heritable, and choosing a high-performing collection to improve the traits is feasible due to their high additive effect, which suggests that there is less environmental influence in the observed variation for traits (Deresa *et al.,* 2023). Broad sense heritability is the ratio of genotypic variance to phenotypic variance while narrow sense heritability is the ratio of additive variance to phenotypic variance and of great importance to plant breeders. Additive variance causes resemblance among relative (Aquaah, 2007). Heritability value > 60% is considered low, 60-80% as moderate and value < 80% is considered as high while GAM value > 15% is considered as low, 15-30% as moderate and < 30% as high (Abrham, 2019). Low and moderate broad and narrow sense heritability was observed in number of fruits per plant, and fruit weight per plant, earlier Deresa *et al.,* (2023), Abrham (2019) and Yunandra (2018) reported same observations for number of fruits per plant and fruit yield. High genetic advance as percentage of mean (GAM) observed for fruit yield per hectare was in agreement with the findings of Abrham (2019) for fresh fruit yield and Deresa *et al.,* (2023) for fruit yield. Low to medium GAM observed for number of fruits per plant and low GAM for fruit weight per plant was in line with Abrham (2019) for number of fruits per plant and Deresa *et al.,* (2023) for number of fruit per plant. Character with low heritability couple with low GAM indicates non-additive gene while characters with high heritability couple with GAM indicate that additive gene control the expression of these characters and can be improve through selection. Phenotypic variance of traits was partitioned into heritable (genotypic variance) and non-heritable components. The magnitude of environmental variance was lower than their genotypic variance for all the traits and hybrids. Hence, the genotypic component of the variation was the major contributor to the total variation in the traits study, similar result have been obtained by Abrham (2019) and Deresa *et al.,* (2023). Dominance and dominance x dominance gene action were found to be positive and higher in magnitude in all the hybrids for number of fruits per plant, fruit weight per plant and fruit yield per hectare indicating hybridization or heterosis breeding as the best breeding method to improve pepper productivity.

Table 1: Estimate of gene effect for number of fruits per plant in the hybrids of pepper

Genotypes	F_2 mean	additive gene effect	dominant gene effect	additive x additive gene effect	additive x dominant gene effect	dominant x dominant gene effect
A♀×B♂	51.00	9.17**	29.49**	17.66**	3.01	-8.31
A♀×C♂	52.33	7.00**	41.67**	26.00**	3.00	-13.98
A♀×D♂	49.33	10.33**	26.85**	18.02**	2.83	-13.70
A♀×E♂	51.33	19.66**	7.01	-3.32	10.33**	16.65*
A♀×F♂	54.00	3.66*	20.66**	10.00	-1.00	-1.33
A♀×G♂	48.00	9.33**	40.66**	32.66**	3.33	-29.32**
B♀×C♂	44.67	-8.34**	42.15**	35.32**	-6.18**	-44.33**
B♀×D♂	41.33	3.63*	43.01**	36.68**	2.32	-48.67**
B♀×E♂	43.00	4.34*	23.48**	17.98**	1.17	-27.00**
B♀×F♂	46.00	-1.33	40.15**	30.66**	0.17	-37.64**
B♀×G♂	47.00	-2.50	28.17**	15.68**	-2.34	-11.03
C♀×D♂	45.33	10.16**	43.85**	34.68**	7.16**	-46.34**
C♀×E♂	42.67	7.00**	26.00**	22.00**	1.67	-28.01**
C♀×F♂	51.00	-1.00	35.99**	26.00**	-1.66	-38.67**
C♀×G♂	51.00	7.66**	26.00**	14.00*	5.66**	-1.60
D♀×E♂	40.67	3.67*	29.16**	24.66**	1.84	-38.33**
D♀×F♂	42.67	-4.67**	40.97**	35.98**	-1.83	-46.31**
D♀×G♂	46.00	2.33	43.49**	32.66**	3.83*	-49.66**
E♀×F♂	40.33	-12.00**	39.02**	33.36**	-8.33**	-44.70**
E♀×G♂	38.00	-7.67**	38.00**	35.34**	-4.34*	-46.69**
F♀×G♂	48.33	5.67**	34.67**	25.34**	4.33*	-35.99**

*,**= significant at (p=0.05) and (p=0.01) respectively, A= Piquante yellow, B=Scotch bonnet, C=Antillais, D=Big sun, E=Tatse, F=Ntuen okpo, G=Efia

Table 2: Estimate of gene effect for fruits weight per plant (g) in the hybrids of pepper

Genotypes	F$_2$ mean	Additive gene effect	Dominant gene effect	Additive x additive gene effect	Additive x dominant gene effect	Dominant x dominant gene effect
A♀×B♂	326.2	-4.25*	107.38**	41.02**	-2.05	-38.17**
A♀×C♂	300.9	6.94**	98.04**	40.04**	2.58	-30.46**
A♀×D♂	277.2	15.21**	109.38**	62.54**	0.89	-53.13**
A♀×E♂	254.4	52.26**	92.90**	49.20**	25.93**	-20.62**
A♀×F♂	284.5	33.86**	81.63**	27.00**	19.84**	-29.52**
A♀×G♂	326.5	13.92**	86.74**	19.16**	10.44**	15.67
B♀×C♂	366.0	8.24**	59.49**	-10.84	1.70	41.37**
B♀×D♂	355.3	32.96**	64.00**	8.20	16.44**	8.14
B♀×E♂	301.2	67.09**	83.19**	34.30**	38.56**	-15.35
B♀×F♂	342.6	34.22**	54.03**	-13.76*	18.00**	36.50**
B♀×G♂	360.1	13.75**	34.11**	-33.46**	8.07**	65.06**
C♀×D♂	334.6	25.77**	43.08**	-18.94**	15.79**	35.43**
C♀×E♂	300.8	51.66**	49.75**	9.40	29.67**	18.86*
C♀×F♂	314.2	18.54**	38.96**	-29.72**	8.86**	54.62**
C♀×G♂	328.7	-2.41	61.63**	-11.28	-1.55	32.45**
D♀×E♂	305.9	33.73**	30.06**	-23.26**	21.72**	62.99**
D♀×F♂	330.2	6.86**	42.17**	-18.80**	7.16**	40.61**
D♀×G♂	322.1	-6.43**	49.85**	-14.54*	4.41*	53.66**
E♀×F♂	317.9	-27.56**	22.07**	-44.16**	-15.25**	89.12**
E♀×G♂	345.9	-57.06**	32.47**	-321.28	-34.21**	-120.79**
A♀×B♂	326.2	-4.25*	107.38**	41.02**	-2.05	-38.17**

*,**= significant at (p=0.05) and (p=0.01) respectively, A= Piquante yellow, B=Scotch bonnet, C=Antillais, D=Big sun, E=Tatse, F=Ntuen okpo, G=Efia

Table 3: Estimate of gene effect for fruits yield per hectare (t/h) in the hybrids of pepper

Genotypes	F$_2$ mean	Additive gene effect	Dominant gene effect	Additive x additive gene effect	Additive x dominant gene effect	Dominant x dominant gene effect
A♀×B♂	13.04	-0.17	4.26	1.62	-0.09	-1.4
A♀×C♂	12.03	0.42	4.14	1.84	0.24	-1.73
A♀×D♂	11.08	0.61	4.45	2.62	0.03	-2.32
A♀×E♂	10.17	2.09**	3.74	2.01	1.04	-1.32
A♀×F♂	11.38	1.50*	3.53	1.36	0.93	-1.48
A♀×G♂	13.05	0.55	3.33	0.78	0.41	0.46
B♀×C♂	14.64	0.35	2.31	-0.50	0.09	1.74
B♀×D♂	14.21	1.32	2.55	0.32	0.66	0.33
B♀×E♂	12.04	2.69**	3.33	1.38	1.55*	-0.67
B♀×F♂	13.70	1.36	2.10	-0.60	0.71	1.47
B♀×G♂	14.40	0.55	1.31	-1.38	0.33	2.65
C♀×D♂	13.38	1.04	1.68	-0.8	0.64	1.47
C♀×E♂	12.03	2.08**	1.93	0.32	1.20	-0.15
C♀×F♂	12.56	0.73	1.52	-1.22	0.34	2.23
C♀×G♂	13.14	-0.09	2.41	-0.50	-0.50	1.37
D♀×E♂	12.23	1.34	1.21	-0.91	0.86	2.52
D♀×F♂	13.21	0.28	1.68	-0.76	0.29	1.62
D♀×G♂	12.88	-0.25	1.98	-0.58	0.19	2.14
E♀×F♂	12.72	-1.11	1.34	-1.36	-0.62	3.54
E♀×G♂	13.83	2.28**	1.25	-1.64	-1.36	4.88
A♀×B♂	13.04	-0.17	4.26	1.62	-0.09	-1.4

*,**= significant at (p=0.05) and (p=0.01) respectively, A= Piquante yellow, B=Scotch bonnet, C=Antillais, D=Big sun, E=Tatse, F=Ntuen okpo, G=Efia

Table 4: Estimate of variance components for number of fruits per plant in pepper genotypes

Genotypes	Ve	Va	Vd	Vg	Vp	Hbs	Hns	$\sqrt{D}/A$	GA	GAM
A♀×B♂	6.38	12.42	1.73	14.15	20.53	68.92	60.5	0.37	6.43	14.72
A♀×C♂	7.57	15.16	1.90	17.06	24.63	69.27	61.55	0.36	7.08	14.25
A♀×D♂	7.98	14.79	2.92	17.71	25.69	68.94	57.57	0.45	7.20	18.31
A♀×E♂	6.35	14.67	2.78	17.45	23.8	73.32	61.64	0.44	7.37	18.90
A♀×F♂	8.40	16.19	3.76	19.95	28.35	70.37	57.11	0.48	7.73	17.57
A♀×G♂	7.12	12.06	4.06	16.12	23.24	69.36	51.89	0.58	6.89	17.23
B♀×C♂	5.98	13.64	2.32	15.96	21.94	72.74	62.17	0.41	7.03	20.28
B♀×D♂	9.20	19.15	2.56	21.71	30.91	70.24	61.95	0.36	8.04	27.21
B♀×E♂	9.93	17.69	2.95	20.64	30.57	67.52	57.87	0.41	7.69	27.46
B♀×F♂	6.68	14.94	1.33	16.27	22.95	70.89	65.10	0.30	7.00	19.09
B♀×G♂	7.81	12.94	4.72	17.66	25.47	69.34	50.80	0.60	7.20	18.78
C♀×D♂	6.84	14.11	1.97	16.08	22.92	70.16	61.56	0.37	6.92	19.4
C♀×E♂	7.16	12.56	1.76	14.32	21.48	66.67	58.47	0.37	6.37	22.22
C♀×F♂	5.69	17.20	1.87	19.07	24.76	77.02	69.47	0.33	7.89	20.06
C♀×G♂	7.29	11.95	2.80	14.75	22.04	66.92	54.22	0.48	6.48	16.07
D♀×E♂	6.92	12.92	1.40	14.32	21.24	67.42	60.83	0.33	6.40	24.93
D♀×F♂	9.32	15.32	2.70	18.02	27.34	65.91	56.08	0.42	7.10	23.41
D♀×G♂	5.79	12.27	2.40	14.67	20.46	71.21	59.97	0.45	6.69	17.61
E♀×F♂	6.08	11.97	3.86	15.83	21.91	72.25	54.63	0.57	6.97	24.43
E♀×G♂	7.15	17.17	3.38	20.55	27.70	74.19	61.99	0.45	8.05	29.69
F♀×E♂	5.85	11.56	3.38	14.94	20.79	71.86	55.6	0.54	6.75	18.13

Where, Ve= environmental variance, Va= additive variance, Vd= dominance variance, Vg= genotypic variance, Vp= phenotypic variance, H_{bs}= broad sense heritability, H_{ns}= narrow sense heritability, $\sqrt{D}/A$ = Degree of dominance, GA=Genetic Advance, GAM= Genetic Advance as percentage of mean, A= Piquante yellow, B=Scotch bonnet, C=Antillais, D=Big sun, E=Tatse, F=Ntuen okpo, G=Efia

Table 5: Estimate of variance components for fruit weight per plant (g) pepper genotypes

Genotypes	Ve	Va	Vd	Vg	Vp	Hbs	Hns	$\sqrt{D}/A$	GA	GAM
A♀×B♂	5.02	7.56	3.54	11.10	16.12	68.86	46.90	0.69	5.70	2.36
A♀×C♂	3.55	10.36	4.87	15.23	18.78	81.10	55.17	0.69	7.25	3.19
A♀×D♂	5.70	12.07	3.03	15.10	20.80	72.60	58.03	0.50	6.82	3.31
A♀×E♂	3.74	5.08	2.77	7.85	11.59	68.83	43.83	0.74	4.76	2.49
A♀×F♂	3.79	7.11	2.58	9.69	13.48	71.88	52.74	0.60	5.44	2.54
A♀×G♂	3.30	18.16	2.57	20.67	23.97	86.23	75.76	0.37	8.69	3.66
B♀×C♂	5.13	9.35	2.25	11.60	16.73	69.34	55.89	0.49	5.84	2.42
B♀×D♂	3.46	9.60	4.23	13.06	17.29	75.53	55.52	0.66	6.47	2.98
B♀×E♂	3.77	7.07	3.99	11.06	14.83	74.58	47.67	0.75	5.92	2.99
B♀×F♂	3.87	11.83	4.68	16.51	20.38	81.01	58.05	0.63	7.54	3.29
B♀×G♂	4.67	12.83	3.11	15.94	20.61	77.34	62.25	0.49	7.23	3.02
C♀×D♂	3.66	7.60	4.69	12.29	15.95	77.05	47.65	0.79	6.35	2.93
C♀×E♂	3.18	9.41	3.34	12.75	15.93	80.04	59.07	0.59	6.58	3.59
C♀×F♂	4.76	8.93	5.01	13.94	18.70	74.55	47.75	0.75	6.65	2.97
C♀×G♂	5.14	13.14	5.35	18.49	23.60	78.25	55.61	0.64	7.84	3.29
D♀×E♂	4.22	10.61	5.10	15.71	19.93	78.83	53.24	0.69	7.26	3.90
D♀×F♂	3.78	11.57	5.66	17.23	21.01	82.01	55.07	0.70	7.75	3.76
D♀×G♂	4.15	13.43	4.81	18.24	22.39	81.46	59.98	0.60	7.76	3.53
E♀×F♂	3.29	16.46	4.15	20.61	23.90	86.23	68.87	0.50	8.68	4.35
E♀×G♂	3.71	11.83	4.68	16.51	20.22	81.65	58.51	0.63	7.56	3.50
F♀×G♂	4.23	13.04	4.45	17.49	21.72	80.52	60.04	0.58	7.73	3.47

Where, Ve= environmental variance, Va= additive variance, Vd= dominance variance, Vg= genotypic variance, Vp= phenotypic variance, H_{bs}= broad sense heritability, H_{ns}= narrow sense heritability, $\sqrt{D}/A$ = Degree of dominance, GA=Genetic Advance, GAM= Genetic Advance as percentage of mean, A= Piquante yellow, B=Scotch bonnet, C=Antillais, D=Big sun, E=Tatse, F=Ntuen okpo, G=Efia

Table 6: Estimate of variance components, for fruit yield per hectare (t/h) in the pepper genotypes

Genotypes	Ve	Va	Vd	Vg	Vp	Hbs	Hns	$\sqrt{D}/A$	GA	GAM
A♀×B♂	2.87	12.04	3.25	15.29	18.16	84.2	66.3	0.52	7.39	76.34
A♀×C♂	3.76	15.58	3.33	18.88	22.64	83.39	68.82	0.46	8.17	89.98
A♀×D♂	3.37	7.98	5.66	13.64	17.01	80.19	46.91	0.84	6.82	83.07
A♀×E♂	3.38	9.92	4.24	14.16	17.54	80.73	56.56	0.66	6.96	91.10
A♀×F♂	2.05	10.9	4.39	15.29	17.34	88.18	62.86	0.63	7.57	88.43
A♀×G♂	2.11	10.71	2.98	13.69	15.80	86.65	67.78	0.53	7.10	75.77
B♀×C♂	2.38	10.11	4.63	14.74	17.12	86.10	59.05	0.68	7.33	75.80
B♀×D♂	2.82	9.61	5.88	15.49	18.31	84.60	52.48	0.78	7.46	85.85
B♀×E♂	2.30	9.81	3.12	12.93	15.23	84.90	64.41	0.57	6.83	86.13
B♀×F♂	2.30	8.91	4.75	13.66	15.96	85.59	55.83	0.73	7.05	76.88
B♀×G♂	2.34	9.83	5.37	15.20	17.54	86.66	56.04	0.74	7.47	77.89
C♀×D♂	2.23	9.04	6.84	15.88	18.11	87.69	49.92	0.87	7.68	88.48
C♀×E♂	2.66	8.75	4.19	12.9	15.60	82.95	56.09	0.69	6.73	91.81
C♀×F♂	2.42	9.27	5.26	14.53	16.95	85.72	54.69	0.75	7.27	81.23
C♀×G♂	2.88	8.93	3.59	12.52	15.4	81.30	57.99	0.63	6.58	68.90
D♀×E♂	2.30	9.36	5.80	15.16	17.46	86.83	53.61	0.79	7.47	100.27
D♀×F♂	2.21	10.34	3.57	13.91	16.12	86.29	64.14	0.59	7.15	86.67
D♀×G♂	3.39	7.95	4.16	12.11	15.50	78.13	51.29	0.72	6.33	71.93
E♀×F♂	2.27	6.79	4.45	11.24	13.96	80.52	48.64	0.81	6.19	77.67
E♀×G♂	2.58	10.85	4.13	14.98	17.56	85.31	61.79	0.62	7.36	85.09
F♀×G♂	2.76	9.18	3.74	12.92	15.68	82.40	58.55	0.64	6.72	75.76

Where, Ve= environmental variance, Va= additive variance, Vd= dominance variance, Vg= genotypic variance, Vp= phenotypic variance, H_{bs}= broad sense heritability, H_{ns}= narrow sense heritability, $\sqrt{D}/A$ = Degree of dominance, GA=Genetic Advance, GAM= Genetic Advance as percentage of mean, A= Piquante yellow, B=Scotch bonnet, C=Antillais, D=Big sun, E=Tatse, F=Ntuen okpo, G=Efia

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