Research Article

Inheritance of Early Maturity in Some Cowpea (*Vigna unguiculata* (L.) Walp.) Genotypes under Rain Fed Conditions in Northern Ghana

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A field experiment was conducted at Savanna Agricultural Research Institute in 2015 cropping season to examine the inheritance of early maturity among an extra-early maturing landrace *Sanzi* and a medium maturing variety *Padi-Tuya* and their progenies. The results indicated highly significant ($P < 0.01$) genetic variations for the maturity indices, namely, days to first flower initiation (DFFI), days to 50% flowering (DFF), days to first pod maturity (DFPM), days to 90% pod maturity (DNPM), and plant height (P_PLT), seed per pod (S_Pod), and hundred seed weight (H_SWT). Heritability estimates for these traits varied from 74% to 99%. No significant differences ($P > 0.05$) were observed between F_1 and RF_1 , implying absence of maternal effect. The segregation ratio in the F_2 population for early and medium maturity fitted into the ratio 3:1, indicating single dominant gene mode of inheritance. Significant positive correlations were found between DNPM, DFFI, DFF, and DFPM; hence selection criteria to improve early maturity of cowpea should focus on these traits. Grain yield also had significant positive correlations with maturity indices indicating high grain yield is associated with late maturity; therefore, high grain yield should be considered alongside early maturity when selecting progenies for earliness.

1. Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is one of the most important and native grain legume crops in sub-Saharan Africa (SSA), which accounts for 64% of the world production [1, 2]. It is predominantly cultivated by resource limited small holder farmers usually women with average farm size of 0.5–1 ha [3, 4]. Cowpea grain (23–25%) and leaves (27–34%) contain valuable amounts of protein and constitute an important protein source in human diets [5, 6]. The grain also contains 1.8% fat and 60.3% carbohydrates and a rich source of calcium and iron [6]. The dry haulms of cowpea are used as fodder for livestock particularly during the dry season when animal feed is scarce. The dropping from the livestock is also used to improve soil fertility, making the crop an essential and integral part of sustainable crop-livestock farming systems in SSA [7, 8]. Cowpea can derive up to

99% of its N nutrition from symbiotic fixation [9] and fix substantial amounts of symbiotic N [10]. In fact, cowpea has been shown to contribute about 240 kg N/ha, with N benefit of 60–70 kg/ha to succeeding crops in rotation in unfertile soils [11].

Cowpea production is constrained by several biotic and a biotic stress factors. Among the abiotic factors, terminal drought which usually occurs during flowering and pod filling stage of the crop could cause as high as 80% yield loss [12]. Climate variability has made the onset and termination of rains unpredictable resulting in a shift to the cultivation of early maturing varieties by farmers [13]. These early maturing varieties are considered climate smart cultivars since they have the ability to escape terminal drought as well as pests and diseases damage that normally occur later in the cropping season [14]. The concept of early maturity in cowpea is a combination of early flower initiation and

short grain filling period [15]. Early maturity constitutes an important adaptation in agroecological zones with short growing seasons particularly in the arid and semiarid tropics where cowpea genotypes that mature between 55 and 60 days are ideal for cultivation [16, 17]. They provide first food sooner than any other crop, thus shortening the hunger period [18]. Early maturing varieties provide additional seed for the main season cropping and are also suitable for rotation with cereals [19]. Reducing crop cycle has helped to avoid terminal drought, incidence of pests and diseases, and unfavorable temperatures during flowering and podding stages [20]. However, most of the early maturing genotypes such as *Sanzi* and *Sumbirizie* which are cultivated by farmers are landraces with either low yields, small grain size, or mottled or brown seed coat colour which are not preferred by consumers. Besides, very few improved cowpea cultivars possessing this trait of earliness are available for cultivation in northern Ghana. There is therefore the need to incorporate the trait with other farmer preferred traits to fill the gap.

Genetic variation and the heritability of that trait are among the key considerations for genetic improvement of crops for any trait [21, 22]. Heritability which is the ability to pass a trait from one generation to the other can be either broad sense (the ratio of the total genetic variance, σ^2_G , to total phenotypic variance, σ^2_P) or narrow sense (the ratio of additive genetic variance, σ^2_A , to the total phenotypic variance, σ^2_P) [23]. Heritability estimates help to understand the genetic bases and the extent to which crop improvement can be achieved through selection [21]. Whereas several studies and progress have been made in understanding the heritability of grain yield and quality of cowpea, little progress has been made on the heritability estimates for early maturity and its related traits [23]. Therefore, heritability estimates for maturity in cowpea can be exploited to provide understanding in the genetic basis of early maturity in the development of cowpea varieties that can be cultivated in the changing climate of the northern Ghana. The objectives of this study were to (i) estimate the heritability of maturity indices in some cowpea genotypes, (ii) determine the type of gene action influencing the inheritance of earliness in cowpea, (iii) determine the contribution of maternal effects on inheritance of early maturity in cowpea, and (iv) determine interrelationships among the maturity indices, yield, and yield components.

2. Materials and Methods

2.1. Location of the Experiment. The study was conducted at the research fields of the CSIR-Savanna Agricultural Research Institute, Nyankpala. SARI is in the Guinea Savanna agroecological zone of Ghana, located on latitude $9^\circ 25'$, 41N, longitude $0^\circ 58'$, 42W, and about 183 m above sea level. The rainfall which normally begins mid-May and ends in early October is unimodal with an average annual rainfall of about 1200 mm [24]. The cropping season begins with the onset of the rains and commences in mid-June and ends in October with the rest of the season being dry and hazy. The mean annual temperature is recorded to be 27.3°C with the hottest part of the season occurring between March and May [24].

The soil is well drained Nyankpala series classified by FAO as Ferric Luvisol. It is brown, fine sandy loam, with low organic matter.

2.2. Plant Materials. Two cultivated varieties *Padi-Tuya*, medium maturing elite cultivar which matures between 70 and 75 days after planting (DAP) and *Sanzi*, and extra-early maturing landrace with maturity period of 45–50 DAP were hybridized to generate the segregating populations. Both direct and reciprocal crosses were made. Eight experimental materials including F_1 , RF_1 , F_2 , RF_2 , BC_1 , RBC_1 , BC_2 , and RBC_2 were developed from the above cross.

2.3. Experimental Procedure. Three experiments were conducted between May 2014 and June 2015. The parents were planted in pots and direct and reciprocal crosses made to produce enough hybrid seeds. Some of the hybrid seeds and their parents were planted. The parents were then backcrossed to the F_1 s and RF_1 s plants to generate BC_1 , RBC_1 , BC_2 , and RBC_2 populations. Some of the F_1 and RF_1 plants were allowed to produce F_2 and RF_2 seeds, respectively, by themselves. In the third experiment, the eight developed populations together with their parents were evaluated under rain fed condition between March 2015 and May 2015.

2.4. Experimental Design. The experimental materials were arranged in a randomized complete block design (RCBD) with three replications. The sample size (number of plants studied) varied as follows: 30 plants for P_1 , P_2 , F_1 , and RF_1 generations, 90 plants for the BC_1 , BC_2 , RBC_1 , and RBC_2 generations, and 300 plants for each of the F_2 and RF_2 generations. The plot size comprised one row each for nonsegregating populations (P_1 , P_2 , F_1 , and RF_1), three rows each for BC_1 , BC_2 , RBC_1 , and RBC_2 generations, and 10 rows each for F_2 and RF_2 generations. Each row (constituting 10 plants) was 2.7 m long with row spacing of 100 cm and a distance of 30 cm between plants. One seed was planted per hill; refilling was done immediately after emergence. Field pests were controlled using K-Optimal (Cyhalothrin 15 g/l + Acetamiprid 20; EC) at the rate of 500 ml per ha at vegetative stage, flowering, and podding. Weeds were manually controlled as and when necessary.

2.5. Data Collected. Data were collected on maturity indices, namely, number of days to first flower initiation (DFFI), as number from day of planting to the day each plant on each plot flowered, number of days to 50% flowering (DFF) from day of planting to the day 50% of the plants on each plot flowered, and number of days to first pod maturity (DFPM) were determined from the day of planting to complete yellowing of first pods on each plant and the number of days to 90% pod maturity (DNDM) was determined from the day of planting to 90% yellowing of pods on each plot. Plant height at flowering (H@F) was measured from the base of each plant to the last terminal bud on the main stem at flowering; plant height at maturity (H@M) was also measured from the base of each plant to the last terminal bud on the main stem at pod maturity; canopy width (CW) was measured as an average of the shortest and the longest canopy

width of each plant. While yield components such as number of pods per plant (N_PLT) were counted, number of seeds per pod (N_SPOD), 10 pods, were randomly selected from each plant and the number of seeds was counted; 100-seed weight (H_WT) was determined in grams from the weight of 100 randomly selected dried seeds and grain yield per plant (G_YD) was determined as average weight of seeds harvested from each plant.

2.6. Statistical Analyses. Data for all the measured variables were subjected to analyses of variance (ANOVA) using Genstat version 12 [25]. Pearson correlation analysis was also performed to determine the association among the different maturity indices. Treatment means were separated using standard error of difference (SED)

2.7. Heritability Estimates. The following traits DFFI, DFF, DFPM, and DNPM were taken on individual plants and the variances calculated using Genstat version 12 [25]. Variance components (additive, dominance, environment, genetic, and phenotypic) were estimated as described by [26, 27], using the following equations:

$$\begin{aligned}\sigma^2_A &= 2F_2 - (\sigma^2_{B1} + \sigma^2_{B2}) \\ \sigma^2_D &= \frac{[(\sigma^2_{B1} + \sigma^2_{B2}) - F_2 - (\sigma^2_{P1} + \sigma^2_{P2} + F_1)]}{3} \\ \sigma^2_E &= \frac{[\sigma^2_{P1} + \sigma^2_{P2} + \sigma^2_{F1}]}{3} \\ \sigma^2_G &= \sigma^2_A + \sigma^2_D \\ \sigma^2_P &= (\sigma^2_{F2}) = \sigma^2_G + \sigma^2_E + \sigma^2_{GE},\end{aligned}\quad (1)$$

where σ^2_A is additive variance, σ^2_D is dominance variance, σ^2_E is environmental variance, σ^2_G is genotypic variance, σ^2_P is phenotypic variance, σ^2_{F1} is variance of F_1 , σ^2_{F2} is variance of F_2 , σ^2_{B1} is variance of BC_1 , σ^2_{B2} is variance of BC_2 , σ^2_{P1} is variance of parent 1, σ^2_{P2} is variance of parent 2.

$$\text{Broad sense heritability } (H^2_b) = \sigma^2_G / \sigma^2_P,$$

$$\text{Narrow sense heritability } (h^2_n) = \sigma^2_A / \sigma^2_P \text{ [26].}$$

2.8. Estimation of Maternal Effects. The maternal effect was investigated by comparing the mean values of F_1 with the mean values of RF_1 using a mean-difference test at 5% level of significance [28].

2.9. Estimation of Inheritance Pattern in Maturity. Chi-square test of significance was used to investigate gene interactions for the F_2 generations. The segregation ratios were analyzed using the χ^2 value which was obtained from the following formula:

$$\chi^2 = \sum \frac{(\text{Observed} - \text{Expected})^2}{\text{Expected}}. \quad (2)$$

In addition, maturity indices such as days to flower first initiation (DFFI) and days to first pod maturity (DFPM) were subjected to frequency distribution analysis to elucidate the inheritance pattern in P_1 , P_2 , F_1 , F_2 , and BC_1 populations in early and medium maturity classes. Data on DFFI was grouped adopting a descriptor developed by the present authors. Data was scored by observing all the plants in each plot in the three replications. Plants which took less than 44 days to develop their first flower (DFFI $\leq$ 44 days) were considered early maturing while those that developed their flowers later (>45 days) were considered medium maturing. On the other hand, plants whose first pod matured in less than 55 days (DFPM $\leq$ 55 days) were considered early maturing and those that matured later (DFPM $>$ 55 days) were recorded as medium maturing, considering the fact that earlier reports classify cowpea genotypes that matured after 80 days as late maturing [29].

3. Results

3.1. Performance of Genotypes. Analysis of variance showed highly significant ($P < 0.001$) differences between the parents and different generations (F_1 , RF_1 , F_2 , RF_2 , BC_1 , RBC_1 , BC_2 , and RBC_2) for DFFI, DFF, DFPM, DNPM, H@F, H@M, CW, N_PLT, N_SPOD, H_WT, and G_YD (Table 1). However, no significant ($P > 0.05$) differences were observed between the F_1 and the RF_1 generations for all the traits. The average number of days to first flower initiation (DFFI) ranged from 29.16 to 41.37 days while days to 50% flowering (DFF) ranged between 33.11 and 44.29 days. *Sanzi* took the lowest number of days to reach DFFI (29.16) and DFF (33.11) while *Padi-Tuya* took the highest number of days to reach DFFI (41.37 days) and DFF (44.29 days). The F_1 plants took 32.12 and 36.48 days to reach DFFI and DFF, respectively, while the F_2 plants took 39.75 and 43.50 days. On the other hand the earlier maturing parent *Sanzi* had an average of 43.73 days for DFPM and 49.33 days for DNPM but the late maturing parent had 63.53 days for (DFPM) and 70.67 days for (DNPM). Also the F_1 plants took an average of 51.56 and 55 days to reach DFPM and DNPM, respectively, while the F_2 plants took 55.70 days and 68.33 days for DFPM and DNPM, respectively. Highly significant ($P < 0.001$) genotypic differences were also observed for the average number of days to first pod maturity and 90% pod maturity with the exception of the following generations: F_1 and RF_1 , BC_1 and BC_2 , RBC_1 and RBC_2 , and F_2 and RF_2 . *Sanzi* took significantly less number of days to reach 90% pod maturity (49.33 DAP) compared with *Padi-Tuya* (70.67 DAP).

Grain yield and yield components showed highly significant ($P < 0.001$) differences among all genotypes studied (Table 1). F_1 had the highest mean grain yield of 3.16 t/ha while *Sanzi* yielded 0.52 t/ha. Mean number of pods per plant ranged from 21.82 (F_2) to 42.56 (BC_2). The F_1 genotype had the highest mean number of seeds per pod of 17.79 and *Padi-Tuya* had the least (15.23). The highest hundred-seed weight of 23.00 g was recorded for *Padi-Tuya* compared with 8.91 g for *Sanzi*.

TABLE 1: Summary statistics for mean of phenotypic traits for the parents and their different generations.

Genotype	DFFI	DFI	DFPM	DNPM	H@F	H@M	CW	P_PLT	S_POD	H_WT (g)	G_YD t/ha
P ₁	41.37	44.29	63.53	70.67	172	40.26	39.3	24.71	15.23	23.00	2.413
P ₂	29.16	33.11	43.73	49.33	737	10.51	104.83	38.50	16.24	8.91	0.520
F ₁	32.12	36.48	51.56	55.00	11.2	26.05	53.13	39.40	17.97	16.83	3.163
RF ₁	31.70	36.11	51.07	54.67	10.7	26.48	53.20	39.33	17.23	16.61	2.890
F ₂	39.75	43.50	55.70	68.33	11.31	29.60	75.98	21.82	16.24	15.93	2.420
RF ₂	39.03	42.03	55.43	69.00	10.39	28.11	74.77	25.53	16.50	15.78	2.157
BC ₁	37.37	41.55	56.07	61.00	12.88	31.84	59.23	27.06	16.47	16.49	2.603
BC ₂	36.82	40.67	53.20	58.33	9.89	24.96	53.57	42.56	17.03	15.61	2.713
RBC ₁	37.07	40.04	54.73	59.67	9.47	22.54	64.70	23.34	17.26	16.02	2.713
RBC ₂	36.16	38.75	51.10	57.00	9.89	23.37	62.53	27.96	17.70	12.15	2.333
Mean	36.054	39.65	53.61	60.30	11.05	26.37	64.1	31.02	16.920	15.73	2.377
S.E.D	0.43	0.69	1.79	1.41	0.73	3.09	4.50	3.83	0.37	0.49	0.13
CV (%)	1.5	2.1	4.1	2.9	8.1	14.4	8.6	15.1	2.7	3.8	6.7
F (0.05)	163.09**	52.63**	15.89**	49.82**	25.32**	11.93**	31.87**	8.61**	9.64**	107.84**	59.73**

DFFI = days to first flower initiation, DFI = days to 50% flowering, DFPM = days to first pod maturity, DNPM = days to 90% pod maturity, H@F = plant height at flowering, H@M = plant height at maturity, CDM = canopy width, P_PLT = pod per plant, S_POD = seed per pod, H_WT = hundred-seed weight (g), G_YD t/ha = grain yield (tons per hectare), SED = standard error of difference, and CV% = coefficient of variation. ** $P \leq 0.01$.

TABLE 2: Estimates of heritability based on variances of DFFI, DFF, DFPM, and DNPM.

Parameter	Variance components					Heritability estimates	
	σ_p^2	σ_g^2	σ_a^2	σ_d^2	σ_e^2	H ² b	h ² n
DFFI	44.88	40.24	38.68	1.56	4.64	89.7	82.2
DFF	4.89	4.84	4.84	-1.95 (0)	1.96	99	99
DFPM	69.63	51.90	51.24	0.66	17.73	74.5	73.6
DNPM	7.65	7.01	7.03	-2.27 (0)	2.92	91.6	91.6

DFFI = days to first flower initiation, DFF = days to 50% flowering, DFPM = days to first pod maturity, DNPM = days to 90% pod maturity, df = degrees of freedom, σ_p^2 = phenotypic variance, σ_g^2 = genotypic variance, σ_a^2 = additive variance, σ_d^2 = dominance variance, σ_e^2 = environmental variance, H²b = broad sense heritability, and h²n = narrow sense heritability.

TABLE 3: Segregation pattern for maturity indices in F₂ and BC₁ populations.

		Early		Medium			χ^2 (cal)	χ^2 (Tab _{0.05,1 df})
		Observe	Expected	Observe	Expected			
DFFI	F ₂	221	225	79	75	3:1	0.27	3.84
DFPM	F ₂	228	225	72	75	3:1	0.20	3.84
DFFI	BC ₁	76	67.5	14	22.5	3:1	1.03	3.84
DFPM	BC ₁	64	67.5	26	22.5	3:1	0.43	3.84

3.2. Maternal Effects. The analysis of variance indicated that there was no significant difference ($P > 0.05$) between the mean values of F₁ and RF₁ for number of days to 50% flowering, number of days to first flower initiation, number of days to 90% pod maturity, number of days to first pod maturity, plant height at maturity (cm), number of pods per plant, hundred-seed weight (g), and grain yield (t/ha) (Table 1).

3.3. Estimates of Variance Components and Heritability. Phenotypic variances ranged from the minimum of 4.89 average number of days to 69.63 for days to first flower initiation (DFFI) and number of days to first pod maturity (DFPM), respectively. Genotypic variances on the other hand varied from 4.84 (DFF) to 51.90 (DFPM). Environmental variance ranged between 1.96 and 17.73 for DFF and DFPM, respectively, while additive variance ranged from 4.84 (DFF) to 51.24 (DFPM), respectively. Dominance variances also ranged from 1.95 (0) to 1.56 for DFF and DFFI, respectively. Estimated heritability values were very high and varied slightly between parameters studied. Broad-sense heritability (H²b) ranged from 74.50 to 99%, for DFFI, DFF, DFPM, and DNPM, while the narrow-sense heritability (h²n) varied from 73.60% to 99% (Table 2).

3.4. The Inheritance Pattern of Maturity in F₂ Population. Segregation ratios, chi-square, and P values for number of days to first flower initiation and number of days to first pod maturity in the F₂ and the BC₁ generation are presented in Table 3. The phenotypic ratio, 3:1, was used to test for goodness of fit of the observed segregation at F₂ and BC₁ generations using the chi-square test. Calculated chi-square values (χ^2) were less than the P values.

Days to first flower initiation varied between minimum of 30 days to maximum of 55 days and DNPM had minimum of 45 days to maximum of 68 days among the F₂ population

evaluated. In the BC₁ generation, the maturity indices ranged between minimum of 31 days and 45 days and maximum of 46 days and 62 days for DFFI and DNPM, respectively (Figure 1). The maturity of the F₁ population varied from 30 days to 35 days for DFFI and from 48 days to 56 days for DFPM. The two parents, P₁ (38–44 days) and P₂ (28–32 days), also differed in their days to first flower initiation (DFFI) as shown in Figure 2. In addition, P₁ (58–68 days) also took a longer time to reach pod maturity (DNPM) than P₂ which too is between 40 and 47 days to reach DFPM (Figures 2 and 3).

3.5. Correlation Analysis. Pearson correlation analysis of maturity, grain yield, and yield-related traits showed significant ($P < 0.01$) correlations among some of the quantitative traits (Table 4). Number of days to 90% pod maturity had highly significant ($P < 0.01$) positive correlation with mean number days to first flower initiation ($r = 0.95$), number of days to 50% flowering ($r = 0.89$), and mean number of days to first pod maturity ($r = 0.82$). This trait also recorded a negative relationship with number of pods per plant ($r = -0.65$) and seed per pod, ($r = -0.46$). Similarly, highly significant positive correlations were found between grain yield and 100-seed weight ($r = 0.61$), number of pods per plant ($r = 0.06$), and plant height at flower and maturity ($r = 0.36$ and $r = 0.45$), respectively. On the other hand, grain yield was negatively correlated with canopy diameter ($r = -0.80$).

4. Discussion

Early maturity constitutes an important adaptation in agroecological zones with short growing seasons particularly in the arid and semiarid tropics where such cowpea genotypes which mature between 55 and 60 days are ideal for cultivation [16, 17].

FIGURE 1: Frequency distribution analysis of DFFI and DNPM for F₂ and BC₁. FIGURE 2: Frequency distribution analysis of DFFI and DNPM for F₁ and Sanzi.

The highly significant differences in the maturity traits (DFFI, DFR, DFPM, and DNPM) among the parents and their generations indicated a high level of genetic variation. This further implies a large scope for breeding and therefore could provide the necessary genetic information for selection for early maturity in cowpea. The phenotypic difference between the parents and their progeny is very important for genetic inheritance studies, aiming to obtain the precise heritability estimates [30]. Most of the genotypes reached maturity in 60 days. Cowpea varieties which mature in less than 60 DAP are classified as extra-early maturing [29]. The values obtained for number of pods per plant were higher than those reported by Bennet-Lartey and Ofori [30] and Egbe et al. [31] but similar to that of Futuless and Bake [32] for Africa. This resulted from hybrid vigor in most of the genotypes; hence the higher grain yields recorded particularly for F₁ and RF₁ and backcrosses. Hundred-seed weight was relatively higher than the values reported by [33] but similar to those of [23, 30]. The result from grain yield (kg/ha) was relatively

higher than the values reported by Egbe et al. [31] and similar to those of Alphonsu et al. [34].

The genetic variance components for number of days to first flower initiation and first pod maturity were positive, except for variance due to dominance for number of days to 50% flowering and that of 90% pod maturity which were negative values and for practical purposes were considered as zero. Negative values for dominance variances which imply the masking effects of genes were also observed in previous studies using populations of cowpea [35]. The values of genetic variance for all the parameters were greater than those observed for the environmental variance. This suggests that the inheritance of maturity in cowpea is more determined by genetic factors rather than the environment and therefore the trait can be improved through selection [35, 36]. Mean number of days to first pod maturity had the highest environmental variance of 17.73, while the mean number of days to first flower initiation was as low as 4.64, indicating that environmental influence on pod maturity is

FIGURE 3: Frequency distribution analysis of DFFI and DNPM for Padi-Tuya.

greater than its influence on flowering, because postflowering environmental conditions could have effect of grain filling.

High narrow sense and broad sense heritability estimates observed suggest that the phenotypes of the traits strongly reflect their genotypes [37]. Similar heritability estimates have been reported for days to flowering and days to pod maturity [2]. On the other hand, a high broad sense heritability of 99% and very low narrow sense heritability estimates of 1.8% for days to pod maturity and 2.0% for days to flowering were reported [17]. The insignificant difference between broad and narrow sense heritability estimates could be attributed to negative dominance variance observed [38]. Broad sense heritability in self-pollinating crops is less informative than narrow sense heritability which is a direct measure of additive variance [39]. High heritability estimates of the trait also suggest that high selection pressure could be imposed in any breeding programme aimed at improving early maturity in cowpea [26] resulting in greater genetic gain. This makes it possible to successfully select important traits for improvement in segregating populations [40]. For this reason, selection for early maturity in cowpea could begin in the F_2 generation where ample variability is observed. Therefore, marker assisted backcrossing, pedigree, and single-seed descent methods could be very useful in selecting for early maturity in cowpea [41]. High broad and narrow sense heritability estimates for maturity indices also suggest that high selection pressure could be imposed for these traits [42].

The observed segregation frequency in the F_2 generation was 3 : 1 for early to medium, respectively. This was significant according to the chi-squares analysis. This implies that inheritance of extra-early maturity in cowpea is under monogenic dominant control. Similar observations were made by Brittingham [43] and Hugo et al. [37]. This indicates that few selection cycles would be necessary to obtain the required accumulation of favourable alleles controlling the inheritance of early maturity in cowpea. Therefore, the development of early maturing cowpea cultivars can be relatively simple through classical breeding strategies such as pedigree and single seed decent.

In addition, the frequency distribution analysis of the 300 F_2 plants evaluated also indicated that 229 representing 76.33% fell within early maturity group while 71 representing 23.66% were in medium maturity group for DFFI. Similar observation was made for BC_1 for the trait. In DFFPM, 222 out of the 300 F_2 plants representing 74% were early maturing and the others were medium maturing; BC_1 population was not much different from that of F_2 .

All the F_1 population were early with means of 32.12 days and 51.56 days for DFFI and DFFPM, respectively; these were closer to the early maturing parent (*Sanzi*), hence elucidation dominant gene effect. About 23% of the medium parent (*Padi-Tuya*) fell within the early maturity group for number of days to first flower initiation but could attain the early maturity status for days to first pod maturity. Earliness is determined by the ability a crop to reach flowering and pod filling in a short period [20]. This means that though some plants of *Padi-Tuya* flowered early, they could not reach early maturity due to long pod filling period required.

The absence in significant differences between the F_1 and the RF_1 populations suggests the absence of maternal effects for inheritance of the maturity indices (DFF, DFFI, DNPM, and DFFPM) in cowpea [40]. The inheritance of these parameters could therefore be attributed to nuclear gene control. For that matter any of the parents could be used as a maternal parent in hybridization programme that focuses on the improvement of maturity in cowpea [29].

Correction analysis suggested that grain yield is significant positively correlated with DFF, DFFPM, HSWT, and P_PLT, indicating that the longer the genotypes takes to flower and/or mature, the higher the grain yield is. Hundred-seed weight was also highly positively correlated with grain yield and DFF and DFFPM and DNPM. This implies that longer grain filling period enables bigger grains to be developed and hence high grain yield. Similar observations were made by Nakawuka and Adipala [44]. These observation notwithstanding would be possible to identify individual plants within the segregation population that will combine early maturity with high grain yield. Single seed descent technique could be employed to obtain cowpea genotypes that combine early maturity with high yielding potential [45].

5. Conclusions

High heritability estimates for the maturity indices indicate possible transfer of the genes that control early maturity to a medium or late maturing variety. The segregation ratio in the F_2 population for early and medium maturity fitted into the ratio, 3 : 1, indicating that maturity in cowpea is conditioned by single dominant gene. Inheritance of early maturity in cowpea is not influenced by maternal effects; hence any of the parents can be used as a maternal parent in hybridization programme for improving early maturity in cowpea. Selection criteria to improve maturity of cowpea should focus on number of days to first flower initiation, number of days to 50% flowering, and number of days to first pod maturity. Grain yield was positively correlated with DFF, DFFPM, HSWT, and P_PLT, indicating that the longer the genotypes takes to flower and/or mature the higher the grain

TABLE 4: Correlation among maturity indices, yield, and yield components.

	DFI	DFI	DFI	DFPM	DNPM	H@F	H@M	CW	P_PLT	S_DP	HSWT	G_YD
DFI	1											
DFI	0.974***	1										
DFPM	0.834***	0.813***	1									
DNM	0.916***	0.894***	0.820***	1								
H@F	0.611***	0.651***	0.761***	0.614***	1							
H@M	0.685***	0.735***	0.787***	0.696***	0.85128	1						
CW	-0.39**	-0.418**	-0.612***	-0.326NS	-0.691***	-0.706***	1					
P_PLT	-0.66***	-0.642**	-0.422*	-0.645***	-0.305NS	-0.303NS	-0.019**	1				
S_PD	-0.314NS	-0.334NS	-0.505***	-0.464***	-0.486***	-0.545***	0.319NS	0.158NS	1			
HSWT	0.613***	0.648***	0.836***	0.653***	0.848***	0.803***	-0.786***	-0.271NS	-0.582NS	1		
G_YD	0.307NS	0.361**	0.446**	0.263NS	0.394**	0.571***	-0.801***	0.059*	-0.240NS	0.609***	1	

* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$, NS: not significant ($P > 0.05$), DFFI = days to first flower initiation, DFF = days to 50% flowering, DFPM = days to first pod maturity, DNPM = days to 90% pod maturity, H@F = plant height at flowering, H@M = plant height at maturity, CW = canopy width, P_PLT = pod per plant, S_PD = seed per pod, HSWT = hundred-seed weight (g), and GYD/Ha = grain yield (tons per hectare).

yield is. The study provides understanding of the genetic basis of inheritance of early maturity in cowpea which can be useful in future breeding programmes.

Abbreviations

F ₁ :	First filial generation
RF ₁ :	Reciprocal cross of first filial generation
F ₂ :	Second filial generation
RF ₂ :	Reciprocal cross of second filial generation
BC ₁ :	First backcross generation
RBC ₁ :	First reciprocal backcross generation
BC ₂ :	Second backcross
RBC ₂ :	Second reciprocal backcross generation
DFFI:	Number of days to first flower initiation
DFF:	Number days to 50% flowering
DFPM:	Number of days to first pod maturity
DNPM:	Number of days to 90% maturity
H@M:	Height at maturity
P.PLT:	Pod per plant
S.Pod:	Seed per pod
H.SWT:	Hundred-seed weight
G.YD:	Grain yield.

Conflicts of Interest

The authors declare that they do not have any conflicts of interest.

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