

Generation Means Analysis of Seed Sucrose Content in Cowpea (*Vigna unguiculata* L. Walp.)

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Abstract: The sucrose concentration of seeds is an important component of the taste in cowpea (*Vigna unguiculata* L. Walp.). The objective of this research was to estimate the heritability, to investigate the mode of genetic control and to evaluate the potential for genetic improvement of sucrose content in cowpea using generation's means analysis. F₁ and F₂ generations as well as backcross populations (BC_{P1} and BC_{P2}) were produced in three hybrid combinations by crosses of four selected cultivars. The sucrose level was measured via a High Performance Liquid Chromatography (HPLC) system. The range of variation in sucrose content among tested varieties was from 1.88 mg/g (Lori) to 5.32 mg/g (C93W-24-125). Broad-sense heritability (h²) was of a moderate 58.50% to high 68.12% value and no transgressive segregation was observed. Narrow-sense heritability (39.47 to 47.83%) and heterosis (-20.00 to -5.94%) values and gene effects analysis suggested that the sucrose content is controlled by additive and non-additive genes. At 10% level of selection, an increase of 19.60 to 33.64% was predicted after one cycle. Epistasis was significant in most of crosses and at least five genes affected the sucrose accumulation in cowpea seeds. These results suggested that breeding for increased sucrose content in the seeds of cowpea can be quite successful through recurrent selection in later generations.

Key words: Genetic improvement, heritability, sweet flavour, *Vigna unguiculata*

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp), an indigenous African annual legume, is a high protein (25%), fiber (6.3%) and low fat (1.9%) vegetable crop having good nutritional qualities (Ehlers and Hall, 1997). About two-thirds of the production and more than three-fourths of the area of production is spread over the vast Sudan Savannah and Sahelian zones of sub-Saharan Africa (Ehlers *et al.*, 2000). Dry grain for human consumption is the principal product of cowpea plant, but leaves, fresh peas, fresh green pods are also consumed (Islam *et al.*, 2008). The nutritional qualities of cowpea grain are influenced by both genotype and environmental conditions (Singh, 2001). In northern Cameroon, most consumers prefer cooked grain with a firm texture (Kitch *et al.*, 1998; Hall *et al.*, 2003). Genotypes are selected based on yield potential, pest resistance, seed quality, maturity period, suitability for dual purpose use, cooking and taste properties (Ehlers and Hall, 1997; Singh, 2001). Cowpea varieties have different taste based mainly on sugars present in the seeds (Kitch *et al.*, 1998; Islam *et al.*, 2008). Farmers who participated in the Institute of

Agricultural Research for Development (IRAD), Cameroon cowpea breeding program noted that a specific line bred by Bean/Cowpea Collaborative Research Support Program (CRSP), 'C93W-24-125B', tasted "sweet" or "good" (Kitch *et al.*, 1998, 2003). Line "C93W-24-125B" was shown to have a sucrose content of about 6% (w/w) compared to about 2% for typical cowpea cultivars (Hall *et al.*, 2003; Kitch *et al.*, 2003). Cameroonian farmers consistently chose this line as being their favourite for its sweet flavour although it had a poor agronomic performance (Ehlers *et al.*, 2000). According to Hall *et al.* (2003) taste panel tests conducted at Purdue University showed that, US tasters chose line 'C93W-24-125B' more than 80% of the time over the conventional varieties. Apparently, the "sweet" trait could be a valuable flavour trait that breeders could use to enhance the desirability of cowpea cultivars for both traditional cowpea consumers and those to whom cowpea is less familiar (Faye *et al.*, 2006). One of the objectives of cowpea improvement is to develop cultivars with greater sucrose content that would confer a distinct sweet taste to the grain (Hall *et al.*, 2003; Faye *et al.*, 2006). The discovery of sweet trait opens up the possibility of

developing new products that are very attractive to consumers and thus larger markets for cowpea (Ehlers *et al.*, 2000; Hall *et al.*, 2003). The sweeter and milder taste of the sweet cowpea could help broaden the number of potential consumers in terms of the consumption of dry grain and in value-added products (Faye *et al.*, 2006). However, a comprehensive assessment of the inheritance of sucrose content in cowpea has not been reported. Studies on the genetics of sucrose trait were conducted in many other cultivated crops like soybean (Kennedy *et al.*, 1985; Maughan *et al.*, 2000; Mebrahtu and Devine, 2009), coffee (Ky *et al.*, 2000), sugarcane (Jackson, 2005), waxy corn (Simla *et al.*, 2009) and sorghum (Audilakshmi *et al.*, 2010). Mebrahtu and Devine (2009) reported that additive and non-additive gene effects were significant for sucrose level in soybean (*Glycine max*) and consequently, the "Single Seed Descent" breeding system appeared as the relevant method of improvement. Knowledge of the genetic basis and heritability of sucrose accumulation is essential for efficient development of superior cultivars. Thus, this study was designated to investigate possible genetic effects on the expression of the sucrose content, to estimate the heritability of the character and the selection gains, and to evaluate the genetic improvement in high sucrose content cowpea germplasm.

MATERIALS AND METHODS

Experimental site: The research was conducted from 2008 to 2010 at the University of Ngaoundéré experimental farm, at Dang, Adamawa region (northern Cameroon), which is intersected by 13°34' East longitude and 7°28' North latitude and has an elevation of 1115.0 m above the mean sea level. This region belongs to the Guinea savannah agroecological zone. The soil is ferruginous type, developed on basalt and at the farm it has a brown reddish clay texture, with relatively high fertility. The climate is characterized by two seasons with an average annual rainfall of 1480 mm that is fairly distributed over the rainy growing period (April to September). The average annual temperature is 22°C, while the annual hygrometry is about 70%.

Genotypes used in the study: Four parents were selected based on their diversity and previously reported levels of sucrose (Kitch *et al.*, 1998; Hall *et al.*, 2003; Kitch *et al.*, 2003). 'K VX 61-1' was a sweet cowpea breeding line developed by the national breeding program in Burkina Faso. 'C93W-24-125' was developed for its high sucrose content by the Institute of Agricultural Research for Development (IRAD, Maroua, Cameroon) through the Bean/Cowpea Collaborative Research Support Program (CRSP). This genotype is small-seeded, late-maturity, photosensitive and has a prostrate growth habit (Ehlers *et al.*, 2000). 'CRSP' and 'Lori Niébé' were improved lines bred by IRAD/CRSP project for their adequate characteristics for making *akara* balls, a value-added

food, but they had poor concentration of sucrose. "CRSP" was derived from a cross between 'VYA' and 'BR1' and had a grain yield averaged 880 kg/ha. 'Lori' was obtained from a single F₄ plant selection from a cross between IITA breeding lines 'IT86D-364' and 'IT81D-1138' and showed grain yield averaged 994 kg/ha.

Combinations and generations: The patterns of inheritance, including genetic effects, were studied in three hybrid combinations obtained from the following crosses: CRSP×K VX 61-1; C93W-24-125×Lori and C93W-24-125×K VX61-1. All crosses were made on plants growing in pots, with emasculation of the flower buds. The F₁ (P₁ ♀×P₂ ♂) and F₁ reciprocal (P₁ ♂×P₂ ♀) seeds were produced for each hybrid combination in rainy season 2008. From August to November 2008, natural self-fertilisation of F₁ hybrids produced F₂ generations, while backcrossing of F₁ to P₁ (BCP₁) and F₁ to P₂ (BCP₂) produced the backcross generations. The process was replicated during the rainy season 2009, so that the seeds of the F₁, F₁ reciprocal, F₂, and backcrosses (BCP₁ and BCP₂) generations could be evaluated under the same cultivation conditions.

Experimental design and sucrose content analysis: In all stages, seeds were sown in plastic pots of 5L capacity. The pots were filled with a mixture of ground and in each sample, 2 g of mineral fertiliser (7% N; 14% P₂O₅; 7% K₂O) were thoroughly mixed with the top 5cm of soil. The experiments were run in a randomized complete block design with 10 replications for the parents and the reciprocal F₁ generations, 15 replications for backcross generations and 25 for F₂ generations. Plants were watered as necessary and a standard insecticide formulation, cypermethrin + dimethoate, at the rate 30 g + 250 g a.i/L was applied at flowering stage to control flower and pod sucking insects' pests. The pods were harvested at maturity; the seeds removed manually and were dried until the average moisture content of 15%. The seeds were analyzed for sucrose via a High Performance Liquid Chromatography (HPLC) system as described by Kennedy *et al.* (1985). Sucrose content was expressed as mg/g.

Data analysis: The means of generations for each combination were subjected to analysis of variance (ANOVA). To test the maternal effect hypothesis, a comparison was made between the means using the *t*-test at 5% significance level for contrasts F₁ vs. F₁ reciprocal. Estimates of the genetic parameters were obtained with the variance of parents P₁ and P₂, F₁, F₂, BCP₁ and BCP₂ generations for each hybrid combination. The broad-sense heritability (h²) and the narrow-sense heritability (h_s²) were estimated using the backcross method (Warner, 1952; Mather and Jinks, 1982):

$$h^2 = s_g^2 / s_p^2 \text{ and } h_s^2 = s_A^2 / s_p^2$$

where, additive variance (s^2_A) = $2s^2_{F_2} - (s^2_{RCP1} + s^2_{RCP2})$; phenotypic variances (s^2_p) = $s^2_{F_2}$; environmental variances in F_2 (s^2_E) = $1/4 (2s^2_{F_1} + s^2_{P_1} + s^2_{P_2})$ and genetic variance (s^2_g) = $s^2_p - s^2_E$ (Wright, 1968).

Heterosis (H%) was quantified as deviation of F_1 value from the mid-parent (MP) and from the better parent values (heterobeltiosis, HB%) as outlined by Fonseca and Paterson (1968):

$$H\% = [(F_1 - MP) / MP] \times 100$$

$$HB\% = [(F_1 - BP) / BP] \times 100$$

where, MP = $(P_1 - P_2) / 2$ and BP = best parent.

The genetic advance (GA) was calculated as per the following formula given by Allard (1960):

$$GA = K \times s_{F_2} \times h_s^2$$

where K = the selection differential in standard units in the present study and it was 1.75 at 10% level of selection as outlined by Allard (1960); s_{F_2} = standard deviation of the phenotypic variance of F_2 and h_s^2 = heritability in narrow sense.

The genetic advance expressed as percentage of mean (GA%) was measured by the following formula:

$$GA\% = (GA \times 100) / X_0;$$

where, X_0 = average of original F_2 plants.

Gene effects based on a six parameters were estimated using the nonweighted generation means analysis describe by Gamble (1962) and are defined as follows: mean [m] = F_2 ; additive [a] = $BC_{P_1} - BC_{P_2}$; dominance [d] = $-0.5P_1 - 0.5P_2 + F_1 - 4F_2 + 2BC_{P_1} + 2BC_{P_2}$; additive×additive [aa] = $-4F_2 + 2BC_{P_1} + 2BC_{P_2}$; additive × dominance [ad] = $-0.5P_1 + 0.5P_2 + BC_{P_1} - BC_{P_2}$ and dominance×dominance [dd] = $P_1 + P_2 + 2F_1 + 4F_2 - 4BC_{P_1} - 4BC_{P_2}$.

The minimum number of genes (N) controlling the trait was estimated following Lande (1981) as:

$$N = (P_2 - P_1)^2 / 8[2s^2_{F_2} - (s^2_{BC_{P_1}} + s^2_{BC_{P_2}})]$$

and according to Mather and Jinks (1982) as follows:

$$N = [0.5(P_2 - P_1)]^2 / [2s\sigma^2_{F_2} - (s^2_{BC_{P_1}} + s^2_{BC_{P_2}})].$$

These effective factor formulas assume that the segregating genes for sucrose content are all located in one parent, not linked, have equal effects, with no genotype × environment effects, no epistatic and dominance effects (Wright, 1968).

RESULTS AND DISCUSSION

Means and their standard errors in parental, F_1 , F_2 and backcross generations for cowpea seed sucrose

concentration are listed in Table 1. The contrast P_1 vs P_2 was significant ($p \leq 0.01$), demonstrating a genetic difference among parental lines of crosses in sucrose content. Among parents, the values of sucrose level ranged from 1.88 mg/g ('Lori') to 5.32 mg/g ('C93W-24-125'). Similar trends were pointed out by Hall *et al.* (2003) and Kitch *et al.* (2003) in cowpea. 'C93W-24-125' and 'KVX 61-1' appeared as sweet genotypes accumulating high proportion of sucrose while 'Lori' and 'CRSP', nonsweet varieties, showed low sucrose content. Islam *et al.* (2008) noted that US cultivars 'Black Crowder', 'Texas Cream 40' and 'Mississippi purple' accumulated high level of sucrose (9.97 to 18.31 mg/g). Analysis of variance showed that sucrose contents significantly differed among generations (Table 1). Since F_2 had a normal distribution, this trait is quantitatively inherited according to Allard (1960) assumption. The F_1 values were slightly different from those of the mid-parents on one hand and were shifted toward the poor parent's values on other hand. In waxy corn, Simla *et al.* (2009) also noted that the seed sucrose in the F_1 -generation of two crosses were significantly lower than its mid-parents values. The above observations suggested that the F_1 values were close to their low parent. In contrast, Audilakshmi *et al.* (2010) noted that in sweet sorghum, the F_1 of crosses for sucrose percentage were tending towards higher percentage parent. Sucrose values of backcross to high parent were higher than those of their F_1 -hybrid but they did not exceed those of their high parent. No cross produced significant transgressive segregant progeny. This finding is in contrast to observations of Mebrahtu and Devine (2009) in certain crosses of soybean. The diversity for sucrose content indicated that hybridization and selection might produce plants with increased seed sucrose content. Sugar accumulation, the key process determining sweetness, is controlled by both translocation of sugars and their metabolism in developing seeds (Islam *et al.*, 2008). The proportion of sucrose is determined primarily by sucrose synthetases enzymes (Bernal-Lugo and Leopold, 1992). No significant difference ($p \geq 0.05$) was observed between F_1 ($P_1 \times P_2$) and reciprocals ($P_2 \times P_1$) suggesting the absence of maternal effects for this character (Table 1). The cowpea seed sucrose content is concentrated mainly on cotyledons, products of fertilization (Islam *et al.*, 2008). For this reason, selection for this trait should begin in F_2 generation where ample variability was observed. Absence of maternal effect has direct implications on the selection process and the progression of segregating populations in genetic improvement programs (Allard, 1960).

The genetic component of variance (s^2_g) was larger than the environmental variance (s^2_E) in all three crosses (Table 2). Heritability values varied slightly between crosses (Table 2). Broad-sense heritability (h^2) ranged from 0.58 to 0.68, and narrow-sense heritability (h_s^2) ranged from 0.39 to 0.48. The genotype had a larger effect

on sucrose content rating than the environment in which the plants are tested. These findings are in agreement with the reports of Ky *et al.* (2000) in coffee, Mebrahtu and Devine (2009) in soybean and Audilakshmi *et al.* (2010) in sorghum. Estimates of narrow-sense heritability indicated that additive effects were primarily responsible for the genetic variation in these hybrids. In the improvement of self-pollinated plants, additive variation is of great importance since it does not segregate from

generation to generation, making it possible to successfully select in segregating populations, since the selective gains will depend only on gametic variation (Warner, 1952). For this reason, backcross, pedigree, single-seed descent or gamete selection methods are recommended for advances the segregating populations (Bernado, 2003). In coffee, Ky *et al.* (2000) noted that sucrose accumulation in seed also showed preponderance of genetic additivity.

Table 1: Mean sucrose content of cowpea seeds and respective standard deviations obtained in parents (P₁ and P₂) and in F₁, F₂ and backcross generations of three hybrid combinations

Parents and generations	Sucrose content of cowpea seeds (mg/g)		
	KVX61 (P ₁) × CRSP (P ₂)	C93W (P ₁) × Lori (P ₂)	C93W (P ₁) × KV × 61 (P ₂)
P ₁ (n = 10)	4.10±0.97 ^a	5.32±0.57 ^a	5.32±0.57 ^a
P ₂ (n = 10)	2.33±0.66 ^c	1.88±0.39 ^d	4.10±0.97 ^b
F ₁ (n = 10)	2.56±0.83 ^c	2.80±0.48 ^c	4.58±0.10 ^b
F ₁ Reciprocal (n = 10)	2.64±0.36 ^c	2.96±0.77 ^c	4.28±0.90 ^b
F ₂ (n=25)	2.85±1.15 ^b	2.68±0.98 ^{cd}	4.51±1.28 ^b
BC _{P₁} (n = 15)	3.66±0.92 ^{ab}	4.13±1.01 ^b	5.02±1.35 ^a
BC _{P₂} (n = 15)	3.01±1.08 ^b	2.00±0.70 ^d	4.36±0.90 ^b
Contrasts and significance of differences			
P ₁ vs. P ₂	1.77**	3.44**	1.22**
F ₁ vs. F ₁ Reciprocal	0.12 ^{ns}	0.16 ^{ns}	0.30 ^{ns}

N: Number of plants sampled in each generation; ns: Not significant; **: Significant at 0.01 probability by t-test; within a cross, means followed by the same letter are not significantly different at 0.05 probability

Table 2: Estimates of means, genetic parameters and prediction of sucrose content gain in cowpea seeds of three hybrid combinations

Genetic parameters and gain	Hybrid combinations for cowpea seeds sucrose		
	KVX61 (P ₁) × CRSP (P ₂)	C93W (P ₁) × Lori (P ₂)	C93W (P ₁) × K × 61 (P ₂)
Parents' means (mg/g)	3.2150	3.6000	4.7100
Phenotypic variance (s ² _p)	1.3225	0.9604	1.6384
Environmental variance (s ² _E)	0.5487	0.3251	0.5222
Genetic variance (s ² _g)	0.7775	0.6615	1.1162
Additive variance (s ² _A)	0.6326	0.4100	0.6435
Broad-Sense heritability (h ²)	0.5850	0.6615	0.6812
Narrow-Sense heritability (h ² _s)	0.4783	0.4270	0.3947
Mid-Parent heterosis (H %)	- 19.00	- 20.00	- 5.94
Heterobeltiosis (HB %)	- 36.58	- 45.86	- 16.72
Minimum value in F ₂ (mg/g)	1.98	1.72	3.18
Maximum Value In F ₂ (mg/g)	4.07	4.67	5.96
Original Mean In F ₂ (mg/g)	2.85	2.68	4.51
Genetic Advance (GA)	0.96	0.73	0.88
Genetic Advance (GA %)	33.64	27.32	19.60
Predicted F ₃ mean (mg/g)	3.81	3.41	5.39

Predicted F₃: Predicted mean of F₃ generation assuming retention of 10% in F₂ with highest sucrose content

Table 3: Estimates of gene effects and the minimum number of effective factors for seed sucrose concentration in three crosses of cowpea

Gene effects parameters and number of genes	Parents of crosses		
	CRSP × KVX61 (P ₂)	C93W × Lori (P ₂)	C93W × KV × 61
Mean [m]	2.85±1.15**	2.68±0.98**	4.51±1.28**
Additive [d]	0.60±0.39*	2.13±0.41**	0.66±0.38*
Dominance [h]	1.33±0.30**	-0.18±0.48	0.44±0.42
Additive × additive [aa]	1.94±0.33**	0.54±0.10	0.68±0.45**
Additive × dominance [ad]	-0.24±0.26	0.31±0.30	0.05±0.25
Dominance × dominance [dd]	-3.65±0.90**	0.16±0.34	-1.20±0.86**
N (Lande, 1981)	0.62	3.54	3.80
N (Mather and Jinks, 1982)	1.23	7.10	7.60
Mean of N.	0.93	5.32	5.70

*: Estimates significantly different from zero at p = 0.05; **: Estimates significantly different from zero at p = 0.01; N: Minimum number of effective genes

In relation to selection gains, assuming retention of 10% plants in F₂ generation with highest sucrose content, gains could be expected, with predicted means of 19.60 to 33.64 after the first selection cycle. Therefore, germplasm selection of cowpea with high sucrose content could be effective in the development of cultivars with high nutritional value that could be used in foods. In this sense, increasing the sucrose content by genetic improvement is a low-cost, high-benefit social strategy for improving the nutritional quality of cowpea seeds.

Conventional heterosis (H%) of -20.00 to -5.94% was observed in these combinations, indicating that F₁ hybrids had lower sucrose content than the mean of the parents (Table 2). Negative percentage of heterobeltiosis (-45.86 to -16.72%) indicated that superdominance hypothesis should not be considered (Fonseca and Paterson, 1968; Audilakshmi *et al.*, 2010). Contrasted reports on heterosis were highlighted for this trait in interspecific cross *Coffea pseudozanguebariae* x *Coffea liberia dewevrei* (Ky *et al.*, 2000) and *Sorghum bicolor* (Audilakshmi *et al.*, 2010). Using the current study, selection for sucrose content may be profitable and feasible in the later segregating populations (Bernado, 2003). The incorporation of sweet genes in combination to increase sweetness is practical in cowpea. The recurrent selection breeding method (Hill, 1996) would be an effective means to transferring the genes for seed sucrose content among cowpea genotypes. Jackson (2005) noted that most sugarcane breeding programs worldwide use recurrent selection for sucrose to increase the sucrose content of new cultivars. However, the high operation cost associated with the measurement of sucrose might preclude its use in practical breeding programs. The correlations between parental sucrose and total sugar means values were positive and significant in soybean (Mebrahtu and Devine, 2009) and in waxy corn (Simla *et al.*, 2009). In soybean, Maughan *et al.* (2000) identified seven genomic regions associated with quantitative trait loci (QTL) controlling sucrose content.

Gene effects were estimated using the nonweighted method of Gamble (1962) and are shown in Table 3. The midpoint ranged from 2.68 to 4.61 for all crosses. For this trait, the additive component [a] was positive and significant for all crosses while the dominant component [d] was positive and significant only for 'CRSP' 'KVX61' cross. The presence of epistasis was usually significant in all crosses except 'C93W-24-125B' x 'Lori'; therefore, genetic model which assume no epistasis do not accurately describe sucrose level in cowpea seeds. Among the interaction components, the fixable additive x additive [aa] effects were nearly always positive compared to dominance x dominance [dd] effects which were generally negative. One form of epistasis, additive x dominance [ad], was not significant in any cross. In general, additive variance was the major component of the

genetic variance. Similar observations were made for sucrose content by Mebrahtu and Devine (2009) in soybean and Audilakshmi *et al.* (2010) in sorghum. Significant estimates of the additive genes effects ([a] and [aa]) were usually positive, indicating that additive effects contribute more to higher sucrose content, in contrast, significant dominance x dominance effects usually reduced the sucrose accumulation. Additive and epistatic gene effects explained most of the genetic variation for sucrose in crosses under investigation. Dominance gene effects were much smaller compared to those of additive and epistatic gene effects. In contrast, generation means analysis revealed the predominance of dominant gene effects for sucrose in corn (Simla *et al.*, 2009). The negative sign associated with dominance x dominance effects, indicated that epistasis reduced sweetness in hybrid combination. Therefore, selection of superior segregants has to be postponed to the later generation until homozygosity is achieved. The breeders' goal should be to achieve homozygosity rapidly while reserving intense selection pressure for later generations. Consequently the 'single seed descent' breeding system (Bernado, 2003) would be most relevant to advance the population to homozygosity.

Estimates of the minimum number of effective factors (genes) for sucrose concentration by Lande (1981) assumption was between 0.62 and 3.80, while with Mather and Jinks (1982) method, the values ranged from 1.23 to 7.60 (Table 3). Dominance and most types of epistasis will bias the estimate of effective factors downward (Wright, 1968). It is assumed that the segregating factors are iso-directionally distributed between the parents and they have equal additive effects. Non-validity of either or both assumptions would result in an underestimation of the true value. It is likely that the estimates of the number of genes were highly biased by the failure to meet the analysis assumptions of no epistasis and no dominance, because some dominance effects were present and epistasis was significant in most of crosses. In addition to lacking of epistasis, the cross 'C93W' x 'Lori' also had little dominance, therefore, estimates of minimum number of effective factors for that cross are likely to be more accurate. The mean number of genes for this cross is estimated to be at least 5 for sucrose content. In other crops, earlier studies revealed that the sucrose content was a polygenic trait (Kennedy *et al.*, 1985; Ky *et al.*, 2000; Maughan *et al.*, 2000; Audilakshmi *et al.*, 2010).

CONCLUSION

From the above study, it is concluded that the genotypes showed greater magnitude of variability for sucrose content indicating ample scope for selection of this important component of taste in cowpea. Our study

highlighted that the investigated trait is genetically controlled. Sucrose content is controlled by additive and epistatic genes and, it can be assumed that it will remain stable under varied environmental conditions. Since, in addition to additivity, epistatic interactions were also observed; one or more cycles of intermating of selected segregants may be adopted to accumulate favourable genes through recurrent result which will result in the improvement of sucrose content. Regarding the genetic advance, from this study, it is possible to increase sucrose content in cowpea seeds by 19-33% through plant breeding. In order to increase the efficiency of breeding and reduce the time to develop an improved variety, high sucrose content will be linked to molecular markers and Marker Assisted Selection (MAS) developed for sweetness in cowpea.

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