

Biological Forum – An International Journal

14(1): 1146-1153(2022)

ISSN No. (Print): 0975-1130 ISSN No. (Online): 2249-3239

Evaluation of Genetic Potential between F₂ and F₃ Generations of Cowpea (Vigna unguiculata L.) Walp.) using Parent Progeny Regression Analysis

V. Manimozhi Selvi^{1*}, A. Nirmalakumari¹, C.R. Anandakumar² and R. Amudha³

¹Centre of Excellence in Millets, Tamil Nadu Agricultural University, Athiyandal, Thiruvannamalai, (Tamil Nadu), India. ²Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, (Tamil Nadu), India. ³Department of Crop Physiology, Horticultural College and Research Institute(Women), Trichy, (Tamil Nadu), India.

> (Corresponding author: V. Manimozhi Selvi*) (Received 04 November 2021, Accepted 19 January, 2022) (Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: The productivity potential of cowpea in Tamil Nadu is low 265 kg/ha as compared to the national productivity. This clearly indicates the necessity to identify the reason for such a low productivity in India and particularly in Tamil Nadu. The limited number of cowpea breeding programs in Tamil Nadu has contributed to the ineffective production. To overcome this issue, the main focus of the present investigation is to identify the promising segregants for further use in future breeding programmes. An investigation was carried out in F_2 and F_3 generations of four inter subspecies crosses of cowpea. The F_2 and F_3 progenies were evaluated along with their parents. The breeding nature of the segregants were investigated by parent progeny regression for the traits viz., days to first flowering, plant height, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, hundred seed weight and single plant yield. Selected single plants based on days to first flowering, number of pods per plant and single plant yield in all cross combinations were forwarded to F₃ generation their performance was studied using parent progeny regression analyses. The evaluation selection response of the selected trait viz., days to first flowering, number of pods per plant and single plant yield using inter generation regression estimates revealed that at positive level of selection for crosses RC 101 \times Vyjayanthi and ACM 05-07 \times Vyjayanthi, correlation and regression coefficients were positive and significant indicating a bright selection for single plant yield at this level. When all these selections are taken into consideration at significant and positive level of correlation and regression were found to be suitable for effortless selection for most of the characters in both crosses RC 101 \times Vyjayanthi and ACM 05-07 \times Vyjayanthi, Hence, these crosses had good chances of yielding better genotypes in case of most unselected traits.

Keywords: Cowpea; Correlation, Path coefficient, Parent progeny regression, (Vigna unguiculata L. Walp).

INTRODUCTION

Cowpea (Vigna unguiculata L. Walp) is a multipurpose, underutilized legume crop mostly grown in dry tropical areas. It is one of the most important food legume crops, exhibits considerable morphological variability in its wild as well as cultivated forms. (Belay and Fisseha 2021). According to FAOSTAT (2017), cowpea was grown on an estimated 11 million ha in Africa in 2017 with most of production confined to West Africa (10.6 million ha), especially in Niger, Nigeria, Burkina Faso, Mali, and Senegal. More than 7.4 million tons of cowpeas are produced worldwide, with Africa producing nearly 5.2 million tons (https://www.iita.org/cropsnew/cowpea/). According to FAOSTAT (2017), over 87% of cowpeas are produced in Africa. However, in South America, Brazil increased cowpea cultivation and the country is now in third place in terms of global production. The grain contains high

protein, carbohydrate, vitamins, and fibre (Hall et al., 2012). It is predominantly cultivated by resource limited small holder farmers usually women with average farm-size of 0.5-1 ha. Cowpea grain (23-25%) and leaves (27-34%) contain valuable amounts of protein and constitute an important protein source in human diets (Owusu et al., 2018).

Success of any breeding programme solely depends on the extent of genetic variability present in the crop. Crop improvement for single plant yield has been through effective use of F₂ and F₃ segregating populations and fixing desirable character combinations.

Parent-offspring regression helps to understand how far the genetic potentials are transferred from one generation to other and a high regression suggests large genetic effect coupled with small environment influence (Bhanu et al., 2019). The success of any recombination breeding programme depends upon 14(1): 1146-1153(2022)

Selvi et al.,

highly variable populations and it lies in the hands of the plant breeder to exercise rigorous selection, to get the best recombinants (Mohammed et al., 2010). The phenotypic expression of a single plant in F_2 is the result of cumulative effect of both genotype and environment. Selection will be effective if only the performance of F_3 lines is more dependable on F_2 performance (Malarvizhi and Rangasamy, 2003). Hence, it is necessary to evaluate as to how far the F₂ values have a bearing on F3 generation mean and whether such parameter can be relied upon for further selection. Parent progeny regression analysis is an effective method for exercising selection in the segregating progenies, only when the performance of the parents in the selection of plants will be effective. Lush (1940) delineated that it was possible to apply selection of best strains based on its genetic potentiality by regressing the progeny mean (F_3) over the values of their corresponding parents (F₂). This study was conducted with the objective of analyzing genetic variability and interrelationship of important yield contributing traits and to identify desirable segregants from each of the four F_2 and F_3 populations. A detailed experiment was carried out to evaluate how far the genetic potential is transferred from F₂ to F₃ generation for single plant yield.

MATERIALS AND METHODS

Pure selfed seeds of the following six varieties, three in dwarf, early flowering with short pod and grain (*V. unguiculata subspecies sinensis*) types and three in climber, late flowering with long pod and vegetable (*V. unguiculata subspecies sequipedalis*) types were collected from Kerala, Tamil Nadu and Rajasthan. The cross combinations were effected, the hybrids (F_1) was studied in the Department of Plant Breeding and Genetics, Agricultural College and Research Institute Madurai during main rainy season. The F_1 seeds from four highly promising heterotic crosses were utilized as the experimental material for the present study of F_2 and F_3 generations.

Evaluation of F₂ generations: The F₂ generation of four cross combinations was raised along with their six parents in a Randomized Block Design replicated twice. A total of 300 plants were raised per cross combinations in 30 rows adopting a spacing of 45 cm between rows and 30 cm between plants in a row. The recommended agronomic practices were followed throughout the crop growth period. Observations were recorded on all the plants in each cross of the F₂ and ten plants in parents. Based on single plant wise F₂ plants are harvested and dried then kept under optimum moisture storage condition. Based on single plant yield wise 30 superior plants were selected and these seed materials were used for source of F₃ generation.

Evaluation of F₃ generation: The F_3 generation consisted of plants chosen based on the single plant yield from four crosses which were raised in F_2 . In F_3 a total of 120 families (30 families from each cross) of four crosses were raised with their six parents in a Randomized Block Design replicated twice. The F_3 generation was raised at the rate of two rows per

progenies (F_2), each rows consisting of ten plants. Each cross had two rows of the respective parents per replication. Observations were recorded in randomly selected five single plants per family and ten plants for each parent per replication. The data recorded on eight quantitative traits in F_2 and F_3 generations were statistically analyzed.

Correlation studies: Phenotypic correlations were computed by using the formula given by Weber and Moorty (1952).

Phenotypic correlation coefficient

$$rp(x,y) = \frac{COV.p_{(xy)}}{\sqrt{\sigma^2 p_x \times \sigma^2 p_y}}$$

Where,

rp(x,y) = phenotypic correlation coefficient between the traits x and y.

COV P (xy) = phenotypic covariance between the traits 'x' and 'y'.

2 Px = phenotypic variance of the trait - 'x'.

2 Py = phenotypic variance of the trait - 'y'

The significance of correlation coefficient was tested by t-test (Nadarajan and Gunasekaran, 2005).

$$t = \frac{r}{SE_r}$$
$$SE_r = \sqrt{\frac{1 - r^2}{N - 2}}$$

Where,

r = correlation coefficient

N = number of observation on the variable X and Y. **Path coefficient analysis:** The relative influence of eight components on yield by themselves (direct effects) and through other traits (indirect effects) was evaluated by the method of path coefficient

analysis as suggested by Dewey and Lu (1959). **Parent progeny regression analysis:** Parent progeny regression analysis involved regression the mean value of a character in the progeny (F_3) upon the value of the respective character in the parent (F_2).

The regression coefficient 'b' was calculated by using the formula (Lush, 1940).

Regression coefficient (b) = $\frac{\text{Sum of products of } F_2 \text{ and } F_3}{\text{Sum of squares of } F_3}$

The significance of 'b' was tested using 't' test (Singh and Chaudary 1985).

$$t = \frac{b}{S.E (b)}$$

S.E (b) = $\sqrt{\frac{SS(F_2) - b^2 SSF_3}{SS(F_3) (n-2)}}$

Where,

S.E(b) = Standard error of regression coefficient

SS (F_2) = Sum of squares of F_2

SS (F_3) = Sum of squares of F_3

n = number of observations

RESULTS AND DISCUSSION

Phenotypic correlation coefficients among yield components in F_2 and F_3 generations of four crosses

are presented in Table 1-4. In the present investigation, number of clusters per plant showed significant and positive association with yield in both F_2 and F_3 generations (in crosses RC101 × Vellayani Jyothica, ACM 05 02 × Ettumanoor local and ACM 05 07 × Vyjayanthi) and (in F_3 of cross RC101 × Vyjayanthi). The trait number of pods per plant showed highly significant and positive correlation with single plant yield in both F_2 and F_3 of all crosses except in F_2 of cross RC101 × Vyjayanthi in which negative association was observed between these two traits. The results indicate, pod length showed, significant and positive association with single plant yield (in F_2 of crosses ACM 05 02 × Ettumanoor local and ACM 05 07 × Vyjayanthi) and (in F_3 of cross RC101 × Vellayani Jyothica). These finding are similar to Baghizadeh *et al.*, (2010); Manggoel *et al.* (2012); Gerrano *et al.* (2015); Mafakheri *et al.* (2017); Owusu *et al.* (2020) in cowpea.

Table 1: Phenotypic correlation coefficients among yield components in F₂ and F₃ generations of cross RC101 **x** Vyjayanthi.

Characters	Generations	Days to first flowering (days)	Plant height (cm)	No. of clusters per plant	No .of pods per plant	Pod length (cm)	No .of seeds per pod	100 seed weight (g)	Single plant yield (g)
Days to first flowering	F ₂	1.000	0.875**	0.121	-0.039	0.179*	0.197**	0.151*	0.115
(days)	F ₃	1.000	-0.111	0.718**	0.732**	0.311*	0.324^{*}	0.829**	0.894**
Plant height (am)	F ₂		1.000	0.037	-0.069	0.205**	0.222**	0.117	0.077
Flant height (Chi)	F ₃		1.000	0.172	0.157	-0.305	-0.352*	-0.001	0.000
No. of closed and a start	F ₂			1.000	0.158*	-0.270**	-0.287**	0.047	-0.113
No. of clusters per plant	F ₃			1.000	0.993**	-0.203	-0.202	0.744**	0.809**
	F ₂				1.000	0.225**	0.209**	0.016	-0.062
No. of pods per plant	F ₃				1.000	-0.196	-0.195	0.748^{**}	0.817**
Dod langth (am)	F ₂					1.000	0.996**	0.144*	0.112
Fou lengui (cm)	F ₃					1.000	0.970**	0.256	0.217
No. of coods per pod	F_2						1.000	0.153*	0.125
No. of seeds per pou	F ₃						1.000	0.272	0.223
100 good weight (g)	F_2							1.000	0.935**
100 seed weight (g)	F ₃							1.000	0.930**
Cincle plant sight (a)	F ₂								1.000
Single plant yield (g)	F ₃								1.000

* Significant at 5 percent level, ** Significant at 1 percent level

Table 2: Phenotypic correlation coefficients among yield components in F₂ and F₃ generations of cross RC101 ★ Vellayani Jyothica.

Characters	Generations	Days to first flowering (days)	Plant height (cm)	No. of clusters per plant	No .of pods per plant	Pod length (cm)	No .of seeds per pod	100 seed weight (g)	Single plant yield (g)
Days to first flowering (days)	F ₂	1.000	0.881**	0.271**	-0.034	0.224**	0.237^{*}	0.131	0.047
Days to first nowening (days)	F ₃	1.000	0.817^{**}	0.652**	0.647**	0.494**	0.551**	0.835**	0.923**
Dignt haight (am)	F_2		1.000	0.221**	0.018	0.186**	0.202**	0.114	0.064
Flaint height (chi)	F ₃		1.000	0.529**	0.517**	0.508**	0.552**	0.744**	0.838**
No. of electory new plant	F ₂			1.000	0.370**	0.681**	0.685**	0.599**	0.549**
No. of clusters per plant	F ₃			1.000	0.984**	0.005	0.012	0.607**	0.699**
	F ₂				1.000	0.374**	0.366**	0.147*	0.149*
No. of pous per plant	F ₃				1.000	0.004	0.005	0.596**	0.699**
Dod longth (am)	F_2					1.000	0.996**	0.139*	0.089
Fod length (cm)	F ₃					1.000	0.960**	0.462**	0.549**
No. of coods per pod	F ₂						1.000	0.147*	0.101
No. of seeds per pou	F ₃						1.000	0.498**	0.584**
100 and weight (g)	F ₂							1.000	0.944**
100 seed weight (g)	F ₃							1.000	0.887**
	F ₂								1.000
Single plant yield (g)	F ₃								1.000

* Significant at 5 percent level, ** Significant at 1 percent level

Table 3: Phenotypic correlation coefficients among yield components in F₂ and F₃ generations of cross ACM 05 02 ★ Ettumanoor local.

Characters	Generations	Days to first flowering (days)	Plant height (cm)	No. of clusters per plant	No .of pods per plant	Pod length (cm)	No .of seeds per pod	100 seed weight (g)	Single plant yield (g)
Days to first	F_2	1.000	0.633**	0.395**	0.398**	0.463	0.460 **	0.725**	0.658**
nowening (days)	F ₃	1.000	-0.109	-0.200	-0.235	0.183	0.165	0.034	-0.056
Diant haight (am)	F ₂		1.000	0.616**	0.626**	0.564**	0.575**	0.745**	0.914**
Plant neight (cm)	F ₃		1.000	0.259	0.273	-0.178	-0.169	0.113	0.156
No. of clusters per	F ₂			1.000	0.986**	0.003	0.017	0.535**	0.688^{**}
plant	F ₃			1.000	0.944**	-0.107	-0.108	0.689**	0.781^{**}
No. of pode per plant	F ₂				1.000	0.009	0.022	0.549**	0.705**
No. of pous per plant	F ₃				1.000	-0.137	-0.130	0.726**	0.816**
Pod length (cm)	F ₂					1.000	0.982**	0.442**	0.606**
-	F ₃					1.000	0.981**	0.288	0.281
No. of souds man and	F ₂						1.000	0.474**	0.612**
No. of seeds per pod	F ₃						1.000	0.303	0.299
100 cood weight (g)	F ₂							1.000	0.826**
100 seed weight (g)	F ₃							1.000	0.907**
Single plant yield (g)	F ₂								1.000
Single plant yield (g)	F ₃								1.000

* Significant at 5 percent level, ** Significant at 1 percent level

Table 4: Phenotypic correlation coefficients among yield components in F₂ and F₃ generations of cross ACM 05 07 **★** Vyjayanthi.

Characters	Generations	Days to first flowering (days)	Plant height (cm)	No. of clusters per plant	No .of pods per plant	Pod length (cm)	No .of seeds per pod	100 seed weight (g)	Single plant yield (g)
Days to first flowering	F ₂	1.000	0.692**	0.600^{**}	0.608^{**}	0.505**	0.510**	-0.239**	0.772^{**}
(days)	F ₃	1.000	0.103	0.675 **	0.674 **	0.122	0.109	0.833**	0.891 **
Plant height (cm)	F ₂		1.000	0.616**	0.614**	0.466**	0.479**	-0.087	0.799**
Flant height (chi)	F ₃		1.000	0.080	0.079	-0.004	0.008	0.036	0.028
No. of chustom non-plant	F ₂			1.000	0.998^{**}	0.034	0.023	0.037	0.779^{**}
No. of clusters per plant	F ₃			1.000	1.000 **	-0.312 *	-0.329 *	0.694**	0.705^{**}
No. of a standard loop	F ₂				1.000	0.034	0.025	0.039	0.783**
No. of pous per plant	F ₃				1.000	-0.310 *	-0.328 *	0.693**	0.704^{**}
Pod longth (am)	F ₂					1.000	0.976^{**}	-0.102	0.525**
Fou lengui (chi)	F ₃					1.000	0.971 **	0.119	0.132
No. of soads per pod	F ₂						1.000	-0.063	0.539**
No. of seeds per pod	F ₃						1.000	0.106	0.125
100 seed weight (g)	F ₂							1.000	0.060
	F ₃							1.000	0.892**
Single plant yield (a)	F ₂								1.000
Single plant yield (g)	F ₃								1.000

* Significant at 5 percent level, ** Significant at 1 percent level

Number of seeds per pod showed positive correlation with single plant yield in all the crosses of both F_2 and F_3 except in crosses ACM 05 02 × Ettumanoor local and ACM 05 07 × Vyjayanthi of F_2 and in cross RC101 × Vellayani Jyothica of F_3 . Also the association was highly significant. Similar positive association was reported by Gerrano *et al.* (2015); Mafakheri *et al.* (2017); Owusu *et al.* (2020); Pandiyan *et al.* (2020) in cowpea. Hundred seed weight and single plant yield showed high significant and positive correlation in both F_2 and F_3 of all crosses except in F_2 of cross ACM 05 07 × Vyjayanthi in which this positive association was not significant. This is in agreement with the reports of Mafakheri *et al.* (2017); Owusu *et al.* (2021) in cowpea for hundred seed weight.

The correlation of days to first flowering, number of clusters per plant, number of pods per plant and

hundred seed weight with single plant yield was highly significant and positive in almost all the crosses for both F_2 and F_3 generation except in F_2 of crosses RC101 × Vyjayanthi and RC101 × Vellayani Jyothica for days to first flowering and cross $\,$ ACM 05 07 \times Vyjayanthi for hundred seed weight and cross RC101 × Vyjavanthi for number of clusters per plant and number of pods per plant. These results indicated that the high yielding ability might be associated with these yield components. In cowpea, positively significant association of seed yield with days to first flowering, number of clusters per plant and number of pods per plant hundred seed weight were observed by several authors Baghizadeh et al. (2010); Manggoel et al. (2012); Gerrano et al. (2015); Mafakheri et al. (2017); Pandiyan et al. (2020); Owusu et al. (2021) in cowpea.

From the above facts, it is clear that the number of clusters per plant, number of pods per plant, number of seeds per pod and hundred seed weight are important for the improvement of yield as these traits exhibited significant and positive association with single plant yield. Therefore, selection of higher number of clusters, higher number of pods, higher number of seeds and hundred seed weight will automatically result in increased single plant yield. Furthermore, increase in pod length had some positive effect on seed yield. Moreover, estimating pod length, counting number of seeds per pod and hundred seed weight in a single plant is laborious. But, selection for number of clusters and number of pods by visual observations in the field is very easy. Therefore, improvement of seed yield in cowpea could be achieved by selecting plants with more number of clusters and more number of pods per plant.

Phenotypic path ways between yield and yield components on single plant yield in F₂ and F₃ generations of four crosses are presented in Table 5-8. The path coefficient analysis showed that number of pods per plant and hundred seed weight exerted the maximum similar contributions to single plant yield with high positive direct effect when compared to other traits in almost all the crosses (except in F₂ of crosses $RC101 \times Vyjayanthi and RC101 \times Vellayani Jyothica$ and in F_3 of cross ACM 05 07 × Vyjayanthi). The total correlation between number of pods per plant and hundred seed weight and single plant yield was highly significant and positive both in F_2 and F_3 of all the cross combinations. High direct effects with maximum contribution of number of pods per plant on single plant yield. These results are in conformity with Gerrano et al. (2015); Mafakheri et al. (2017); Pandiyan et al. (2020); Owusu et al. (2021) in cowpea.

From the traced out pathways and associations it was found that, number of clusters per plant, number of pods per plant, number of seeds per pod and hundred seed weight were showed higher total associations in almost all the crosses in both generation. Above these traits exhibited a high positive direct effect on single plant yield. They also exhibited significant indirect contribution on yield through component traits could be used as yield determinants for further improvement in the population.

Table 5: Phenotypic path ways between yield and yield components on single plant yield in F_2 and F_3 generations of cross RC101×Vyjayanthi

Characters	Generation	Days to first flowering (days)	Plant height (cm)	No. of clusters per plant	No .of pods per plant	Pod length (cm)	No .of seeds per pod	100 seed weight (g)	Single plant yield (g)
Days to first flowering	F ₂	0.074	-0.073	-0.021	0.002	-0.024	0.015	0.143	0.115
(days)	F ₃	0.297	-0.001	-0.045	0.215	0.040	-0.029	0.416	0.894^{**}
Plant height (cm)	F ₂	0.064	-0.084	-0.006	0.003	-0.028	0.017	0.111	0.078
	F ₃	-0.033	0.007	-0.011	0.046	-0.039	0.031	0.000	0.000
No. of clusters per	F ₂	0.009	-0.003	-0.172	-0.006	0.036	-0.022	0.045	-0.113
plant	F ₃	0.213	0.001	-0.063	0.292	-0.026	0.018	0.373	0.809^{**}
No. of pode per plant	F ₂	-0.003	0.006	-0.027	-0.038	-0.030	0.016	0.015	-0.062
No. of pous per plant	F ₃	0.218	0.001	-0.062	0.294	-0.025	0.017	0.375	0.817^{**}
Pod longth (am)	F ₂	0.013	-0.017	0.046	-0.009	-0.135	0.076	0.137	0.112
Fou lengui (ciii)	F ₃	0.092	-0.002	0.013	-0.058	0.129	-0.085	0.129	0.217
No. of coads per pod	F ₂	0.015	-0.019	0.050	-0.008	-0.135	0.077	0.145	0.125
No. of seeds per pod	F ₃	0.096	-0.0002	0.013	-0.057	0.125	-0.088	0.137	0.223
100 good weight (g)	F ₂	0.011	-0.010	-0.008	-0.001	-0.020	0.012	0.950	0.935**
100 seeu weight (g)	F ₃	0.246	0.000	-0.047	0.220	0.033	-0.024	0.502	0.930**

Residue effects $F_2 = 0.305$, $F_3 = 0.265$ * Significant at 5 percent level, ** Significant at 1 percent level

Table 6: Phenotypic path ways between yield and yield components on single plant yield in F_2 and F_3 generations of cross RC101×Vellavani Jvothica.

Characters	Generations	Days to first flowering (days)	Plant height (cm)	No. of clusters per plant	No .of pods per plant	Pod length (cm)	No .of seeds per pod	100 seed weight (g)	Single plant yield (g)
Days to first flowering	F ₂	-0.162	0.080	0.012	-0.001	-0.160	0.155	0.121	0.047
(days)	F ₃	0.285	0.121	-0.051	0.226	0.041	0.070	0.231	0.923**
Blant height (am)	F ₂	-0.143	0.091	0.010	0.003	-0.1323	0.133	0.105	0.064
Plant height (cm)	F ₃	0.233	0.148	-0.042	0.181	0.042	0.070	0.205	0.838**
No. 6 lost services and	F ₂	-0.044	0.020	0.046	0.006	-0.484	0.450	0.556	0.549**
No. of clusters per plant	F ₃	0.186	0.079	-0.079	0.344	0.000	0.001	0.168	0.699**
No. of node non-plant	F ₂	0.006	0.002	0.017	0.015	-0.2664	0.240	0.136	0.149**
No. of pods per plant	F ₃	0.185	0.077	-0.078	0.350	0.000	0.001	0.165	0.699**
De 11 au de (com)	F ₂	-0.036	0.017	0.031	0.006	-0.712	0.654	0.1290	0.089
Pod length (cm)	F ₃	0.141	0.075	0.000	0.001	0.083	0.121	0.128	0.549**
No. of coords man mod	F ₂	-0.038	0.018	0.032	0.005	-0.709	0.657	0.136	0.101
no. of seeds per pod	F ₃	0.157	0.082	-0.001	0.002	0.080	0.126	0.138	0.584^{**}
100 seed weight (g)	F ₂	-0.021	0.010	0.028	0.002	-0.099	0.096	0.927	0.944**
	F ₃	0.238	0.110	-0.048	0.209	0.038	0.063	0.276	0.887^{**}

Residue effects $F_2 = 0.311$, $F_3 = 0.242$ * Significant at 5 percent level, ** Significant at 1 percent level

Biological Forum – An International Journal 14(1): 1146-1153(2022)

Characters	Generations	Days to first flowering (days)	Plant height (cm)	No. of clusters per plant	No .of pods per plant	Pod length (cm)	No .of seeds per pod	100 seed weight (g)	Single plant yield (g)
Days to first	F ₂	-0.041	0.217	-0.039	0.179	0.215	-0.074	0.201	0.658^{**}
flowering (days)	F ₃	0.042	-0.001	0.309	-0.467	0.043	0.003	0.015	-0.056
Plant height	F ₂	-0.026	0.343	-0.060	0.282	0.262	-0.093	0.207	0.914**
(cm)	F ₃	-0.005	0.012	-0.400	0.543	-0.042	-0.003	0.051	0.156
No. of clusters	F ₂	-0.016	0.211	-0.098	0.444	0.001	-0.003	0.148	0.688^{**}
per plant	F ₃	-0.009	0.003	-1.457	1.989	-0.027	-0.002	0.330	0.803**
No. of pods per	F ₂	-0.016	0.215	-0.096	0.450	0.004	-0.004	0.152	0.705^{**}
plant	F ₃	-0.010	0.003	-1.458	1.988	-0.032	-0.002	0.328	0.816^{**}
Pod length	F ₂	-0.019	0.194	0.000	0.004	0.464	-0.158	0.123	0.606^{**}
(cm)	F ₃	0.008	-0.002	0.165	-0.273	0.235	0.019	0.130	0.281
No. of seeds	F ₂	-0.019	0.197	-0.002	0.010	0.455	-0.161	0.131	0.612^{**}
per pod	F ₃	0.007	-0.002	0.166	-0.259	0.231	0.019	0.136	0.299
100 seed	F_2	-0.030	0.256	-0.052	0.247	0.205	-0.076	0.277	0.826^{**}
weight (g)	F ₃	0.001	0.001	-1.065	1.444	0.068	0.006	0.451	0.907**

Table 7: Phenotypic path ways between yield and yield components on single plant yield in F_2 and F_3 generations of cross ACM 05 02 × Ettumanoor local.

* Significant at 5 percent level, ** Significant at 1 percent level

Table 8: Phenotypic path ways between yield and yield components on single plant yield in F_2 and F_3 generations of cross ACM 05 07 Vyjayanthi.

Characters	Generations	Days to first flowering (days)	Plant height (cm)	No. of clusters per plant	No .of pods per plant	Pod length (cm)	No .of seeds per pod	100 seed weight (g)	Single plant yield (g)
Days to first	F_2	0.112	0.129	-0.204	0.563	-0.038	0.233	-0.024	0.772**
flowering (days)	F ₃	0.435	-0.005	0.742	-0.636	-0.008	0.017	0.346	0.891**
Plant height	F ₂	0.078	0.187	-0.209	0.569	-0.035	0.219	-0.009	0.799**
(cm)	F ₃	0.045	-0.047	0.088	-0.075	0.000	0.001	0.015	0.028
No. of	F ₂	0.067	0.115	-0.340	0.924	-0.003	0.011	0.004	0.779^{**}
clusters per plant	F ₃	0.294	-0.004	1.099	-0.943	0.021	-0.050	0.288	0.705**
No. of pods	F ₂	0.068	0.115	-0.339	0.926	-0.003	0.011	0.004	0.783**
per plant	F ₃	0.293	-0.004	1.099	-0.943	0.021	-0.050	0.288	0.704^{**}
Pod length	F ₂	0.057	0.087	-0.011	0.031	-0.075	0.446	-0.010	0.525**
(cm)	F ₃	0.053	0.000	-0.343	0.293	-0.067	0.147	0.049	0.132
No. of seeds	F_2	0.057	0.089	-0.008	0.023	-0.073	0.457	-0.006	0.539**
per pod	F ₃	0.047	0.000	-0.362	0.309	-0.065	0.152	0.044	0.125
100 seed	F_2	-0.027	-0.016	-0.013	0.036	0.008	-0.029	0.101	0.060
weight (g)	F ₃	0.362	-0.002	0.762	-0.654	-0.008	0.016	0.415	0.892**

* Significant at 5 percent level, ** Significant at 1 percent level Residue effects $F_2 = 0.301$, $F_3 = 0.351$

The inter generation correlations between F_2 and F_3 mean values and regression of F₃ on F₂ for all the traits are presented in Table 9. In the present study, the selection response of the selected traits (days to first flowering, number of pods per plant and single plant yield) days to first flowering showed highly significant positive correlation and regression were observed in cross RC $101 \times$ Vyjayanthi (b=0.61, r=0.77). However, at cross ACM 05-07 × Vyjayanthi (b=0.87, r=0.77) registered highly significant and positive correlation with high regression value. Non significant positive correlation and regression were observed in cross ACM $05-02 \times$ Ettumanoor local (b=0.14, r=0.16) and non significant negative regression and correlation were observed in cross RC 101 × Vellavani Jyothica (b=-0.04, r=0.06). Among the crosses, cross ACM 05-07 \times Vyjayanthi (b=0.70, r=0.71) recorded a highly significant positive correlation and regression and cross RC 101 × Vyjayanthi (b=0.43, r=0.34) showed only a significant positive correlation and regression for number of pods per plant. Non significant positive correlation and regression have also observed in cross ACM 05-02 \times Ettumanoor local (b=0.38, r=0.20) whereas, cross RC $101 \times$ Vellavani Jyothica (b=-0.04, r=0.03) recorded non significant correlation and regression values in negative direction for this trait. The cross ACM 05-02 × Ettumanoor local (b=0.58, r=0.47) registered a significant positive correlation and regression for single plant yield. At cross RC 101 \times Vyjavanthi (b=0.69, r=0.84) and cross ACM 05-07 \times Vyjayanthi (b= 0.96, r=0.98) recorded highly significant positive correlation with high regression value. Non significant negative correlation and regression were also exhibited by cross RC 101 \times Vellavani Jvothica (b=-0.56, r=0.34) for this same trait. Similar finding has been reported by Kalaiyarasi and Palanisamy (2000); Bhanu et al. (2019) in cowpea.

Days to first flowering, number of pods per plant and single plant yield was showed significant positive correlation and regression for crosses RC 101 imesVyjayanthi and ACM 05-07 \times Vyjayanthi; and significant correlation and regression for cross ACM 05-02 Ettumanoor local at positive level. The chances of identifying the superior genotypes at this level, for

Selvi et al.,

Biological Forum – An International Journal 14(1): 1146-1153(2022)

crosses RC 101 \times Vyjayanthi and ACM 05-07 \times Vyjayanthi were high. Here, even phenotypic selection could lead to better results. These results indicated the selection would be more effective, when exercised at these levels for respective crosses. These results are in agreement with the findings of Mafakheri *et al.* (2017); Pandiyan *et al.* (2020); Owusu *et al.* (2021) in cowpea.

Also negative and non significant correlation and regression were recorded for single plant yield in cross RC 101 \times Vellayani Jyothica. It revealed that, selection is not effective for single plant yield based on the individual of this cross. So it could be effective for other traits (Smalley *et al.* 2004). When unselected traits are taken into consideration, at positive level,

significant positive associations were observed in cross ACM 05-07 × Vyjayanthi for all the characters, except plant height and hundred seed weight and in cross RC 101 × Vyjayanthi for most of the characters, except plant height, pod length and hundred seed weight. While in cross ACM 05-02 Ettumanoor local recorded significantly positive correlation and regression for plant height and hundred seed weight. These results indicated that selection will be more effective when exercised for the respective crosses. The selection importance of these traits had been already suggested by Gerrano *et al.* (2015); for number of clusters per plant and number of pods plant; Mafakheri *et al.* (2017) for number of seeds per pod; Owusu *et al.* (2021) for hundred seed weight in cowpea.

 $\label{eq:F2} Table 9: Parent progeny \ Correlation \ (r) \ and \ Regression \ coefficients \ (b) \ between \ F_2 \ and \ F_3 \ generations \ of four \ inter \ crosses \ of \ cowpea.$

Characters		RC101 x Vyjayanthi	RC101 x Vellayani Jyothica	ACM 05 02 🗙 Ettumanoor local	ACM 05 07 x Vyjayanthi
Days to first flowering (days)	r	0.77**	0.06	0.16	0.77^{**}
Days to first nowering (days)	b	0.61**	-0.04	0.14	0.87^{**}
Plant height (am)	r	0.25	0.22	0.37*	0.10
Flait height (chi)	b	-0.19	-0.31	0.34^{*}	0.39
No. of eluctor per plent	r	0.42^{*}	0.19	0.20	0.81**
No. of cluster per plant	b	0.44^{*}	-0.17	0.21	1.32**
No. of non-nlout	r	0.34*	0.03	0.20	0.71**
No. of pos per plant	b	0.43*	-0.04	0.38	0.70^{**}
Ded lan oth (and)	r	0.23	0.02	0.15	0.78**
Pod length (cm)	b	0.22	0.01	-0.19	0.96**
No. of coods per ped	r	0.84**	0.23	0.05	0.73**
No. of seeds per pou	b	0.93**	-0.16	0.08	0.90**
100 and main t (a)	r	0.16	0.05	0.59**	0.05
100 seed weight (g)	b	0.11	-0.11	0.68^{**}	-0.12
Single plant yield (g)	r	0.84**	0.34	0.47^{*}	0.98**
Single plant yield (g)	b	0.69**	-0.56	0.58^{*}	0.96**

* Significant at 5 percent level, ** Significant at 1 percent level

The evaluation of the selection response of the selected traits viz., days to first flowering, number of pods per plant and single plant yield using inter generation regression estimates revealed that at positive level of selection for crosses RC101 \times Vyjayanthi and ACM 05 $07 \times V$ via vanthi, correlation and regression coefficients were positive and significant indicating a bright selection for single plant yield at this level. When all these selections are taken in consideration at significant and positive level of correlation and regression were found to be suitable for effortless selection for most of the characters in both crosses $RC101 \times Vyjayanthi$ and ACM 05 07 \times Vyjayanthi. Hence, among the four crosses RC101 \times Vyjayanthi and ACM 05 07 \times Vyjayanthi had good chances of yielding better genotypes in case of most selected traits.

CONCLUSION

It may be concluded that, number of clusters per plant, number of pods per plant, number of seeds per pod and hundred seed weight were the yield contributing traits and by performance, the crosses RC101 \times Vyjayanthi and ACM 05 07 \times Vyjayanthi were superior and desirable characters like dwarf, early duration and long purple pod inherited to their progenies in later generation.

FUTURE SCOPE

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. The study provides understanding of the genetic basis of inheritance of early maturity, dwarf and long purple pod in cowpea which can be useful in future breeding programmes.

REFERENCES

- Baghizadeh, A., Taleei, A. and Ghasemi, E. (2010). Evaluation of genetic variability for yield and some of quantitative traits in Iran cowpea collection. *Agric. Biol. J. N. Am.*, 1(4): 625-629.
- Bhanu, A. N., Singh, M. N., and Srivastava, K. (2019). Genetic analysis of gene-specific resistance to mungbean yellow mosaic virus in mungbean (*Vigna* radiata). Plant Breeding, 138(2): 202-206.
- Belay, F., and Fisseha, K. (2021). Genetic variability, heritability, genetic advance and divergence in Ethiopian cowpea [Vigna unguiculata (L) Walp] landraces. J. Agric. Sc. Food Technol., 7(1): 138-146.
- Dewey, D. R. and Lu, K. H. (1959). Correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, 51(9): 515-518.
- Gerrano, A. S., Adebola, P. O., Jansen van Rensburg, W. S., and Laurie, S. M. (2015). Genetic variability in

cowpea (Vigna unguiculata (L.) Walp.) genotypes. South African Journal of Plant and Soil, 32(3): 165-174.

- Hall, A. (2012). Phenotyping cowpeas for adaptation to drought. *Frontiers in physiology*, *3*, 155. (<u>https://www.iita.org/cropsnew/cowpea/</u>).
- Lush, J. L., 1940. Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proc. American Soc. Animal Prod.*, 33: 293-301.
- Kalaiyarasi, R., & Palanisamy, G. A. (2000). Parent-progeny regression analysis and variability studies in cowpea (Vigna unguiculata (L.) Walp.). Legume Research-An International Journal, 23(4), 237-240.
- Mafakheri, K., Bihamta, M. R., and Abbasi, A. R. (2017). Assessment of genetic diversity in cowpea (Vigna unguiculata L.) germplasm using morphological and molecular characterisation. Cogent Food & Agriculture, 3(1): 1327092.
- Malarvizhi, D. and Rangasamy, P. (2003). Character association and component analysis in F₂ generation of cowpea (*Vigna unguiculata* L. Walp). *Legumes Res.*, 26(4): 264-267.
- Manggoel, W., Uguru, M. I., Ndam, O. N., and Dasbak, M. A. (2012). Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [Vigna unguiculata (L.) Walp] accessions. Journal of Plant Breeding and Crop Science, 4(5): 80-86.
- Mohammed, M. S., Russom, Z. and Abdul, S. D. (2010). Inheritance of hairiness and pod shattering, heritability and correlation studies in crosses between cultivated cowpea (*Vigna unguiculata* (L.) Walp.) and its wild (var. pubescence) relative. *Euphytica.*, 171: 397-407.

- Nadarajan, N. and Gunasekaran, M. (2005). *Quantitative Genetics and Biometrical Techniques in Plant Breeding*. Kalyan Publishers, Ludhiana.
- Owusu, E. Y., Akromah, R., Denwar, N. N., Adjebeng-Danquah, J., Kusi, F., and Haruna, M. (2018). Inheritance of early maturity in some cowpea (Vigna unguiculata (L.) Walp.) genotypes under rain fed conditions in Northern Ghana. Advances in agriculture.
- Owusu, E. Y., Mohammed, H., Manigben, K. A., Adjebeng-Danquah, J., Kusi, F., Karikari, B., and Sie, E. K. (2020). Diallel Analysis and Heritability of Grain Yield, Yield Components, and Maturity Traits in Cowpea (Vigna unguiculata (L.) Walp.). The Scientific World Journal.
- Owusu, E. Y., Karikari, B., Kusi, F., Haruna, M., Amoah, R. A., Attamah, P., and Issahaku, M. (2021). Genetic variability, heritability and correlation analysis among maturity and yield traits in Cowpea (Vigna unguiculata (L) Walp) in Northern Ghana. Heliyon, 7(9): e07890.
- Pandiyan, M., Vaithilingan, M., Krishnaveni, A., Sivakumar, P., Sivakumar, C., Jamuna, E., and Senthilkumar, P. (2020). Genetic Variability Studies on Cowpea Genotypes. Int. J. Curr. Microbiol. App. Sci., 9(6): 3794-3797.
- Singh, R. K. and Chaudhary, B. D. (1985). *Biometrical Methodes in Quantitative Genetic analysis*. Kalyani Publishers, New Delhi.
- Smalley, M. D., Daub, J. L. and Hallauer, A. R. (2004). Estimation of heritability in maize by parent off spring regression. *Maydica.*, 49(3): 221.
- Weber, C. R. and Moorthy, B. R. (1952). Heritable and Non Heritable relationships and variability of oil content and Agronomic characters in the F₂ generation of soybean crosses. *Agron. J.*, 44: 209.

How to cite this article: V. Manimozhi Selvi, A. Nirmalakumari, C.R. Anandakumar and R. Amudha (2022). Evaluation of Genetic Potential Between F_2 and F_3 Generations of Cowpea (*Vigna unguiculata* L.) Walp.) Using Parent Progeny Regression Analysis. *Biological Forum – An International Journal*, 14(1): 1146-1153.