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Article · May 2019

DOI: 10.2298/JAS1901053A

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MORPHO-GENETIC VARIABILITY IN F₂ PROGENY COWPEA
GENOTYPES TOLERANT TO BRUCHID
(*CALLOSOBRUCHUS MACULATUS*)

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Abstract: *Callosobruchus maculatus* Fab. is a major threat to cowpea production reducing the quality, quantity and market value of cowpea grains. A cheap and easy identification method would be a valuable tool in identifying and breeding resistant genotypes in the vast cowpea germplasm. Hence, the purpose of the study was to identify and evaluate the genetics of cowpea traits between resistant and susceptible plant genotypes to *C. maculatus*. Contrasting qualitative and quantitative traits in *C. maculatus* resistant and susceptible parents were evaluated in 72 F₂ progeny cowpea plants. Heritability, segregation and association of investigated traits with the *C. maculatus* resistant performance of the F₂ cowpea genotypes were evaluated to determine closely related traits with *C. maculatus* resistance. Results from the study showed high heritability for all cowpea quantitative traits except leaf petiole length. Both Mendelian inheritance and non-Mendelian inheritance were observed among qualitative traits. However, association evaluation between cowpea traits and mean bruchid development period, percentage adult emergence and oviposition preference were weak ($r < 0.5$) and not significant ($p < 0.05$). This indicates that *C. maculatus* resistance in cowpea may be attributed to factors other than morphological variations.

Key words: *Callosobruchus*, cowpeas, variability, susceptibility, resistant, morphology

Introduction

Cowpea (*Vigna unguiculata* L. Walp.) is an important warm season grain legume cultivated in over 65 countries covering Asia and Oceania, the Middle East,

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Southern Europe, Africa, southern USA and Central and South America (Singh, 2005). Over 80% of dry cowpea produce comes from three countries (Nigeria, Niger and Burkina Faso) of West Africa that cover nearly 83% of the global cowpea area (Popelka et al., 2006). For this reason, cowpea remains the primary source of income for small-scale farmers practising agriculture in dry savannah of sub-Saharan Africa (Kamara et al., 2012).

Cowpea feeds millions of people in developing worlds with an annual world-wide production estimated around 4.5 metric tonnes on 12–14 million ha (Diouf, 2011). It is favoured by farmers because of its ability to maintain soil fertility (Blade et al., 1997, Muchero et al., 2009). It is a nitrogen-fixing plant, and when used in rotation with cereal crops, it can help restore soil fertility (Sanginga et al., 2003). Similarly, it is a source of income (Singh, 2002; Timko et al., 2007), and it is used as animal fodder (Deshpande et al., 2011). In addition, comparably high yields in harsh environments where other food legumes do not thrive (Shimingani and Shimelis, 2011) have made it a crop of choice for many farmers in the sub-Saharan regions. Despite this, it has been revealed that the mean grain yield of cowpea in a typical sub-Saharan African farmer's field is about 495 kg ha⁻¹, much lower than what is obtained under experimental conditions (FAO, 2012).

Callosobruchus maculatus Fab. is considered the most important and common pest of cowpea in storage both in Africa and Asia (Deshpande et al., 2011). Infestation by this insect pest starts on the field, but heavy damage is done during storage. The larvae of the *C. maculatus* feed on the seed contents and estimates of storage losses are highly variable ranging widely from 4% to 100% due to perforations, thus reducing the degree of usefulness and making the seeds unfit either for planting or human consumption reducing its market values (Oluwafemi, 2012; Mofunanya and Namgbe, 2016).

The use of resistant cultivars is still the best method to manage *C. maculatus* infestation (Tripathy, 2016). Although only three cowpea accessions (TVu2027, TVu11952, TVu11953) have been identified to have moderate resistance to *C. maculatus*, there has been a recent report showing that two of the accessions (TVu2027, TVu11952) have shown reduced resistance to *C. maculatus* damage (Amusa et al., 2014). Therefore, the need to identify and breed alternative sources of *C. maculatus* resistance to bruchid damage cannot be overestimated. Furthermore, easy identification of resistant accessions without bioassays has been difficult. Hence, the purpose of the study was to evaluate the genetics of cowpea traits between resistant and susceptible plant genotypes to *C. maculatus*, and find the association of these traits with *C. maculatus* resistance.

Materials and Methods

Collection of samples and bioassay

C. maculatus resistant (TVu11953) and susceptible (Ife Brown) cowpeas were collected for the study from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria and the Institute of Agricultural Research and Training (IAR&T), Moor Plantation, Ibadan, Nigeria respectively. They were screened for *C. maculatus* resistance to ascertain their tolerance level according to the method of Amusa et al. (2014). Seventy-two (72) F₂ segregating populations from the reciprocal crosses between TVu11953 and Ife Brown were developed for the study. The cowpea samples were verified for *C. maculatus* resistance accordingly. Mean development period (MDP), percentage adult emergence (PAE) and oviposition preference were used as measures for *C. maculatus* resistance in the study (Amusa et al., 2014).

Morphological evaluation of collected samples

Seeds of 72 F₂ segregating populations developed above were collected and planted in plastic buckets of 2-kg pots at equidistance from each other arranged in a randomised complete block design with three replications in the screen house, IAR&T, Ibadan, Oyo State (Latitude: 7° 22' 35.2" N, Longitude: 3° 50' 34.4" E). Ten (10) replicated pots of cowpea grains for each of TVu11953 and Ife Brown parent genotypes were planted alongside the 72 F₂ genotypes and normal agronomic practices were carried out throughout the duration of the study. Phenotypic evaluations of the parent cowpea genotypes (TVu11953 and Ife Brown) were done to identify variation in quantitative and qualitative traits between TVu11953 and Ife Brown genotypes according to Cowpea Descriptors of the International Board for Plant Genetic Resource (IBPGR, 1983). Significantly different traits between both parents were phenotyped on the F₁ and F₂ segregation generation plants.

Data collection and analysis

Differentiating qualitative traits between TVu11953 and Ife Brown were identified by observation while t-test was used to identify differentiating quantitative traits of cowpea measured. Differences were considered significant at the 5% significance level. Heritability evaluation was done on significantly different quantitative traits of parent cowpea genotypes measured in the F₂ progeny population according to Boopathi (2013). Qualitative traits of cowpea were subjected to the chi-square goodness of fit to determine the segregation pattern in

F₂ cowpea population and the chi-square test for independent assortment was used to determine association between qualitative traits and bruchid resistant traits.

Results and Discussion

Morphological differences between TVu11953 and Ife Brown bruchids

Differences both in qualitative and quantitative traits were observed between TVu11953 and Ife Brown parent cowpea genotypes in the study. Observable qualitative trait differences included seed shape, seed colour, pod shape, photoperiod sensitivity, flower colour and seed size (Table 1). Significant cowpea quantitative trait differences in the study included terminal leaflet length ($t = 3.11$, $p < 0.01$), leaf petiole length ($t = 2.64$, $p < 0.05$), pod length ($t = 24.23$, $p < 0.01$), pod width ($t = 3.91$, $p < 0.01$), seed length ($t = 6.52$, $p < 0.01$), seed width ($t = 4.44$, $p < 0.01$), seed thickness ($t = 3.94$, $p < 0.01$) and 100-seed weight ($t = 20.44$, $p < 0.01$) (Table 2). Cobbinah et al. (2011) have reported diverse phenotypic variations among cowpea accessions. Variations observed in this study were similar to such variations that have been reported for seed coat colour, pod shape, flower colour, flowering time, flowering initiation, terminal leaflet length, terminal leaflet width, leaf petiole length, pod length, pod width, seed length, seed width, seed thickness and 100-seed weight (Timko et al., 2007; Cobbinah et al., 2011).

Table 1. Qualitative traits of cowpea genotypes which show differences between TVu11953 and Ife Brown cowpeas.

Characters of cowpea	TVu11953	Ife Brown
Source	IITA	IAR&T
Source status	<i>C. maculatus</i> resistant	<i>C. maculatus</i> susceptible
Study status	<i>C. maculatus</i> resistant	<i>C. maculatus</i> susceptible
Seed shape	Kidney	Rhomboid
Seed coat colour	Mottle red	Brown
Pod shape	Curved	Straight
Days to the 1 st flowering	65 days	45 days
Days to 50% flowering	70 days	50 days
Photoperiod sensitivity	Photoperiod sensitive	Photoperiodic neutral
Flower colour	Purple	White
Seed size	Large	Small

IITA: International Institute of Tropical Agriculture, Ibadan; IAR&T: Institute of Agricultural Research and Training, Ibadan.

Table 2. Quantitative traits of cowpea genotypes which show differences between TVu11953 and Ife Brown bruchids.

Characters	TVu11953	Ife Brown	t-test
Terminal leaflet length (cm)	15.43	13.51	3.11**
Leaf petiole length (cm)	8.36	11.43	2.64*
Pod length (cm)	7.08	11.05	24.23**
Pod width (mm)	6.00	7.90	3.91**
Seed length (mm)	10.63	7.98	6.52**
Seed width (mm)	7.47	5.77	4.44**
Seed thickness (mm)	5.93	4.38	3.94**
100-seed weight (g)	26.32	15.23	20.44**

* $p < 0.05$; ** $p < 0.01$.

Segregation of qualitative traits in F₁ and F₂ cowpea populations Segregation of cowpea seed shape

Both TVu11953 and Ife Brown were true breeding for kidney and rhomboid seed shapes respectively. F₁ generation seeds from reciprocal crosses showed that all seeds from TVu11953 mother plants had kidney-shaped seeds while rhomboid seed shape was observed in all seeds from Ife Brown mother plants. However, the F₂ seeds from TVu11953 mother plant lines were all kidney-shaped, but Ife Brown mother plant lines produced 707 kidney-shaped seeds and 601 rhomboid-shaped seeds. Furthermore, the kidney-shaped seed exhibited complete dominance on the TVu11953 mother plant line with the absence of the rhomboid-shaped seeds. Seed shape analysis from pooled F₂ sampled seeds showed a monogenic pattern of inheritance ($\chi^2(3:1) = 0.72$, $p > 0.05$) with kidney shape dominant over rhomboid shape (Table 3).

Table 3. A segregation pattern of seed shape in F₁ and F₂ cowpea generations.

Crosses (♀ × ♂)	F ₁ seeds		F ₂ seeds		$\chi^2(1:3)$	$\chi^2(3:1)$
	Kidney	Rhomboid	Kidney	Rhomboid		
P ₁ × P ₂	32	0	1025	0	-	-
P ₂ × P ₁	0	75	707	601	588.79**	306.12**
Total	32	75	1732	601	3016.72**	0.72

** $p < 0.01$; χ^2 : Chi-square; ♀: Maternal plant; ♂: Paternal plant; P₁: TVu11953; P₂: Ife Brown.

The presence of F₁ hybrid seed shapes conforming to the seed shape of their mother plants shows the presence of a maternal influence on the inheritance of seed

shape in cowpea while the segregation pattern of seed shape in the F₂ cowpea population corroborates with the work of Meena and Kumar (2014) who reported 3:1 monogenic inheritance of seed shape in F₂ segregation population of chickpea. However, the result of this study did not corroborate with the findings of Hossain et al. (2010) who reported that seed shape was controlled by two genes in soybean and chickpea and a segregation ratio of 9:7 in their study.

Segregation of cowpea seed coat colour

Seed coat colour is a major trait that affects consumer acceptability in cowpea. Its preference and use patterns differ from one region to another (Egbadzor et al., 2015). Both TVu11953 and Ife Brown were true breeding for mottled red and brown seed coat colours. Maternal effect was observed in seed coat colour segregation with F₁ seeds produced from maternal plants resembling maternal seeds. F₁ hybrid seeds from TVu11953 mother plants were all mottled in colour while seeds from Ife Brown mother plants were all brown in colour (Table 4). However, the presence of intermediates in the F₂ seed population showed that seed colour may be controlled by more than one gene.

Table 4. A segregation pattern of seed colour in F₁ and F₂ cowpea generations.

Crosses (♀ + ♂)	F ₁ Seeds		F ₂ Seeds			χ^2 (1:3)	χ^2 (3:1)	χ^2 (1:2:1)
	Mot	Brown	Mot	Int	Brown			
P ₁ x P ₂	32	0	707	318	0	1057.17**	19.84**	-
P ₂ x P ₁	0	75	1	706	601	588.79**	306.12**	
Total	32	75	708	1025	601	-	-	43.96**

** $p < 0.01$; χ^2 : Chi-square; ♀: Maternal plant; ♂: Paternal plant; P₁: TVu11953; P₂: Ife Brown; Mot: Mottled red; Int: Intermediate colour.

F₂ seeds from TVu11953 mother plant lines produced 707 seeds with mottled red colour and 318 seeds which showed an intermediate colour. The segregation pattern of seed coat colour on both TVu11953 and Ife Brown plants significantly deviated from Mendelian segregation ratio for monogenic recessive and dominant inheritance respectively ($p < 0.01$). Similarly, dihybrid inheritance analysis of seed coat colour in pooled sampled seeds from both TVu11953 and Ife Brown mother plants also showed a significant deviation from the expected 1:2:1 ratio (Table 4). Cowpeas have been reported to show varied seed coat colours ranging from white to cream to brown to black each controlled by genes with maternal effects (Drabo et al., 1988; de Castro et al., 2013). These authors have showed that five major genes interact to produce ten different seed coat colours in cowpea. Their works have also showed that all colour genes could be recessive to give red seeds while

the absence of seed coat pigmentation results in cream or white seeds. Epistasis interactions in the genes responsible for seed coat colour in cowpea have also been reported (Kongjaimun et al., 2012; Lachyan and Dalvi, 2015).

Segregation of cowpea pod shapes

Both TVu11953 and Ife Brown were true breeding for curved and straight pod shapes. The presence of curved and straight pods in hybrid plants of TVu11953 and Ife Brown mother plants respectively shows that pod shape inheritance may be maternally influenced in the F₁ generation. In the F₂ generation, both TVu11953 and Ife Brown mother plant lines produced both curved and straight pods. The presence of 111 curved and 38 straight pods in the TVu11953 mother line revealed a dominance of monogenic inheritance for curved pods over straight pods ($\chi^2(3:1) = 0.02$, $p > 0.05$). This is similar to the works of Nwofia (2014) who reported that coiled shaped pods were dominant over the straight shape pods in the F₂ generation of cowpea. However, the pooled samples showed a pod shape segregation pattern with a goodness of fit to expected ratio of 9:7 for straight pods to curved pods ($\chi^2(9:7) = 3.08$, $p > 0.05$) (Table 5). This signifies the presence of epistasis interaction of duplicate recessive genes for straight-shaped pods from the pooled samples in the F₂ generation pods. Uguru (1995a) reported that there were evidences that pod shape in cowpea was governed by two loci, *PP* and *VV* for coiled and straight pod shapes, the former being dominant and epistatic over the latter.

Table 5. A segregation pattern of pod shape in F₁ and F₂ cowpea generations.

Crosses (♀ + ♂)	F ₁ pods		F ₂ pods		χ^2 (1:3)	χ^2 (3:1)
	Curved	Straight	Curved	Straight		
P ₁ x P ₂	21	0	111	38	194.69**	0.02
P ₂ x P ₁	0	45	25	174	16.42**	413.75**
Total	21	45	136	212	36.80**	239.46**

** $p < 0.01$; χ^2 : Chi-square; ♀: Mother (recipient) plant; ♂: Father (donor) plant; P₁: TVu11953; P₂: Ife Brown.

Segregation of cowpea photoperiod sensitivity

The time of flowering is an important agronomic trait as it affects both adaptation of a variety to a particular agro-ecological zone and also its productivity (Ishiyaku et al., 2005). The onset of flowering in cowpea is modulated by a photoperiod which has a significant effect on phenology in all cowpea genotypes (Nuhu and Mukhtar, 2013). Some authors have indicated the photoperiod to be the

most important environmental variable affecting flowering time and that most cultivated cowpeas in west Africa were photoperiod sensitive (Craufurd et al., 1996). TVu11953 was observed to be photoperiod sensitive initiating its flowers only between October and February while Ife Brown was photoperiod insensitive, flowering throughout the year of planting regardless of planting time. The initiations of flowers in TVu11953 and Ife Brown were averagely 65 and 45 days respectively after sowing. This corroborates with the works of Craufurd et al. (1996) and Manggoel and Uguru (2011) who stated that cowpea genotypes with mean first flowering greater than 45 days were photoperiod sensitive while those that flowered less than 45 days were photoperiod insensitive or neutral.

Table 6. A segregation pattern of photoperiod sensitivity among F₁ and F₂ cowpea generations.

Crosses (♀ + ♂)	F ₁ plants		F ₂ plants		χ^2 (1:3)	χ^2 (3:1)
	PHS	PHN	PHS	PHN		
P ₁ x P ₂	24	0	24	0	-	-
P ₂ x P ₁	0	53	0	49	-	-
Total	24	53	24	49	2.42	69.08*

* $p < 0.05$; χ^2 : Chi-square; ♀: Mother (recipient) plant; ♂: Father (donor) plant; P₁: TVu11953; P₂: Ife Brown; PHN: photoperiod neutral; PHS: photoperiod sensitive.

The presence of photoperiod sensitivity in plant individuals from photoperiod sensitive maternal plants both in the F₁ and F₂ generation cowpea plants showed photoperiod sensitivity to be maternally influenced. This is similar to the reports of Manggoel and Uguru (2011) who showed that flowering time as an indication of the photoperiod was maternally influenced. They stated that the wide gap in days to first flowering between the photoperiod sensitive and photoperiod neutral cowpea accessions can be linked to different factors other than Mendelian inheritances. The maternal inclination with respect to the number of days to flowering in the offspring implies that progenies from crosses with photoperiod sensitive accessions as maternal parents will not flower until a certain critical photoperiod is attained. However, pooled results of observations from F₂ generation plants showed a goodness of fit to expected 3:1 ratio for photoperiod neutral to photoperiod sensitive ($\chi^2(3:1) = 2.42$, $p > 0.05$) (Table 6). This did not corroborate with the work of Sene (1967) who reported that photoperiod sensitivity was controlled by a single gene completely dominant over the photoperiod neutral gene in cowpea. The result from the segregation pattern observed among pooled sampled F₂ plants might be due to the unequal number of plants examined from both maternal lines. However, if the same number of plants were pooled together from maternal lines and examined, the goodness of fit would result in a ratio of 1:1, indicating that the

trait was maternally inherited. Earlier works of Ishiyaku et al. (2005) have suggested polygenic control with epistasis gene action while the work of Kongjaimun et al. (2012) reported ten QTLs responsible for flowering time in cowpea.

Segregation of cowpea flower colours

Sangwan and Lodhu (1998) have stated that flower colour is less influenced by environment variations and that they are used as markers in the identification of species or varieties. The observation of purple flowers on hybrid plants from seeds of both parental maternal lines in the F₁ generation shows purple colouration of cowpea flowers to be dominant over white flower colourations. In the F₂ generation, purple flowers showed a dominant segregation pattern over the white-coloured flowers ($\chi^2(3:1) = 0.11, p > 0.05$) (Table 7). This result is similar to the works of Cobbinah et al. (2011) who also reported a higher frequency of cowpea plants with the purple flowers than with the white flowers in the F₂ plants generated from a cross between purple-flowered and white-flowered cowpea accessions. Uguru (1995b) observed a partial colour dominance of purple petal colour over white petal colour in a cross of white and purple petal coloured parents. Sangwan and Lodhu (1998) have reported that inheritance of flower colour in cowpea showed a monogenic inheritance with purple flowers dominant over white flowers both in F₂ and backcross populations evaluated in their study.

Table 7. A segregation pattern of flower colours in F₁ and F₂ cowpea generations.

Crosses (♀ + ♂)	F ₁ plants		F ₂ plants		χ^2 (1:3)	χ^2 (3:1)
	Purple	White	Purple	White		
P ₁ x P ₂	24	0	24	0	-	-
P ₂ x P ₁	53	0	32	17	42.46*	2.46
Total	77	0	56	17	104.11*	0.11

* $p < 0.05$; χ^2 : Chi-square; ♀: Mother (recipient) plant; ♂: Father (donor) plant P₁: TVu11953; P₂: Iife Brown.

Phenotypic evaluation and heritability of quantitative traits in the F₂ cowpea populations

Genetic variability is the basic information needed for breeders to improve crops by adopting the appropriate method of selection based on the variability that exists in the plant material (Sharma et al., 2017). Phenotypic evaluation of the F₂ plants showed variation to be the highest in leaf petiole length in the F₂ population followed by 100-seed weight and the lowest in seed width. The heritability

estimates are important genetic parameters that play a significant role in selection of different cowpea genotypes from a population (Manggoel et al., 2012). Heritability was high for all traits evaluated in the F₂ population except for leaf petiole length which had the lowest heritability of 45% compared to 100-seed weight which had the highest heritability of 96% (Table 8). This is similar to reports of Omoigui et al. (2006) and Inuwa et al. (2012) who also reported similar high heritability for 100-seed weight. However, the high heritability for pod length ($H^2 = 75\%$) observed in this study did not corroborate with the report of Omoigui et al. (2006) who reported a moderate heritability of 43% for pod length in their study. The low heritability observed in leaf petiole length corroborates with the findings of Inuwa et al. (2012). High broad-sense heritability values usually indicate the predominance of additive gene action in the expression of the traits (Manggoel et al., 2012).

Table 8. Quantitative traits evaluated in F₂ cowpea population.

Traits	Parents		Mean	F ₂ generation			H ²
	TVu11953	Ife Brown		Min–Max	SD	CV	
TLL	15.43	13.51	11.42	5.40–17.40	2.08	18.25	86
LPL	8.36	11.43	8.06	3.10–13.30	2.18	27.00	45
PDL	7.08	11.05	10.75	5.00–15.80	2.05	19.02	75
PDW	6.00	7.90	7.24	4.88–12.60	0.90	12.45	94
SDL	10.64	7.98	9.25	6.80–11.44	0.98	10.62	89
SDW	7.47	5.77	6.26	4.57–7.65	0.57	9.19	92
SDTK	5.93	4.38	4.78	3.78–5.79	0.48	9.95	88
100SDWT	26.32	15.23	17.46	9.80–27.87	3.79	21.72	96

Min: Minimum; Max: Maximum; SD: Standard deviation; CV: Coefficient of variation (%); H²: Heritability (%); TLL: Terminal leaflet length (cm); LPL: Leaf petiole length (cm); PDL: Pod length (cm); PDW: Pod width (mm); SDL: Seed length (mm); SDW: Seed width (mm); SDTK: Seed thickness (mm); 100SDWT: 100-seed weight (g).

Correlation between cowpea quantitative traits and *C. maculatus* resistance

Contrasting quantitative traits between TVu11953 and Ife Brown were correlated with *C. maculatus* resistant measures (mean development period and percentage adult emergence) in the F₂ segregating population. Terminal leaf length, seed length, seed weight and seed thickness had a negative correlation with the mean development period (-0.05, -0.04, -0.03, -0.05, respectively). Other quantitative traits showed a positive correlation with the percentage adult emergence of *C. maculatus* insects in the F₂ generation. Terminal leaflet length, leaf petiole length, pod length, pod width and seed thickness showed a negative

correlation with the number of eggs laid by *C. maculatus* insects in the study on F₂ generation seeds evaluated (Table 9). Several authors have reported bruchid resistance to be associated with several phenotypic traits in related crop species. These include seed size, seed coat texture, seed thickness and seed colour in mungbean and green gram varieties (Mei et al., 2009; Gupta and Apte, 2016; Soumia et al., 2017). Though both positive and negative associations were observed between the contrasting traits and *C. maculatus* resistance measures in the study, these relationships were weak and not significant. They can therefore not be used in predicting *C. maculatus* tolerance levels in cowpea genotypes.

Table 9. Cowpea quantitative trait correlations with mean development period, percentage adult emergence of insects and the number of eggs laid by *C. maculatus*.

Characters	MDP	PAE	ESD
Terminal leaflet length (cm)	-0.05	0.12	-0.06
Leaf petiole length (cm)	0.13	0.08	-0.02
Pod length (cm)	0.00	0.14	-0.28
Pod width (mm)	0.08	0.32	-0.28
Seed length (mm)	-0.04	0.09	0.10
Seed width (mm)	-0.03	0.08	0.10
Seed thickness (mm)	-0.05	0.23	-0.15
100-seed weight (g)	0.04	0.14	0.02

MDP: Mean insect development period; PAE: Percentage adult emergence; ESD: Number of eggs laid (Oviposition).

The test of independent assortment between *C. maculatus* resistance and some cowpea traits

Genotype resistance when employed as an option to minimise cowpea losses caused by *C. maculatus* during storage is the best alternative to manage *C. maculatus* damage (Tripathy, 2016). The development of resistant cultivars is, however, still very limited, since few high resistance sources have been identified (Singh et al., 1985; Dongre et al., 1996). The segregations of several contrasting traits between the TVu11953 and Ife Brown genotypes were tested for association segregation of *C. maculatus* resistance measured by MDP. All the traits evaluated showed independent segregation assortment with MDP in the F₂ population evaluated (Table 10). Similarly, independent assortment between PAE with these contrasting traits between TVu11953 and Ife Brown was analysed to check for segregation association with *C. maculatus* resistance. The analysis showed that none of the traits evaluated had a significant association with PAE (Table 11).

Table 10. The test of independent assortment of cowpea traits with the bruchid mean development period.

Traits	Phenotype	MDP		χ^2	<i>p</i>
		Resistant	Susceptible		
Seed coat colour	Mottled	0	19	2.37	0.34
	Intermediate	2	34		
	Brown	2	15		
Seed shape	Kidney	1	37	1.31	0.34
	Rhomboid	3	31		
Photoperiod sensitivity	PHS	1	24	0.18	0.67
	PHN	3	44		
Flower colour	Pink	3	52	0.01	0.95
	White	1	16		
Seed weight	Large	0	26	2.39	0.29
	Small	4	42		

χ^2 : Chi-square; *p*: Probability value; MDP: Mean development period; PHS: Photoperiod sensitive; PHN: Photoperiod neutral.

Table 11. The test of independent assortment of traits with the bruchid percentage adult emergence.

Traits	Phenotype	PAE		χ^2	<i>p</i>
		Resistant	Susceptible		
Seed coat colour	Mottled	0	19	4.54	0.10
	Intermediate	2	34		
	Brown	3	14		
Seed shape	Kidney	1	37	2.32	0.18
	Rhomboid	4	30		
Photoperiod sensitivity	PHS	1	24	0.51	0.65
	PHN	4	43		
Flower colour	Pink	4	51	0.04	0.84
	White	1	16		
Seed size	Large	0	26	3.01	0.15
	Small	5	41		

χ^2 : Chi-square; *p*: Probability value; PAE: Percentage adult emergence; PHS: Photoperiod sensitive; PHN: Photoperiod neutral.

Conclusion

The identification of discriminating traits between *C. maculatus* resistance and susceptibility in cowpea would be an added tool for easy identification and breeding of *C. maculatus* resistant genotypes. Contrasting morphological traits between *C. maculatus* resistant and susceptible genotypes in this study showed a low correlation and no association with *C. maculatus* resistance. This indicates that

C. maculatus resistance is not solely dependent on seed traits as suggested by some authors for related crops. There is a need therefore to employ other more technical approaches that would better help in *C. maculatus* resistant genotype selection among cowpea germplasm lines.

Acknowledgements

The authors wish to acknowledge the Central Research Committee, University of Lagos for providing funds (CRC No. 2013/04) for the study, the International Institute of Tropical Agriculture, Ibadan (IITA) and the Institute of Agricultural Research and Training, (IAR&T), Moor Plantation, Ibadan, Nigeria for providing the seeds of the accessions used for the study and IAR&T for allowing the use of their facilities for the research.

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Received: July 11, 2018

Accepted: December 13, 2018

MORFO-GENETSKA VARIJABILNOST KOD GENOTIPOVA VIGNE F₂
GENERACIJE POTOMSTVA TOLERANTNIH NA VIGNIN ŽIŽAK
(*CALLOSOBRUCHUS MACULATUS*)

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R e z i m e

Callosobruchus maculatus Fab. predstavlja najveću pretnju proizvodnji vigne, smanjujući kvalitet, količinu i tržišnu vrednost zrna. Metoda jeftine i jednostavne identifikacije bila bi dragoceno sredstvo u identifikaciji i oplemenjivanju otpornih genotipova u obimnoj germplazmi vigne. Stoga, svrha ovog istraživanja bila je da se identifikuje i proceni genetika osobina vigne između biljnih genotipova otpornih i osetljivih na *C. maculatus*. Kontrastne kvalitativne i kvantitativne osobine kod otpornih i osetljivih roditelja na *C. maculatus* procenjene su kod 72 biljke vigne F₂ generacije potomstva. Heritabilnost, segregacija i asocijativnost ispitivanih osobina sa performansama genotipova vigne F₂ generacije otpornim na *C. maculatus* su ocenjeni, kako bi se odredile blisko povezane osobine sa otpornošću na *C. maculatus*. Rezultati istraživanja pokazali su visoku heritabilnost za sve kvantitativne osobine vigne, osim dužine peteljke lista. Mendelovsko i ne-Mendelovsko nasleđivanje primećeno je među kvalitativnim osobinama. Međutim, asocijativna procena između osobina vigne i prosečnog perioda razvoja bruhide, procenta pojave odraslih jedinki i sklonosti ovipoziciji bila je slaba ($r < 0,5$) i nije bila značajna ($p < 0,05$). Ovo ukazuje na to da se otpornost prema *C. maculatus* kod vigne može pripisati faktorima, koji se ne odnose na morfološke varijacije.

Ključne reči: *Callosobruchus*, vigne, varijabilnost, osetljivost, otpornost, morfologija.

Primljeno: 11. jula 2018.
Odobreno: 13. decembra 2018.

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