Gene Actions and Combining Ability Analysis for Some Seed Characters in *Citrullus Mucosospermus* (Fursa)

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Abstract In order to suggest breeding strategies to improve *Citrullus mucosospermus* (Fursa), 4×4 complete diallel cross design involving *Bebu*, *Wlêwlê small seeds* 1 (*Wss1*), *Wlêwlê small seeds* 2 (*Wss2*) and *Wlêwlê small seeds* 3 (*Wss3*) genotypes was used to assess combining ability and gene actions involved in the inheritance of six seed traits. The F_1 direct and reciprocal crosses plus the parental inbred lines coming from these cultivars were grown in a randomized complete block design with three replications. The results indicated the existence of genetic variation between parental lines for all investigated seed traits. Combining ability analysis exhibited the involvement of both additive and non-additive types of gene actions in the expression of all studied traits, suggesting, doing the selection in *C. mucosospermus* heterogeneous populations for improving these seed traits. Non-additive gene actions were predominant in the inheritance of investigated traits indicating the possibility of the heterosis exploitation or the postponement of selection to later generations for improving genetically these traits. *Bebu* appeared the best general combiner for Mass of fresh seed, Mass of dry seed, Mass of 100 seeds, seed length and seed width while, *Wss1* and *Wss2* are the best combiners for percentage of seed integuments. Therefore, parental lines *Bebu*, *Wss1, Wss2* and crosses with high significant specific combining ability effects are proposed for their incorporation in *C. mucosospermus* breeding programs. The presence of both GCA and SCA effects suggests the use of recurrent reciprocal selection to improve *C. mucosospermus* seed traits.

Keywords: Bebu, breeding strategies, combining ability, gene actions, Wlêwlê small seeds

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1. Introduction

Citrullus mucosospermus (Fursa), the so-called *Egusi melon* belongs to *Cucurbitaceae* family [1] and is native to West Africa where it was domesticated [2]. In Côte d'Ivoire, it is the most oleaginous cultivated cucurbit species. *C. mucosospermus* is prized for its oleaginous seeds. Like other oleaginous cucurbits, its oilseeds are consumed as soup thickener [3,4]. Oil extracted from *C. mucosospermus* seeds is comestible and is used in cosmetology and pharmaceutic industries [5,6,7]. Seeds are rich in nutrients such as carbohydrates (10.45 - 26.30%), proteins (21.78 - 30.42%) and lipids (41.78 - 56.08%) [8]. In addition, seed oil were found to be rich in various unsaturated fatty acids, which possess potential health benefits [6].

In spite of its economic, cultural, therapeutic, nutritive importance, *C. mucosospermus* is a neglected and an underutilized crop because of a deficiency of research and development. Consequently, there is lack of information about genetics and breeding of this important crop in many African countries, particularly in Côte d'Ivoire [9,10]. For instance, yields of different cultivars despite their good adaptation to extremely divergent agro-ecosystems are low [3] and vary from 0.10 to 0.31 t ha^{-1} [11]. *C. mucosospermus* productivity must be improved genetically in consideration of its numerous qualities. The improvement of the production and the uses of this important crop can result in food security and income generation for peasants [12].

The choice of the most efficient breeding program for genetic improvement of one trait depends on the knowledge of the type of gene actions involved in its inheritance and the genetic control of related trait. One of

the biometrical techniques available to plant breeders to obtain information's on the type of gene actions involved in expression of trait in the crop species is diallel analysis [13], which reportedly provided early information on the genetic behavior of a group of parents and their hybrid combinations in the first generation [14]. Diallel analysis represents the best strategy for determining the general (GCA) and specific (SCA) combining abilities which help to identify the best parents and hybrid combinations and, provide sufficient genetic data about character inheritances [15,16,17]. Indeed, the significance of the GCA reflects additive gene actions while, the significance of SCA reflects the non-additive genetic effects which indicates relevant non-allelic interactions [16,18,19]. The non-significant of both GCA and SCA values indicates epistasis gene effects play a remarkable role in determining these characters [20,21]. If several studies on GCA and SCA in other *Cucurbitaceae* species have been realized [22-27], it is not the case for *C. mucosospermus*.

This study aims to assess the genetic control of some important seed traits and to study combining abilities (GCA and SCA effects) of four parental lines and their F_1 hybrids in order to suggest breeding strategies for *C. mucosospermus*.

2. Materials and Methods

2.1. Plant Material

Combining ability and gene action analysis were done using four *Citrullus mucosospermus* (Fursa) accessions collected from four regions of Côte d'Ivoire (Table 1).

The genotypes *Bebu* (*B*), *Wlêwlê small seeds* 1 (*Wss1*), *Wlêwlê small seeds* 2 (*Wss2*) and *Wlêwlê small seeds* 3 (*Wss3*) were chosen basing on a wide range of morphological diversity in fruit and seed characteristics that prominently distinguish one line from another.

Each of four accessions (*B* and *Wss1, Wss2, Wss3*) was purified after four generations of self-pollination to obtain inbred lines, which were planted during the period from January to April 2016 for crossing. At flowering, these four parental inbred lines were crossed in complete diallel cross design to produce 12 F_1 hybrid descents.

2.2. Experimental Design and Data Collection

Parents and their 12 F_1's hybrid descents were evaluated at field from May to August 2016 in a randomized complete block design with three replications at Kononfla city located at altitude 243 m above sea level between latitude 6° 37′ 18″ North - longitudes 5° 54′ 37″ West. The mean annual temperature fluctuates from 25 to 30 °C and average of annual rainfall varying between 1500 to 2000 mm. The experimental field area was 2067 m² (53 m × 39 m) and divided into three blocks with 16 plots per block. The area of one plot was 32 m² (8 m × 4 m) and the distance between two plots is 1 m. Only one F_1 family or parental line was sowed by hand on 3 rows within a plot with plant spacing of 2 m × 2 m. Two weeks after sowing, the most vigorous seedlings were selected per hole by separating. The experimental field was regularly weeded during the vegetative growth stage.

Ten plants were selected randomly in each plot giving 30 plants per family for data collection. Six traits (Table 2) related to seeds were collected from three fruits of each randomly selected plant.

Table 1. Description of parental *C. mucosospermus* accessions used for complete diallel cross

Accession names	Origin of collection	Accession codes	Main fruit and seed characteristics
Bebu	Korhogo (North of Côte d'Ivoire)	B	Large and green fruit with large seeds
Wlêwlê small seeds 1	Béoumi (Center of Côte d'Ivoire)	Wss1	Small and white fruit with small seeds
Wlêwlê small seeds 2	Gohitafla (West-Center of Côte d'Ivoire)	Wss2	Small and green fruit with small seeds
Wlêwlê small seeds 3	Tanda (East of Côte d'Ivoire)	Wss3	Medium and green fruit with small seeds

Table 2. Seeds traits evaluated with their measurement methods

Seed traits (unit)	Codes	Measurement methods
Mass of fresh seeds (g)	**MfS**	Mass of fresh seeds extracted directly per fruit determined with precision balance (*Ohaus adventurer balance*; 0,001 g sensibility).
Mass of dry seeds (g)	**MdS**	Mass of seeds from the same fruit dried in natural condition and weighed at regular intervals of two days during two weeks with precision balance (*Ohaus adventurer balance*; 0,001 g sensibility), until a constant mass. Seeds were considered dry when mass stayed constant between two consecutive interval measurements. The last measurement corresponded to dry seed mass per fruit.
Mass of 100 seeds (g)	**MS_{100}**	A batch of 100 dry seeds per fruit weighed with precision balance (*Ohaus adventurer balance*; 0,001 g sensibility).
Percentage of seed integument (%)	**PSi**	For each fruit, a batch of 20 undecorticated dry seeds (seeds with integuments, $M_{20}UD$) was weighed with precision balance (*Ohaus adventurer balance*; 0,001 g sensibility). Seeds where then decorticated and weighed again to determine the mass of the batch of 20 decorticated dry seeds (seeds without integuments, $M_{20}D$). Then seed integument percentage was calculated according to formula: $PSi = [(M_{20} UD - M_{20} D) \times 100] / M_{20} UD$.
Seed length (mm)	**SL**	Was determined as the distance between the seed base and its opposite apex measured on 20 seed samples extracted in three fruits per plant.
Seed width (mm)	**SW**	Was determined as the lateral diameter measured on 20 seed samples extracted in three fruits per plant.

2.3. Data Analysis

Mean values of the parents and their F_1 hybrids were calculated for all studied traits. Analysis of variance (ANOVA) and the post ANOVA test (Turkey test) were performed at 0.05 level of probability to test differences among treatment means. All statistic tests were performed using R Software version 3.3.1 (R Development Core Team 2011).

The analysis of variance of GCA, SCA and reciprocal effects and their respective effect estimates were carried out according to [28] model 1 method 1. The statistical model for the mean value of a cross (i × j) in Griffing's analysis is:

$$Y_{ij} = m + g_i + g_j + s_{ij} + \frac{1}{bc}\sum e_{ijkl} \qquad (1)$$

Where Y_{ij} is the mean of $(i×j)^{th}$ cross over replications k (k = 1, 2, . . ., b); m is the general population mean; g_i and g_j is the GCA effects of ith and j^{th} parent respectively; s_{ij} is the SCA effect of the cross between the ith and the jth parents; e_{ijkl} is the environmental effect that is associated with i_{jkl} observations; b is the number of replication; and c is the number of samples per replication.

The significance of the estimates of variance due to GCA and SCA was tested using F-values at threshold probabilities of 1% and 5%, while significance of estimates of GCA and SCA was tested using their respective standard error according to [28].

The genetic components were estimated according to [29]:

$$\sigma^2_{GCA} = \frac{(MS_{GCA} - MS_{error})}{6n} \qquad (2)$$

$$\sigma^2_{SCA} = MS_{SCA} - MS_{error} \qquad (3)$$

Where σ^2_{GCA} is the component due to GCA; σ^2_{SCA} is the component due to SCA; MS_{GCA} is the variance due to GCA, MS_{SCA} is the variance due to SCA, MS_{error} is the mean error, and n is the number of replications.

The ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ was estimated to assess gene actions such as additive and dominance effects. More $\sigma^2_{GCA}/\sigma^2_{SCA}$ is raised, more the additive effects of the genes are more important.

3. Results and Discussion

3.1. Mean Values of the Parental and F_1 Descents for Six Seed Traits

Table 3 presents the mean values of seed characters of *C. mucosospermus* parental lines and their F_1 hybrids from diallel cross.

The results showed that *Bebu* (*B*) seed characters differed significantly from these of *Wlêwlê small seeds* (*Wss*) cultivars for all studied traits. Indeed, *B* stands out from accessions of *Wss* cultivars by large seeds (long and wide seeds), by higher mass of fresh seeds (MfS), mass of dry seeds (MdS), mass of 100 seeds (MS_{100}) and percentage of seed integuments (PSi) (Figure 1). [10] reported similar results about mean values of seed traits in *B* and *Wss* accessions. The results also revealed that *Wss* accessions (*Wss1, Wss2* and *Wss3)* were distinct one from other, indicating existence of variability among them.

Indeed, *Wss3* stands out from two other accessions of *Wss* according to higher MfS, PSi and wider seeds. Accessions of *Wss1* and *Wss2* are different from each according to MS_{100}, Seed length (SL) and Seed width (SW).

The comparison of agronomic performance of F_1 hybrids revealed that hybrids *B × Wss3 and Wss3 × B* recorded the highest values for trait MfS, MdS, MS_{100} and PSi expressions. Progenies *B × Wss1, Wss1 × B, B × Wss2 and Wss2 × B* exhibited high values for SL and SW expressions. [26] suggested that progenies with high agronomic performance value for some traits could be selected as candidate genotypes in breeding programs aiming these traits enhancement. Elsewhere, some F_1 hybrids presented mean values equal or superior to those of their best parents for some traits suggested complete or super dominance. This is the case of hybrids from direct and reciprocal crosses *B × Wss1, B × Wss2, B × Wss3* and *Wss2 × Wss3* for traits MfS and MdS, of hybrids from direct and reciprocal crosses *Wss1 × Wss3* and *Wss2 × Wss3* for MS_{100}, and of hybrids from crosses that involved *Wss3* as one of the parents for PSi. The complete or super dominance observed in these crosses for these characters indicates the heterosis effect. Even if the expression of heterosis in one crop implies the potential of producing superior cultivars through selection in segregating populations or heterosis breeding [30,31], it is not the case for PSi. Indeed, high mean values for PSi, which express the impediment to decorticate seeds, were not desirable. On the other hand, the lower values express easiness to decorticate seeds were desirable. Thus, crosses with low mean values for PSi could be selected as candidate genotypes for the reduction of seed integuments in breeding programs of *C. mucosospermus*.

Figure 1. Form of parental seeds (**B** = *Bebu*; **Wss1** = *Wlêwlê small seeds* 1, **Wss2** = *Wlêwlê small seeds* 2, **Wss3** = *Wlêwlê small seeds* 3)

3.2. Analysis of Variance of GCA and SCA and Gene Actions

The mean squares from analyses of variances for general (GCA) and specific (SCA) combining abilities as well as the ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ are presented in Table 4.

The data showed that mean squares due to general and specific combining abilities were highly significant (P < 0.001) for all evaluated traits suggesting the presence of both additive and non-additive genetic variance in the expression of these traits. The presence of both additive and non-additive gene actions in the inheritance of these traits indicates that selection may be used in *C. mucosospermus* heterogeneous populations for improving these traits [32]. In concrete terms, the use of reciprocal recurrent selection and/or

bi-parental mating suggested for the improvement efficiently of the traits [33,34]. For all studied traits, the magnitude of SCA variance was higher than GCA variance. The ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ ranged from 0.01 to 0.05, which means non-additive effects played a larger role than additive effects in the expression of these traits. The preponderance of non-additive gene actions in the inheritance of these traits suggests the possibility of the heterosis exploitation [19,35], or the postponement of selection to later generations for improving genetically these traits [36,37].

Table 3. Means performance of four *C. mucosospermus* inbred lines and their hybrids F$_1$ for studied traits

Genotypes		MfS (g)	MdS (g)	MS$_{100}$ (g)	PSi (%)	SL (mm)	SW (mm)
Parental inbred lines							
B		64.85 ± 16.30b	30.12± 8.83bc	16.34± 0.84a	34.58 ± 4.17c	16.16 ± 0.64a	9.84 ± 0.38a
Wss1		32.45 ± 5.98fg	15.10± 3.04g	4.87± 0.42fg	17.88 ± 3.22h	11.04 ± 0.47e	4.47 ± 0.27h
Wss2		30.57 ± 7.53g	14.89± 3.63g	3.90± 0.31i	17.15 ± 3.92h	10.08 ± 0.39gh	3.80 ± 0.46i
Wss3		37.75 ± 9.28def	16.91± 4.39fg	4.95± 0.48f	20.27 ± 3.22g	9.91 ± 0.51h	5.34 ±0.33g
F$_1$ descents							
B × Wss1		59.24 ± 15.84 b	27.07± 7.42c	9.09± 0.52cd	24.87 ± 2.77ef	13.25 ± 0.64c	7.13 ± 0.54c
Wss1 × B		59.65 ± 12.12b	27.32± 6.13c	9.22± 0.75c	24.10 ± 4.45f	13.33 ± 0.46c	7.56 ± 0.41b
B × Wss2		63.02 ± 15.60b	29.57± 8.02bc	8.85± 0.50d	26.25 ± 3.03def	13.32 ± 0.44c	6.79 ± 0.42d
Wss2 × B		63.19 ± 12.75b	31.61± 6.94b	8.97± 0.72cd	26.97 ± 4.20de	13.63 ± 0.53b	6.93 ± 0.40cd
B × Wss3		80.88 ± 14.72a	36.94± 7.54a	10.25± 0.64b	42.72 ± 3.44a	12.56 ± 0.53d	6.66 ± 0.37de
Wss3 × B		82.11 ± 18.60a	36.38± 8.97a	9.96± 0.78 b	42.53 ± 4.28a	12.54 ± 0.43d	6.50 ± 0.28e
Wss1 × Wss2		35.11 ± 8.06efg	16.60 ± 3.75fg	40.31gh	17.22 ± 5.73h	10.77 ± 0.50f	4.48 ± 0.3 h
Wss2 × Wss1		34.48 ± 8.54efg	16.88 ± 4.57fg	4.52± 0.47g	17.26 ± 5.26h	10.88 ± 0.44ef	4.33 ± 0.29h
Wss1 × Wss3		40.82 ±11.60de	19.41 ± 6.28ef	5.76± 0.45e	27.40 ± 4.94d	10.82 ± 0.43ef	5.29 ± 0.22g
Wss3 × Wss1		43.78±12.33cd	20.69 ± 6.07de	5.61± 0.50e	27.22 ± 6.31d	10.71 ± 0.61f	5.25 ± 0.31g
Wss2 × Wss3		47.82 ± 10.84c	23.05 ± 5.47d	5.86± 0.77e	36.87 ± 4.96b	10.28 ± 0.43g	5.63 ± 1.75f
Wss3 × Wss2		47.50 ± 11.53c	22.29 ± 5.71de	5.80± 0.48e	36.70 ± 4.31bc	10.09 ± 0.28gh	5.25 ± 0.36g
Test	**F**	159.36	124.02	2786.1	354.09	1165.2	659.9
	p	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001

Means within a same column followed by the same letter are not significantly different (p = 0.05) according to Turkey' HSD test. B = Cultivar Bebu; Wss1= Wlêwlê small seeds 1; Wss2 = Wlêwlê small seeds 2; Wss3 = Wlêwlê small seeds 3; MfS = Mass of fresh seeds; MdS = Mass of dry seeds; MS$_{100}$= Mass of 100 seeds; PSi = percentage of seed integuments; SL = seeds length; SW = seeds width.

Table 4. Analysis of variance of GCA and SCA, and gene effects for six seed traits in a four-parent diallel cross

Sources of variance	df	MfS	MdS	MS$_{100}$	PSi	SL	SW
GCA	3	1038.10**	204.28**	50.14**	217.64**	15.23**	10.68**
SCA	6	1437.54**	308.03**	56.16**	455.09**	97.32**	27.10**
Error	30	4.23	1.13	0.01	0.62	0.01	0.01
σ^2_{GCA}		57.44	11.29	2.79	12.06	0.85	0.59
σ^2_{SCA}		1190.79	261.86	53.78	337.53	98.89	27.24
$\sigma^2_{GCA}/ \sigma^2_{SCA}$		0.04	0.04	0.05	0.03	0.01	0.02

: significant at 1%. **MfS = Mass of fresh seeds; **MdS** = Mass of dry seeds; **MS$_{100}$** = Mass of 100 seeds; **PSi** = percentage of seed integument; **SL** = seeds length; **SW** = seeds width; σ^2_{GCA}= Component due to GCA mean squares; σ^2_{SCA}= Component due to SCA mean squares.

Table 5. GCA and SCA effects of four *C. mucosospermus* inbred lines and their hybrids for all studied traits

	MfS	MdS	MS$_{100}$	PSi	SL	SW
GCA of parents						
B	15.77**	7.09**	3.72**	4.58**	2.03**	1.70**
Wss1	-9.20**	-4.28**	-1.34**	-5.77**	-0.36**	-0.58**
Wss2	-7.42**	-2.83**	-1.61**	-3.05**	-0.69**	-0.83**
Wss3	0.85[ns]	0.02[ns]	-0.77**	4.25**	-0.98**	-0.30**
Standard error	0.63	0.33	0.03	0.24	0.02	0.03
SCA of crosses						
B × Wss1	1.43[ns]	0.33[ns]	-0.63**	-1.82**	-0.22**	0.27**
B × Wss2	3.30**	2.28**	-0.61**	-2.41**	0.30**	0.03[ns]
B × Wss3	13.42**	5.50**	-0.25**	6.30**	-0.34**	-0.78**
Wss1×Wss2	-0.03[ns]	-0.20[ns]	0.10**	-1.44**	0.04[ns]	-0.14**
Wss1×Wss3	-0.80[ns]	0.26[ns]	0.39**	1.33**	0.27**	0.19**
Wss2×Wss3	2.78*	1.43*	0.80**	8.09**	0.02[ns]	0.61**
Standard error	1.15	0.59	0.06	0.44	0.05	0.05

ns: no significant; *and **: significant at 5% and at 1% respectively. **B** = Cultivar Bebu ; **Wss1**= Wlêwlê small seeds 1 ; **Wss2 =** Wlêwlê small seeds 2 ; **Wss3 =** Wlêwlê small seeds 3 ; **MfS** = Mass of fresh seeds ; **MdS** = Mass of dry seeds ; **MS$_{100}$** = Mass of 100 seeds ; **PSi** = percentage of seed integuments ; S**L** = seeds length ; **SW** = seeds width.

3.3. General and Specific Combining Ability Effects for Studied Traits

Results about GCA effects reveal that *B* has recorded the highest significant positive values of GCA for all studied traits while *Wss1* and *Wss2* obtained significant negative values of GCA for PSi. In addition, *Wss3* has significant positive values of GCA for PSi (Table 5). Positive values of GCA for PSi expressing the difficulty to decorticate seeds were not desirable and the negative values expressing the easiness to decorticate were desirable. Thus, *B* was the best general combiner for all studied traits except for PSi that the best general combiners were *Wss1* and *Wss2*. These three inbred lines (B, *Wss1* and *Wss2*) could be used in *C. mucosospermus* breeding programs. In fact, genotypes with significant GCA effects for a trait indicate that these genotypes contain more genes with additive effects [23,38], suggesting this trait is heritable and these genotypes have high potential for generating superior offspring [27]. Consequently, these genotypes could be used as a good parent for this trait in a breeding program designed to improve that trait [24,29,38]. High significant values of GCA for one trait reveals that selection and hybridization methods would result in interesting genetic improvement for this trait thanks to desirable genes accumulation of two parents in the targeted genotype [17,26,30]. Thus, parental lines *B* (for MfS, MdS, MS$_{100}$, SL and SW) and *Wss1* and *Wss2* (for PSi) can be used in recombination breeding programs to accumulate their favorable genes responsible for increasing seed yield in promising pure lines.

The estimates of SCA revealed that *B × Wss2*, *B × Wss3* and *Wss2 × Wss3* crosses had the highest positives significant values of SCA for MfS and MdS. For MS$_{100}$, higher significant positive estimated values of SCA were recorded in *Wss1 × Wss2*, *Wss1 × Wss3* and *Wss2 × Wss3* progenies. The best combinations for PSi were B × *Wss1*, B × *Wss2* and *Wss1 × Wss2* crosses since they presented negative significant values of SCA. Crosses B × *Wss2* and *Wss1 × Wss3* showed the highest positive significant estimates of SCA for SL while *Wss2 × Wss3*, B × *Wss1* and *Wss1 × Wss3* crosses exhibited the positive significant estimates of SCA for SW (Table 5). Thus, crosses with significant SCA effects involved parents with various types of general combining ability effects (high x low and low x low). Combinations exhibiting significant positive SCA effects for a trait have the potentials of producing good segregants for selections for these attributes in the higher generations [27]. [19] reported that the most favorable combination is the cross having the greatest SCA, in which at least one parent has greater GCA and is divergent in relation to the other parent of the crossing. [39] emphasized that the diversity in parental GCA-effects plays an important role for the production of F$_1$ hybrids with significant positive SCA effects. In fact, great positive significant SCA effects for one trait, obtained in crosses which were involving one progenitor with high GCA effect (high x low), suggested the involvement of additive x dominance gene interactions in this trait expression [38]. When one parent with high GCA crosses another with low GCA gives high SCA effect, this cross could be advanced further for the isolation of transgressive segregants in order to develop good inbred lines [25].

Indeed, these promising crosses may be improved through conventional breeding methods such as bi-parental mating and diallel selective mating, thereafter followed by pedigree method of selection, so as the tight linkage, if any, may be broken and transgressive segregants may be isolated [15]. High significant SCA values resulting from crosses, which involved both parents with low GCA effects, were also observed. This fact is the result of the presence of epistasis (non-allelic interaction) at heterozygous loci, which is not fixed, so it is suggested utilizing these crosses through single plant selection in the later generations [38].

4. Conclusion

In the present study, parental lines shown genetic variation for all examined traits. Both additive and dominance components of variation were highly significant for all studied traits indicating that selection may be used in *C. mucosospermus* heterogeneous populations for improving these traits. Non-additive gene actions play an important role in the inheritance of all studied traits, which suggests the possibility of the heterosis exploitation or the postponement of selection to later generations for improving genetically these traits. Among parental lines, *B* is the best general combiner for MfS, MdS, MS$_{100}$, SL and SW while, *Wss1* and *Wss2* are the best combiners for PSi. For each studied trait, at least two crosses with high significant SCA effects were observed. It is suggested that *C. mucosospermus* breeders can improve the potential of seed crop by selecting very promising lines in respect of seed traits. Therefore, we suggested parental lines *B, Wss1, Wss2* and crosses with desirable significant SCA effects for their including in *C. mucosospermus* breeding programs. Cause of the presence of both GCA and SCA effects, recurrent reciprocal selection can be used to improve *C. mucosospermus*.

Acknowledgements

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