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Correlation and Path Coefficient Analysis among Seed Yield Traits of Mung Bean (*Vigna radiata* L.) Accessions in Ethiopia

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Authors' contributions

This work was carried out in collaboration among the three authors. In addition all the authors read and approved the final manuscript.

Research Article

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ABSTRACT

Aims: This study was conducted to evaluate the association of different yield related traits to seed yield of mungbean

Place and Duration of Study: The study was conducted at the Haramaya University Rare research site and Hirna Research site during the 2012 cropping season.

Methodology: Randomized Complete Block Design with three replications was used for both locations. Each genotype was planted on a 1.2 X 2m plot consisting of four rows, which accommodates ten plants per row and thus 40 plants per plot.

Results: The result showed that seed yield per plot was significantly associated with harvest index, seed yield per plant and biomass at both locations. However, at Hirna, number of secondary branches and number of pods per plant were also significantly associated with seed yield per plot. Path analysis indicated that harvest index and biomass were the main determinants of yield per plot at both Hirna and Rare. Analysis over locations also supported that harvest index and biomass are the main determinant of yield per plot.

Conclusion: The present investigation indicated that a large scope of simultaneous improvement in seed yield through selection could be achieved using the traits identified as predictors of yield in mungbean.

Keywords: *Correlation; direct effect; indirect effect; mung bean; path coefficient.*

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1. INTRODUCTION

Mungbean (*Vigna radiata* L.) is a warm season annual herb that belongs to the family fabaceae and is botanically recognized as *Vigna radiata* L. Wilczek [1,2]. It is one of the leading pulse crops in India and an important food legume of many tropical and sub-tropical parts of the world. It is grown mostly in rotation with cereals. It has the diploid chromosome number $2n = 22$ [3].

The short duration it needs to grow as well as its wide adaptability together with the easier way of its digestibility when it is compared to black gram, makes mung bean cultivation to spread all over the world [4]. It has the potential to make up the gap of protein shortage since its seeds are rich in protein and amino acids, thus serve as a valuable protein source for human consumption. The world annual production area of mung bean is about 5.5 million ha [5], with a rate increase of 2.5% per annum [6].

Generally mungbean is mostly grown under dry land farming systems where erratic rains often expose the crop to moisture stress [7]. July-August is the main growing season and harvesting is done in October. Mungbean is basically grown as a mixed-, inter-, and relay crop [8, 9].

Mungbean is an excellent source of protein (27%), and its essential amino acid composition (9.59 mg/100 g) compares favorably with that of soybean and kidney bean [10,11]. Mungbean occupies an important position due to its high seed protein content and ability to restore the soil fertility through symbiotic nitrogen fixation [12].

Mungbean cultivation is gaining popularity day by day among the farmers and Ethiopia's mung bean export has grown slightly to 1363 tons in 2002 from 822 tons in 2001 [13]. Though its production in Ethiopia is very negligible when it is compared to other pulse crops, small holder farmers in drier marginal environments in Ethiopia grow mung bean and it has been an important grain legume for resource poor farmers in these areas. It is important to develop a high yielder variety so that the farmers will be able to get maximum product and stable yield in their environments.

Seed yield in mung bean is a complex character like other crops, and is determined by various components and influenced by many other important yield contributing characters controlled by polygenes and also environmental factors [14]. Selection is an integral part of a breeding program by which genotypes with high productivity in a given environment could be developed. However, selection for high yield is made difficult because of its complex nature. Therefore, only little progress could be made over a long span of time through direct selection for yield. Indirect selection through yield components has been proved more effective [15]. This selection criterion takes into account the information on interrelationship among agronomic characters, their relationship with grain yield as well as their direct influence on grain yield. Nevertheless, selection for yield *via* highly correlated characters becomes easy if the contribution of different characters to yield is quantified using path coefficient analysis [16].

Generally, Knowledge of the extent and pattern of variability, particularly of genetic variability present in a population of a given crop is absolutely essential for further improvement of the crop. Similarly, information on the extent and nature of interrelationship among characters help in formulating efficient scheme of multiple trait selection. In Ethiopia, there is no

information on these aspects of mungbean. Therefore, there is a need to generate information on interrelationships of yield and yield related traits among mungbean genotypes. Having this in mind this study was carried out to study associations among yield and yield related traits in mung bean.

2. MATERIALS AND METHODS

2.1 The Experimental Site

The field experiment was carried out at two sites, Haramaya University Rare research site and Hirna research site, Ethiopia during the main rainy season from July to September 2012. The Haramaya University Rare research site is found at an altitude of 1950m with latitude of 9.0°N and longitude of 42.0°E. The place has a mean maximum and minimum temperature of 28.5°C and 12.6°C respectively and has an average annual rainfall of about 790 mm [17]. The soil is characterized as a fluvisol and slightly basic with pH of 7.75 [18]. Whereas the Hirna research site is situated at a latitude of 9°13'N and longitude of 41°6'E has an altitude of 1870 meters above sea level [19]. The soil of this research site is vertisol with a pH value of 6.75. It receives mean annual rainfall of 990-1100 mm and has mean annual temperature of 24°C.

2.2 Experimental Materials

For this study thirteen mungbean (*Vigna radiata*.L) accessions were used. The accessions were MB6148-05-12, MONG WHOLE, BLACK BEAN, ASHA, MH-85-11, MBBR-1, MB6173B-33, SHOWA ROBIT, MH-97-6, EGYPT, GOFA LOCAL, KENYA and NV26. These accessions were obtained from Melkassa Agricultural Research Center (MARC).

2.3 Experimental Design and Procedures

Randomized Complete Block Design (RCBD) with three replications was used for both locations. Each genotype was planted on a 1.2 X 2m plot consisting of four rows, which accommodates ten plants per row and thus 40 plants per plot. A distance of 1m was maintained between the plots and row to row spacing was 40cm. Plant to plant spacing was twenty centimeter. The weeding activities were carried out after two to three weeks from sowing and no fertilizer was applied.

2.4 Data Collection

According to [20], the pre and post harvesting observations were recorded as the means from five randomly selected plants from each genotype in each replication for all characters studied except days to flowering and days to maturity, which were determined on plot basis.

1. **Days to flowering:** number of days from planting to a stage where 50% of the plants in a plot produced flower.
2. **Days to maturity:** the number of days from planting to a stage when 90% of the plants in a plot produced matured pods.
3. **100 Seed weight:** the average weight in grams of 100 randomly taken seeds from each plot.

4. **Biomass yield per plant:** the weight in grams recorded by weighing the total above ground biomass harvested from each experimental plot at the time of harvest.
5. **Harvest Index:** average seed yield is divided by the average biological yield.

$$\text{Harvest Index (HI)} = \frac{\text{Seed yield (g)}}{\text{Biomass yield (g)}}$$

6. **Seed yield (kg/ha):** seed yield of the plants from each plot was determined and converted to kg/ha.
7. **Number of seeds per pod:** the mean number of seeds per pod obtained from each plant at harvest.
8. **Plant height:** the height in centimeters from the ground level to the tip of the plant at maturity recorded as the averages of the sample plants from each plot.
9. **Number of secondary branches per plant:** number of secondary branches on each plant.
10. **Number of primary branches per plant:** number of primary branches on each plant.
11. **Number of pods per plant:** the mean number of pods obtained from each plant at harvest after maturity.
12. **Number of seeds per plant:** the mean number of seeds per plant obtained from each plant at harvest.
13. **pod length:** each pod length of the plant sample was measured and averaged for the number of the sample.

2.5. Data Analysis

2.5.1. Estimation of phenotypic and genotypic correlations

Phenotypic and genotypic correlations between yield and yield related traits were estimated using the method described by [21].

$$r_{pxy} = \frac{COV_{pxy}}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$

Where: r_{pxy} = phenotypic correlation coefficient between character x and y

COV_{pxy} = phenotypic covariance between character x and y

σ^2_{px} = phenotypic variance for character x

σ^2_{py} = phenotypic variance for character y

$$r_{gxy} = \frac{COV_{gxy}}{\sqrt{\sigma^2_{gx} \cdot \sigma^2_{gy}}}$$

Where; r_{gxy} = genotypic correlation coefficient between character x and y

COV_{gxy} = genotypic covariance between character x and y

σ^2_{gx} = genotypic variance for character x

σ^2_{gy} = genotypic variance for character y

The coefficient of correlations was tested using tabulated r-value at g-2 degrees of freedom, where 'g' is number of genotypes at 5% level of significance.

2.5.2 Path coefficient analysis

Path coefficient analysis was worked out using the method suggested by [16] using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effect of yield related traits (yield components) on seed yield and oil contents of the seed based on the following relationship:

$$r_{ij} = p_{ij} + \sum r_{ik}p_{kj}$$

Where: r_{ij} = mutual association between the independent character (i) and dependent character viz. seed yield (j) as measured by the correlation coefficient. p_{ij} = component of direct effects of independent character (i) and dependent character (j) as measured by the path coefficient and $\sum r_{ik}p_{kj}$ = Summation of components of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent character (k).

The contribution of the remaining unknown factors (effect) was measured as the residual effect (R_E) which is calculated as:

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

The magnitude of R_E indicates that how best the causal factors accounts for the variability of the dependent factor [22]. That is if the value of R_E is small (for instance near zero) the considered dependant character (for example seed yield) is fully explained by the variability of the considered independent character, where as the higher R_E value indicates effects some other factors which have not been considered, but need to be included in the model to account fully for the variation in the dependent character. Four different types of yields as seed yield per plot, seed yield per plant, fatty oil content and essential oil content were used as dependent characters separately for path coefficient analysis and the remaining characters were used as independent variables as required.

3. RESULTS AND DISCUSSION

3.1 Correlation Studies

The possibility of high yield through yield attributes as primary interest in crop improvement requires understanding the amount and the magnitude of correlations among various yield traits. Estimates of correlation coefficient at phenotypic and genotypic level for individual locations are given in Table 1 and 2.

Table 1. Estimates of Correlation coefficients at phenotypic (above diagonal) and Genotypic (below diagonal) levels of 13 characters in mung bean germplasm accessions at Hirna

Variable	NPB	NSB	PH	PPP	SPP	BMYP	SPPD	DF	DM	HSW	HI	PL	YLD
NPB		0.930**	0.842**	0.475*	0.511*	0.545*	0.546*	0.441*	0.650**	0.142	0.350*	0.236	0.527*
NSB	0.977**		0.795**	0.570*	0.573*	0.603**	0.530*	0.325*	0.592**	0.265	0.481*	0.290	0.618**
PH	0.886**	0.857*		0.364*	0.462*	0.588*	0.626**	0.201	0.448*	0.225	0.346*	0.335*	0.544*
PPP	0.515	0.621*	0.376		0.891**	0.612**	0.326	0.140	0.291	0.353*	0.457*	0.234	0.652**
SPP	0.556*	0.656*	0.493*	0.904**		0.722**	0.647**	-0.056	0.130	0.322*	0.521*	0.516*	0.747**
BMYP	0.690*	0.754*	0.680*	0.710*	0.879**		0.608**	0.010	0.181	0.336	0.446*	0.458*	0.814**
SPPD	0.564*	0.582*	0.695	0.351	0.676*	0.848*		-0.257	-0.074	0.183	0.429*	0.671**	0.604**
DF	0.476	0.380	0.231	0.152	-0.082	-0.007	-0.304		0.835**	-0.233	-0.018	-0.536*	-0.027
DM	0.673*	0.623*	0.455	0.308	0.137	0.208	-0.083	0.859		-0.139	0.132	-0.365*	0.199
HSW	0.202	0.293	0.241	0.441	0.430	0.425	0.275	-0.256	-0.148		0.210	0.138	0.295
HI	0.561*	0.631*	0.436	0.634*	0.749*	0.726*	0.566*	-0.025	0.164	0.148		0.523*	0.819**
PL	0.265	0.302	0.329	0.235	0.563*	0.538*	0.783	-0.560*	-0.400	0.136	0.632*		0.584
YLD	0.699*	0.771*	0.628*	0.758*	0.912**	0.921**	0.772*	-0.040	0.229	0.329	0.908**	0.658*	

Where, NPB=Number of primary branches, NSB=Number of secondary branches, PH=plant height, PPP=Pod per plant, SPP=Seed per pod, BMYP=Biomass yield, SPPD= Seed per pod, DF=Days to flowering, DM=Days to maturity, HSW= 100 seed weight, HI= Harvest index, PL= Pod length, YLD (kg/ha) = yield in (kg/ha), *and **at 5% and 1% probability level respectively

Table 2. Estimates of Correlation coefficients at phenotypic (above diagonal) and Genotypic (below diagonal) levels of 13 characters in mungbean germplasm Accessions at Rare

Variable	NPB	NSB	PH	PPP	SPP	BMYP	SPPD	DF	DM	HSW	HI	PL	YLD
NPB		0.445*	0.517*	0.425*	0.392*	0.151	0.256	0.131	0.273	0.128	0.244	0.079	0.156
NSB	0.648*		0.635**	0.216	0.211	0.237	0.475*	0.17	0.499*	0.142	0.496*	0.239	0.379*
PH	0.713*	0.799*		0.598**	0.477*	0.432*	0.433*	-0.049	0.242	0.367*	0.546*	0.291	0.517*
PPP	0.615*	0.334	0.712*		0.880**	0.655**	0.241	0.102	0.077	0.209	0.379*	0.214	0.518*
SPP	0.504	0.280	0.618*	0.914**		0.656**	0.405*	-0.2529	-0.073	0.203	0.419*	0.412*	0.567*
BMYP	0.331	0.229	0.607*	0.772*	0.781*		0.192	0.425*	-0.168	0.419*	0.245	0.393	0.708**
SPPD	0.301	0.567*	0.438	0.201	0.381	0.229		-0.379*	0.023	0.256	0.411*	0.648**	0.388*
DF	0.147	0.218	-0.049	-0.189	-0.358	-0.489	-0.423		-0.763**	-0.526*	-0.181	-0.670**	-0.409*
DM	0.396	0.563*	0.323	0.100	-0.086	-0.207	0.003	0.811*		-0.326*	0.123	-0.475*	-0.145
HSW	0.115	0.216	0.406	0.274	0.311	0.541*	0.295	-0.609*	-0.334		0.244	0.534*	0.359*
HI	0.504	0.567*	0.608*	0.509*	0.567*	0.252	0.562*	-0.199	0.149	0.268		0.459*	0.743**
PL	0.189	0.272	0.331	0.161	0.429	0.379	0.712*	-0.717*	-0.494	0.599*	0.533*		0.617**
YLD	0.499	0.478	0.679*	0.710*	0.830*	0.738*	0.609*	-0.519*	-0.161	0.465	0.793*	0.716*	

Where, NPB=Number of primary branches, NSB=Number of secondary branches, PH=plant height, PPP=Pod per plant, SPP=Seed per pod, BMYP=Biomass yield, SPPD= Seed per pod, DF=Days to flowering, DM=Days to maturity, HSW= 100 seed weight, HI= Harvest index, PL= Pod length, YLD (kg/ha) = yield in (kg/ha), *and **at 5% and 1% probability level respectively

3.1.1 Correlation coefficients of seed yield per plot with other traits at Hirna and Rare

At Hirna (Table 1), seed yield per ha showed positive and highly significant association with seeds per plant ($r=0.912^{**}$), biomass yield per plant ($r=0.921^{**}$) and harvest index ($r=0.908^{**}$) at a genotypic level. High significance of seeds per plant, biomass yield per plant and harvest index shows that any improvement of these traits may result in an increment of seed yield. Similar results were reported by [23] where positive and significant association of seed yield with most of the traits in mung bean was observed. [24] also reported positive correlation of seed yield with seeds per plant, seeds per pod and harvest index. Though non-significant, the association of days to maturity and 100 seed weight with seed yield per plot was positive. This indicates these characters could be useful for improvement of yield through selection.

Seed yield per plot also showed negative and non-significant association with days to flowering. The trend was same for the associations of seed yield per plot with other traits through the values of phenotypic correlation coefficients which were lower than corresponding genotypic correlation.

At Rare, the other location (Table 2), seed yield per plot showed positive and highly significant association with pod length ($r=0.617^{**}$), harvest index ($r=0.743^{**}$) and biomass yield ($r=0.708^{**}$) at phenotypic level. The other traits showed positive and significant association, however their significance level was not as higher as it was observed at Hirna. This difference may be due to the environmental influence. The correlation coefficients of these traits and other traits like plant height ($r=0.679^*$), pods per plant ($r=0.710^*$), seeds per plant ($r=0.830^*$) and seeds per pod ($r=0.609^*$) with seed yield per plot at genotypic level were also high. This result was supported by [25,26,27,28] who reported positive correlation of pods per plant, seeds per plant, 100 seed weight and seeds per pod with seed yield. At both genotypic and phenotypic level days to flowering and days to maturity had negative association with seed yield. This result was in line with a report by [29] who found negative genotypic and phenotypic correlation of days to flowering and days to maturity with seed yield at three locations. This may be related to the fact that when days to maturity increases, the phenology of the crop enters into the dry spell, which in turn leads to loss in yield.

In all locations genotypic correlation was greater in magnitude than the corresponding phenotypic correlation. Generally, positive and significant association of pairs of characters at both phenotypic and genotypic level justified the possibility of correlated response to select while the negative correlations prohibit the simultaneous improvement of those traits.

In a combined analysis of the two locations (Table 3), a genotypic correlation coefficient of seed yield was highly significant and positive with seeds per plant ($r=0.920^{**}$), biomass yield ($r=0.920^{**}$) and harvest index ($r=0.923^{***}$). The partitioning of these correlations showed that seeds per plant, biomass yield and harvest index exhibited high direct effects on seed yield. Therefore, beside selection for yield *per se* which are practicing in breeding program of most crops, this study showed that selection for yield in mungbean may be done through these characters. This result is in agreement with [24] who reported positive correlation of seed yield with seeds per plant, seeds per pod and harvest index. Whereas at the phenotypic level, secondary branches ($r=0.654^{**}$), plant height ($r=0.702^{**}$), pods per plant ($r=0.702^{**}$), seeds per plant ($r=0.752^{**}$), biomass yield ($r=0.818^{**}$), seeds per pod ($r=0.542^{**}$), pod length ($r=0.592^{**}$) and harvest index ($r=0.839^{**}$) were highly significant and positively correlated with seed yield while primary branches per plants ($r=0.352^*$) and 100 seed weight ($r=0.263^*$) were positive and significant. Therefore, any improvement of these characters would result a

substantial increment on seed yield. Similar findings were reported previously by [26,27,28]. From the results of correlation coefficients it can be concluded that indirect selection for any character with a significantly positive association with yield would improve the productivity of mungbean crop.

3.2. Path Analysis

The phenotypic and genotypic correlations were further analyzed by path coefficient analysis, which involves partitioning of the correlation coefficients into direct and indirect effects through alternate characters or pathways. Such analysis leads to identification of important component traits useful in indirect selection complex traits like yield. Since a character like seed yield is dependent on several mutually associated component characters and change in any one of the components is likely to affect the whole network of cause and effect relationship.

3.2.1 Estimates of direct and indirect effects of various characters on seed yield per plot at Hirna

The path analysis revealed that at genotypic level, maximum positive direct effect was exerted on seed yield per plot by number of primary branches, plant height and pods per plant. This indicates that the high yielding mungbean could be obtained by selecting pods per plants, plant height and primary branches. In addition, positive indirect effect through all characters except 100 seed weight and days to flowering was also observed on seed yield per plot. So, direct and indirect selection through these characters should be effective. These findings are in line with the report of [30] who suggested that pods per plant should be given priority in selecting for high yielding varieties in mungbean as it had positive direct and indirect effects on seed yield. In addition, Seeds per plant, harvest index and biomass affected seed yield positively and directly as well as indirectly via all characters except via 100 seed weight which showed a negative effect indicating that part of variability observed in seed yield could be explained by those traits. [31] and [32] also showed that seed yield can be directly and positively influenced by biomass yield in mungbean. Days to flowering and 100 seed weight had negative direct effect on seed yield. The residual (0.0015) indicated that characters which included in genotypic path analysis explained (99.8%) of the total variation in seed yield.

At the phenotypic level the direct and indirect effect as shown on Table 4 revealed that pods per plant, number of primary branches, biomass and plant height had positive direct influence on seed yield and also they had negative indirect effect via number of secondary branches and days to flowering. Biomass yield and harvest index had high direct effect on seed yield with positive significance value indicating that, improvement of these characters will increase seed yield. Similarly [33] and [34], reported that there was a positive direct effect of 100 seed weight, seeds per pod and pods per plant on seed yield in mungbean. However, seed yield was affected negatively directly and indirectly by the number of secondary branches and days to flowering.

Table 3. Estimates of Correlation coefficients at phenotypic (above diagonal) and Genotypic (below diagonal) levels of 13 characters in mungbean germplasm accessions combined for the two locations

Variable	NPB	NSB	PH	PPP	SPP	BMYP	SPPD	DF	DM	HSW	HI	PL	YLD
NPB		0.66**	0.47**	0.444**	0.448**	0.352*	0.397*	0.265*	0.374*	0.164	0.312*	0.168	0.352*
NSB	0.928**		0.71**	0.554**	0.55**	0.581**	0.541**	0.196	0.456*	0.205	0.59*	0.334*	0.654**
PH	0.910**	0.908**		0.617**	0.584**	0.613**	0.494**	-0.044	0.199	0.195	0.603**	0.382*	0.702**
PPP	0.543*	0.601*	0.5917*		0.908**	0.71**	0.361*	-0.008	0.184	0.279*	0.550**	0.306*	0.702**
SPP	0.543*	0.595*	0.605*	0.893**		0.757**	0.573**	-0.160	0.09	0.269*	0.585**	0.506**	0.753**
BMYP	0.629*	0.669*	0.729*	0.814*	0.929**		0.453**	-0.163	0.04	0.319*	0.530**	0.452**	0.818**
SPPD	0.526	0.579*	0.588*	0.329	0.638*	0.712*		-0.320*	0.040	0.233*	0.474**	0.678**	0.542**
DF	0.319	0.347	0.158	-0.029	-0.277	-0.303	-0.356		0.704**	-0.351*	-0.119	-0.593**	-0.181
DM	0.557*	0.572*	0.410	0.162	0.028	0.011	0.017	0.842*		-0.273*	0.151	-0.295*	0.084
HSW	0.222	0.282	0.435	0.423	0.455	0.677*	0.328	-0.441	-0.375		0.218	0.346*	0.263*
HI	0.616*	0.635*	0.587*	0.675*	0.795*	0.753*	0.583*	-0.085	0.171	0.219		0.53**	0.839**
PL	0.249	0.262	0.314	0.155	0.543	0.591*	0.801*	-0.668*	-0.411	0.396	0.578*		0.592**
YLD	0.686*	0.714*	0.704*	0.755*	0.920**	0.920**	0.762*	-0.247	0.089	0.426	0.923**	0.697*	

Where, NPB=Number of primary branches, NSB=Number of secondary branches, PH=plant height, PPP=Pod per plant, SPP=Seed per pod, BMYP=Biomass yield, SPPD= Seed per pod, DF=Days to flowering, DM=Days to maturity, HSW= 100 seed weight, HI= Harvest index, PL= Pod length, YLD (kg/ha) = yield in (kg/ha), *and **at 5% and 1% probability level respectively

3.2.2 Estimates of direct and indirect effects of various characters on seed yield per plot at Rare

At Rare, the path coefficient analysis at genotypic level revealed that biomass had the maximum positive direct effect followed by harvest index. The positive correlation of harvest index and biomass with seed yield was also highly significant. The positive direct effect of biomass on seed yield is in accordance with the previous report by [35]. Characters like primary and secondary branches affected seed yield positively both directly and indirectly via all characters except days to maturity and 100 seed weight. This shows that increasing number of branches directly and indirectly increases seed yield. [36] also reported that primary branches per plant, number of secondary branches and seeds per pod have a direct effect on seed yield of mungbean. Days to maturity had negative direct and indirect effect on seed yield through all characters except via seeds per pod, biomass yield, 100 seed weight and pod length while 100 seed weight showed a negative effect via days to flowering and days to maturity indirectly. The residual effect of 0.000009 suggested that about 99.9% of variation in seed yield per plot was accounted for by the characters included in the present study.

At the phenotypic level, as it is shown on Table 5, direct and indirect path analysis revealed that biomass and harvest index had high positive direct effect on seed yield as well as they had significant and positive correlation with seed yield. The present finding was in agreement with the report of [37] who reported positive direct effect of biological yield and harvest index on seed yield. In addition, plant height, seeds per pod, pod length, pods per plant and seeds per plant had positive direct effect on seed yield. Number of secondary branches, days to maturity and 100 seed weight had negative direct effect on seed yield. However, negative direct effect of 100 seed weight and days to maturity on seed yield is counter balanced by positive indirect effect. This indicated that this trait is not directly associated with yield. Basically selection directly through this character resulting in poor seed yield, so indirect causal factors must be considered especially for the traits contributing positively.

In a combined analysis of the two locations, path analysis showed at the phenotypic level, harvest index and biomass yield had high positive direct effect on seed yield as well as their correlation was significant and positive with seed yield ($r=0.839^{**}$ and $r=0.818^{**}$ respectively) (Table 6). Pods per plant, biomass yield, harvest index, plant height and seeds per plant had positive effect on seed yield both directly and indirectly but they had negative effect on seed yield only via days to 100 seed weight and number of primary branches. The positive direct and indirect effect of these characters indicates that they are main contributors to yield. This finding is in accordance with the report of [32,37,38]. The residual effect (0.261) indicating appropriateness of characters chosen was 73.9% of the total variation in seed yield. Hence biomass yield, harvest index and pods per plant are the most important yield contributing components as they recorded high direct and indirect effects towards seed yield in mungbean. Number of primary branches, days to maturity and 100 seed weight had negative direct effect on seed yield but their indirect effect were positive through days to flowering and days to maturity for 100 seed weight and via all traits except harvest index for days to maturity. It can be concluded that characters with positive effects should be significantly considered in selection criteria for yield improvement in mungbean breeding programs.

Table 4. Estimates of direct (bold-diagonal values) and indirect effects (off-diagonal values) at phenotypic levels of 12 traits on seed yield per plot in mungbean at Hirna

Variable	NPB	NSB	PH	PPP	SPP	BMYP	SPPD	DF	DM	HSW	HI	PL	rp
NPB	0.203	-0.279	0.021	0.109	0.080	0.278	0.034	-0.082	0.154	0.0001	0.190	0.019	0.527*
NSB	0.189	-0.301	0.19	0.131	0.089	0.308	0.022	-0.061	0.141	0.0003	0.261	0.051	0.618**
PH	0.171	-0.239	0.024	0.084	0.072	0.300	0.040	-0.037	0.106	0.0003	0.187	0.027	0.544*
PPP	0.096	-0.172	0.009	0.232	0.139	0.312	0.020	-0.026	0.069	0.0004	0.248	0.019	0.652**
SPP	0.104	-0.173	0.012	0.206	0.157	0.368	0.041	0.010	0.030	0.0004	0.282	0.042	0.747**
BMYP	0.111	-0.182	0.015	0.142	0.113	0.512	0.038	-0.003	0.043	0.0004	0.242	0.083	0.814**
SPPD	0.111	-0.159	0.016	0.076	0.102	0.311	0.064	0.048	-0.018	0.0002	0.232	0.055	0.604**
DF	0.089	-0.098	0.005	0.033	-0.009	0.005	-0.016	-0.189	0.198	-0.0003	-0.009	-0.044	-0.027
DM	0.132	-0.178	0.012	0.067	0.020	0.093	-0.005	-0.158	0.238	-0.0002	0.072	-0.302	0.199
HSW	0.029	-0.080	0.006	0.082	0.051	0.172	0.012	0.044	-0.033	0.0001	0.114	0.011	0.295
HI	0.071	-0.145	0.009	0.106	0.082	0.228	0.027	0.003	0.032	0.000	0.543	0.043	0.819**
PL	0.048	-0.087	0.009	0.054	0.081	0.235	0.043	0.101	-0.087	0.000	0.2844	0.083	0.584

Where: NPB= Number of primary branches, NSB= Number of secondary branches, PH= Plant height, PPP= Pod per plant, SPP= Seed per plant, BMYP= Biomass yield, SPPD= Seed per pod, DF=Days to flowering, DM= Days to maturity, HSW= 100 Seed weight, HI= Harvest index, PL= Pod length. *, ** indicated the significance of phenotypic correlation coefficient at 5% and 1% probability level respectively Residual=0.239

Table 5. Estimates of direct (bold-diagonal values) and indirect effects (off-diagonal values) at phenotypic levels of 12 traits on seed yield per plot in mungbean at Rare

Variable	NPB	NSB	PH	PPP	SPP	BMYP	SPPD	DF	DM	HSW	HI	PL	rp
NPB	0.020	-0.057	0.011	0.003	0.099	0.114	0.025	0.034	-0.054	-0.017	0.164	0.018	0.156
NSB	0.009	-0.129	0.013	0.001	0.053	0.179	0.046	0.044	-0.098	-0.019	0.033	0.054	0.379*
PH	0.010	-0.082	0.021	0.004	0.121	0.327	0.043	-0.013	-0.047	-0.050	0.367	0.066	0.517*
PPP	0.008	-0.028	0.012	0.006	0.223	0.495	0.024	-0.026	-0.015	-0.028	0.255	0.048	0.518*
SPP	0.008	-0.027	0.010	0.005	0.254	0.496	0.040	-0.065	0.014	-0.028	0.282	0.093	0.567*
BMYP	0.003	-0.030	0.009	0.004	0.166	0.757	0.019	-0.109	0.033	-0.057	0.165	0.098	0.708**
SPPD	0.005	-0.061	0.009	0.002	0.103	0.145	0.099	-0.098	0.005	-0.035	0.276	0.147	0.388*
DF	0.003	-0.022	-0.001	-0.001	-0.064	-0.322	-0.037	0.257	-0.150	0.071	-0.130	-0.150	-0.409*
DM	0.005	-0.064	0.005	0.001	-0.019	-0.127	-0.002	0.196	-0.196	0.044	0.083	-0.110	-0.145
HSW	0.003	-0.018	0.007	0.001	0.051	0.317	0.025	-0.135	0.064	-0.136	0.164	0.121	0.359*
HI	0.005	-0.064	0.011	0.002	0.106	0.186	0.040	-0.046	-0.024	-0.033	0.673	0.104	0.743**
PL	0.002	-0.031	0.006	0.001	0.105	0.298	0.064	-0.172	0.093	-0.073	0.309	0.227	0.617**

Where: NPB=Number of primary branches, NSB=Number of secondary branches, PH= Pant height, PPP= Pod per plant, SPP= Seed per plant, BMY= Biomass yield, SPPD= Seed per pod, DF= Days to flowering, DM= Days to maturity, HSW=100 Seed weight, HI=harvest index, PL=Pod length. *, ** indicated the significance of phenotypic correlation coefficient at 5% and 1% probability level respectively Residual=0.305

Table 6. Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level of 12 traits on seed yield per plot in mungbean accessions combined for the two locations

	NPB	NSB	PH	PPP	SPP	BMYP	SPPD	DF	DM	HSW	HI	PL	rp
NPB	-0.043	0.047	0.005	0.025	0.014	0.160	0.003	0.017	0.006	-0.007	0.169	0.019	0.352*
NSB	-0.028	0.072	0.007	0.031	0.018	0.277	0.004	0.011	0.026	-0.008	0.317	0.038	0.654**
PH	-0.021	0.052	0.009	0.034	0.019	0.303	0.004	0.004	0.010	-0.009	0.355	0.046	0.702**
PPP	-0.019	0.040	0.006	0.055	0.029	0.345	0.003	0.002	0.010	-0.012	0.310	0.036	0.702**
SPP	-0.019	0.039	0.006	0.049	0.032	0.364	0.005	0.013	0.003	-0.011	0.331	0.059	0.753**
BMYP	-0.015	0.041	0.006	0.039	0.024	0.485	0.004	0.012	0.002	-0.012	0.277	0.049	0.818**
SPPD	-0.017	0.039	0.005	0.021	0.019	0.219	0.008	0.024	0.000	-0.010	0.275	0.078	0.542**
DF	-0.011	0.012	-0.001	-0.002	-0.006	-0.087	-0.003	0.068	0.044	0.015	-0.096	-0.070	-0.181
DM	-0.015	0.031	0.002	0.009	0.002	0.016	-0.000	0.048	-0.061	0.012	0.063	-0.037	0.084
HSW	-0.007	0.015	0.002	0.016	0.009	0.149	0.002	-0.026	0.018	-0.040	0.115	0.041	0.263*
HI	-0.014	0.042	0.006	0.031	0.019	0.248	0.004	-0.012	-0.007	-0.009	0.542	0.061	0.839**
PL	-0.007	0.024	0.004	0.017	0.016	0.213	0.006	-0.042	0.020	-0.015	0.296	0.113	0.592**

NPB= Number of primary branches, NSB= Number of secondary branches, PH= Plant height, PPP= Pod per plant, SPP= Seed per plant, BMY= Biomass yield, SPPD= Seed per pod, DF=Days to flowering, DM= Days to maturity, HSW= 100 Seed weight, HI= Harvest index, PL= Pod length, rg= genotypic correlation with seed. *, ** indicated the significance of phenotypic correlation coefficient at 5% and 1% probability level respectively Residual=0.261

4. CONCLUSIONS

Mungbean is an economically important short duration legume crop in Ethiopia. However, there is lack of information on extent of genetic diversity and there is a need to study associations among seed yield and yield related traits to design effective breeding strategies. Keeping this in view the present investigation was undertaken on 13 accessions of mung bean. These accessions were evaluated at the Haramaya University Rare research site and Hirna research site during 2012 cropping season. Data on 13 traits, namely, days to flowering, days to maturity, hundred seed weight, biomass yield per plant, harvest index, seed yield per plot, number of seeds per pod, plant height, number of secondary branches, number of primary branches, number of pods per plant, number of seeds per plant and pod length were recorded at both the locations. Seed yield per plot was found to be significantly associated with seed yield per plant, harvest index and biomass at both locations. However, plant height had highly significant correlation with seed yield per plot at Rare while it was not associated with seed yield per plot at Hirna. In combined analysis over locations, seed yield per plot was positively and significantly associated with biomass and harvest index, whereas it had negative association with days to flowering. Path analysis for yield per plot showed that harvest index, biomass and seed yield per plant were the important determinants of seed yield at Hirna. At Rare also, harvest index and biomass were found to be the important traits determining yield per plot. Analysis over locations further supported the importance of harvest index and biomass as predictor of yield per plot. Generally, there was a significant variation between accessions at both sites and it is useful to determine genetic and environmental influence on the relationship of seed yield and yield related traits. Considering the yield performance at two locations, maximum value of yield in kilogram per hectare was recorded for GOFA LOCAL at Hirna whereas, NV26 at Rare location. For this accessions attention is to be given when improvement of seed yield in mungbean is required. In conclusion, the present investigation indicated that there is a wide range of genetic variability and diversity in mungbean germplasm though the present investigation was conducted on only a part of it. There is large scope of simultaneous improvement in seed yield through selection. However, it would be worthwhile to study more available germplasm over years and locations to identify more diverse accessions as well as to confirm the importance of the traits identified as predictors of yield.

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COMPETING INTERESTS

There are no competing interests in relation to any financial and personal relationships with other people or organizations that in one way or the other which inappropriately influence our work.

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