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Correlation and Path Coefficient Analyses of Cowpea (*Vigna unguiculata* L.) Landraces in Ethiopia

Tesfaye Walle[1], Firew Mekbib[2], Berhanu Amsalu[3], Melaku Gedil[4]

[1]Department of Plant Sciences, Wolkite University, Wolktie, Ethiopia
[2]School of Plant Sciences, Haramaya University, Dire Dawa, Ethiopia
[3]Melkassa Agricultural Research Center, Adama, Ethiopia
[4]International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria
Email: firew.mekbib@gmail.com

Abstract

Understanding the nature and extent of association between yield and yield related traits is the prerequisite study for any underutilized crop improvements of sustainable genetic enhancement. However, there is a lack of sufficient information on seed yield and related trait correlation and path coefficient analysis of cowpea in Ethiopia. To fill the existing knowledge gap, the present study was conducted to determine the nature and extent of phenotypic and genotypic correlation and path coefficient analysis among 18 quantitative traits. A total of 324 cowpea landraces were tested in 18 × 18 simple lattice design at Melkassa Agricultural Research Center and Miesso sub center during 2016 cropping season. The magnitude of genotypic correlations was higher than phenotypic correlations in most traits at both locations; this implies that the traits under consideration were genetically controlled. Seed yield was positively and highly significantly correlated with most of the traits at phenotypic and genotypic levels, indicating the presence of strong inherited association between seed yield and the other 17 traits. Almost all traits genotypic direct and indirect effects were higher than the phenotypic direct and indirect effects; this indicated that the other traits had a strong genetically inherited relationship with seed yield. Genotypic path coefficient analysis revealed that days to flowering, biomass and harvest index at Miesso, and seed thickness, plant height, days to maturity and biomass at Melkassa had relatively high positive direct effect on seed yield. However, seed width and hundred seed weight had exerted negative direct effect on seed yield at each location. Phenotypic path coefficient analysis showed that biomass and harvest index had exerted high positive direct effect on seed yield at both locations.

From these results it can be concluded from this study that seed yield in cowpea can be improved by focusing on traits pod length, seed length, seed thickness, seed width, biomass and harvest index at both locations. The information obtained from this study can be used for genetic enhancement of cowpea thereby developing high yielding varieties.

Keywords

Direct Effect, Genotypic Association, Indirect Effect, Phenotypic Association, Seed Yield

1. Introduction

Cowpea (*Vigna unguiculata* L.) is the most economically important indigenous African grain legume producing a source of economic livelihood and nutritional well-being for rural poor and urban consumers [1] [2].

Cowpea plays a critical role in the lives of millions of people in Africa and other parts of the developing world, where it is a major source of dietary protein that nutritionally complements staple low-protein cereal and tuber crops, and is a valuable and dependable commodity that produces income for poor farmers [2] [3]. It is also a cheap source of many other nutrients; it is known as vegetable meat [4] [5] [6].

Cowpea is primarily grown in drier regions of the world where it is one of the most drought tolerant food legumes [4] [5]. This drought tolerant crop is nutritious and highly palatable as the leaves, seeds, fresh pods and flowers are consumed [5] [7]. However, grain yield is complex trait because this trait is governed by many minor genes effects and is often confounded by interaction of morphological, physiological and biochemical characters of the crop with the environment thus making genetic improvement of these traits in crops a slow and difficult process [8] [9].

Therefore, understanding the nature and intensity of association between two or more quantitative traits between yield and yield contributing traits, correlation simply measures that mutual relationship between yield and yield contributing traits. Thus, correlation helps in the selection of superior genotype from diverse genetic populations [10]. However, in correlation studies indirect associations become more complex and confusing but path analysis helps to avoid this complication by measuring the direct influence of one trait on other and permits the partitioning of given correlation coefficients into its components of direct and indirect effects [10] [11]. The path coefficient analysis is an effective means of analyzing direct and causes of association and permits the critical examination of the specific traits that produce a given correlation. The path analysis provides information about magnitude and direction of direct and indirect effect of the yield components, which cannot be provided by correlation [12] [13].

In Ethiopia, cowpea is grown in southern and eastern Tigray zone, north and south Wollo zone, east and west Haraghe zone, Ethio-Somali region, Afar region, Wolayita zone and Jinka zone. Dray cowpea seed used for human consumption is the most important product of the cowpea plant; these grains can either be boiled or "nifiro" or converted into other food products like "Shiro" and "Kollo". In Gambella region used for nutritious vegetable soup; the young seedling, leaves, green pod and peas are used for salad in vegetarian diets as well as different dishes in the area. In addition to human consumption cowpea haulms and chaff are used as livestock feeds in all producing regions and are also beneficial in maintaining soil fertility thus making it an important component of any cropping system. Those regions adversely affected by erratic rainfall patterns [14] [15]. Compared to the other pulse crop cowpea can grow in sandy soils having low water-holding capacity in these drier regions [16]. For that reason, early maturing cowpea landraces can provide food earlier than any other crop (56 days after planting), thereby shortening the "hunger period" that often occurs prior to harvest of other crops in farming communities, an insurance crop in producing regions of the country.

However, lack of sufficient information on seed yield and related trait correlation and path coefficient analysis of cowpea in Ethiopia. Therefore, the objectives of present study were to determine the nature and extent of phenotypic and genotypic correlations among 18 quantitative traits of 324 cowpea landraces and to identify the most important traits for indirect selection in future cowpea breeding programs.

2. Materials and Methods

2.1. Descriptions of the Study Area

The field experiment was conducted from July to November 2016 at Melkassa Agricultural Research Center (MARC) and Miesso during the main cropping season. MARC is located at 39°12'N and 8°24'E and 1550 meters above sea level (masl) and received five months mean rainfall of 140.96 mm (total 704.8 mm). The minimum and maximum temperatures were 14.35°C and 28.22°C, respectively. The soil texture of the field site was Andosoil with the pH 7.6. The second testing site (Miesso) is located at 9°14'N (Latitude) and 40°45'E (Longitude) and 1470 meters above sea level (masl) received five months mean rainfall of 84 mm (total 420 mm). The minimum and maximum temperatures were 15.2°C and 31.1°C, respectively. The soil texture of the field site was Vertisols.

2.2. Experimental Materials

A total of 324 cowpea landraces collected from different agro ecological regions of Ethiopia. 72, 55, 52, 50, 14, and 68 landraces were collected from Oromia, Amhara, Gambella, SNNP, Tigray regions, and Unknown (the landraces had no passport data), respectively. Of these, 311 landraces were obtained from Melkassa Agricultural Research Center (MARC), Ethiopia. Five landraces of Ethiopian

origin were obtained from International Institute of Tropical Agriculture (IITA), while the rest eight are improved (released) varieties.

2.3. Experimental Design and Procedures

The experiments were laid out using 18×18 simple lattice design. The plot size was 2 m long, 0.75 m between rows and 0.2 m between plants. It consists two rows accommodating 10 plants per row. The distance between plots, intra blocks and replications was 1 m, 1.5 m and 2 m, respectively. The data were collected from the two rows.

2.4. Data Collection

The quantitative data were collected according to the descriptor of cowpea (*Vigna unguiculata*) developed by the International Board for Plant Genetic Resources [17]. The data were collected from the plot basis are; days to flowering (days), days to maturity (days), grain filling period (days), seed length (mm), seed thickness (mm), seed width (mm), hundred seed weight (g), seed yield per plot (g), biomass (g) and harvest index (%). The data were collected from on the plant basis are; plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, pod clearance (cm), pod length (cm), pod width (mm), peduncle length (cm), number of pods per peduncle, terminal leaflet length (cm), terminal leaflet width (cm) and number of racemes per plant. Digital Vernier caliper [18] used for pod width, seed length, seed thickness and seed width data measurements.

2.5. Data Analyses

The data were subjected to analysis of variance to check the presence of variation among the genotypes for the tested traits and then based on the ANOVA result; all highly significant traits were promoted for correlation and path coefficient analyses. Phenotypic and genotypic correlations between yield and yield related traits were estimated using the method described by [19] as:

The phenotypic correlation coefficient $\left(rp_{xy} \right) = \dfrac{Cov_{pxy}}{\sqrt{\left(\sigma^2 px \right)\left(\sigma^2 py \right)}}$

The genotypic correlation coefficient $\left(rg_{xy} \right) = \dfrac{Cov_{gxy}}{\sqrt{\left(\sigma^2 gx \right)\left(\sigma^2 gy \right)}}$

where, r_{pxy} is phenotypic correlation coefficient and Genotypic correlation coefficient (rg_{xy}) between character x and y; Cov_{pxy} and Cov_{gxy} are phenotypic covariance and genotypic covariance between character *x* and *y*; σ^2_{gx} and σ^2_{gy} are genotypic variances traits *x* and y; σ^2_{px} and σ^2_{py} are phenotypic variances of traits *x* and *y*, respectively. The coefficient of correlation was tested using tabulated value at $n - 2$ degree of freedom, at 5% and 1% probability level, where n is the number of treatments (landraces) as described by [20]. META-R Version 6.01 [21] was employed for phenotypic and genotypic correlation coefficient analysis.

Microsoft Excel computer program was employed for phenotypic and genotypic path coefficient analysis as well as estimation of residual effect. Path coefficient analysis was conducted as suggested by [22] using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effects of yield and other traits based on the following relationship.

$$R_{ij} = P_i j + \sum r_{ik} P_k$$

where, r_{ij} is mutual association between the independent character (i) and dependent traits (i) as measured by correlation coefficients, p_{ij} is components of direct effects of the independent traits (i) on the dependent traits (j), $\sum r_{ik} P_k$ = summation of components of indirect effect of a given independent character (i) on the dependent traits (j) via all other independent traits (k).

The residual effect (R) was estimated using the formula shown below [22].

$R = \sqrt{1 - R^2}$ Where, $R^2 = \sum r_{ij} p_{ij}$.

3. Results and Discussion

3.1. Genotypic and Phenotypic Correlations Coefficient Analysis

Estimates of phenotypic and genotypic correlation coefficients between each pair of traits are presented in Table 1 and Table 2. In the present investigation, the analysis of correlation in each location showed that the magnitudes of genotypic correlation coefficients (r_g) were higher than the phenotypic correlation coefficients (r_{ph}) except in few cases, indicating the presence of strong inherent association among these traits due to genetic factors and the preponderance of genetic variance in expression of traits in line with this, [23] in cowpea, [24] in barley, [25] in wheat and [26] in chickpea. In this study, at both locations, almost all other traits showed that significantly positive correlation with seed yield at genotypic level. This positive genetic correlation between seed yield and other desirable traits makes selection easy for improving both the traits simultaneously. A similar finding was reported by [27]. In general, these genetic relationships of traits may result from pleiotropic effects of a gene, linkage of two genes, linkage disequilibrium, and epistatic effects of different genes or due to the environmental influences [28] [29].

3.1.1. Correlations of Seed Yield with Other Traits

Seed yield is a complex trait and that is set by the interactive effects of several yield associated traits that area unit successively influenced by their genetic structures and also the environmental factors. Thus, the direct measurement and improvement of seed yield itself are also may be ambiguous due to the influence of the environmental factors and the nature of genetic makeup of the yield trait. Therefore, it is essential to investigate information the relative contribution of various components to yield performance. The simple genotypic and phenotypic correlation is a vital tool for this goal because the understanding of correlation is key one choice is to be created on many traits at a time through some contemporary selections of cowpea. In this study, the results of seed yield showed

Table 1. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among 20 traits studied at Miesso.

Traits	DF	GFP	DM	PH	PdL	NRPP	NPPPd	TLW	PL	PdW	nsPP	SL	SW	ST	HSW	Yld	BM	HI
DF		−0.31**	0.87**	0.20**	0.01 ns	−0.04 ns	−0.05 ns	0.12*	0.30**	0.38**	0.37**	0.24**	0.20**	0.16**	0.20**	−0.17**	0.02 ns	−0.34**
GFP	−0.37**		0.18**	0.14*	0.07 ns	−0.09 ns	−0.14*	0.25**	−0.31**	−0.48**	−0.33**	−0.14*	−0.16**	−0.15*	−0.27**	−0.47**	−0.46**	−0.34**
DM	0.65**	0.46**		0.26**	0.02 ns	−0.11*	−0.11 ns	0.21**	0.14*	0.13*	0.19**	0.17**	0.13**	0.09 ns	0.06 ns	−0.41**	−0.23**	−0.54**
PH	0.15*	0.00 ns	0.14 ns		−0.14**	0.06*	0.08 ns	0.17**	0.14*	0.13**	0.24**	0.09**	0.05*	0.08 ns	0.04 ns	0.00**	0.22**	−0.22**
NPPP	−0.14*	−0.04 ns	−0.17**	−0.18**		0.60**	0.55**	−0.20**	0.09 ns	−0.04 ns	0.03 ns	0.03 ns	0.02 ns	0.05 ns	0.00 ns	0.25**	0.14*	0.31**
PdL	−0.01 ns	−0.07 ns	−0.08 ns	0.06 ns	0.56**		0.40**	0.18**	0.21**	0.18**	0.12**	0.17**	0.16**	0.16**	0.14**	0.31**	0.51**	0.20**
NPPPd	−0.04 ns	−0.02 ns	−0.05 ns	0.00 ns	0.18**	0.11*		−0.12*	0.23**	0.31**	0.18 ns	0.11**	0.21*	0.26**	0.18 ns	0.29**	0.37**	−0.05**
TLW	−0.02 ns	0.05 ns	0.02 ns	0.00 ns	−0.02 ns	0.02 ns	0.00 ns		0.15*	0.15*	−0.22**	0.52**	0.25**	0.27**	0.36**	0.22**	0.16**	0.48**
PL	0.22**	−0.08 ns	0.13 ns	0.09 ns	0.12 ns	0.11 ns	0.11 ns	0.08 ns		0.83**	0.80**	0.72**	0.83**	0.82**	0.74**	0.23**	0.36**	0.09*
PdW	0.26**	−0.14**	0.13 ns	0.06 ns	0.09 ns	0.04 ns	0.09 ns	0.04 ns	0.72**		0.75*	0.73**	0.85**	0.81**	0.83**	0.28**	0.38**	0.16**
nsPP	0.27**	−0.12**	0.16**	0.15**	0.03 ns	0.06 ns	0.10 ns	−0.07 ns	0.75**	0.61 ns		0.37**	0.54**	0.54*	0.42 ns	0.14**	0.31**	−0.02**
SL	0.17**	−0.08	0.10 ns	0.06 ns	0.11 ns	0.08 ns	0.05 ns	0.19**	0.62**	0.60 ns	0.31**		0.89**	0.88**	0.92**	0.34**	0.50**	0.22**
SW	0.18**	−0.08 ns	0.10 ns	0.05 ns	0.09 ns	0.05 ns	0.11 ns	0.11*	0.69**	0.70**	0.43**	0.84**		1.00**	0.89**	0.40**	0.51**	0.26**
ST	0.15*	−0.09 ns	0.07 ns	0.05 ns	0.10 ns	0.06 ns	0.12 ns	0.11*	0.69**	0.66 ns	0.42**	0.84***	0.97**		0.89**	0.40**	0.53**	0.30**
HSW	0.16**	−0.11 ns	0.06 ns	0.04 ns	0.09 ns	0.03 ns	0.09 ns	0.14 ns	0.62**	0.69**	0.35**	0.81**	0.79**	0.77**		0.32**	0.43**	0.25**
Yld	−0.13*	−0.19**	−0.28**	0.02 ns	0.18**	0.16**	0.15*	0.07 ns	0.21**	0.21 ns	0.14**	0.26**	0.32**	0.32**	0.25**		1.00**	0.91**
BM	0.00 ns	−0.21**	−0.16**	0.10 ns	0.19**	0.12*	0.15*	0.05 ns	0.23**	0.23 ns	0.18**	0.28**	0.35**	0.35**	0.26**	0.76**		0.84**
HI	−0.18	−0.08 ns	−0.24**	−0.09 ns	0.13*	0.13*	0.05*	0.09 ns	0.10**	0.12*	0.00 ns	0.15*	0.19**	0.21**	0.16**	0.72**	0.26**	

DM = days to flowering, DM days to maturity, GFP = grain filling period, PH = plant height, NPBPP = number of primary branches per plant, NPPP = number of pods per plant, NSPP = number of seeds per pod, PC = pod clearance, PL = pod length, PdW = pod width, PdL = peduncle length, NPPPd = number of pods per peduncle, TLL = terminal leaflet length, TLW = terminal leaflet width and NRPP = number of racemes per plant, HSW = hundred seed weight, SL = seed length, ST = seed length, SW = seed width, Yld = seed yield per plot, BM = biomass and HI = harvest index.

significant and positive genotypic and phenotypic correlations with biomass and harvest index at both environments (Table 1 and Table 2). This indicated that the traits are significantly important for improvement of cowpea yield through direct selection. The present findings were in accordance with the findings of [30] [31] in cowpea landraces.

On the other hand, seed yield showed negative and highly significant genotypic and phenotypic correlation with days to flowering, days to maturity and grain filling period at Miesso (Table 1). The traits like seed length, seed thickness, seed width, hundred seed weight, number of pods per plant, number of seeds per pod, pod length, peduncle length, number of pods per peduncle and number of racemes per plant had highly significant and positive correlation with seed yield at genotypic and phenotypic levels. These results put forward that easy simultaneous improvement in any of these traits will lead to increase through direct selection for seed yield of cowpea. These genotypic and phenotypic correlations indicate that the extent to which the corresponding traits are under the control of the same set of genes having a physiological basis for their expression. In the present result in line with [26] [31] [32] [33], who reported positive and

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Table 2. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among 18 traits studied at Melkassa.

Traits	DF	GFP	DM	PH	PdL	NRPP	NPPPd	TLW	PL	PdW	NSPP	SL	SW	ST	HSW	Yld	BM	HI
DF		0.20**	0.96**	0.45**	0.09 ns	0.12*	−0.67**	0.19**	0.73**	0.57**	0.34**	0.54**	0.58**	0.53**	0.86**	0.30**	0.35**	0.20**
GFP	−0.02 ns		0.46**	0.09 ns	0.48**	−1.00**	0.24**	0.47**	−0.19**	−0.71**	−0.28**	−0.14*	−0.43**	−0.35	0.28**	−0.06 ns	0.10 ns	−0.21**
DM	0.80**	0.58 ns		0.47**	0.20**	−0.15*	−0.59**	0.29**	0.61**	0.38**	0.24**	0.47**	0.43**	0.41**	0.83**	0.26**	0.38**	0.13*
PH	0.18**	0.06 ns	0.19**		0.14*	−0.13*	−0.71**	0.09 ns	0.04 ns	0.18**	0.20**	0.17**	0.05*	0.06**	0.35**	0.13*	0.12**	0.19**
PdL	0.06 ns	0.09 ns	0.11 ns	0.15**		0.25**	0.27**	−0.43**	−0.10 ns	0.28**	0.25**	0.24**	0.18***	0.11*	−0.26**	0.14*	0.24**	0.11 ns
NRPP	0.00 ns	−0.11 ns	−0.07 ns	0.06 ns	0.08 ns		−0.11**	−0.25**	0.33**	0.58	0.34**	0.29**	0.33**	0.49**	0.25**	0.17**	0.16**	0.11**
NPPPd	−0.25**	0.07 ns	−0.16**	−0.06 ns	0.11 ns	0.06 ns		−1.00**	−1.00**	−0.86**	−1.00**	−0.51**	−0.64**	−0.51**	−1.00**	−0.25**	−0.25**	−0.29**
TLW	0.04 ns	0.05 ns	0.07 ns	0.18**	0.02 ns	0.13**	−0.10 ns		0.05 ns	0.62**	−0.02 ns	0.41**	0.38**	0.45**	1.00**	0.38**	0.49**	0.30**
PL	0.38**	−0.04 ns	0.28**	0.06 ns	0.11 ns	0.16**	−0.18	0.12*		0.85**	0.65**	0.94**	0.99**	1.00**	0.50**	0.47**	0.56**	0.31**
PdW	0.31**	−0.02 ns	0.23**	0.05 ns	0.10 ns	0.16**	−0.19	0.17**	0.46**		0.52**	0.74**	0.83**	0.81**	0.74**	0.62**	0.60**	0.68**
NSPP	0.18**	−0.03 ns	0.13*	0.02 ns	0.09 ns	0.07 ns	−0.16**	−0.10 ns	0.29**	0.27**		0.22**	0.32**	0.21**	0.04 ns	0.30**	0.26**	0.39**
SL	0.36**	−0.002 ns	0.29**	0.07 ns	0.11*	0.14*	−0.17**	0.20**	0.53**	0.45**	0.11 ns		0.83**	0.86**	1.00**	0.48**	0.47**	0.45**
SW	0.40**	−0.04 ns	0.30**	0.01 ns	0.09 ns	0.21**	−0.19**	0.17**	0.55**	0.47**	0.19	0.77**		0.99**	1.00**	0.50**	0.44**	0.50**
ST	0.37**	−0.02 ns	0.29**	0.00 ns	0.05 ns	0.22**	−0.16**	0.17**	0.54**	0.45**	0.13*	0.78**	0.91**		1.00**	0.48**	0.47**	0.44**
HSW	0.19**	0.03 ns	0.17**	0.07 ns	0.01 ns	0.04 ns	−0.11*	0.13*	0.20**	0.19**	0.03 ns	0.37**	0.40**	0.40**		0.29**	0.10**	0.38**
Yld	0.17**	−0.01 ns	0.13*	0.07 ns	0.15*	0.16**	−0.02 ns	0.14*	0.35**	0.31**	0.19**	0.39**	0.41**	0.38**	0.07**		0.95**	0.99**
BM	0.21**	−0.01 ns	0.16**	0.02 ns	0.09 ns	0.11**	−0.04 ns	0.09 ns	0.29**	0.24**	0.14*	0.32**	0.33**	0.33**	0.03**	0.78**		0.89**
HI	0.09 ns	−0.01 ns	0.06 ns	0.10 ns	0.16**	0.14*	−0.02 ns	0.13*	0.26**	0.28**	0.18**	0.32**	0.35**	0.30**	0.08**	0.82**	0.31**	

DM = days to flowering, DM days to maturity, GFP = grain filling period, PH = plant height, NPBPP = number of primary branches per plant, NPPP = number of pods per plant, NSPP = number of seeds per pod, PC = pod clearance, PL = pod length, PdW = pod width, PdL = peduncle length, NPPPd = number of pods per peduncle, TLL = terminal leaflet length, TLW = terminal leaflet width and NRPP = number of racemes per plant , HSW = hundred seed weight, SL = seed length, ST = seed length, SW = seed width, Yld = seed yield per plot, BM = biomass and HI = harvest index.

highly significant genotypic association between seed yield with hundred seed weight, seed per pod, pod length and number of pod per plant. [34] had also reported positive and highly significant genotypic and phenotypic correlation between seed yield with a number of pods per plant and hundred seed weight. [35] reported significant positive correlation of grain yield with number of pod per plant. At Melkassa, days to maturity, grain filling period and number of pods per peduncle had a weak negative correlation with seed yield at the phenotypic level (Table 2). However, the rest traits showed significant and positive correlation with seed yield per plot at the phenotypic level. This result indicates the inherent association between the studied traits with seed yield and the presence of greater opportunities for genetic improvement of cowpea yield through direct phenotypic selection. This result partly in line with [26] who found a positive correlation between grain yield and number of peduncles per plant, number of pod per plant and hundred seed weight in cowpea. Similarly, [36] reported positive correlation of seed yield with number of pods per plant.

Seed yield per plot showed intermediate positive and highly significant corre-

lation with seed length, seed length, seed width, number of seeds per pod and number of pods per plant at genotypic and phenotypic levels (Table 2). Traits like pod clearance, peduncle length, terminal leaflet length and terminal leaflet width showed positive and highly significant correlation with seed yield per plot at genotypic and phenotypic levels. Over all, the present study suggested the presence of strong inherent association among the studied traits and due to this phenotypic selection may be rewarding for the improvements of cowpea. These results were in harmony with the findings of [30] [31] [35] [36] [37] [38].

Generally, at both locations, almost all traits found to have highly significant and positive correlation with seed yield per plot at genotypic and phenotypic levels. It implies that there is an enormous chance of exploiting the potential of these traits for effective selection in cowpea improvement programme.

3.1.2. Correlation among Yield Related Traits

At Miesso, days to maturity was significantly and positively correlated with days to flowering, grain filling period at genotypic and phenotypic levels. This result in agreement with [39] who reported days to flowering, plant height and number seed per pod were positive genotypic and phenotypic correlated with days to maturity. Similarly, [27] reported days to maturity had positive genotypic and phenotypic correlation with days to flowering, plant height, pod length, number of seed per pod and hundred seed weight. However, days to maturity was negatively correlated with number of pod per peduncle, number of pod per plant, number of racemes per plant and harvest index. The present result in line with [27] also reported that number of pod per plant negatively correlated with days to maturity. Significantly high and positive correlations were observed between pod length with days to flowering, pod width, number of seeds per pod seed, seed thickness, seed length, seed width and hundred seed weight. The findings are in close harmony with the result of [27] who reported days to flowering, days to maturity, plant height, number of seed per pod and hundred seed weight were positively correlated with pod length at genotypic and phenotypic level. [39] also reported positive phenotypic and genotypic correlation of pod length with days to flowering, plant height, number of seed per pod and number seed per pod. Similarly, harvest index was significantly and positively correlated with the number of racemes per plant, number of pods per plant, peduncle length, pod length, pod width, seed length, seed thickness seed width and hundred seed weight at genotypic and phenotypic levels. Conversely, [30] reported days to maturity, pod length, number of seed per pod and biomass were negatively correlated with harvest index at genotypic level. However, days of flowering, grain filling period and plant height were negatively correlated with harvest index at genotypic and phenotypic levels (Table 1). [39] also reported harvest index was negatively correlated with days to flowering, plant height and biomass at phenotypic level; while days to flowering, plant height, hundred seed weight and biomass had positive genotypic correlation with harvest index. Number of pods per plant was significantly and positively correlated with peduncle length and num-

ber of racemes per plant. This result in line with [38] who reported that number of pods per plant had positive phenotypic and genotypic correlated with plant height, pod length number of seed per pod while number of pods per plant had negative correlation with days to flowering, days to maturity and hundred seed weight at phenotypic and genotypic levels.

In the present study, all the traits, except days to maturity and grain filling period showed positive phenotypic and genotypic correlations with biomass. Some of these had significant positive correlations. It is in harmony with [31] [37] [38] who reported highly significant and positive genotypic and phenotypic correlation of biomass with number of seeds per pod and pod length. In the contrary, number of seeds per pod was significantly and negatively correlated with days to flowering at genotypic and phenotypic levels [37] [38]. These positive and significant correlations showed the presence of inherited genetic associations between biomass and other traits. Therefore, there is a greater chance to develop high yielder cowpea variety through direct selection by using biomass and harvest index and other positively correlated traits with seed yield. The relationship between seed yield per plot and biomass was highly significant and strongly positive correlation at phenotypic and genotypic levels. This implies that selection based on these traits except days to maturity and grain filling period would enhance the genetic potentials of yield increment in cowpea through direct selection.

At Melkassa, all traits, except number of pods per peduncle and peduncle length showed positive and highly significant correlation with days to flowering at genotypic level. The traits like days to maturity, plant height, pod length, peduncle length, number of seeds per pod, seed length, seed thickness, seed width and hundred seed weight were also showed positive and highly significant correlation with days to flowering at the phenotypic level. This result in line with [31] reported days to flowering positively correlated with days to maturity and plant height at genotypic and phenotypic levels. Conversely [11] who reported pod width, pod width length and hundred seed weight were negatively correlated with days to flowering. On the other hand, numbers of seed per plant and biomass showed negatively phenotypic and genotypic correlated with days to flowering. [27] also reported days to maturity, plant height, pod length, number of seed per pod and hundred seed weight were positively correlated with days to flowering at phenotypic and genotypic levels. Positive and highly significant genotypic and phenotypic correlations were recorded between days to maturity and plant height, terminal leaflet width, number of seeds per pod, seed length, seed thickness, seed width, and hundred seed weight. On the contrary, [40] reported days to maturity negatively correlated with plant height, hundred seed weight and biomass at phenotypic and genotypic levels. However, grain filling period negatively correlated with days to maturity at genotypic level.

All traits, except the number of seeds per pod, number of racemes per plant and peduncle length significantly high and positive correlated with the number of pods per peduncle at genotypic and phenotypic levels. Highly significant and

positive correlations were recorded between a number of pods per peduncle and number of seeds per pod, pod width, seed length, seed thickness, seed width, hundred seed weight, biomass and harvest index at genotypic and phenotypic levels. This result in line with, [23] reported number of pods per plant, pod length terminal leaflet length and terminal leaflet width were positive genotypic and phenotypic correlation with number of pods per peduncle. Similarly, positive and highly significant genotypic and phenotypic correlations were recorded between peduncle length and number of seeds per pod, seed length, seed thickness, seed width, hundred seed weight, and biomass and harvest index. [11] reported pod length, pod width and number of seed per pod were positively correlated with number of pods per peduncle at genotypic and phenotypic levels. All the traits, except number of seeds per pod and number of pods per peduncle were showed highly significant and positively phenotypic and genotypic correlations with seed length (Table 2).

Hundred seed weight showed perfect and highly significant correlation with terminal leaflet width ($r_g = 1.00$), number of pods per peduncle ($r_g = -1.00$), seed length ($r_{ph} = 1.00$), seed thickness ($r_{ph} = 1.00$) and seed width ($r_{ph} = 1.00$). In addition, the trait like grain filling period, plant height, peduncle length and number of racemes per plant showed positive and highly significant correlation with hundred seed weight at the phenotypic level (Table 2). Previous studies in cowpea also revealed positive genotypic and phenotypic correlations between hundred seed weight and days to maturity, days to flowering, pod length and biomass [40]. However, on the contrary to the present results, [39] reported negative correlations between hundred seed weight and days to flowering, days to maturity, plant height, number of pods per plant, pod length and number of seeds per pod. In the present study, number of seeds per pod, seed length, seed thickness and seed width showed positive and highly significant phenotypic and genotypic correlation with biomass. Harvest index was positive and highly significant correlations with number of seeds per pod, seed length, seed thickness, seed width, biomass and harvest index at both levels. On the contrary, [40] reported days to maturity, pod length, plant height, number of seeds per plant, hundred seed weight and biomass were positively correlated with harvest index at genotypic and phenotypic levels.

3.2. Path Coefficient Analysis

Path coefficient analysis has been used to evaluate selection criteria in several crops. This technique is useful in determining the direct influence of one variable on another and also separates the correlation coefficient into its components of direct and indirect effects [41]. The genotypic and phenotypic correlation coefficients were further divided into direct and indirect effects using path coefficient analysis which involves partitioning of the correlation coefficients into direct and indirect effects through alternate traits or pathways. Such analysis leads to the identification of important component traits useful in indirect selection of complex traits like yield and other complex traits. In this study, seed yield

per plot was considered as a complex dependable trait (resultant) while the rest of the variables that were positively correlated with grain yield were used as causal (independent) traits of the 18 traits on seed yield (Tables 3-6).

3.2.1. Genotypic Path Coefficient Analysis of Seed Yield with Other Traits

The results of genotypic path coefficient analysis of seed yield with other 18 traits Miesso and Melkassa are presented in Table 3 and Table 4. According to [41] who classified path coefficients (0.00 - 0.09) negligible, (0.10 - 0.19) low, (0.20 - 0.29) moderate, and (0.30 - 0.99) high and more than 1.00 is very high. The present investigation, seed thickness followed by days to maturity and plant height had exerted high and positive direct effect on seed yield at Miesso (Table 3), indicating that direct selection for these three traits in order to improve seed yield of cowpea. Likewise, [7] [10] [11] [42] reported that plant height exhibited positive direct effect on seed yield in cowpea. However, seed width, grain filling period and hundred seed weight had exerted negative direct effect on seed yield.

Table 3. Genotypic path coefficient analysis for direct (bold diagonal) and indirect effect (off diagonal) 19 traits at Miesso.

Traits	DF	GFP	DM	PH	PC	NPPP	PdL	NRPP	NPPPd	TLW	PL	PdW	NSPP	SL	SW	ST	100S	BM	HI
DF	**−0.635**	0.198	−0.552	−0.127	−0.188	0.119	−0.006	0.027	0.031	−0.077	−0.193	−0.240	−0.237	−0.151	−0.125	−0.101	−0.127	−0.013	0.218
GFP	0.198	**−0.813**	−0.147	−0.116	0.071	0.024	−0.057	0.071	0.112	−0.206	0.252	0.391	0.270	0.117	0.131	0.122	0.216	0.374	0.273
DM	−0.706	−0.147	**0.499**	0.015	−0.013	0.003	0.000	0.002	0.004	0.016	−0.049	−0.094	−0.064	−0.018	−0.016	−0.012	−0.028	−0.005	0.059
PH	0.100	0.071	0.128	**0.565**	0.412	−0.195	−0.078	0.035	0.043	0.094	0.082	0.071	0.134	0.051	0.027	0.043	0.020	0.124	−0.125
PC	0.168	−0.049	0.132	0.412	**−0.451**	0.001	−0.152	−0.088	−0.089	0.024	−0.081	−0.041	−0.070	−0.072	−0.044	−0.057	−0.045	−0.111	−0.048
NPPP	0.085	0.013	0.098	0.156	0.001	**0.360**	0.121	0.070	0.071	−0.019	0.065	0.032	0.056	0.058	0.035	0.045	0.036	0.088	0.038
PdL	0.003	0.025	0.008	−0.050	0.121	0.202	**0.373**	0.197	0.150	0.067	0.077	0.066	0.043	0.062	0.058	0.059	0.053	0.188	0.075
NRPP	−0.016	−0.033	−0.042	0.023	0.073	0.224	0.197	**−0.255**	0.024	0.017	0.017	0.008	0.014	0.013	0.010	0.012	0.005	0.019	0.014
NPPPd	0.013	0.035	0.027	−0.019	−0.050	−0.141	−0.103	−0.094	**−0.310**	0.036	−0.073	−0.095	−0.055	−0.034	−0.064	−0.081	−0.057	−0.115	0.016
TLW	−0.037	−0.079	−0.064	−0.051	0.016	0.061	−0.055	−0.081	0.036	**0.039**	0.006	0.006	−0.009	0.021	0.010	0.011	0.014	0.006	0.019
PL	0.012	−0.012	0.005	0.006	0.007	0.004	0.008	0.010	0.009	0.006	**−0.167**	−0.138	−0.133	−0.120	−0.138	−0.137	−0.123	−0.060	−0.015
PdW	−0.063	0.080	−0.022	−0.021	−0.015	0.006	−0.029	−0.020	−0.051	−0.024	−0.138	**0.286**	0.215	0.210	0.245	0.231	0.236	0.110	0.047
NSPP	0.107	−0.095	0.054	0.068	0.045	0.009	0.033	0.062	0.051	−0.063	0.229	0.215	**−0.309**	−0.114	−0.168	−0.166	−0.131	−0.094	0.007
SL	−0.073	0.044	−0.051	−0.028	−0.049	−0.009	−0.051	−0.060	−0.034	−0.162	−0.222	−0.226	−0.114	**0.152**	0.135	0.134	0.140	0.076	0.033
SW	0.030	−0.025	0.020	0.007	0.015	0.003	0.024	0.023	0.031	0.038	0.126	0.130	0.083	0.135	**−1.550**	−1.544	−1.384	−0.793	−0.400
ST	−0.246	0.233	−0.140	−0.117	−0.195	−0.084	−0.247	−0.281	−0.408	−0.426	−1.274	−1.250	−0.832	−1.366	−1.544	**2.240**	1.993	1.180	0.669
HSW	0.449	−0.596	0.134	0.079	0.222	−0.010	0.317	0.174	0.413	0.815	1.650	1.849	0.951	2.069	2.000	1.993	**−0.730**	−0.317	−0.185
BM	−0.015	0.335	0.166	−0.161	−0.179	−0.106	−0.369	−0.212	−0.270	−0.120	−0.262	−0.280	−0.223	−0.365	−0.374	−0.385	−0.317	**0.446**	0.375
HI	−0.153	−0.150	−0.242	−0.099	0.047	0.139	0.090	0.094	−0.024	0.213	0.040	0.073	−0.010	0.098	0.115	0.133	0.113	0.375	**0.158**
Rg	0.30**	−0.06 ns	0.26**	0.13*															

Residual = 0.147. DM = days to flowering, DM days to maturity, GFP = grain filling period, PH = plant height, NPBPP = number of primary branches per plant, NPPP = number of pods per plant, NSPP = number of seeds per pod, PC = pod clearance, PL = pod length, PdW = pod width, PdL = peduncle length, NPPPd = number of pods per peduncle, TLL = terminal leaflet length, TLW = terminal leaflet width and NRPP = number of racemes per plant, HSW = hundred seed weight, SL = seed length, ST = seed length, SW = seed width, Yld = seed yield per plot, BM = biomass and HI = harvest index.

Table 4. Genotypic path coefficient analysis for direct (bold diagonal) and indirect effect (off diagonal) 17 traits at Melkassa.

Traits	DF	GFP	DM	PH	PdL	NRPP	NPPPd	TLW	PL	PdW	NSPP	SL	SW	ST	HSW	BM	HI	r_g
DF	**1.852**	0.379	1.770	0.839	0.161	0.214	−1.234	0.356	1.354	1.053	0.636	1.007	1.079	0.977	1.588	0.649	0.377	−0.17**
GFP	0.092	**0.450**	0.208	0.041	0.215	−0.450	0.106	0.212	−0.085	−0.317	−0.124	−0.063	−0.194	−0.159	0.126	0.044	−0.095	−0.47**
DM	−1.947	−0.940	**−2.037**	−0.951	−0.411	0.313	1.196	−0.600	−1.251	−0.774	−0.496	−0.964	−0.868	−0.828	−1.683	−0.782	−0.270	−0.41**
PH	0.037	0.007	0.038	**0.081**	−0.290	0.272	1.454	−0.176	−0.078	−0.359	−0.406	−0.344	−0.094	−0.123	−0.705	−0.235	−0.391	0.00**
PdL	0.000	0.002	0.001	0.001	**0.005**	0.001	0.001	−0.002	0.000	0.001	0.001	0.001	0.001	0.001	−0.001	0.001	0.000	0.25**
NRPP	−0.004	0.035	0.005	0.005	−0.009	**−0.035**	0.004	0.008	−0.011	−0.020	−0.012	−0.010	−0.012	−0.017	−0.009	−0.006	−0.004	0.31**
NPPPd	−0.029	0.010	−0.026	−0.031	0.012	−0.005	**0.044**	−0.044	−0.044	−0.038	−0.044	−0.022	−0.028	−0.022	−0.044	−0.011	−0.013	0.29**
TLW	0.011	0.028	0.017	0.005	−0.025	−0.015	−0.059	**0.059**	0.003	0.037	−0.001	0.024	0.022	0.027	0.059	0.029	0.018	0.22**
PL	0.047	−0.012	0.039	0.002	−0.007	0.021	−0.064	0.003	**0.064**	0.054	0.041	0.060	0.064	0.064	0.032	0.036	0.020	0.23**
PdW	−0.024	0.030	−0.016	−0.008	−0.012	−0.025	0.037	−0.027	−0.036	**−0.043**	−0.022	−0.032	−0.036	−0.035	−0.031	−0.026	−0.029	0.28**
NSPP	−0.007	0.006	−0.005	−0.004	−0.005	−0.007	0.020	0.000	−0.013	−0.011	**−0.001**	−0.002	−0.002	−0.002	−0.001	−0.001	−0.001	0.14**
SL	0.009	−0.002	0.008	0.003	0.004	0.005	−0.008	0.007	0.016	0.012	0.004	**0.017**	0.014	0.014	0.017	0.008	0.007	0.34**
SW	−0.047	0.035	−0.035	−0.004	−0.015	−0.027	0.052	−0.031	−0.081	−0.068	−0.026	−0.07	**−0.082**	−0.080	−0.082	−0.036	−0.040	0.40**
ST	0.055	−0.037	0.043	0.006	0.012	0.051	−0.053	0.047	0.105	0.085	0.023	0.090	0.1034	**0.105**	0.105	0.049	0.046	0.40**
HSW	−0.041	−0.013	−0.039	−0.016	0.012	−0.012	0.047	−0.047	−0.024	−0.035	−0.002	−0.05	−0.047	−0.047	**−0.047**	−0.005	−0.018	0.32**
BM	0.206	0.058	0.226	0.068	0.144	0.096	−0.145	0.291	0.331	0.354	0.150	0.274	0.261	0.274	0.058	**0.588**	0.523	0.43**
HI	0.094	−0.097	0.061	0.088	0.050	0.049	−0.132	0.138	0.145	0.313	0.181	0.207	0.228	0.202	0.177	0.408	**0.459**	0.25**

Residual = 0.212. DM = days to flowering, DM days to maturity, GFP = grain filling period, PH = plant height, NPBPP = number of primary branches per plant, NPPP = number of pods per plant, NSPP = number of seeds per pod, PL = pod length, PdW = pod width, PdL = peduncle length, NPPPd = number of pods per peduncle, TLL = terminal leaflet length, TLW = terminal leaflet width and NRPP = number of racemes per plant, HSW = hundred seed weight, SL = seed length, ST = seed length, SW = seed width, Yld = seed yield per plot, BM = biomass and HI = harvest index.

On the contrary, [7] [10] [27] [43] reported that hundred seed weight had high direct positive effect on seed yield per plant at genotypic levels. With respect to indirect effect, hundred seed weight and biomass positive and highest contribution to seed yield per plot via seed length and seed thickness, respectively. The residual effect (0.147) indicates that traits which are included in the genotypic path coefficient analysis explained by 85.3% of the total variation in seed yield. Similar reports were reported by [10] [11].

At Melkassa, the residual effect (0.212) indicated that traits which are included in the genotypic path analysis explained 78.8% of the total variation on seed yield. Days to flowering followed by biomass and harvest index exerted a positive direct effect on seed yield. [43] [44] reported that days to flowering had high positive direct effects on seed yield in cowpea. On the other hand, days to maturity, seed width and hundred seed weight had showed the negative direct effect on seed yield (Table 4). The traits days to maturity, pod length, peduncle length, seed length and hundred seed weight were exhibited high and positive indirect effect via days to flowering on seed yield. Similarly, [11] reported that pod length exerted high positive indirect effect on seed yield. However, number of pods per peduncle exerted a negatively indirect effect through days to flowering (−1.233)

Table 5. Phenotypic path coefficient analysis for direct (bold diagonal) and indirect effect (off diagonal) 19 traits at Miesso.

Traits	DF	GFP	DM	PH	PC	NPPP	PdL	NRPP	NPPpd	TLW	PL	PdW	NSPP	SL	SW	ST	HSW	BM	HI
DF	**−0.027**	0.010	−0.018	−0.004	−0.004	0.004	0.000	0.003	0.001	0.001	−0.006	−0.007	−0.007	−0.005	−0.005	−0.004	−0.004	0.000	0.005
GFP	0.006	**−0.017**	−0.008	0.000	0.001	0.001	0.001	0.000	0.000	−0.001	0.001	0.002	0.002	0.001	0.001	0.002	0.002	0.003	0.001
DM	−0.019	−0.014	**−0.030**	−0.004	−0.003	0.005	0.002	0.003	0.001	−0.001	−0.004	−0.004	−0.005	−0.003	−0.003	−0.002	−0.002	0.005	0.007
PH	0.007	0.000	0.007	**0.045**	0.033	−0.008	0.003	0.002	0.000	0.000	0.004	0.003	0.007	0.003	0.002	0.002	0.002	0.004	−0.004
PC	−0.006	0.002	−0.004	−0.028	**−0.039**	−0.005	−0.010	−0.006	−0.003	0.000	−0.005	−0.002	−0.004	−0.003	−0.003	−0.003	−0.002	−0.006	−0.002
NPPP	−0.003	−0.001	−0.004	−0.004	0.003	**0.024**	0.011	0.014	0.005	−0.001	0.001	0.000	0.000	0.000	0.000	0.000	−0.001	0.001	0.005
PdL	0.000	0.002	0.002	−0.001	−0.006	−0.011	**−0.024**	−0.011	−0.004	0.001	−0.003	−0.002	−0.001	−0.003	−0.002	−0.002	−0.002	−0.004	−0.003
NRPP	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NPPpd	−0.001	−0.001	−0.002	0.000	0.003	0.007	0.006	0.004	**0.037**	0.000	0.004	0.003	0.004	0.002	0.004	0.004	0.003	0.005	0.002
TLW	0.000	−0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**−0.012**	−0.001	0.000	0.001	−0.002	−0.001	−0.001	−0.002	−0.001	−0.001
PL	0.004	−0.001	0.002	0.001	0.002	0.001	0.002	0.002	0.002	0.001	**0.017**	0.012	0.013	0.011	0.012	0.012	0.011	0.004	0.002
PdW	−0.002	0.001	−0.001	−0.001	−0.001	0.000	−0.001	0.000	−0.001	0.000	−0.006	**−0.009**	−0.005	−0.005	−0.006	−0.006	−0.006	−0.002	−0.001
NSPP	0.011	−0.005	0.007	0.006	0.005	0.000	0.001	0.003	0.004	−0.003	0.031	0.025	**0.041**	0.013	0.018	0.017	0.014	0.007	0.000
SL	0.010	−0.005	0.006	0.004	0.005	0.000	0.006	0.005	0.003	0.011	0.037	0.036	0.019	**0.060**	0.051	0.050	0.049	0.017	0.009
SW	0.020	−0.010	0.011	0.005	0.008	−0.001	0.010	0.005	0.012	0.013	0.078	0.079	0.048	0.096	**0.113**	0.109	0.089	0.039	0.022
ST	−0.027	0.017	−0.012	−0.010	−0.012	−0.001	−0.019	−0.011	−0.023	−0.020	−0.126	−0.122	−0.077	−0.154	−0.178	**−0.184**	−0.142	−0.064	−0.038
HSW	−0.001	0.001	0.000	0.000	0.000	0.000	−0.001	0.000	−0.001	−0.001	−0.004	−0.005	−0.002	−0.006	−0.006	−0.005	**−0.007**	−0.002	−0.001
BM	0.002	−0.126	−0.100	0.059	0.090	0.038	0.116	0.073	0.089	0.033	0.140	0.139	0.110	0.174	0.212	0.211	0.157	**0.611**	0.159
HI	−0.101	−0.047	−0.133	−0.050	0.31	0.113	0.073	0.073	0.027	0.052	0.054	0.66	−0.001	0.082	0.109	0.116	0.090	0.259	**0.561**

Residual = 0.337. DM = days to flowering, DM days to maturity, GFP = grain filling period, PH = plant height, NPBPP = number of primary branches per plant, NPPP = number of pods per plant, NSPP = number of seeds per pod, PC = pod clearance, PL = pod length, PdW = pod width, PdL = peduncle length, NPPPd = number of pods per peduncle, TLL = terminal leaflet length, TLW = terminal leaflet width and NRPP = number of racemes per plant, HSW = hundred seed weight, SL = seed length, ST = seed length, SW = seed width, Yld = seed yield per plot, BM = biomass and HI = harvest index.

and its association with seed yield (r_g = −0.25**). In contrast, [26] found that number of pod per peduncle exerted high direct effect of seed yield at genotypic level. Biomass exerted the second highest positive direct effect (0.588) on seed yield. Peduncle length (0.331), pod width (0.354) and harvest index (0.523) had also exhibited highly positive indirect effect via biomass on seed yield. Though biomass exhibited negatively indirect effect through days to maturity (−0.782) and its association with seed yield remained positive and highly significant (r_g = 0.38**). Harvest index had highly favorable direct effect (0.459) and high favorable indirect effect via days to biomass (0.523), flowering (0.377) and pod width (0.313) and contributed to its strong positive significant association with grain yield (r_g = 0.99**). However, it exerted the highest indirect effect (−0.391) through plant height and day to maturity (−0.270). These results in harmony with the findings of [30] [45] who reported that biomass and harvest index exhibited the highest positive direct effect on seed yield, whereas days to maturity contributed negative direct effect on seed yield.

Table 6. Phenotypic path coefficient analysis for direct (bold diagonal) and indirect effect (off diagonal) 17 traits at Melkassa.

Traits	DF	GFP	DM	PH	PdL	NRPP	NPPpd	TLW	PL	PdW	NSPP	SL	SW	ST	HSW	BM	HI
DF	**−0.051**	0.001	−0.041	−0.009	−0.003	0.000	0.013	−0.002	−0.019	−0.016	−0.009	−0.019	−0.020	−0.019	−0.010	−0.011	−0.004
GFP	0.001	**−0.036**	−0.021	−0.002	−0.003	0.004	−0.002	−0.002	0.001	0.001	0.001	0.000	0.001	0.001	−0.001	0.000	0.000
DM	0.049	0.035	**0.061**	0.012	0.006	−0.004	−0.010	0.004	0.017	0.014	0.008	0.018	0.018	0.018	0.011	0.010	0.004
PH	0.000	0.000	0.000	**−0.002**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PdL	−0.001	−0.001	−0.002	−0.002	**−0.016**	−0.001	−0.002	0.000	−0.002	−0.002	−0.001	−0.002	−0.001	−0.001	0.000	−0.001	−0.003
NRPP	0.000	0.000	0.000	0.000	0.000	**−0.001**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NPPpd	−0.004	0.001	−0.003	−0.001	0.002	0.001	**0.016**	−0.002	−0.003	−0.003	−0.003	−0.003	−0.003	−0.003	−0.002	−0.001	0.000
TLW	0.000	0.000	0.000	0.001	0.000	0.001	−0.001	**0.005**	0.001	0.001	−0.001	0.001	0.001	0.001	0.001	0.001	0.001
PL	0.008	−0.001	0.006	0.001	0.002	0.003	−0.004	0.003	**0.021**	0.010	0.006	0.011	0.012	0.012	0.004	0.006	0.006
PdW	−0.002	0.000	−0.001	0.000	−0.001	−0.001	0.001	−0.001	−0.003	**−0.006**	−0.002	−0.003	−0.003	−0.003	−0.001	−0.001	−0.002
NSPP	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**−0.001**	0.000	0.000	0.000	0.000	0.000	0.000
SL	−0.004	0.000	−0.003	−0.001	−0.001	−0.001	0.002	−0.002	−0.006	−0.005	−0.001	**0.000**	0.000	0.000	0.000	0.000	0.000
SW	0.001	0.000	0.001	0.000	0.000	0.001	−0.001	0.000	0.001	0.001	0.000	0.002	**0.003**	0.002	0.001	0.001	0.001
ST	−0.002	0.000	−0.001	0.000	0.000	−−0.001	0.001	−0.001	−0.003	−0.002	−0.001	−0.004	−0.005	**−0.005**	−0.002	−0.002	−0.002
HSW	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**	0.000	0.000
BM	0.122	−0.006	0.094	0.012	0.054	0.064	−0.021	0.054	0.170	0.139	0.079	0.187	0.193	0.193	0.018	**0.583**	0.179
HI	0.057	−0.005	0.042	0.062	0.105	0.093	−0.011	0.082	0.169	0.181	0.115	0.208	0.226	0.191	0.055	0.199	**0.647**

Residual = 0.122. DM = days to flowering, DM days to maturity, GFP = grain filling period, PH = plant height, NPBPP = number of primary branches per plant, NPPP = number of pods per plant, NSPP = number of seeds per pod, PC = pod clearance, PL = pod length, PdW = pod width, PdL = peduncle length, NPPPd = number of pods per peduncle, TLL = terminal leaflet length, TLW = terminal leaflet width and NRPP = number of racemes per plant, HSW = hundred seed weight, SL = seed length, ST = seed length, SW = seed width, Yld = seed yield per plot, BM = biomass and HI = harvest index.

Generally, the residual effects were low (0.147, 0.212) these indicated that traits which were included in the genotypic path analysis explained 85.3% and 78.8% of the total variation on seed yield at Miesso and Melkassa, respectively, indicating that the independent traits were explained the dependent trait (seed yield) more than two third (2/3); therefore, the genotypic path coefficient analysis based selection for cowpea improvement is very appropriate. [46] reported that the residual value is small (for instance, nearly zero) the dependent trait considered (seed yield) is fully explained by the other independent traits. The estimation of direct and indirect effects was more pronounced in the genotypic path than the phenotypic path. This analysis confirmed that day to flowering, days to maturity, plant height seed thickness, biomass and harvest index produced high positive direct effect on seed yield, appeared to be the prominent traits when selecting for seed yield in cowpea landraces. Therefore, the present study put forward that days to flowering, days to maturity, plant height seed thickness, biomass and harvest index exerted highest direct effect on seed yield and it should be given maximum consideration for total yield improvement as the appropriate selection indices. The selection procedure should be formulated so that the advance in one component is not risked by the deterioration effect of the other. Therefore, the results of the path coefficient analysis indicated that seed width, hundred seed weight, biomass and harvest index were the main determinants of seed yield.

3.2.2. Phenotypic Path Coefficient Analysis of Seed Yield with Other Traits

The results of phenotypic path coefficient analysis of seed yield with other 18 traits at Miesso and Melkassa are presented in **Table 5** and **Table 6**. Biomass (0.611) followed by harvest index (0.561) and seed width (0.113) had exerted high positive direct effect on seed yield. Similar to the present findings, [30] [45] reported that the highest positive direct effect on seed yield per plant was exhibited by biomass and harvest index. Biomass had high favorable direct effect and high favorable indirect effect via harvest index, seed width and seed width and contributed to its strong positive association with seed yield (r_{ph} = 0.76) at Miesso. Biomass (0.259) had exhibited considerable positive indirect effect on seed yield via harvest index [27] [47] [48]. However, seed thickness (−0.184) had negative indirect effect on seed yield via biomass, but positive and significant phenotypic correlation with seed yield (r_{ph} = 0.32). This result indicated that phenotypic path coefficient analysis explained by 66.3% of the total variation in seed yield.

Similarly, at Melkassa, harvest index (0.647) followed by biomass (0.583) and days to maturity (0.061) had exerted positive and favorable direct effect on seed yield. [30] [47] observed that the biomass and harvest index had the highest direct effect on seed yield in cowpea. Association of biomass with grain yield was significantly positive. Harvest index can be considered of the important yield component exerted the second highest positive direct effect (0.583) on seed yield. It had also exhibited very high positive indirect effect via seed length (0.208), seed width (0.226) and biomass (0.199). In addition to the direct and indirect effect of harvest index had also strong and highly significant correlation with seed yield (r_{ph} = 0.82). These results are in accordance with the findings of [30] [33] [45] [47] reported biomass (0.199) had considerable positive indirect effect on seed yield. The residual effect (0.122) indicates that traits which are included in the phenotypic path coefficient analysis explained by 87.8% of the total variation in seed yield.

Generally, the present investigation suggests that days to maturity, biomass, harvest index, and seed width should be given as the most reliable selection indices for effective improvement in cowpea as the appropriate selection indices. The selection procedure should be formulated so that to proceed in one component is not exposed by the deterioration effect of the other. Therefore, Path analysis indicated that days to maturity, biomass, harvest index and seed width were the main determinants of seed yield. Thus, these traits should be given more emphasis during selection for yield improvement in cowpea.

4. Conclusions

The present study revealed that the magnitude of the genotypic correlations was higher than the phenotypic correlations in most traits. Traits depict the existence of strong inherent association among traits due to the genetic control. In addition to these, the present study showed the masking effects of the environmental

factors were too little. In this study, the results of seed yield showed significant and positive genotypic and phenotypic correlations with length, seed thickness, seed width, hundred seed weight, biomass and harvest index at both locations. This indicated that the traits were significantly important for direct selection. Hence, improving one or more traits could result in high seed yield in cowpea. On the other hand, days to flowering, grain filling period and days to maturity were negative phenotypic and genotypic correlation with seed yield at Miesso. However, days to flowering and days to maturity had positive phenotypic and genotypic correlation with seed yield at Melkassa.

Genotypic path coefficient analysis revealed that days to flowering, biomass and harvest index had relatively high positive direct effect on seed yield at Miesso, and seed thickness, plant height, days to maturity and biomass at Melkassa had relatively high positive direct effect on seed yield. However, seed width and hundred seed weight had exerted negative direct effect on seed yield at each location. At phenotypic path coefficient analysis showed that biomass and harvest index had exerted high positive direct effect on seed yield at both locations. In general, this study clearly stated background information on correlation and path coefficient analysis of seed yield with other yield related traits. Therefore, the present results consider as benchmark information for future high take molecular based analysis and genome wide association study for identifying important traits for cowpea seed yield improvement.

Acknowledgements

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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