

Crossing potential in the production of persistent green seeds in *Cowpea* using *gt* and *gc* genes

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ABSTRACT

Eight cowpea genotypes (*Vigna unguiculata* (L.) Walp.) combined in two sets of crosses were studied to evaluate parent's potential and effects of genes for green testa (*gt*) and green cotyledon (*gc*) on days to first flowering (NDF), one hundred seed weight (SW) and dry seed yield per plant (SYP). Moreover, this study contributed to the identification of the best combinations of parents to form a population with wide genetic base for selecting lines having seeds with green color that persist to dryness. Two crosses segregating for both *gt* and *gc* genes were studied in Experiment 1, and a 3 x 5 partial diallel was studied in Experiment 2. In Experiment 1, the F₂ generation of AU-GC-67 x Bettergreen had higher genetic variance than AU-78.1 x Bettergreen for the three traits. Results also showed that the genes *gt* and *gc* individually or in combination did not affect the characters studied. In Experiment 2, the effects of general combining ability (GCA) were higher than those of specific combining ability (SCA), indicating that the additive genetic effects were predominant in the expression of the three traits. Parents with the greatest GCA effects were: AR-92-537 and AU-GC-67 for earliness; AU-KPH-9/9-1 and Royal Blackeye for lateness; Colossus 80 for large seeds and AU-KPH-9/9-1, Colossus 80, Royal Blackeye and Bettergreen for seed yield per plant. According to the mean and the GCA of the parents and the mean and the genetic variance of the F₂ generation, the crosses AU-GC-67 x AU-KPH-9/9-1, AU-78.1 x AU-KPH-9/9-1, AU-78.1 x Colossus 80, Bettergreen x AUBe, Bettergreen x Royal Blackeye and Bettergreen x Colossus 80 are the most promising/highly recommended to build a population with a wide genetic base for selection of high yielding lines with persistent green seeds.

KEY WORDS: Cowpea genetics, green testa, green cotyledon, vegetable breeding.

INTRODUCTION

Visual appearance is very important for agricultural products like cowpea [*Vigna unguiculata* (L.) Walp.] which are marketed as dry seeds, fresh pods, frozen seeds or canned seeds. In all these cowpea products, seed color has an important visual appeal, particularly for dry seed form, since it is the quality factor that the consumer first notices (Francis, 1980).

Most modern American cultivars grown for seed can be classified as blackeye, pinkeye, cream, or crowder. Each type produces seeds with a distinctive appearance and flavor, and appeals to a unique market segment. Two other types, yardlong beans and snap type cultivars, are grown to a limited extent (Fery, 1990). Nevertheless, the packing process for the frozen trade requires a cultivar that retains its green seed color regardless of its stage of maturity (Chambliss, 1974). Also, in the Brazilian northeastern

market, the light green seed color has high commercial value, due to its attractive appearance in fresh and dry seeds (Freire Filho et al., 1981).

Two recessive genes for green color in cowpea dry seeds have been found: *gt* (green testa) (Chambliss, 1974) and *gc* (green cotyledon) (Fery et al., 1993). These genes are the result of two natural mutations from Ala. 963.8 and Carolina Cream, respectively. The latter resulted from the Ala. 963.8 x Floricream cross (Fery and Dukes, 1984).

Currently, there are two cultivars with the *gtgt* genotype: Freezegreen, cream type (Chambliss, 1979), and Genegreen, blackeye type (Chambliss and Hunter, 1992), four cultivars with the *gcgc* genotype: Bettergreen, cream type (Fery et al., 1993), Charleston Greenpack, pinkeye type (Fery, 1998), Petite-N-Green, pinkeye type (Fery, 1999) and Green Pixie, cream type (Fery, 2000) and only one cultivar with *gtgtgcgc* genotype, Green Dixie Blackeye, blackeye

type (ARS News & Information, 2000). Fery (1990) pointed out that the incorporation of *gt* gene into blackeye, pinkeye, and cream cultivars is currently an important goal of several cowpea breeding programs in the United States. In addition, Fery et al. (1993) anticipated the extensive use of 'Bettergreen' as a parent in breeding programs.

The objectives of this study were to investigate two groups of parents combined in two sets of crosses to determine parent's potential, the effects of the *gt* and *gc* genes individually and in combination, on flowering, seed size and yield, and the best parent combinations to build a population for the selection of lines with green seeds that persist to dryness.

MATERIAL AND METHODS

Eight parents were selected. Three of green seed genotypes (parent group 1), AU-GC-67 (blackeye type) and AU-78.1 (cream type), with green testa and cream cotyledons (genotype *gtgtGcGc*), and Bettergreen (cream type) cultivar (Fery et al., 1993) with cream testa and green cotyledons, (genotype *GtGtgcc*). Five of a common seed genotypes (parent group 2) with cream, white or brown testa and cream cotyledons (genotype *GtGtGcGc*), composed of two blackeye types, AUBe (Chambliss and Hunter, 1991) and Royal Blackeye (Lancaster et al., 1988); two crowder types Colossus 80 (Fery and Dukes, 1982) and AU-KPH-9/9-1, from the Auburn University cowpea breeding program, both having brown seeds; and one line pinkeye type AR-92-537, from the University of Arkansas cowpea breeding program.

The eight parents were used in two sets of crosses. In Set 1, two crosses were made within parent group 1 (green seed genotypes): AU-GC-67 x Bettergreen and AU-78-1 x Bettergreen, and F_1 , F_2 and backcrossed populations were obtained. In Set 2, 15 crosses were made between parent group 1 (green seed genotypes) and parent group 2 (common seed genotypes) in a 3 x 5 partial diallel cross.

Experiment 1 and Experiment 2 were comprised of crosses from Set 1 and Set 2, respectively. These two experiments were initiated in the field in 15-16 May, 1995, at the E.V. Smith Research Center, Shorter, Alabama (32° 36' N, 85° 50' W and altitude of 200 m asl), in a Norfolk fine sandy loam soil (Thermic Typic Kandiudults; USDA taxonomy). A randomized complete block design with six replications was used for both experiments. Single-row plots (between row 1.0 m and length of row of 7.2 m), with 12 seeds per row in Experiment 1 were used. Parents and F_1 seeds

were sown in one row per replication, backcrosses seeds in two rows per replication, and F_2 seeds in four rows per replication. Data were collected from 10 competitive plants per row for all generations. In Experiment 2, parents and F_2 seeds were sown in one-row plots of 9.0 m of length and 1.0 m between row with 15 seeds per row. Data were collected from 12 competitive plants in the row. In this experiment, the cowpea cultivar Pickworth was used as common border for all plots and blocks. Weeds were controlled with herbicides and hand hoeing. An irrigation gun was used to insure the crop received at least one inch of water per week.

Data were recorded for number of days to first flower (NDF), 100 seeds weight (SW), and seed yield per plant (SYP). The methodology presented by Mather and Jinks (1982) and Ramalho et al. (1993) was used for the ANOVA in Experiment 1. The "Partial-ST" model of Geraldi and Miranda-Filho (1988) was used for the of partial diallel analysis in Experiment 2. The general linear model analysis from Statistical Analysis System (SAS) Institute, Cary, NC. was used to analyze the data from both experiments.

An estimate of the average degree of dominance (Mdd) in Experiment 1 was calculated according to Mather and Jinks (1982) and Ramalho et al. (1993), using the formula: $Mdd = (2 V_D / V_A)^{0.5}$; where V_D : dominance genetic variance, and V_A : additive genetic variance. The broad sense heritability (H^2) and the narrow sense heritability (h^2) were estimated using the formulas:

$$H^2 = V_G(F_2) / V_P(F_2) \text{ and}$$

$$h^2 = V_A(F_2) / V_P(F_2),$$

where $V_G(F_2)$: genetic variance of the F_2 generation and $V_P(F_2)$ = phenotypic variance of the F_2 generation.

The genetic coefficient of variation (GCV) was calculated using the formula:

$$GCV = \sqrt{V_G(F_2)} / m(F_2);$$

where $\sqrt{V_G(F_2)}$: genetic standard deviation of the F_2 generation and $m(F_2)$: mean of the F_2 generation.

The expected genetic gain due to selection (GS) was estimated using the formula presented by Jonhson et al. (1955):

$$GS = i V_A(F_2) \sqrt{V_P(F_2)} / V_P(F_2);$$

where, $i = 1.755$ is the selection differential, expressed in phenotypic standard deviation, with the expectation

in the case of 10% selection, and $\sqrt{V_P(F_2)}$: phenotypic standard deviation of the F_2 generation.

RESULTS AND DISCUSSION

Experiment 1

The ANOVA showed that populations and their components, parents, backcrosses and the contrast of parents versus F_1 were statistically different ($P < 0.01$) for the traits NDF, SW and SYP. Differences were also found in F_1 for NDF, and in the contrast parents + F_1 vs F_2 + backcrosses for SW.

The parents and the F_1 phenotypic variances were interpreted as environmental variances, and, since the parents were pure lines, they were expected to have no genetic variability. Among the parents, AU-CG-67 had the highest phenotypic variance for all three characters. Except $BC_1[F_1(P_1 \times P_3) \times P_1]$ for NDF and $BC_1[F_1(P_2 \times P_3) \times P_3]$ for SW, the F_2 generation of the cross AU-GC-67 x Bettergreen had the highest phenotypic and genotypic variances for all three traits (Table 1).

The genetic parameters estimated for both crosses are presented in Table 2. Regardless of the error in estimating the genetic parameters, the total genetic variance and the additive genetic variance for SW and SYP for the cross AU-GC-67 x Bettergreen were higher than the observed values for the cross AU-78.1 x Bettergreen, which had the highest dominance

genetic variance for SYP. The high variances found in the parents, F_1 and backcrosses compared to F_2 variance precluded estimation of some genetic parameters for NDF in both crosses. There was partial dominance for SW in both crosses and for SYP in AU-GC-67 x Bettergreen and overdominance for SYP in AU-78.1 x Bettergreen. In both crosses, broad sense heritability (H^2) was intermediate for NDF (0.40 and 0.33), and high for SW (0.88 and 0.89) and SYP (0.73 and 0.69). Narrow sense heritability (h^2) was high in both crosses for SW (0.87 and 0.64) and for SYP (0.63) in AU-GC-67 x Bettergreen, and intermediate for SYP (0.32) in AU-78.1 x Bettergreen. The Genetic Coefficient of Variation (CGV) in both crosses was low for NDF (4.45 and 3.10) and ranged from average to high for SW (20.81 and 17.41) and SYP (30.78 and 27.53). The genetic gain due to selection (GS) for SW (4.07) and SYP (23.53) in the cross AU-GC-67 x Bettergreen was higher than in the cross AU-78.1 x Bettergreen, 2.62 and 10.71 respectively, reflecting the differences in the magnitude of the additive genetic variances between the crosses.

The additive genetic effects for SW in both crosses were more important than the effects due to dominance, which agrees with Drabo et al. (1984) and Singh and Dabas (1992). For SYP, the additive genetic effects predominated in the cross AU-GC-67 x Bettergreen, whereas in the cross AU-78.1 x Bettergreen the dominance genetic effects were more important, which are similar to the results obtained by Singh and Dabas

Table 1. Number of plants (n), mean (m), phenotypic variance (VP) and genetic variance (VG) within populations for number of days to first flower (NDF), weight of one hundred seeds (SW) and dry seed yield per plant (SYP) in two cowpea crosses segregating for the *gt* and *gc* genes.

Populations	n	NDF (day)			SW (g)			SYP (g)		
		m	Vp	Vg	m	Vp	Vg	m	Vp	Vg
AU-GC-67 (P1)	54	42.6	6.9	-	14.6	0.9	-	58.3	106.7	-
AU-78.1 (P2)	39	45.0	1.7	-	15.0	0.4	-	41.6	64.2	-
Bettergreen (P3)	37	47.0	5.9	-	8.8	0.5	-	46.8	55.8	-
$F_1(P1 \times P3)$	33	46.9	6.8	-	13.8	0.9	-	67.7	194.5	-
$F_2(P1 \times P3)$	200	45.6	10.6	4.1	12.1	7.1	6.3	58.5	443.5	324.5
$BC_1F_1(P1 \times P3) \times P1$	83	45.0	8.8	0.9	13.9	1.2	0.3	72.2	230.3	111.3
$BC_1F_1(P1 \times P3) \times P3$	79	47.0	7.2	2.6	10.8	6.9	6.1	54.3	374.3	255.3
$F_1(P2 \times P3)$	41	49.3	6.0	-	13.3	0.9	-	67.5	211.2	-
$F_2(P2 \times P3)$	210	47.3	6.3	2.2	12.7	5.5	4.9	57.0	356.3	245.9
$BC_1F_1(P2 \times P3) \times P2$	86	46.5	8.5	4.3	14.2	1.1	0.5	57.8	274.6	164.2
$BC_1F_1(P2 \times P3) \times P3$	93	48.0	5.4	1.2	11.0	6.3	5.7	57.2	322.6	212.2
MSD ^{1/}		2.8			1.2			14.8		

^{1/}MSD: Minimum significant difference at the 5% level of probability by the Tukey test.

Table 2. Genetic variance (V_G), additive variance (V_A), dominant variance (V_D), environmental variance (V_E), medium degree of dominance (Mdd), broad sense heritability (H^2), narrow sense heritability (h^2), genetic coefficient of variation (GCV), genetic gain due to selection (GS) for number of days for first flower (NDF), weight of one hundred seeds (SW) and dry seed yield per plant (SYP) in two crosses of cowpea segregating for the *Gt* and *Gc* genes.

Parameters	Characters		
	NDF	SW	SYP
AU-GC-67 x Bettergreen			
F ₂ mean	45.60	12.05	58.51
V _G	4.14	6.28	324.54
V _A	-	6.18	282.46
V _D	-	0.10	42.08
V _E	6.21	0.80	119.00
Mdd	-	0.18	0.54
H ²	0.40	0.88	0.73
h ²	-	0.87	0.63
CVG (%)	4.45	20.81	30.78
GS	-	4.07	23.53
GS (% of mean)	-	33.84	40.22
AU-78.1 x Bettergreen			
F ₂ mean	47.27	12.65	56.95
V _G	2.15	4.85	245.88
V _A	-	3.49	115.29
V _D	-	1.35	130.59
V _E	4.19	0.60	110.39
Mdd	-	0.88	1.50
H ²	0.33	0.89	0.69
h ²	-	0.64	0.32
CVG (%)	3.10	17.41	27.53
GS	-	2.62	10.71
GS (% of mean)	-	20.71	18.82

(1992). The best response to selection for the improvement of SYP was obtained from AU-GC-67 x Bettergreen once the additive genetic effects were greater for this cross. This result is in agreement with Lelely (1975) and Aryeety and Laing (1973) that found H² values of 0.68 and 0.63 for SW and SYP, respectively. As for SYP, the H² in both crosses was relatively high when compared with the values of 0.54 and 0.35, found by Bapna and Joshi (1973) and Kheradnam and Niknejad (1974), respectively. The narrow sense heritability (h²) for SW was high in both crosses when compared to the h² value of 0.37 obtained by Aryeety and Laing (1973). H² in SYP was high in AU-GC-67 x Bettergreen and intermediate in AU-78.1 x Bettergreen.

The GCV in both crosses was high for SW (20.81 and 17.41) and SYP (30.78 and 27.53). The same was observed for the expected genetic gain due to selection, indicating that there is enough genetic variability in both crosses to improve SW and SYP, but especially in AU-GC-67 x Bettergreen, where the GS for SW and SYP were about twice as much as those in AU-78.1 x Bettergreen.

Analysis of the segregating classes for green seed color in F₂ generations showed that there were no differences by the "t" test for NDF, SW and SYP when progenies with cream testa and cream cotyledons (genotypes *Gt_Gc_*) were compared to progenies with green testa and cream cotyledons (genotype *gtgtGc_*), cream testa and green cotyledons (genotype *Gt-gcgc*) and green testa plus green cotyledon (genotype *gtgtgcgc*) (Table 3). Nevertheless, there were variations in green color

Table 3. Number of plants (n), population mean (m), phenotypic standard deviation (SD) and value for t test for segregating classes for *gt* and *gc* genes compared to *Gt_Gc_* class within F₂ generations for number of days to first flower (NDF), one hundred seeds weight (SW) and dry seed yield per plant (SYP) in the cowpea crosses AU-GC-67 x Bettergreen and AU-78.1 x Bettergreen.

Generation/ Genotype	n	NDF (day)			SW (g)			SYP (g)		
		m	SD	t ^{1/}	m	SD	t ^{1/}	m	SD	t ^{1/}
F ₂ (P1xP3)										
<i>Gt_Gc_</i>	96	45.7	3.5		11.9	2.9		57.4	22.1	
<i>GtgtGc_</i>	33	44.6	3.7	1.6 ^{ns}	11.5	3.0	0.7 ^{ns}	60.0	24.0	0.6 ^{ns}
<i>Gt_gcgc</i>	44	46.3	2.6	1.9 ^{ns}	12.4	2.2	1.2 ^{ns}	60.7	19.8	0.9 ^{ns}
<i>gtgtgcgc</i>	11	45.5	2.9	0.3 ^{ns}	11.5	2.1	0.4 ^{ns}	58.5	17.9	0.2 ^{ns}
F ₂ (P2xP3)										
<i>Gt_Gc_</i>	128	46.9	2.8		12.5	2.2		59.0	20.3	
<i>GtgtGc_</i>	34	47.8	2.4	1.7 ^{ns}	13.0	2.6	1.0 ^{ns}	58.2	18.6	0.2 ^{ns}
<i>Gt_gcgc</i>	38	47.6	2.7	1.4 ^{ns}	12.8	2.4	0.6 ^{ns}	53.6	16.7	1.8 ^{ns}
<i>gtgtgcgc</i>	10	47.1	3.5	0.2 ^{ns}	12.6	2.8	0.1 ^{ns}	49.5	15.7	1.4 ^{ns}

^{1/} Value of t test; ^{ns} Not significant at the 5% level of probability by the t test.

intensity. The seeds from the double recessive genotypes (*gtgtgcgc*) had a deeper green color than those from the single recessive genotypes (*gtgt* or *gcgc*). Fery and Dukes (1994) reported similar findings. The green color appears deeper with white or cream backgrounds, and there is little variation within each background. A hypothesis postulates that genes with minor effects contribute to the reduction or intensification of the expression of the genes *gt* and *gc*. If this hypothesis is confirmed, green testa and cotyledon color will be intensified further through selection.

Experiment 2

There were significant differences among populations ($P < 0.01$) for all three traits investigated (Table 4). This was also true for the components of the populations: parent group 2, parents versus crosses, crosses and general combining ability (GCA) for parent group 2. Parent group 1 versus parent group 2 and GCA of parent group 1 were statistically different ($P < 0.01$) for NDF and SW. Specific combining ability (SCA) was statistically different ($P < 0.01$) for NDF only. This indicates that there were significant genetic differences in parent group 1 for NDF and SW, but not for SYP. In parent group 2, there were genetic differences for all the three characters. Parental groups were genetically different for NDF and SW, but not for SYP. The significant difference ($P < 0.01$) for parents versus crosses suggests that new genetic combinations can be different from the parents, even for SYP where the two groups of parents did not differ from each other. The GCA was statistically significant ($P < 0.01$) in parent group 1 for NDF and SW and in parent group 2 for all three characters. This indicates that only parent group 2 had genetic differences in GCA for SYP. The SCA was very small when compared to the GCA, and was significant ($P < 0.01$) for NDF only (Table 4).

Parents AU-GC-67 and AR-92-537 contributed to the reduction of NDF, while Bettergreen, AU-KPH-9/9-1 and Royal Blackeye contributed to the increase of NDF. The SW was reduced by AU-78.1 and AR-92-537 and increased by AU-GC-67 and Colossus 80. For SYP there were significant difference ($P < 0.01$) in GCA only in the Parent group 2. AU-KPH-9/9-1, Colossus 80 and Royal Blackeye had the greatest positive GCA for SYP (Table 5).

The means for NDF and SW in the F_2 were located between the parental extremes, but were higher than the best parent for SYP in seven crosses. Some crosses

also had high genetic variance for all three traits, indicating the presence of wide genetic variability (Table 6). For NDF and SW the parental means were larger than the F_2 means. The GCV was low for NDF (5.36) and moderate for SW (10.37) and SYP (12.15) (Table 7). Parent group 2 had wider genetic background for SYP than parent group 1. The highly significant differences among crosses ($P < 0.01$) and

Table 4. Analysis of variance for number of days for first flower (NDF), weight of one hundred seeds (SW) and dry seed yield per plant (SYP) for two groups of parents and their F_2 generations in a 3 x 5 cowpea partial diallel cross.

Source of variation	df	Mean squares		
		NDF (days)	SW (g)	SYP (g)
Populations	22	8.92 ^{1/}	8.02 ^{1/}	96.91 ^{1/}
Parent group (1)	2	4.06 ^{1/}	12.76 ^{1/}	30.31
Parent group (2)	4	20.92 ^{1/}	16.49 ^{1/}	148.67 ^{1/}
Par. (1) vs Par. (2)	1	5.72 ^{1/}	44.84 ^{1/}	0.31
Parents vs Crosses	1	6.74 ^{1/}	1.01 ^{1/}	812.90 ^{1/}
Crosses	14	6.57 ^{1/}	2.79 ^{1/}	47.39 ^{1/}
GCA Par. (1)	2	9.23 ^{1/}	7.81 ^{1/}	16.28
GCA Par. (2)	4	15.85 ^{1/}	5.52 ^{1/}	106.07 ^{1/}
SCA	8	1.26 ^{1/}	0.18	25.83
Error	110	0.31	0.14	9.85

^{1/} Significant by F test at probability level of 0.05.

Table 5. Estimates of general combining ability (GCA) for parents group 1 (g_i) and parents group 2 (g_j), and error of estimates of the $s(g_i)$ and $s(g_j)$ for number of days to first flower (NDF), weight of one hundred seeds (SW) and dry seed yield per plant (SYP) for eight parents and their F_2 generations in a 3 x 5 cowpea partial diallel cross.

Populations	NDF (day)	SW (g)	SYP (g)
GCA parent group 1 (g_i)			
AU-GC-67 (P1)	-1.2395	0.9553	-2.0040
AU-78.1 (P2)	-0.2140	-1.4146	0.5071
Bettergreen (P3)	1.4536	0.4593	1.4969
GCA parent group 2 (g_j)			
AUBe (P4)	-0.0907	-0.8286	-2.4278
AR-92-537 (P5)	-3.4443	-1.5353	-9.1168
Royal Blackeye (P6)	1.6686	0.0113	1.8990
AU-KPH-9/9-1 (P7)	2.2072	0.2946	5.8924
Colossus 80 (P8)	0.6591	2.0580	3.7534
$s(g_i)$	0.2025	0.1388	1.1459
$s(g_j)$	0.2864	0.1962	1.6205

Table 6. Number of plants (n), population mean (m), phenotypic variance (VP), and genotypic variance (VG) within populations for number of days to first flower (NDF), one hundred see weight (SW) and dry seed yield per plant (SYP) for parents and their F₂ generations a 3 x 5 cowpea partial diallel cross.

Populations	n	NDF (day)			SW (g)			SYP (g)		
		m	Vp	Vg	m	Vp	Vg	m	Vp	Vg
AU-GC-67 (P1)	54	44.5	7.4	-	15.0	0.9	-	44.0	98.4	-
AU-78.1 (P2)	50	45.5	5.1	-	15.3	0.3	-	34.0	69.1	-
Bettergreen (P3)	41	48.5	7.0	-	9.0	1.2	-	35.1	120.0	-
AUBe (P4)	45	45.7	3.8	-	15.0	1.4	-	36.6	89.0	-
AR-92-537 (P5)	54	41.9	4.9	-	13.2	0.7	-	19.8	24.3	-
Royal Blackeye(P6)	53	51.0	2.8	-	17.6	0.8	-	52.3	75.0	-
AU-KPH-9/9- 1(P7)	42	53.6	3.1	-	22.3	1.2	-	34.8	220.7	-
Colossus 80 (P8)	38	47.8	4.6	-	21.9	2.1	-	46.2	261.7	-
1 x 4	58	47.7	8.4	2.8	15.3	4.8	3.6	47.4	149.9	56.2
1 x 5	61	40.9	6.0	-	14.4	5.5	4.4	40.2	133.5	72.1
1 x 6	61	47.2	12.1	7.1	16.3	3.0	2.8	56.2	114.9	28.2
1 x 7	54	48.2	10.2	5.0	16.4	4.2	3.5	58.2	273.1	117.4
1 x 8	60	44.8	6.9	0.9	18.4	5.6	4.1	57.5	261.6	81.5
2 x 4	48	45.4	5.0	0.5	15.9	4.5	3.5	46.0	187.5	108.3
2 x 5	51	42.9	5.4	0.4	14.9	3.7	3.2	35.1	92.0	45.3
2 x 6	61	47.3	5.4	1.4	16.6	3.1	2.5	46.9	134.4	62.4
2 x 7	59	48.7	9.3	5.2	16.6	3.8	3.0	55.9	274.7	129.9
2 x 8	60	45.6	7.4	2.6	19.3	3.6	2.3	58.2	261.3	95.9
3 x 4	60	46.2	7.1	1.7	13.4	9.3	8.0	50.5	212.3	107.8
3 x 5	58	44.5	10.7	4.7	13.2	5.5	4.5	48.7	94.9	22.8
3 x 6	57	49.1	6.3	1.4	14.3	4.0	3.0	53.8	173.6	76.1
3 x 7	64	48.4	8.1	3.1	15.0	7.0	5.8	45.8	260.4	90.0
3 x 8	42	50.1	14.7	8.8	15.7	13.8	12.3	46.8	283.1	92.2
MSD ¹		2.9			1.9			16.5		

¹ MSD - Minimum significant difference between means at the 5% level of probability by the Tukey test.

the high means and genetic variances in many crosses indicated that a wide range of combinations of the two groups of parents produce segregating generations with a wide genetic base. In both groups of parents that contributed to the increase of NDF and SW also contributed to the increase of SYP with the exception of AU-GC-67. Parents that contributed to the reduction of NDF and SW also contributed to the reduction of SYP, except for AU-78.1.

The effects of GCA were larger than the effects of SCA for all traits, except for SYP in Parent group 1, indicating that additive genetic effects were more important than dominance genetic effects. Tikka et al. (1976), using a diallel, found similar results for flower initiation in F₁ and F₂ generations. Similar results were obtained for SW and SYP in the F₁ generation by Singh and Jain (1972) and Lal et al. (1975) and Jatarsa (1980) for SYP. Imrie and Bray (1983) using F₂ populations observed that additive genetic effects were more important for SW and SYP, whereas dominance genetic effects were more

important for NDF.

Considering the genetic material obtained by the current study, for short-term objectives, the selection to improve plant yield and green seed color can start

Table 7. Phenotypic variance (VP), genetic variance (VG) and genetic coefficient of variation (GCV) for number of days to first flower (NDF), one hundred seeds weight (SW) and dry seed yield per plant (SYP) estimate in F₂ generation from a 3 x 5 cowpea partial diallel cross.

Parameters	NDF (day)	SW (g)	SYP (g)
Parents mean	47.34	16.15	37.92
F ₂ mean	46.60	15.70	50.41
Vp	39.43	16.78	284.36
Vg	6.26	2.65	37.54
GCV (%)	5.36	10.37	12.15

in F_2 and backcrosses from Experiment 1, which are segregating for both *gt* and *gc* genes. To achieve medium-term objectives, crosses can be made between the best F_2 populations using the parental groups of Experiment 2 to combine both *gt* and *gc* genes in a population with a wide genetic base. Using means and GCA of parents and means and genetic variances of crosses as selection criteria, the best crosses are: AU-GC-67 x AU-KPH-9/9-1, AU-78.1 x AU-KPH-9/9-1, AU-78.1 x Colossus 80, Bettergreen x AUBe, Bettergreen x Royal Blackeye and Bettergreen x Colossus 80.

RESUMO

Potencial de cruzamentos para produção de sementes de cor verde persistente em caupi usando os genes *gt* e *gc*

Dois grupos de parentais de caupi [*Vigna unguiculata* (L.) Walp.] reunidos em dois conjuntos de cruzamentos foram estudados para avaliar o potencial dos parentais e os efeitos dos genes “green testa” (*gt*) e “green cotyledon” (*gc*) nos caracteres número de dias para a antese da primeira flor (NDF), peso de 100 sementes (SW) e produção de semente seca por planta (SYP); e identificar as melhores combinações de parentais para formar uma população de base genética ampla para selecionar linhas com sementes de cor verde persistente após a secagem. Dois cruzamentos segregando para os genes *gt* e *gc* foram estudados no Experimento 1 e um cruzamento dialélico parcial 3 x 5 foi estudado no Experimento 2. No Experimento 1, a geração F_2 do cruzamento AU-GC-67 x Bettergreen apresentou variância genética mais alta que o cruzamento AU-78-1 x Bettergreen para os três caracteres. Os resultados também indicaram que os genes *gt* e *gc* individualmente ou em combinação não afetaram os caracteres em estudo. No Experimento 2 os efeitos da Capacidade Geral de Combinação (CGC) foram maiores que os da Capacidade Específica de Combinação (CEC), indicando que os efeitos genéticos aditivos foram predominantes na expressão dos três caracteres. Os parentais com maior CGC foram: AR-92-537 e AU-GC-67 para precocidade; AU-KPH-9/9-1 e Royal Blackeye para ciclo longo; Colossus 80 para semente grande; e AU-KPH-9/9-1, Colossus 80, Royal Blackeye e Bettergreen para produtividade por planta. Considerando a média e a CGC dos parentais e a média e a variância genética das gerações F_2 os cruzamentos AU-GC-67 x AU-KPH-9/9-1, AU-78.1 x AU-KPH-9/9-1, AU-78.1 x

Colossus 80, Bettergreen x AUBe, Bettergreen x Royal Blackeye e Bettergreen x Colossus 80 são os mais promissores para a formação de uma população com base genética ampla para seleção de linhagens com alto potencial de produtividade e com grãos de cor verde persistente após a secagem.

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