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DETERMINATION OF COMBINING ABILITY AND HERITABILITY FOR CANNING QUALITY TRAITS IN COMMON BEAN

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ABSTRACT

Breeding for common bean (*Phaseolus vulgaris* L.) genotypes with optimal canning quality holds the potential for increased dry bean consumption among middle-class income urban dwellers in sub-Saharan Africa (SSA). Understanding the genetic control of canning quality traits is central for the improvement of common bean genotypes for desired canning quality. The objective of this study was to determine the combining ability and heritability of canning quality traits (CQTs) in common bean; and to establish entry points for effective breeding for these traits. A population from two contrasting parents for canning quality traits was developed and progressed to F2. The F2:F4 seed was evaluated for CQTs at three months post-harvest. Substantial variation was observed among the canning quality traits tested, including the general appearance of the canned beans, seed coat colour retention namely, clumping, free starch, splitting, and hydration coefficient. Canning quality traits encompassed a spectrum of both additive and non-additive effects. Promising combiners for CQTs were identified among the parents, KK8 and MAC 13, suggesting their potential for utilisation in breeding programmes. Moderate to high Baker's ratio (BR = 0.41-0.94) values were observed for some CQTs and narrow sense heritability (h^2 = 0.47-0.66). Canning quality traits exhibited substantial broad sense heritability (H^2) values, ranging from 0.6 to 0.92. These findings provide valuable entry points for breeding programmes focused on improving common bean for canning quality.

Key Words: Baker's ratio, broad sense heritability, *Phaseolus vulgaris*

RÉSUMÉ

La sélection de génotypes de haricots communs (*Phaseolus vulgaris* L.) avec une qualité de conserve optimale est offre le potentiel pour la consummation de haricots secs qui est augmenté parmi les citadins à revenus de la classe moyenne en Afrique subsaharienne (ASS). Il est essential de comprendre le contrôle génétique des caractères de qualité de mise en conserve pour l'amélioration des génotypes de haricots communs pour obtenir la qualité de mise en conserve souhaitée. L'objectif de cette étude était de déterminer la capacité de combinaison et l'héritabilité des caractères de qualité de mise en conserve (CQT) du haricot commun; et établir des points d'entrée pour une sélection efficace de ces caractères. Une population issue de deux parents contrastés pour les caractères de qualité de conservation a été développée et a progressé jusqu'à F2. Les graines F2:F4 ont été évaluées pour les CQT trois mois après la récolte. Une variation substantielle a été observée parmi les caractéristiques de qualité de mise en conserve testées, notamment l'apparence générale des haricots en conserve, la rétention de la couleur de l'enveloppe des graines, à savoir l'agglutination, l'amidon libre, le fractionnement et le coefficient d'hydratation. Les caractéristiques de qualité de la mise en conserve englobaient un spectre d'effets à la fois additifs et non additifs. Des combinateurs prometteurs pour les CQT ont été identifiés parmi les parents, KK8 et MAC 13, suggérant leur potentiel d'utilisation dans les programmes de sélection. Des valeurs modérées à élevées du ratio de Baker (BR = 0,41-0,94) ont été observées pour certains CQT et une héritabilité au sens étroit (h^2 = 0,47-0,66). Les caractères de qualité de mise en conserve présentaient des valeurs d'héritabilité au sens large (H^2) substantielles, allant de 0,6 à 0,92. Ces résultats constituent des points d'entrée précieux pour les programmes de sélection axés sur l'amélioration de la qualité du haricot commun pour la mise en conserve.

Mots Clés: Ratio de Baker, héritabilité au sens large, *Phaseolus vulgaris*

INTRODUCTION

Dry beans (*Phaseolus vulgaris* L.) are a staple food in sub-Saharan Africa (SSA), providing starch, protein, fiber and minerals including iron, zinc, potassium, selenium, molybdenum, vitamins (thiamine, vitamin B6) and folate (Costa *et al.,* 2006). Beans are consumed as boiled green leaves, green immature pods and/or dry grains in different forms. Beans are boiled and eaten alone as sauce, mixed with other sauces like ground nuts and vegetables, removing the seed coat after boiling, and mashing, boiling in combination with other foods such as banana and potato (Katungi *et al*., 2009).

The fresh form is generally preferred over the dry form, but it takes a short time before beans dry. Thus beans are commonly consumed as boiled dry grain since fresh beans are difficult to store (Katungi *et al*., 2009).

Dry beans are primarily consumed in unprocessed forms, which is economically advantageous, being 55% cheaper than the least expensive processed bean product (Monitor Group for the Rwanda Ministry of Agriculture and Livestock, 2012).

The SSA region is experiencing a surge in the number of middle-income consumers, particularly among urban dwellers, who are willing to pay a premium for the convenience of pre-cooked and canned beans (Aseete *et al*., 2018; Mukankusi *et al*., 2022). As the demands of modern living continue to evolve, canned beans present an appealing alternative to the time-consuming process of cooking dry beans, adding value by providing a semi-prepared option with reduced cooking requirements (Zanovec *et al*., 2011). Furthermore, canned beans have the potential to bring about a range of benefits, from elevated product value to enhanced profitability for farmers and processors (Pan, 2010). As such, the development of common bean varieties with optimal canning quality

characteristics is pivotal for the development of the bean subsector.

Effective breeding strategies necessitate a comprehensive understanding of combining ability and mode of inheritance. Inheritance studies are imperative for plant breeders as they illuminate how traits are passed from one generation to the next. Combining ability, coupled with heritability, forms the foundation of genetic analyses for crop traits (Ma Teresa *et al*., 1994). The objective of this study was to determine the combining ability and heritability of canning quality traits (CQTs) in common bean to lay entry points for effective breeding for the desired canning quality.

MATERIALS AND METHODS

Population development. Population development was done in a screen house and F3 evaluated in the field, both at the National Crops Resources Research Institute (NaCRRI), at Namulonge in Uganda.

A modest screen house covered with an insect screening net material to provide environmental modification and protection from severe weather conditions, especially excessive heat that would cause flower abortion as well as the exclusion of pests, was used.

The Institute is located in central Uganda at latitude 0°32'N and longitude 32°53'E; with an altitude of 1150 meters above sea level. The Institute falls in a bimodal rainfall region, with March to May as the first season and September to December as the second rainy season. Altogether, the mean annual rainfall is 1270 mm and mean temperature is 22.5 °C (Nsubuga *et al.,* 2011; UNMA, 2020).

A 2 x 4 crossing block was established with two buckets per genotype. Five-liter buckets, filled with 3 kg of loam soil, were used. Five seeds per bucket were planted, and these were later thinned to 4 seedlings. The North Carolina 2 mating design was used, whereby the genotypes with good canning quality traits served as males; while those with poor canning quality, traits as females (Table 1). F1 seed was advanced to F2. At F2, 5 plants were selected and harvested individually, the F3 seed from these individual plants was planted in the field at NaCRRI in 2021 (season B).

The experiment was laid out in a Randomised Complete Block Design (RCBD), with a plot of 2 rows of 1 m length, and replicated twice. All the recommended agronomic practices such as weeding, spraying, and staking were done to ensure proper growth of the trial. The F4 seed was then harvested in bulk from each plot, dried, sorted and stored at room temperature (22^{o}C) for about 3 months.

Before the actual canning process, water absorption capacity of seed samples was determined by the Hydration Coefficient (HC). From each field plot, 100 g dry seed samples were placed in nylon mesh bags and soaked in distilled water for 16 hours. Water was removed, and the bean samples allowed to drain from paper towels for about 3 minutes. The HC was then calculated as the ratio of the soaked bean weight to the weight of the dry sample.

The canning process. The amount of beans to be canned was determined using Equation 1.

$$\text{Beans to be canned} = \frac{90 \text{ g (i.e. solids required)}}{1 - \left(\frac{MC\%}{100}\right) \text{ (i.e. solids at a given moisture content)}} \quad \text{..... Equation 1}$$

Moisture content (MC%) of each seed sample, was determined using a 6095-moisture analyser (SINARTM AgriProto, made in England).

Cold soaking. The seed samples to be canned per variety were placed in mesh bags, and soaked in a solution of calcium chloride for 12 hours. The solution was prepared by adding

TABLE 1. Characteristics of parental genotypes used in hybridisation for canning quality traits

Genotype	Seed coat colour	Colour code	Seed size	Reaction to cooking time	Country where released
SMR-53	Maroon	4	Small	Good	Ghana
KK8	Red mottled	10	Big	Good	Kenya
MAC 13	Red mottled	10	Big	Poor	Uganda, Rwanda, Burundi
NABE 9C	Cream with dark blue speckles	21	Big	Poor	Uganda
94GERM	Blue	11	Big	Poor	Uganda landrace
SMR 116	Red	6	Small	Poor	CIAT

0.28 g of calcium chloride in one liter of distilled water and stirring very well before immersing the beans in it.

Hot soaking. The cold-soaked beans were transferred into a pre-heated solution of calcium chloride prepared as described for cold soaking above. The beans were maintained in this hot solution at 87 ^{O}C for 30 minutes. Temperature was monitored by a thermometer, to ensure it remained stable as required. The mesh bags were then removed from the boiler, cooled under running tap water for about 3 minutes, and allowed to drain for 10 minutes.

The weight of hot-soaked bean samples was determined before transferring the samples into labeled glass jars of 500 ml capacity. The glass jars were then filled with boiling brine, which was prepared by adding 2.8 g of calcium chloride and 150 g of sucrose (sugar) into 10 liters of distilled water. The mixture was well stirred to ensure its proper dissolution. The solution was then boiled in a normal saucepan at 87 ^{O}C until all the glass jars were filled with brine.

The glass jars containing the canning samples were filled with boiling brine, using a measuring cup. To prevent the glass jars from breaking due to abrupt temperature changes, they were placed in hot water during the process of brine addition. The sealed glass jars were placed in an autoclave, which was heated at 121 ^{O}C for 45 minutes. After cooking, the glass jars were allowed to cool under tap running water and then stored on shelves for 1 month before evaluation.

For evaluation, the canned beans were poured onto wide plastic plates, ensuring that the brine (canning medium) and cooked bean grains (Fig. 1) were viewed properly to ease the evaluation process.

Canning quality parameters. Canned beans were evaluated for clumping, seed coat colour retention, appearance, viscosity (brine clarity), bean splitting and free starch. Free starch was evaluated using a panel of eight trained persons

Figure 1. Canned bean genotypes displaying how both the grain and brine were properly visible to the evaluation panel.

on a scale of 1 to 5 rating; where 1 = poor and 5 = excellent, based on a modified Michigan State University (MSU) bean canning protocol (Uebersax and Hosfield, 1985).

After evaluation, the canned samples were washed and rinsed on plastic sieves using clean tap water and allowed to drain for about a minute. Then, the canned bean net weight was determined. The coefficient of washed-drained solids was determined by dividing the washed–drained solids' weight by the soaked weight of the sample.

$$WDC = \frac{\text{Washed drained solid's weight}}{\text{Soaked weight}} \quad \text{... Equation 2}$$

Data analysis. Data collected were subjected to analysis of variance (ANOVA) using R package (Version 4.1.3) fitting the following statistical model:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + R_k + e_{ijk} \quad \text{... Equation 3}$$

Where:

μ is the grand mean, g_i and g_j are the general combining ability (GCA) effects of the i^{th} and j^{th} parents, respectively; s_{ij} is the specific combining ability (SCA) effect for the hybrid between the i^{th} and j^{th} parents which was considered as a fixed effect; R_k is replication means effect and e_{ijk} is experimental error.

The variance components were partitioned into additive and dominant effects (Mather and Jinks, 1982). The significant genotype means were compared using the Least Significant Differences (LSD) at 5% level of significance.

Bakers' ratio and heritability. The relative importance of additive *versus* non-additive gene effects was determined according to the ratio established by Baker (1978). All negative values of estimated variance components were considered as zero in the formulas for Narrow and Broad sense heritability (Wang *et al.*,

1992). Baker's ratios were used to predict the performance of crosses based on GCA values (the importance of additive and non-additive gene effects). The closer the ratio is to 1, the greater the reliability of predicting performance based on GCA (Baker, 1978). Baker's ratio and heritabilities were estimated on an entry-mean basis following Equations 4 - 6:

$$BR = \frac{(\sigma_e^2\ \mathrm{GCA1} + \sigma_e^2\ \mathrm{GCA2})}{(\sigma_e^2\ \mathrm{GCA1} + \sigma_e^2\ \mathrm{GCA2} + \sigma_e^2\ \mathrm{SCA}).}$$

…..…….. Equation 4

$$\mathrm{h}^2 = \frac{(\sigma_e^2\ \mathrm{GCA1} + \sigma_e^2\ \mathrm{GCA2}\ )}{(\sigma_e^2\ \mathrm{GCA1} + \sigma_e^2\ \mathrm{GCA2} + \sigma_e^2\ \mathrm{SCA} + \sigma_e^2\ /\mathrm{n.reps}}$$

.....…….. Equation 5

$$\mathrm{H}^2 = \frac{(\sigma_e^2\ \mathrm{GCA1} + \sigma_e^2\ \mathrm{GCA2} + \sigma_e^2\ \mathrm{SCA}\ )}{(\sigma_e^2\ \mathrm{GCA1} + \sigma_e^2\ \mathrm{GCA2} + \sigma_e^2\ \mathrm{SCA} + \sigma_e^2\ /\mathrm{n.reps}}$$

…….....……..…… Equation 6

RESULTS

Significant variation was observed among tested lines for all phenotyped traits, except the washed drained coefficient and washed drained weight (Fig. 2). There were also significant GCA and SCA estimates for several canning quality parameters. In terms of GCA, canning traits particularly the general appearance of canned beans, clumping, free starch and hydration coefficient displayed significant outcomes (GCA and SCA), for both female and male parents (Table 2).

Heritability for canning quality traits. Moderate to high Baker's ratios were obtained for key canning traits namely, hydration coefficient, seed coat colour retention, free starch, clumping, washed drain weight and viscosity (Table 3). However, the Baker's ratio (BR) was comparatively low for the appearance trait. In terms of narrow sense heritability, free starch and viscosity displayed moderate levels; while clumping and washed drain weight, exhibited a moderately high heritability estimate. Broad sense heritability values were consistently high, ranging from 7 to 9.2, except for viscosity, which showed a moderate value of 0.59 (Table 3).

Parental GCA effects. There were significant positive GCA effects for canning quality traits, concerning parent KK8 (Table 4). The effects were significant, notably for the appearance of the canned sample, clumping, seed coat colour retention, hydration coefficient and washed drain coefficient. Positive GCA effects, though not significant (P>0.05), were also evident for viscosity and washed drain coefficient. On the other hand, KK8 exhibited negative GCA effects for splitting and free starch.

The other male parent, SMR-53, exhibited effects that were the reverse of those of KK8. Among the female parents, 94 GERM displayed positive though non-significant GCA effects (P>0.05) for seed coat colour retention, free starch, splitting, and washed drain coefficient. Only hydration coefficient demonstrated significant GCA effects (Table 4).

MAC 13, a female parent, yielded positive GCA effects for seed coat colour retention, splitting and washed drain coefficient; with free starch and splitting exhibiting statistical significance. Positive GCA effects for traits, *viz:* clumping, viscosity, washed drain weight, and washed drain coefficient, were observed for the female parent, NABE 9C; although none of these effects were significantly different. Similarly, the female parent, SMR116, exhibited positive GCA effects for a range of traits, including appearance, clumping, free starch, splitting, viscosity, hydration coefficient, and washed drain weight; although none of these were statistically significant (Table 4).

Parental SCA effects. Significant positive SCA effects were observed in specific parent combinations (Table 5). Notably, a positive

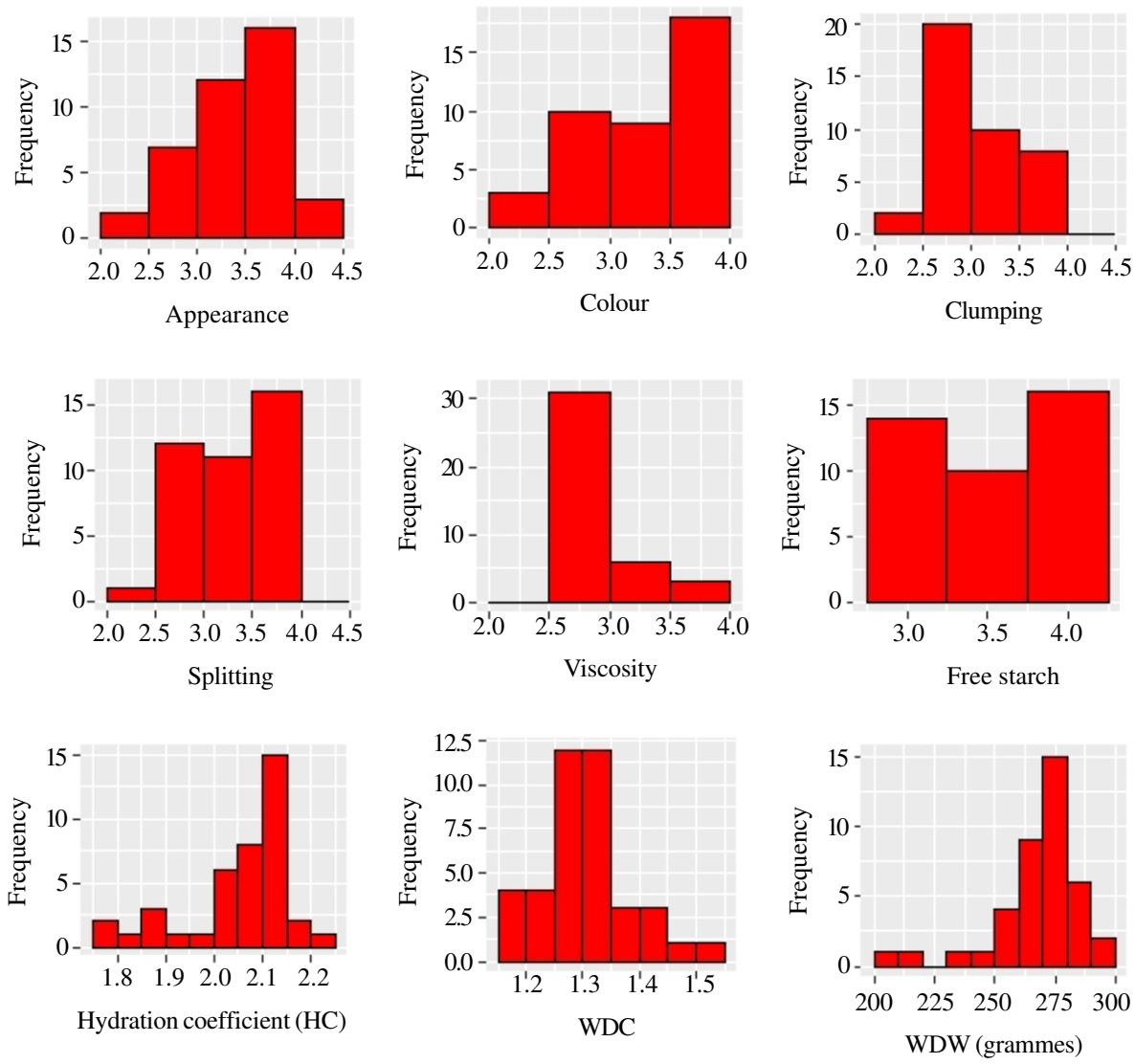

Figure 2. Frequency distribution for the performance of canning quality traits.

SCA effect was detected between male parent KK8 and NABE 9C for both appearance and seed coat colour retention. Conversely, the second male parent, SMR-53, exhibited significant positive SCA effects with MAC13 for appearance and free starch. Additionally, SMR-53 displayed significant positive SCA effects with both 94 GERM and SMR 116, encompassing free starch and splitting (Table 5).

DISCUSSION

The significant differences noted among the F3 progeny in all the canning quality traits (Fig. 2), underscored the substantial genetic variability within the test parent population. This variability bodes well for potential improvement efforts through selective breeding strategies (Singh *et al.*, 2023), implying that there is a possibility of selecting

TABLE 2. Mean Square values for canning quality traits

	APPEAR	CLUMP	COL	FS	SPLIT	VISC	HC	WDW	WDC
REP	0.61	0.20	1.01	0.20	0.05	0.00	0.13	1017.50	0.06
Female	0.05	0.10	0.30	1.48***	1.02***	0.30*	0.04*	1918.10	0.01
Male	2.81***	3.20***	2.11*	0.80*	0.05	0.05	0.06*	6228.70*	0.00
F.M	2.05***	0.40*	0.95*	0.90**	1.35***	0.08	0.04*	946.10	0.03*
F.M.line	0.4*	0.31*	0.52	0.22	0.28*	0.19*	0.02	292.70	0.01
Error	0.20	0.10	0.30	0.17	0.15	0.08	0.01	759.50	0.00

REP = Replication, F.M = Female.Male, F.M.Line, Female. Male. Line, APPEAR = appearance, CLUMP = clumping, COL = colour, FS = Free starch, SPLIT = splitting, VISC= viscosity, HC = hydration coefficient, WDC = washed drain coefficient, WDC = washed drain coefficient

TABLE 3. Variance components and heritability for canning quality traits

	V.CCAF	V.CGCAM	V.CSCA	Error	BR	NSH	BSH
APPEA	-0.04	0.33	0.92	0.20	0.24	0.22	0.92
CLUP	0.00	0.39	0.15	0.10	0.72	0.66	0.91
COL	0.00	0.23	0.32	0.30	0.41	0.32	0.79
FS	0.33	0.08	0.36	0.17	0.53	0.47	0.90
SPLT	0.22	-0.01	0.60	0.15	0.25	0.23	0.91
VISC	0.06	0.00	0.00	0.08	0.94	0.56	0.59
HC	0.01	0.01	0.01	0.01	0.47	0.38	0.81
WDW	289.65	683.65	93.30	759.50	0.91	0.67	0.74

V.CGAF =Variance component General combining ability Female parent; V.CGCAM = Variance component General combining ability Male parent; V.CSCA = Variance component Specific Combining Ability; BR = Baker's ratio; NSH = Narrow Sense Heritability; BSH = Broad Sense Heritability; APPEA = Appearance; CLUP = Clumping; COL = Colour; FS = Free Starch; SPLT = Splitting; VISC = Viscosity; HC = Hydration co-efficient; WDW = Washed Drain Weight

TABLE 4. Cross means, GCA values, SE's & Grand mean

Cross	Appear	Clump	Colour	Starch	Splt	Vis	HC	WDW	WDC
KK8x94GERM	3.4	3.4	3.6	3.2	3.4	3.2	3.4	279.7	1.31
KK8xMAC13	3.2	3.4	3.6	3.9	3.9	3	3.9	270.3	1.27
KK8xNABE9C	4	3.8	3.8	3.2	3.4	3.2	3.4	282.2	1.32
KK8xSMR 116	3.7	3.4	3.7	3.4	3.3	3.3	3.3	274.3	1.32
Mean KK8	3.58	3.5	3.7	3.4	3.5	3.2	3.5	276.6	1.30
GCA (KK8)	0.19*	0.2**	0.16*	-0.1	-0.03	0.03	0.03*	8.8*	0.00
SMR 53x94GERM	3.3	3	3.5	3.9	3.9	3	3.9	264.9	1.22
SMR 53xMAC13	3.5	3.2	3.7	3.7	3.5	3	3.5	236	1.35
SMR 53xNABE9C	2.8	3	2.9	3.1	3	3.5	3	261.8	1.33
SMR 53xSMR 116	3.2	3.2	3.3	3.8	3.8	3.2	3.8	273.3	1.28
Mean SMR 53	3.2	3.1	3.3	3.63	3.55	3.125	3.55	276.6	1.30
GCA (SMR53)	-0.19*	-0.2**	-0.16*	0.1	0.03	-0.03	-0.03*	-8.8*	-0.01
Mean 94GERM	3.4	3.2	3.55	3.55	3.65	3.1	3.65	272.3	1.27
GCA 94GERM	-0.04	-0.1	0.04	0.03	0.13	-0.05	0.05*	4.5	-0.04
Mean MAC13	3.35	3.3	3.65	3.8	3.7	3	3.7	253.2	1.31
GCA MAC13	-0.04	0	0.14	0.28*	0.18*	-0.15	-0.03	-14.6	0.00
Mean NABE9C	3.4	3.4	3.35	3.15	3.2	3.25	3.2	272	1.33
GCA NABE9C	0.012	0.1	-0.16	-0.38	-0.33	0.1	-0.33	4.2	0.03
Mean SMR 116	3.45	3.3	3.5	3.6	3.55	3.25	3.55	273.8	1.30
GCA SMR 116	0.062	0	-0.01	0.07	0.02	0.1	0.02	6	0.00
SE (GCAm)	0.07	0.06	0.13	0.07	0.06	0.04	0.01	4.36	0.02
SE (GCAf)	0.01	0.07	0.13	0.09	0.07	0.06	0.03	6.16	0.03
SE (Cross)	0.17	0.15	0.2	0.13	0.14	0.11	0.04	7.4	0.03
Grand mean	3.388	3.3	3.51	3.53	3.53	3.15	3.53	267.8	1.3

Appear = Appearance; Clump = Clumping; Splt = Splitting; Vis = Viscosity; HC = Hydration coefficient; WDW = Washed Drain Weight; WDC = Washed Drain coefficient

genotypes and families from within this population for improving canning quality traits.

General and specific combining ability. The canning quality traits appearance, clumping, seed coat colour retention, free starch, splitting and hydration coefficient exhibited significant differences in both General Combining Ability (GCA) and Specific Combining Ability (SCA). This underscores the dual roles of both additive and non-additive gene actions in the genetic control of these canning quality traits. For washed drain weight and washed drain coefficient, the effects were attributed solely to additive and non-additive gene action respectively. These observations confirm the findings of Wassimi *et al*. (1990), whereby GCA effects were significant for certain traits, and both additive and non-additive effects influenced the expression of specific canning traits. This indicates that both genotype selection and hybridisation could be successfully employed in breeding for these traits (Acquaah, 2007).

GCA and SCA effects. Male parent KK8, emerged as a promising candidate for improving the general appearance of canned beans, clumping, seed coat colour retention, hydration coefficient and washed drained

TABLE 5. SCA effects of dry bean canning quality traits

Traits	Female Male	94GERM	MAC 13	NABE9C	SMR 116
APPEA	KK8	-0.14	-0.34**	0.41**	0.06
	SMR 53	0.14	0.34**	-0.41**	-0.06
CLUP	KK8	0.00	-0.10	0.20	-0.10
	SMR 53	0.00	0.10	-0.20	0.10
COL	KK8	-0.11	-0.21	0.29*	0.04
	SMR 53	0.11	0.21	-0.29*	-0.04
FS	KK8	-0.25*	0.20	0.15	-0.10
	SMR 53	0.25*	-0.20	-0.15	0.10
SPLT	KK8	-0.23*	0.23	0.23	-0.23*
	SMR 53	0.23*	-0.23	-0.23	0.23*
VISC	KK8	0.08	-0.03	-0.08	0.03
	SMR 53	-0.08	0.03	0.08	-0.03
WDC	KK8	0.04	-0.05	-0.01	0.01
	SMR 53	-0.04	0.05	0.01	-0.01
HC	KK8	-0.05	0.03	0.05	-0.03
	SMR 53	0.05	-0.03	-0.05	0.03
WDW	KK8	-1.40	8.30	1.40	-8.30
	SMR 53	1.40	-8.30	-1.40	8.30

APPEAR = appearance, CLUMP = clumping, COL = colour, FS = Free starch, SPLIT = splitting, VISC = viscosity, HC =, hydration coefficient, WDC = washed drain coefficient, WDC = washed drain coefficient

coefficient, as it exhibited positive and significant GCA effects for these traits (Table 4). This implies that it contributed positively to their increased mean performance. Among the female parents, 94 GERM and MAC 13, showed potential as good combiners for hydration coefficient, free starch, and splitting. These observations suggest that the male parent, KK8, and female parents (94 GERM and MAC 13) could be strategically utilised in hybridisation programmes aimed at enhancing canning quality traits (Jacinto *et al*., 2003; De la Cruz-Lázaro *et al*., 2010; Ferrari *et al*., 2018). Families, KK8 X NABE 9C, for appearance and seed coat colour retention; SMR-53 X MAC13 for appearance, SMR-53 X 94 GERM for free starch and splitting; and SMR-53 and SMR116 for splitting; which displayed significant SCA for different canning quality traits, could be utilised in hybridisation to improve these traits (De la Cruz-Lázaro *et al.,* 2010; Ferrari *et al*., 2018).

Baker's ratio (BR), Narrow sense heritability (h^2) and Broad sense (H^2). The substantial Baker's ratio values for clumping, viscosity, and washed drain weight, alongside moderate values for free starch and hydration coefficient (Table 3), suggest the prevalence of additive genetic effects in influencing these traits (De la Cruz-Lázaro *et al*., 2010; Ferrari *et al.,* 2018). These outcomes indicate that the genetic value of a cross can be reliably predicted based on the GCA values of the parents, facilitating the selection of parent pairs for generating breeding populations with desired traits. The moderate to moderately high narrow sense heritability (h^2) estimates for free

starch, viscosity, clumping and washed drain weight, further emphasize the role of additive gene action in the inheritance of these traits. Comparable findings have been reported by Walters *et al.* (1997) for visual appearance and washed drain weight. The high Baker's ratios for viscosity and washed drain weight, provide additional evidence of significant contribution of additive gene effects in governing these traits.

The consistently high Broad-Sense Heritability estimates (Table 3) indicating overall predictability based on total genetic variance divided by phenotypic variance, suggest that the observed genetic variability primarily stems from variability among the cross means and that the testing approach employed accurately estimate the genetic value of a cross (Falconer and Mackay, 1996; Acquaah, 2007). The heritability values obtained in the present study, underscores the potential for genetic improvement through selective breeding endeavors, as traits demonstrating higher heritability estimates are more likely to respond positively to breeding efforts.

CONCLUSION

Both additive and non-additive genetic effects are important in controlling most canning quality traits in common bean *via* clumping, seed coat colour retention, free starch, splitting and hydration coefficient. This implies that both genotype selection and hybridisation can be utilised for the improvement of canning quality traits in future breeding programs. The study further identifies parental genotypes, KK8 and MAC 13, as promising combiners for canning quality traits and Specific parent combinations; KK8 X NABE 9C, SMR-53 X MAC13, SMR-53 X 94 GERM, and SMR-53 X SMR 116, for possible trait enhancement through hybridisation. We recommend testing for canning quality traits at a higher generation that would allow production of sufficient seed for testing and confirmation of the observed results in different locations

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