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Studies of Gene Effects on Yield and Yield Components in "Egusi" Melon (*Colocynthis citrullus* L.)

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ABSTRACT

Estimates of gene effects for number of fruits/plant, weight of fruits/plant, average fruit weight, seed yield/plant, number of seeds/plant, seed yield/fruit, number of seeds/fruit and 100-seed weight were made on "Egusi" melon (*Colocynthis citrullus* L.). The dominance (*d*) gene effect was more important than the additive (*a*) gene effect in the inheritance of these attributes. The epistatic gene effects made a high contribution and the dominance × dominance (*dd*) gene effect exhibited greater influence among the epistatic genes in most of the attributes. The implications of these findings are discussed and Reciporal Recurrent Selection is suggested as the breeding method for the improvement of these attributes.

Keywords: additive, dominance, epistatic gene action

INTRODUCTION

"Egusi" melon (*Colocynthis citrullus*) is a popular crop in Nigeria and other West African countries. The seed of "Egusi" melon is rich in oil and protein and is one of those crops that furnishes the human diet with good quality and quantity proteins. Among the Cucurbitaceae, *C. citrullus* is the most import in terms of oil and protein quantity of the seeds (Oyenuga and Fetuga 1964; Girgis and Said 1968; Oyolu and Macfarlene 1982; Nwokolo and Sim 1987). Very little research has been done to improve the production of this important crop. There is a complete dearth of information on its genetics. Knowledge of the nature and magnitude of various genetic components controlling the yield and some of its attributes in this crop is necessary. This is so since the success in a crop improvement programme depends on these. Gamble (1962) had noted the importance of the estimation of gene effects in the formulation of a breeding procedure for quantitative genetic traits such as yield. He said that the magnitude of the different gene effects indicates their relative importance in the inheritance. Additive and dominance gene effects have been shown as the major components of gene effects (Lal *et al.* 1975; Jatasra 1980; Chatrath *et al.* 1986). Gamble (1962), however noted the importance of epistatic gene effects on the inheritance of different quantitative characters. The objective of this study is to estimate the gene effects and thereby propose a breeding programme for the improvement of yield in this crop.

MATERIALS AND METHODS

The experiment was carried out in the Department of Crop Science Experiment Farm, Faculty of Agriculture, University of Nigeria, Nsukka. The materials used in this study consisted of 8 inbred lines of "Egusi" melon cultivars; NS.B, NS.W, NS.R, NS.E, NS.E, OV.1, Sewere, W.SE and B.SE (**Table 1**). The following crosses were made; NS.B × NS.W, NS.R × NS.E, W.SE × Sewere, OV.I × W.SE and OV.I × B.SE. The F_1s were selfed and crossed to their respective parents to obtain the F_2s, BC_1s and BC_2s. The inbred parents, F_1s, F_2s, BC_1s and BC_2s of each cross were evaluated in a randomized complete block design (RCBD) with three replications. Each block was divided into six plots, each containing one of the six genotypes. Each plot measured 6 m × 6 m and the "Egusi" melon was planted at 0.5 m × 0.5 m spacing.

Data on number of fruits/plant, weight of fruits/plant, average fruit weight, seed yield/plant, number of seed/plant, seed yield/fruit, number of seeds/fruit and 100-seed weight were collected.

The estimates of various gene effects were obtained following the relationship given by Gamble (1962) as follows:

$$m = \overline{F}_2$$

$$a = \overline{P_1F_2} - \overline{P_2F_2}$$

$$d = \tfrac{1}{2}\overline{P_1} - \tfrac{1}{2}\overline{P_2} + \overline{F}_1 - 4\overline{F_2} + 2\overline{P_1F_1} - 2\overline{P_2F_1}$$

$$aa = -4\overline{F_2} + 2\overline{P_1F_1} + 2\overline{P_2F_1}$$

$$ad = -\tfrac{1}{2}\overline{P_1} + \tfrac{1}{2}\overline{P_2} + \overline{P_1F_1} - \overline{P_2F_1}$$

$$dd = \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{P_1F_1} - 4\overline{P_2F_1},$$

where the parameters *m*, *a*, *d*, *aa*, *ad* and *dd* represent the mean, additive, dominance, additive × additive, additive × dominance, dominance × dominance gene effects, respectively.

$$\sigma_a^2 = \sigma^2 P_1F_1 - \sigma^2 P_2F_1$$

$$\sigma_D^2 = \tfrac{1}{4}\sigma^2 P_1 + \tfrac{1}{4}\sigma^2 P_2 + \sigma^2 F_1 + 16\sigma^2 F_2 + 4\sigma^2 P_1F_1 + 4\sigma^2 P^2 P_2F_1$$

$$\sigma^2 aa = 16\sigma^2 F_2 + 4\sigma^2 P_1\ F_1 + 4\sigma^2 P_1F_1$$

$$\sigma^2 ad = \tfrac{1}{4}\sigma^2 P_1 + \sigma^2 P_1F_1 - \sigma^2 P_2F_1$$

$$\sigma^2 dd = \sigma^2 P_1 + \sigma^2 P^2 + 4\sigma^2 F + 16\sigma^2 F_2 + 16\sigma^2 F_1$$

The "t" test was used as test statistics based on the following relationship:

$$\pm t = \frac{gene\ effect}{\sqrt{\text{var}iance\ of\ \ gene\ effect}}\ .$$

RESULTS

For number of fruits/plant additive gene effect had a low magnitude relative to the mean of the F_2 (**Table 2**). It was negative in NS.B × NS.W, NS.R × NS.E and OV.I × B.SE

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Table 1 Description of the inbred lines of Egusi melon (*Colocynthis citrullus* L.) used in the study.

Inbred lines	Fruit description	Seed description
NS.B	Blue, large	Thin skin, sharp edge
NS.W	White, large	Thin skin, sharp edge
NS.R	Round, large	Thin skin, sharp edge
NS.E	Elongated, large	Thin skin, sharp edge
OV.I	Mottled, large	Thin skin, sharp edge
Sewere	White, small	Thin skin, sharp edge
W.SE	Mottled, small	Thin skin, white encrusted edge
B.SE	Striped, small	Thin skin, black encrusted edge

Table 2 Estimates of the six gene effects for number of fruits/plant in the five crosses.

Gene effect	Crosses				
	NS.B × NS.W	NS.R × NS.E	W.SE × Sewere	OV.I × W.SE	OV.I × B.SE
m	2.51*	1.66*	1.85*	2.27*	2.83*
a	-0.11*	-0.41*	0.48*	0.02^{ns}	-0.57*
d	0.47*	-1.29*	-0.09^{ns}	0.68^{ns}	3.66^{ns}
aa	-1.59^{ns}	0.90*	-0.20*	-0.64*	1.14*
dd	4.82**	0.91**	1.69^{ns}	2.77*	1.49*
ad	0.26*	-0.29*	0.69^{ns}	-0.06*	-0.115*

* and ** = significant at 5% and 1% probability levels, respectively; ns = non-significant effect.

Table 3 Estimates of the six gene effects for weight of fruits (kg)/plant in the five crosses.

Gene effect	Crosses				
	NS.B × NS.W	NS.R × NS.E	W.SE × Sewere	OV.I × W.SE	OV.I × B.SE
m	2.87*	2.21*	1.86*	2.73**	2.31*
a	0.15^{ns}	-0.62**	0.42*	0.48**	0.55*
d	0.21*	-1.54^{ns}	0.19*	1.50^{ns}	5.80*
aa	-2.62*	0.74^{ns}	0.36*	-0.44*	3.68*
dd	8.81*	0.41^{ns}	1.98^{ns}	2.72^{ns}	-2.29^{ns}
ad	0.72*	0.1^{ns}	0.39*	2.70^{ns}	-0.54^{ns}

* and ** = significant at 5% and 1% probability levels, respectively; ns = non-significant effect.

Table 4 Estimates of the six gene effects for average fruits weight (kg) in the five crosses.

Gene Effect	Crosses				
	NS.B × NS.W	NS.R × NS.E	W.SE × Sewere	OV.I × W.SE	OV.I × B.SE
m	1.21*	1.39*	51.47*	1.32*	0.84*
a	0.11*	-0.08^{ns}	15.48^{ns}	0.25^{ns}	-0.16*
d	-0.46^{ns}	-0.35**	42.54*	-0.03*	0.48*
aa	-0.50*	-0.51^{ns}	5.36^{ns}	-0.18**	0.55*
dd	1.41^{ns}	0.09*	8.16*	0.06^{ns}	-0.56^{ns}
ad	0.12^{ns}	0.15^{ns}	15.63^{ns}	0.13**	-0.09^{ns}

* and ** = significant at 5% and 1% probability levels, respectively; ns = non-significant effect.

Table 5 Estimates of the six gene effects for seed yield (g)/plant in the five crosses.

Gene Effect	Crosses				
	NS.B × NS.W	NS.R × NS.E	W.SE × Sewere	OV.I × W.SE	OV.I × B.SE
m	46.34*	37.61**	384.34**	58.00*	40.49**
a	-0.49*	-14.19**	127.77**	16.15*	16.54**
d	2.51^{ns}	21.66*	275.10*	48.22*	73.46**
aa	-49.34**	1.82*	35.50*	-11.87^{ns}	19.96**
dd	164.98**	46.36^{ns}	70.32*	70.25**	59.64*
ad	16.18*	-0.72*	124.64*	14.02*	13.46**

* and ** = significant at 5% and 1% probability levels, respectively; ns = non-significant effect.

Table 6 Estimates of the six gene effects for number of seeds/plant in the five crosses.

Gene Effect	Crosses				
	NS.B × NS.W	NS.R × NS.E	W.SE × Sewere	OV.I × W.SE	OV.I × B.SE
m	350.39**	295.65**	31.65**	452.61**	423.11*
a	5.14**	-118.21**	6.13^{ns}	83.89*	87.44*
d	88.37**	94.40^{ns}	1.85^{ns}	313.00*	332.84**
aa	-311.16**	-38.40**	-13.98^{ns}	-44.26**	-93.28**
dd	1169.09*	431.02**	10.11^{ns}	657.56	677.49*
ad	124.66**	-28.16*	3.77*	70.65**	90.75*

* and ** = significant at 5% and 1% probability levels, respectively; ns = non-significant effect.

and positive in the other two crosses. It was also lower than the dominance gene effect in all the crosses except in W.SE × Sewere and was significant on all crosses but OV.I × W.SE. The dominance gene effect was low relative to the mean of the F_2 in all crosses except OV.I × B.SE where dominance was higher than the mean effect. The dominance gene action was also negative on NS.R × NS.E and W.SE × Sewere and positive on the other three crosses. Among the epistatic gene effects, the dominance × dominance gene effect had the highest magnitude.

The estimate of gene effect on weight of fruits/plant (**Table 3**) indicates that the additive gene effect was positive in all crosses except OV.I × B.SE. It was also low in magnitude and significant in all except NS.B × NS.W. The dominance gene effect was higher in magnitude than the additive effect in all the crosses except W.SE × Sewere. It was also positive in all crosses except NS.R × NS.E. The dominance gene effect was significant in all crosses. The epistatic gene effects showed relatively high magnitude in most of the crosses.

On average, for fruit weight (**Table 4**), the additive gene effect was low in magnitude relative to the mean of F_2. It was however, higher than dominance gene effect in OV.I × B.SE. It was negative only in NS.R × NS.E and OV.I × B.SE. The dominance gene effect had relatively high magnitude in some of the crosses and was positive only in W.SE × Sewere and OV.I × B.SE. Among the epistatic gene effects the dominance × dominance gene effect recorded higher magnitude in NS.B × NS.W and OV.I × B.SE, while the additive × additive gene effect was higher in OV.I × W.SE and NS.R × NS.E.

The additive gene effect was lower than the dominance effect on seed yield/plant in all the crosses (**Table 5**). It was negative only in NS.B × NS.W and NS.R × NS.E and statistically significant in all crosses. The dominance gene effect was positive in all the crosses and significant except on NS.B × NS.W for the same yield attribute. It had the highest magnitude in W.SE × Sewere and OV.I × B.SE. Among the epistatic gene effects the dominance × dominance gene effect had the highest magnitude in all crosses except W.SE × Sewere where additive × dominance gene effect had higher magnitude.

The additive gene effect was negative and high in number of seeds/plant in NS.R × NS.E and W.SE × Sewere, and was higher than dominance gene effect in these crosses (**Table 6**). It was also positive in all the crosses except in NS.R × NS.E. The additive gene effect was significant in all crosses. The dominance gene effect was positive and significant in all the crosses. Among the epistatic gene effect, the dominance × dominance gene effect showed highest magnitude except in W.SE × Sewere where it was lower than the additive × additive gene effect. It also recorded non-significant effect in this cross.

The result obtained in seed yield/fruit (**Table 7**) shows that the additive gene effect has low magnitude relative to the mean of F_2. It was however higher than dominance gene effect in W.SE × Sewere. It was significant in all crosses and only negative in NS.R × NS.E. The dominance gene effect recorded highest magnitude in OV.I × W.SE and was relatively high in other crosses except in W.SE × Sewere. The dominance gene effect was only negative in NS.B × NS.W and NS.R × NS.E. The epistatic gene effects showed relative high magnitude in the crosses.

Additive gene effect recorded low magnitude in number

Table 7 Estimates of the six gene effects for seed yield (g)/fruit in the five crosses.

Gene Effect	Crosses				
	NS.B × NS.W	NS.R × NS.E	W.SE × Sewere	OV.I × W.SE	OV.I × B.SE
m	18.97**	23.99**	235.77**	26.85**	15.66**
a	0.70*	-2.76**	43.26*	5.41*	5.29*
d	-6.33*	-6.69**	24.26*	10.70**	9.94**
aa	-10.44*	-12.40*	-82.56*	1.14*	7.42
dd	30.17*	17.18*	49.09*	-3.36*	-7.59^{ns}
ad	5.52*	2.06**	21.84**	5.25*	9.92*

* and ** = significant at 5% and 1% probability levels, respectively; ns = non-significant effect.

Table 8 Estimates of the six gene effects for number of seed/fruit in the five crosses.

Gene effect	Crosses				
	NS.B × NS.W	NS.R × NS.E	W.SE × Sewere	OV.I × W.SE	OV.I × B.SE
m	145.96**	187.71**	1.09*	213.37**	162.92**
a	2.30*	-28.52*	0.03*	21.26**	30.25*
d	-35.79*	-100.92**	-0.36^{ns}	39.19**	-30.8^{ns}
aa	-61.72**	-133.60*	-30.44^{ns}	-21.44*	-93.28**
dd	200.26*	0197.92**	0.92*	40.80^{ns}	-28.81*
ad	35.50^{ns}	-02.83**	-0.03^{ns}	-22.54^{ns}	-6.40*

* and ** = significant at 5% and 1% probability levels, respectively; ns = non-significant effect.

Table 9 Estimates of six gene effects for 100-seed weight (g) in the five crosses.

Gene effect	Crosses				
	NS.B × NS.W	NS.R × NS.E	W.SE × Sewere	OV.I × W.SE	OV.I × B.SE
m	13.41*	12.97*	13.41*	12.95*	10.17*
a	0.33^{ns}	0.50*	-0.88^{ns}	0.21*	2.11*
d	- 2.34^{ns}	3.38**	-0.05*	-0.44^{ns}	6.75*
aa	- 2.62*	2.32^{ns}	1.72^{ns}	-0.73^{ns}	6.22*
dd	3.35^{ns}	- 3.93^{ns}	-3.66^{ns}	0.87*	- 5.34*
ad	0.84^{ns}	1.19^{ns}	-0.58^{ns}	-0.01^{ns}	0.90^{ns}

* and ** = significant at 5% and 1% probability levels, respectively; ns = non-significant effect.

of seeds/fruit (**Table 8**), but had the highest magnitude in OV.I × B.SE among the gene effects. It was also significant in all the crosses and positive in all except in NS.R × NS.E. The dominance gene effect has high magnitude in comparison with the other gene effects. It was also negative in all crosses except OV.1 x W.SE. Among the epistatic gene effects the dominance × dominance gene effect was the highest in most of the crosses while the additive × dominance gene effect had the least magnitude. They were also significant in most crosses.

Estimate of gene effect in 100-seed weight revealed that additive gene effect was low in magnitude but higher than the dominance gene effect in W.SE × Sewere (**Table 9**). It was positive in all crosses except W.SE × Sewere. The dominance gene effect also had low magnitude relative to the mean of F_2. The dominance gene effect was significant in NS.R × NS.E, W.SE × Sewere and was only positive in NS.R × NS.E and OV.1 x B.SE. The epistatic gene effects were also relatively low in all crosses except OV.I × B.SE. They were non-significant in most of the crosses.

DISCUSSION

The estimates of gene effects measure the effect of the variable loci. The low magnitude of the additive gene effect recorded in most of the attributes appeared to suggest minimal contribution of the additive (*a*) gene effect on the inheritance of these attributes. It was however noted that for seed yield/plant the additive gene effect was higher than in other attributes. The dominance (*d*) gene effect contributed more to the inheritance of most of the yield attributes than the additive gene effect in all the crosses. This shows that the dominance gene effect is more important in the inheritance of these characters in "Egusi" melon. It was also noted that the dominance gene effect was negative in some of the attributes, which implies that it contributed diminishing effect on the attributes. However, on seed yield/plant, it was positive in all crosses indicating an enhancing effect on seed yield/plant and other attributes where it was positive. Rakhi and Rajamony (2005) have suggested that yield in culinary melon (*Cucumis melo* L.) could be improved through selection because of high additive gene effect on yield. This was supported by the finding of Feyzian *et al.* (2009) that additive gene effects controlled average fruit weight and yield in melon. Zalapa *et al.* (2006) added that additive gene effects were most important in governing number of primary branches and yields/plant in melon. They further reported that days to anthesis, fruit weight/ plant and average fruit weight are controlled by dominance and epistatic genetic effects. The dominance gene effect has also been implicated in controlling fruit enlargement in melon (Fernández-Silva *et al.* 2009).

The high magnitude of the additive × additive (*aa*), additive × dominance (*ad*) and dominance × dominance (*dd*) gene effects in most of the attributes relative to mean effect indicates that epistatic gene effects contributed greatly to the inheritance of these attributes (Hayman 1958). For example, the non-additive gene effect appeared to contribute more than the additive gene effect in the inheritance of most of the attributes studied, an indication that their inheritance is controlled by many loci. The dominance × dominance gene effect was higher than that of other epistatic effects. Considering the sign of the dominance and dominance × dominance gene effects, the epistatic gene interaction was of the complimentary type in seed yield/plant in all crosses (Mather and Jinks 1971).

CONCLUSION

The important part of this crop is the seed, which is consumed in many forms and which also contains oil and a good array of amino acids. Considering this fact, breeding procedures that may lead to high seed production should be used. Such breeding procedure as reciprocal recurrent selection may be adopted which according to Comstock *et al.* (1949), Uguru and Uzo (1991) is the best for inheritance that is more of dominance and epistatic gene effects.

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