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Germplasm evaluation and enhancement for the development of cowpea (*Vigna unguiculata* (L.) Walp dual-purpose F₂ genotypes

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Cowpea is an important grain legume as well as fodder crop, especially in the dry regions of South Africa. The production of this crop has been below average because of low genetic variation and cultivation of poor-yielding varieties which have not been improved. The potentials of cowpea F2 generation arising from crosses made from 55 exotic parental lines, introduced into South Africa were determined. F₁ lines derived from the crosses were advanced to F₂ lines in the glass-house, and the segregating F2 families were further evaluated in the field with their parental lines. The following data were collected from the progeny: number of pods per plant, 100 seed-weights, fodder yield, grain yield and harvest index. Results showed that F2 lines exhibited significant differences on all the parameters studied thus indicating the presence of genetic variability among the segregating progeny. Number of pods per plant, 100 seed-weight and harvest index showed higher significant differences. The F2 lines obtained a significant increase in number of pods per plant as compared to their parents, thus indicating the potentials of progeny for higher pod production. Harvest index for F2 lines varied between 0.16 and 0.60 (dual-purpose type), and are mostly medium cowpea types with dual purpose characteristics for producing grain for human consumption and fodder for livestock. These parameters should therefore receive highest priority in developing high yielding dual-purpose varieties. There are several promising F₂ progenies which performed exceedingly well over the parents, so further screening is essential until their full potential is attained.

Key words: Vigna unguiculata, germplasm, harvest index, dual-purpose, 100 seed-weights, segregating population.

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp) is one of the most widely adapted; drought- tolerant, versatile, and nutritious grain legumes (Ehlers and Hall 1997, Purseglove, 1974). Dry grain and fodder are two most important yield components of cowpea (Mahalakshni, 2004). Cowpea is consumed in many forms: young leaves, green pods and green seeds are eaten as vegetables whereas dry seeds

are used in a variety of food preparations. Cowpea is a staple food in many regions of Africa. Its desirability reflects the fact that the leaves, immature pods, fresh seeds (southern pea or "green pods"), and the dry grain are popularly eaten or marketed. Some varieties have a short cycle and mature early and thus are able to provide food during the hungry period, usually at the end of the wet season when food availability can become extremely scarce in semi arid regions of Sub-Saharan Africa (Singh et al., 2003).

The dry grains are commonly milled and consumed in numerous traditional main dishes of Africa as porridge and bread, food to young children as weaning food, and eaten as processed snack foods. Cowpea grains as well

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as the vegetative parts make major nutritional contributions to diets, and they are also suitable for canning (Singh et al., 2003). Cowpea grain contains about 25% protein and 64% carbohydrates (Bressani, 1985). Just like cowpea grains and leaves, the nutritive value of cowpea haulms is very high. The crude protein content ranges from 13 - 17%, with high digestibility and low fibre. Furthermore, cowpea has the ability to fix atmospheric nitrogen, which allows it to grow on, and improve nitrogen-impoverished soils (Steel, 1972). Thurling and Ratinam (1987) reported that a program of yield improvement would be based on hybridization between two or more selected genotypes. Accurate selection of parent is normally difficult because the yields of potential parents rarely provide an effective basis for identifying the genotypes with the greatest potential for generating superior lines when crossed.

Thus, it is usually necessary to evaluate various types of crossbred populations prior to making any decision regarding parental combinations. This requirement has stipulated considerable research into the value of measurements from early crossbred generations (F_1 - F_3) as predictors of cross potential. In the improvement of agronomic traits in self pollinating crops, selection for the trait may be conducted from as early as among the F_2 and F_3 lines derived from crosses between two inbred parents. Success in early generation selection in the breeding program depends on accurate estimation of differences between the lines in the heterogeneous population, and the assumption that these differences will persist when testing is conducted on descendant lines that are approaching homozygosity (Padi, 2007).

In the past, farmers cultivate two main types of cowpea; early maturing varieties, grown for grain and late maturing varieties that are grown for fodder production. The dry season or off-season in South Africa is characterized by scarcity in good quality fodder and it is during this period that farmer's need most high quality fodders for livestock to enable the animal sustain their fat reserve in order to cope against winter. Unfortunately the existing varieties grown by farmers cannot sustain or meet this requirement because they are low yielding, pest susceptible and unimproved. For cowpea to contribute meaningfully to food security there is need to develop dual-purpose varieties that give reasonable grain and fodder yields, and also maximize the output from land and labor.

This study was undertaken to cross a set of parental lines from ARC germplasm, and evaluate the performances of F_2 families for the development of dual-purpose cowpea types.

MATERIALS AND METHODS

The trials making up this study were conducted under glasshouse conditions in winter and in the field during summer, at the Agricultural Research Council (ARC), Potchefstroom, South Africa. The

cowpea used in this study was obtained from the ARC (Potchefstroom) cowpea germplasm bank. Thirty-four improved cowpea lines from ARC were used to form the crossing parents.

Development of cowpea first and second generations

During the 2006/2007 summer growing season, the 34 parental lines were planted in plastic pots. Two seeds were planted per pot with controlled glasshouse temperatures of 20 - 30 °C. Specific pairwise crosses were made out among the 34 lines in the glasshouse during 2007/2008. Matured flowers were emasculated in the evening and pollinated in the morning using forceps for opening the flowers. Tags were used to identify the crossed plants. During the developmental stage of the crossed plants, talstar insecticide was applied weekly to control any insect in the glasshouse that could cause damage. The plants were watered only when necessary, and weeds were controlled by hand.

The F_1 seeds were multiplied in the glasshouse. Talstar® (insecticide) was sprayed 7- day intervals to control aphids, mites and any opportunistic insect pests. Weeds were controlled by hand pulling as and when necessary throughout the growing period. Thirty families were selected from the crosses. The selection criterion was based on the suitability (grain, fodder and dual-purpose) class, number of days to flowering and physiological maturity and the available seed obtained at F_1 (Table 1).

Field study and layout

Parental genotypes used to develop hybrids and their F_2 lines were evaluated in the field trial that was conducted at Potchefstroom to measure the performances of the F_2 progeny in comparison with their parents. The F_2 families and their parental lines were used for the field experiment. The soil was prepared by a plough followed by disking. A ridger was used to prepare the planting area, and a spacing of one meter between adjacent ridges was used. Planting was done on December 6, 2007 at Potchefstroom. The crop was sown on ridges, 7 m long with an inter-row spacing of 1 m and an intra-row spacing of 20 cm (with an expected number of 35 plants per plot).

The experiment was laid out in a randomized complete block design with four replicates. The total experimental area measured 31 × 64 m. The 64 entries used were randomized within each replicate using Microsoft Excel 2008. Weeds were controlled using Gramaxone as a crop pre-emergence treatment and hand-hoeing. Insect protection of one spray of Talstar® per week was applied to avoid insect damage. Data was taken on the following agronomic traits: number of days to 50% flowering, number of days to 50% maturity, biomass, pod length, number of pods per plant, grain yield and harvest index.

RESULTS AND DISCUSSION

There was significant variation observed among the genotypes for all the parameters that were measured. Number of days to 50% flowering ranged from 61 to 71 days for the progeny and 51 to 80 days for the parental lines. IT99K-409-8 × Mamlaka flowered in 61 days while Adom and IT95K-1491 were the two parental lines that flowered early (Table 2). The wide range in days to flowering in the F_2 families indicate that significant variation and that progress could be made in selecting for different maturity groups in cowpeas. Differences in

S/N	Name	No. of days to flowering	No. of days to maturity	100 seed wt	Suitability class
1	Glenda	58	87	12.99	Dual-purpose
2	ITOOK-1263	74	99	15.50	Dual-purpose
3	IT98D-1399	56	87	14.97	Grain
4	IT82D-889	58	89	14.03	Grain
5	IT81D-1228	58	89	9.50	Grain
6	Mamlaka	59	92	10.81	Grain
7	2246	57	95	13.99	Grain
8	IT98K-412-13	76	99	21.95	Grain
9	IT98K-166-4	52	97	13.38	Grain
10	Queenam	58	99	13.51	Grain
11	TVX-3236	72	103	9.83	Grain
12	IT99K-409-8	58	103	14.88	Grain
13	Danila	85	102	12.62	Fodder
14	IT89KD-288	72	104	20.24	Fodder
15	Ngoji	64	97	16.36	Fodder
16	IT97K-499-35	68	105	14.22	Fodder
17	ITOOK-835-45	75	105	12.63	Fodder
18	IT98K-205-9	74	107	14.41	Fodder
19	IT99K-7-21-2-2	61	107	15.50	Fodder
20	2020	66	114	14.35	Fodder

number of days to flowering was due sensitivity to photoperiod, thus indicating that the lines responded differently to photoperiod. The same findings of differences to flowering were reported by Amanullah and Hatam (2000), and Adeyanju et al. (2007) reported similar transgressive segregation for flowering days. The number of days to maturity ranged from 92 to 109 for the parental lines and 95 to 108 days for the progeny. IT98K-962 × Queenam matured early, and was followed by IT99K-409-8 × Mamlaka and IT98K-205-9 × Mamlaka which matured in 61 and 62 days respectively (Table 2). This variations signified the existence of different cowpea types: early, dual-purpose and fodder, genotypes among the progeny; that is, early genotypes, that reached maturity within 90 days, medium maturing (dual purpose) genotypes had a crop cycle between 90 and 100 days, and lastly the late maturity genotypes that reached maturity after 109 days. This also shows that the genotypes can be selected based on the farmers needs.

The pod length for the parental lines ranged from 13.94 m to 18.47 cm, Queenam produced the longest pod (18.47 cm) among the parents; the shortest pod (13.94 cm) was obtained from IT98K-406-2. The pod length ranged from 13.16 to 17.12 cm for the progeny and the longest pod length was obtained from 2246 \times 2020, while the shortest was measured for Danila \times 2020 (Table 3). Means of best six progeny out of 30 were consistently higher than the parents, and 10 progeny also had more improved pod length than one of the parents or mean of

both parents that constituted the family. The results indicated heterosis and inheritance of longer pods by F2 generations over their parents. Harzra et al., (1993) investigated the inheritance of pod length in cowpea and found that length was inherited quantitatively in F2 populations. The number of pods per plant for the F₂ lines ranged between 24 and 45, as well as 23 and 41 among the parents (Table 3). The highest number of pods per plant was obtained by IT99K-409-8 x IT89KD-288 and 2246 × 2020 with 45 pods per plant while IT97K-497-2 recorded the highest number of pods per plant among the parental lines. IT99K-718-6 × IT98K-166-4 produced the lowest number of pods among the genotypes and the parental lines (IT97K-499-35 and IT99K-409-8) recorded the lowest variation for this parameter. The variation in the number of pods per plant among F₂ lines was possibly attributed to heterosis for this trait. It can also be inferred that the two progeny (2246 \times 2020 and 99K-409-8 \times 288) with erect and semi-erect plant type produced more pods (45 and 47 respectively per plant, while those with prostrate plant type produced less number of pods per plant. Padi (2008) stated that the results of poor set of pods could have been attributed to some segregates that were late in flowering and end up setting few pods. There were high significant differences observed among the F₂ generations with respect to 100 seed weight. Hundred-seed weight ranged from 10.84 g to 16.47 g for the F2 lines, and 9.29 to 20.52 g for the parental lines as shown in Table 4. There was transgressive segregation for 100

Table 2. Number of days to 50% flowering and pod maturity of F₂ lines evaluated in Potchefstroom in 2007/08.

Cross	#day's 50% Flowering	# days to Pod maturity
IT98K-962 × 2246	64 (61)	98 (98)
IT99K-718-6 × IAR-1696	67 (65)	103 (106)
ITOOK-1263 × IT98K-406-2	66 (69)	105 (103)
IT99K-7-21-2-2 × IT99K-573-1-1	68 (64)	103 (101)
ITOOK-1263 × Ngoji	66 (66)	105 (100)
IT98K-962 × IT93K-625	62 (65)	101(98)
IT99K-573-1-1 × IT82D-889	69 (60)	104 (96)
IT99K-573-1-1 × IT86D-719	68 (69)	106 (98)
IT98K-412-13 × TVX-3236	67 (69)	98 (101)
IT99K-718-6 × IT98K-166-4	71 (56)	107 (101)
IT99K-573-1-1 × 92KD-263-4-1	70 (64)	101(101)
IT98K-628 × Glenda	64 (66)	101(96)
IT98K-962 × Mamlaka	65 (61)	100 (96)
IT97K-499-35 × IT90K-284-2	63 (66)	102 (99)
IT97K-499-35 × IT98D-1399	65 (54)	102 (99)
IT99K-409-8 × IT81D-1228	69 (59)	101(97)
IT98K-962 × 2246	64 (61)	98 (98)
IT99K-491-7 × IT81D-1228	67 (61)	101(99)
ITOOK-835-45 × IT81D-1228	69 (70)	107 (100)
IAR-1696 × TVX-3236	65 (70)	103 (105)
99K-409-8 × Mamlaka	61 (59)	95 (92)
IT97K-497-2 × Mamlaka	62 (65)	101(92)
ITOOK-1263 × Mamlaka	67 (63)	104 (97)
IT97K-499-35 × Adom	62 (57)	102 (97)
IT98K-205-9 × Mamlaka	63 (65)	96 (98)
IT95K-1491 × IAR-1696	61 (64)	98 (105
IT99K-409-8 × IT89KD-288	62 (66)	102 (102)
ITOOK-1263 × ITOOK-835-45	67 (71)	107 (104)
2246 × 2020	68 (61)	104 (103)
Danila × 2020	71 (72)	108 (100)
Over-all Mean	62 (64)	100 (100)
CV (%)	4.4	4.7
S.E.	2.86	4.77
(P≤ 0.05)	0.01	0.01

DFF = Number of days to 50% flowering; #days maturity = number of days to pod maturity; CV = coefficient of variation; S.E. = standard error.

seed-weights with seven F_2 lines performing better than their mean parental values, and 14 out of 30 had heavier weights than the parents (better single parent value). IT89KD-288 and IT99K-573-1-1 were the better performing parents for this trait, and IT98K-962 \times Queenam, and IT99K-718-6 \times IAR-1696 were the two high best yielding F_2 generations. IT81D-1228 and Danila produced the lowest seed weight of 9.29 and 9.93 g, while Danila \times 2020 and 2246 \times 2020 produced the lowest seed weight of 10.84 and 11.84 g, respectively.

The total grain yield of the F₂ generations ranged from 1, 6130 to 4, 6660 kg-ha (Table 4), and that of parental

lines ranged from 1, 3100 kg-ha to the highest of 5, 7880 kg-ha. The highest yielding F_2 lines were IT99K-573-1-1 \times 889, and TV \times -3236 attained the highest yield among the parents. The lowest yielding F_2 lines were Danila \times 2020 and IT99K-718-6 \times IT98K-166-4 with a yield of 1, 6130 and 1, 6480 kg-ha respectively. This was possibly due to the fact that the two parents used for the crosses were fodder producing varieties and they were late maturing genotypes. The wide range in grain yield by the F_2 lines with means exceeding that of the parents indicate that the progenies with grain size larger than the parents could be selected without loss of yield potential

Table 3. Pod length and number of pods per plant of F2 lines evaluated in Potchefstroom in 2007/08.

Cross	Pod length	#Pods/plant
IT98K-962 × IT84S-2246	15.13 (15.20)	36 (35)
IT99K-718-6 × IAR-1696	13.98 (15.66)	32 (39)
ITOOK-1263 × IT98K-406-2	15.78 (13.77)	36 (29)
IT99K-7-21-2-2 × IT99K-573-1-	14.89 (15.84)	27 (29)
ITOOK-1263 × Ngoji	14.58 (14.45)	31 (31)
IT98K-962 × IT93K-625	16.08 (15.42)	32 (29)
IT99K-573-1-1× IT82D-889	14.61 (16.19)	34 (29)
IT99K-573-1-1 × IT86D-719	16.96 (14.81)	30 (29)
IT98K-412-13 × TVX-3236	15.60 (14.52)	29 (31)
IT99K-718-6 × IT98K-166-4	15.17 (15.92)	24 (37)
IT99K-573-1-1 × 92KD-263-4-1	14.53 (15.28)	38 (28)
IT98K-628 × Glenda	17.12 (14.49)	30 (32)
IT98K-962 × Mamlaka	13.92 (14.64)	32 (29)
IT97K-499-35 × IT90K-284-2	15.59 (14.96)	35 (28)
IT97K-499-35 × 98D-1399	14.07 (15.08)	33 (24)
IT99K-409-8 × IT81D-1228	15.29 (14.90)	33 (27)
IT98K-962 × IT84S-2246	15.13 (15.11)	36 (35)
IT99K-491-7 × IT81D-1228	15.60 (15.87)	45 (31)
ITOOK-835-45 × IT81D-1228	15.88 (15.77)	33 (29)
IAR-1696 × TVX -3236	14.42 (14.87)	32 (33)
IT99K-409-8 × Mamlaka	15.96 (14.23)	26 (25)
IT97K-497-2 × Mamlaka	15.89 (15.09)	34 (28)
ITOOK-1263 × Mamlaka	16.60 (13.86)	28 (28)
IT97K-499-35 × Adom	14.43 (14.16)	32 (26)
IT98K-205-9 × Mamlaka	14.94 (14.75)	35 (29)
IT95K-1491 × IAR-1696	14.11 (14.99)	30 (32)
IT99K-409-8 × IT89KD-288	13.92 (15.14)	47 (29)
ITOOK-1263 × ITOOK-835-45	15.60 (14.85)	28 (28)
IT84S-2246 × 2020	17.01 (16.19)	45 (38)
Danila × 2020	13.16 (16.74)	29 (35)
Over all Mean	15.35 (15.09)	33 (30)
CV (%)	11.9	29.5
S.E.	1.82	9.70
(P≤0.05)	0.01	0.01

POD/PLNT= Number of pods per plant; CV = coefficient of variation; S.E. = standard error.

even at further generation. This is supported by Padi (2008). Muhammad et al., (1994) and Ombakho and Tyagi (1987) who reported that variation in cowpea yield was mainly due to number of pods per plant, number of seeds per pod, pod length and seed weight. Padi (2007) also confirmed that a progeny that exhibited distinguished performance at F₂ also sustained their performance at advanced homozygous generation. This means that

selection for high performance at the F_2 can be used for selection for later generation. In conclusion, significant heterosis was exhibited among F_2 families compared to their better parents. Seven F_2 families exhibited heterosis for pod length, four for grain yield and seventeen for fodder yield out of thirty families that constituted the segregating population. However, ten families for pod length, eight for fodder and twelve for grain yield

Table 4. 100 seed-weight and grain yield of F2 generations evaluated in Potchefstroom in 2007/08.

Cross	100-seed wt (g)	Grain yield (kg/ha)
IT98K-962 × IT84S-2246	13.81 (14.85)	1972.0 (2202.31)
IT99K-718-6 × IAR-1696	16.64 (13.63)	2886.0 (3807.55)
ITOOK-1263 × IT98K-406-2	16.47 (15.86)	3086.0 (2455.87)
IT99K-7-21-2-2 × IT99K-573-1-	16.21 (18.62)	2690.0 (2641.05)
ITOOK-1263 × Ngoji	16.13 (16.37)	2273.0 (2883.17)
IT98K-962 × IT93K-625	15.71 (15.22)	2804.0 (3460.84)
IT99K-573-1-1 × IT82D-889	15.58 (16.63)	4666.0 (3462.24)
IT99K-573-1-1 × IT86D-719	15.57 (16.14)	3339.0 (3334.73)
IT98K-412-13 × TVX-3236	15.12 (14.32)	3546.0 (2739.11)
IT99K-718-6 × IT98K-166-4	14.50 (14.50)	1648.0 (2207.56)
IT99K-573-1-1 × 92KD-263-4-1	14.22 (15.93)	3387.0 (2564.47)
IT98K-628 × Glenda	14.22 (13.42)	2661.0 (3468.97)
IT98K-962 × Mamlaka	14.17 (12.76)	2427.0 (3632.76)
IT97K-499-35 × IT90K-284-2	14.10 (15.66)	2339.0 (2695.21)
IT97K-499-35 × IT98D-1399	14.08 (14.41)	2036.0 (2980.43)
IT99K-409-8× IT81D-1228	13.99 (11.02)	2087.0 (1849.90)
IT98K-962 × IT84S-2246	13.81 (14.85)	1972.0 (2202.33)
IT99K-491-7 × IT81D-1228	13.60 (11.58)	1633.0 (3083.01)
ITOOK-835-45 × IT81D-1228	13.53 (10.32)	1987.0 (2037.24)
IAR-1696 ×TVX-3236	13.48 (11.40)	2767.0 (3818.17)
IT99K-409-8 × Mamlaka	13.44 (11.48)	3174.0 (3700.57)
IT97K-497-2 × Mamlaka	13.42 (11.88)	3960.0 (5227.02)
ITOOK-1263 × Mamlaka	13.16 (14.09)	2788.0 (3887.82)
IT97K-499-35 × Adom	12.99 (14.14)	2145.0 (3236.61)
IT98K-205-9 × Mamlaka	12.86 (12.08)	2379.0 (4337.14)
IT95K-1491 ×IAR-1696	12.78 (14.44)	2771.0 (2593.47)
IT99K-409-8 × IT89KD-288	12.48 (16.64)	2928.0 (1885.18)
ITOOK-1263 × ITOOK-835-45	12.15 (14.66)	1836.0 (2637.74)
IT84S-2246 ×2020	11.84 (13.34)	2366.0 (2222.15)
Danila × 2020	10.84 (11.11)	1613.0(1676.04)
Overall Mean	14.17 (14.04)	2870.0 (2964.37)
CV (%)	9.6	38.9
S.E.	1.35	1033.3
(P≤ 0.05)	0.01	0.01

SW= 100 seed weight; GY= grain yield; CV = coefficient of variation; S.E. = standard error.

performed better than one better parent that was involved in the cross, and in some cases their performance was better than the mean of both parents. Several of these progeny that exhibited excellent performance will be selectable at advanced homozygous generation.

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