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Genetic Variability and Association among Seed Yield and Yield Related Traits in Ethiopian Mustard (*Brassica Carinata* A. Braun) At Haramaya University, Raare Site, Eastern Ethiopia

Naol Bayou Shiferaw*

Genetics, Ethiopian Biodiversity Institute, P.O. Box 487 Addis Ababa, Ethiopia

**Corresponding author*

Abstract

Ethiopian mustard (*Brassica Carinata* A. Braun) or gomenzer is an oilseed crop that is well adapted to the highlands of Ethiopia. Cultivation of Ethiopian mustard, as an oilseed, requires genetic improvement which relies on its genetic diversity and interrelationships among traits. The present study had objectives, to assess the extent and pattern of genetic variability in Ethiopian mustard genotypes, to estimate heritability and genetic advance under selection, to estimate the association among seed-yield and yield related traits and partition the genetic correlation coefficients into direct and indirect effects. A total of 25 accessions of Ethiopian mustard originating from diverse agro ecological locations of Ethiopia were used for this study in RCBD. Among the tested genotype there were three released varieties. The genotypes were obtained from Holleta Agricultural Research Centers of Ethiopia. Data were collected on 11 characters. The analysis of variance showed highly significant ($p<0.01$) difference for all characters, indicating the existence of variability and the potential for selection and improvement within characters. High phenotypic coefficient of variation (PCV) was recorded for seed yield per plot, biomass per plot and seed yield per plant. The magnitude of PCV and genotypic coefficient of variation (GCV) were high for seed yield per plot, biomass per plot and secondary branch per plant. High heritability estimate was coupled with high genetic advance as percent of mean for biomass per plot and seed yield per plot. This indicates the effectiveness of selection to improve these two characters. Correlation and path coefficient analysis were used to determine characters associations. Seed yield per plot showed positive and significant associations with biomass per plot, harvest index per plot, plant height, harvest index per plant and seed yield per plant. This indicated that simultaneous improvement of seed yield per plot and these characters is possible. Among the characters considered, day to flowering exhibited negative correlation with seed yield per plot. Correlation and path coefficient analysis of seed yield per plot and seed yield per plant revealed that biomass and harvest index had strong and positive correlations and also exerted favorable direct effects on seed yield at phenotypic and genotypic levels. Selection for biomass and harvest index therefore can be very useful for seed yield improvement. Furthermore, plant height and 1000-seed weight could be useful for indirect selection of seed yield.

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Introduction

Mustard belongs to the family Cruciferae (Brassicaceae) (Williams, 1989). The Brassicaceae family (genus *Brassica)* as a whole is believed to have originated around the Mediterranean, Eastern Afghanistan, the adjoining portion of Pakistan and North-Eastern Africa (Hemigway, 1976). It has about 338 genera and 3709

species (Warwick *et al.,* 2006). About 159 species are included in the genus *Brassica* (Zhou *et al.,* 2006). The genus includes six economically important species namely, *B. rapa, B. oleracea, B. nigra B. juncea, B. napus and B. carinata* (Daweny and Robbelen, 1989).

B. carinata was given this name for the first time by A. Braun in 1841(Daweny and Robbelen, 1989). The species is known to have various scientific synonyms like *Brassica intergrifolia* Var. Carrinata (West) Rupr (1860), *Melanosinapis abyssinica* Hort. ex Regel, *Sinapis abyssinica* A. Braun (1856) (Edwards *et al.,* 2000). Present day evidence suggest that, the amphidiploids *B.carinata* (BBCC n=2x=17) is originated from a natural cross between *B. nigra* (BB n=8) and *B. oleracea* (CC n=9), followed by chromosome doubling, in the highland of Ethiopia and the Mediterranean coast (Mizushina, 1980). It is self-pollinating amphidiploids species (Doweny and Robbelen, 1989). Under open field conditions, an average of 30% out-crossing may result from pollination by wind and/or insects.

Brassica species were considered as species with fixed taxonomic entities and, alien gene transfer among different genomes were thought to be impossible. But attempts by Sinskaia in 1927, proved it wrong (Ahmed *et al.,* 2002). He attempted a cross between *Brassica* species, but successful result was obtained by that of Karpechenko (Ahmed *et al.,* 2002). Karpenchenko successfully synthesized *Raphano brassica*: the first inter-generic fertile hybrid of *Raphanus sativus* and *B. oleracea* in 1928 (Ahmed *et al.,* 2002). In addition, the self-compatibility and out-crossing ability makes the anther derived homozygous lines to be part of the mass and recurrent selection that improves even other *Brassica* species (Ahmed *et al.,* 2002).

Globally, among oilseed crops, Ethiopian mustard ranks 3rd after soybean and oil palm in production of vegetable oils. In the production of oil seed proteins it ranks 5th (Kauser *et al.,* 2006). In Pakistan, *Brassica Carinata* ranks second after cottonseed as source of vegetable oil (Khan *et al.,* 2008). In 2011-2012, rapeseed and Ethiopian mustard were planted over 216.5 thousand hectares which produced about 191.9 thousand tons, with an average yield of 886 kg hec. Out of this, 34% of the total edible oil was produced locally, while the remaining 66% were imported with a cost of 2.611 billion Birr (ESOP, 2011-2012). The cause of the lower edible oil is the non availability of high yielding lines (Nassimi *et al.,* 2006).

Ethiopian mustard is mainly grown in Arsi, Bale, Sidamo, Gonder, Gojam, Wollo, Shoa and Wallega. It is often grown on well-drained and organic matter rich soil close to homesteads. Ethiopian mustard is well adapted to cool, long growing season and high rainfall areas at elevation between 2200 and 2800 meters above sea level. In these areas, the temperature and rainfall range from 12 to 18ºC and 600 to 900 mm, respectively during the growing season (i.e., June to December). It grows well in either a heavy sandy loam or light clay soils with a good drainage system (Nigussie, 2001).

Ethiopian mustard is native to Ethiopian highlands and its cultivation is thought to have been started around 4000 years B.C. It is third in production next to Niger seed (*Guizotia abyssinica*) and Linseed (*Linum ustatisumum*) (Alemayehu and Becker, 2002; Schippers, 2002). *Brassica Carinata* is a conventional African vegetable, previously collected from the wild for human consumption (Schippers, 2002). In the Ethiopian highlands it is cultivated as an oil and leafy vegetable crop (Schippers, 2002). Ethiopian mustard is cultivated as an option to the traditional mustard especially for low rainfall areas of the world. In its area of adoption, it possesses acceptable yield levels as well as resistance to diverse biotic and abiotic stresses. Furthermore, with good drought resistance and low pod-shattering tendency, *B. carinata* could be developed as an oilseed crop in Canada to diversify and stabilize oilseed production (Getinet *et al.,* 1996).

In Ethiopia, cultivation and usage of *B. carinata* is an old practice. The crop is traditionally used for many purposes, such as greasing traditional bread-baking (clay pan), curing diseases and as a source of vegetable relish (Nigussie, 2001). Especially for the small-scale farmers, it is a food security crop, because it is a source of food and income during shortages that mostly occurs at middle of main rainy season. It is the only crop that can be consumed by defoliating its leaves or sold to generate income after a month of sowing. In many parts of the country, boiled and chopped leaves are mixed with butter, and served along with cheese and *'kitifo' (*slightly cooked, heavily chopped, and buttered beef). Bottom stalks remaining after harvesting can be used for fences or firewood. Similarly, the upper-branched parts are often used for making brooms that are used to clean floors.

Ethiopian Mustard oil, which is very often adulterated with oils from Niger seed (*Guizotia abyssinica*) or Linseed (*Linum ustatissimum*), is the main commercial

product (Nigussie, 2001). On the other hand, the oil shows physical and chemical properties suitable for bio-diesel (Cardone *et al.,* 2003) which can also potentially contribute to the economic development of the country. Additional advantage of Ethiopian mustard is also immense in the farming system once seedling is established, as a potential rotational-crop for cereals and pulses. This would increase crop diversity, reduce chemical use and thereby increase profits (Gan *et al.,* 2007). In addition, the residual defatted meal of *B. carinata* can be used as a soil amendment for plant defence due to the highly biologically active compounds in the meal.

Major production constraints of the Ethiopian mustard are: lack of high yielding, early maturing varieties, high erucic acid (C22: 1) content in seed oil and high glucosinolate content in the meal (EARO, 2000). Therefore, in order to enhance its cultivation, developing early and high yielding varieties remains the breeding policy to achieve agronomic objectives. Assessing the extent and pattern of genetic variability of Ethiopian mustard genotypes is a prerequisite which may help in identifying important genotypes for improvement of Ethiopian mustard. A number of methods have been used for analysis of genetic variability (Melchinger *et al.,* 1999).

The genetic potential and the environment to which the crop is subjected determine the yield ability of any crop. Improving any or all of these factors will lead to increase in yield.

Hence, at both national and regional levels, research efforts are going on to improve the genetic potential and management practices of Ethiopian mustard to overcome the above indicated yield-limiting factors (Nigussie, 2001).

Inter-specific hybridization can easily be forced in the family Brassicaceae where gene flow is very limited under natural conditions (Sandhu and Gupta, 2000). The level of genetic diversity performance has been proposed as a predictor of F1 performance and heterosis. Genetic variability plays an important role in plant breeding because hybrids between lines of diverse origins generally display a greater heterosis than those between closely related parents (Karkoo, *et al.,* 2000).

Achievement of any crop improvement depends upon the presence of genetic variability, heritability, correlation as well as genetic gain in selection (Khan *et al.,* 2006). Heritability is a key of transmissibility of traits and as such partition the total variance into genetic and environmental components (Marwede *et al.,* 2004). Plant traits having satisfactory variability, high heritability and genetic advance would be an effective tool for crop improvement (Aytac and Kinaci, 2009).

Additive genes are considered to control traits with high heritability and genetic advance and the phenotypic selection thus would be effective (Ghosh and Gulati, 2001; Khulbe *et al.,* 2000; Aytaç and Kinaci, 2009). Developing high yielding varieties need critical evaluation of existing genetic variability, heritability and genetic advance (Choudhary *et al.,* 1999; Kakroo *et al.,* 2000).

In any crop improvement program, the first thing that the breeder looks into is the existence of genetic variability for characters of interest (Aytac and Kinaci, 2009). This estimate brings about the evaluation of genetic and environmental effects, aiding in selection. Evaluation of heritability can also be used to predict genetic advance under selection, so that the plant breeder can be hopeful of progress from various types and intensities of selection. Hence, estimation of the extent and pattern of genetic variability existing in the available germplsm is essential to breeders (Khulbe, *et al.,* 2000).

The existence of variation alone in the population is not sufficient for improving desirable characters. High heritability (transfer of characters from generation to generation and/or from parent to offspring) is also needed to have better opportunity to select directly for the characters of interest. This is mainly because of the opportunity associated with high heritability in correct identification and measurement of the genotypes based on phenotypic values and in avoiding errors in genotypic classification, the expected gain under a particular selection system supplies the practical information on the amount of genetic progress. It is also essential to predict the amount of genetic gain that could be expected from selection of some top genotypes for the character of interest (Aytac and Kinaci, 2009).

With increase in the number of characters, however, there exists some amount of interdependence. Under such complex situations, path coefficient analysis could be used for the identification of the direct and indirect causes of association, and it can measure the relative importance of each character (Nigussie *et al.,* 1996). Information on the above genetic aspects can help plant breeders to identify important germplasm and selection

criteria in the crop breeding programs. Several genotypes have been tested in the national research project of Ethiopian mustard (Nigussie, 2001). However, information in these materials in the aforementioned aspects is limited despite their paramount importance. Keeping in view the importance of edible oil and its shortage in the country, an experiment was conducted to screen lines derived from *B. carinata*. The present study was conducted with the objectives. General objective: To evaluate genetic variability, heritability, genetic advance and correlation among seed yield and yield related traits of Ethiopian mustard genotypes.

The specific objectives of the study are to assess the extent and pattern of genetic variability among Ethiopian mustard genotypes, estimate the heritability and genetic advance under selection for important agronomic traits, and evaluate the association between seed yield and yield-related characteristics through correlation analysis. Furthermore, the study aims to partition the genetic correlation coefficients into their direct and indirect effects using path coefficient analysis to identify the key traits contributing to seed yield improvement and to provide a scientific basis for effective selection in Ethiopian mustard breeding programs.

Materials and Methods

Experimental Site

Field experiment was conducted at Haramaya University, Rare site during main cropping season of 2014. The Rare research site is located at 1980 m.a.s.l; 9^0 26'N latitude and 42^0 3'E longitudes. The site has a bimodal rainfall distribution and is representative of semi-arid tropical belt of eastern Ethiopia and is characterized by a sub-humid type of climate with an average annual rainfall of about 790 mm, annual mean temperature of 17 ^{0}C with mean minimum and maximum temperature of 3.8 and 25 ^{0}C, respectively (Tekalign and Hammes, 2005).

Experimental Materials

For this study, 25 germplasm accessions of Ethiopian mustard originating from diverse agro ecological locations of Ethiopia were used. Among the tested genotype there were three released varieties. The genotypes were obtained from Holeta Agricultural Research Center of Ethiopia. Description of the genotypes is depicted in Table 1.

Experimental Design

The experiment was carried out using randomized complete block design (RCBD) with two replications. Each genotype was planted in a plot size of 1.6m by 2m long. The distances between plots, rows, plant and replications were 1m, 40cm, 20cm and 2m, respectively. The rates of fertilizer application was 40.3 kg/ha and 150 Kg/ha Urea and DAP respectively. Fertilizers were applied at one time at sowing and the seed rate was 3g per plot based on the national seed rate recommendation of 10 Kg/ha for each genotype. Seed and fertilizer were drilled uniformly by hand. Other cultural practices were followed as recommended for the area (Nigussie, 2001).

Data Collection

Data was collected on plot and plant basis as shown below.

Description of data that was collected on blot basis

- **Days to 50% flowering (DF)**: The number of days from the date of sowing to the date at which about 50% of the plants in a plot showed blooming on about 50% of their flower buds.
- **Biomass per plot (BM/P)**: The total above ground biological yield in grams was obtained from each plot at harvest and expressed in grams.
- **Harvest index per plot (HI/P)**: The fraction of dry seed in the above ground biological yield on a plot basis.
- **Thousand seed weight (TSW)**: The weight in grams of 500 seeds randomly sampled from each plot and was multiplied by two in each line of replication. Then weight in grams was recorded.
- **Seed yield per plot (SY/P)**: Seed yield per plot was measured in grams after moisture of the seed is adjusted to 7%.

Description of data collected on five randomly selected plants

- **Primary branches per plant (PB/PL)**: The average number of primary branches from 5 plants.
- **Secondary branches per plant (SB/PL)**: The average number of secondary branches formed on primary branches/plant.
- **Plant height (PH)**: The height of plants in each plot was measured in centimeters from the ground surface to the top of the main stem at maturity.

- **Biomass per plant (BM/PL)**: The total above ground biological yield in grams was measured for a single sampled plant and expressed in grams.
- **Harvest index per plant (HI/PL)**: The fraction of seed yield in the above ground biomass on a single plant basis was computed from 5 random plants.
- **Seed yield per plant (SY/PL)**: The total seed obtained from five randomly selected plants was weighted and expressed in grams.

Methods of Data Analysis

Analysis of variance (ANOVA)

Data was subjected to analysis of variance using the procedures outlined by Gomez and Gomez (1984). SAS computer software version 9.2 (SAS, 2008) was used for statistical data analysis. Analyses of covariance were done for each pair of characters to obtain the sum of cross products to be used in covariance calculation. The randomized complete block design analysis of variance was used to derive variance components as structured below in Table 2 (Cochran and Cox, 1975). To test the statistical significance of the treatments, one way factorial analysis of variance (ANOVA) was used. The level of significance was ($P<0.05$). Experimental design document was organized and categorized based on the objectives of the study

RCBD ANOVA was computed using the following model

$$Y_{ij} = \mu + r_j + g_i + \varepsilon_{jj}$$

Where, Y_{ij} = the response of trait Y in the i^{th} genotype and the j^{th} replication.
μ = the grand mean of trait Y
r_j = the effect of the j^{th} replication.
g_i = the effect of the i^{th} genotype
ε_{ij} = experimental error effect

Estimation of phenotypic and genotypic variances

The phenotypic and genotypic variance of each trait was estimated from the randomized complete block design analysis of variance. The expected mean squares under the assumption of random effects model was computed from linear combinations of the mean squares and the phenotypic and genotypic coefficient of variations were computed as per the methods suggested by Burton and Devane (1953).

Genotypic variance $(\sigma^2 g) = \frac{msg - mse}{r}$ or $\sigma^2 g) = (\sigma^2_t - \sigma^2_e)$

Environmental variance $(\sigma^2 e) = ms_e$

Where, ms_g and ms_e are the mean sum of squares for the genotypes and error in the analysis of variance, respectively. σ^2_t= mean square of treatment and r is the number of replications. Then, the phenotypic variance was estimated as the sum of the genotypic and environmental variance.

Phenotypic variance $(\sigma^2 p) = \sigma^2_g + \sigma^2_e$

The covariance components were also estimated in similar fashion as the variance components.

Estimation of genotypic and phenotypic coefficient of variability

The genotypic and phenotypic coefficients of variability were undertaken according to the formulae of Singh and Chaundary (1977).

Genotypic Coefficient of Variation (GCV) = (σ_g /grand mean) x 100

Phenotypic Coefficient of Variation (PCV) = (σ_p/grand mean) x 100

Where, σ_g and σ_p are genotypic and phenotypic standard deviations, respectively.

Estimation of heritability and genetic advance

Heritability ($h^2 b$) in broad sense for all characters was computed using the formula adopted by Falconer and Mackay (1996), as follows:

Heritability in broad sense $(h^2_b) = (\sigma^2 g/\sigma^2_p)$ x 100

Estimate of expected genetic advance

Then, the genetic advance for selection intensity (k) at 5% (2.06) was estimated by following the formula of Johnson *et al.,* (1955b).

$GA = k^* \sigma_p * h^2 b$
Where, GA represents the expected genetic advance under selection; σ_p is the phenotypic standard deviation, $h^2 b$ is heritability in broad sense and k is selection intensity.

The genetic advance as percent of population mean was also estimated by following the procedure of Johnson *et al.,* (1955b).

Genetic advance per population mean = (GA/grand mean)*100

Association analysis

Genotypic correlation

Both genotypic and environmental effects and genotypic correlation, which the inherent association between two variables, were estimated by the formula of (Al- Jibouri *et al.,* 1958):

r_g= Gcovx.y/ √ ($\sigma^2_{gx}.\sigma^2_{gy}$)

Where, r_g=genotypic correlation coefficient
Gcovx.y =genotypic co-variance between variables x and y
σ^2_{gx} =genotypic variance for variable x
σ^2_{gy}= genotypic variance for variable y

Phenotypic correlation

r_p= Pcovx.y/ √ ($\sigma^2_{px}.\sigma^2_{py}$).

Where,
r_{ph} = phenotypic correlation coefficient
Phcovx.y = phenotypic co-variance between variables x and y
σ^2_{px} = phenotypic variance for variable x
σ^2_{py}= phenotypic variance for variable y

Path coefficient analysis

The path coefficient analysis were done using the formula of Dewey and Lu (1959) and with statistical package developed by Doshi (1991) using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effects of yield components on seed yield based on the following relationship.

$r_{ij} = P_{ij} + \Sigma r_{ik} P_{kj}$

Where, r_{ij} is Mutual association between the independent variable(character) (i) and dependent variable (j) as measured by correlation coefficient; P_{ij} is component of direct effect of the independent variable (i) on the dependent variable (j) as measured by path coefficient; and $\Sigma r_{ik} P_{kj}$ is summation of components of indirect effects of a given independent character.

Result and Discussion

The Analysis of Variance

The analysis of variance for the 11 characters studied is given in Table 3. All the characters showed highly significant ($p \leq 0.01$) difference among the tested genotypes. The significance of genotype difference for the different characters indicates the presence of genetic variability for each of the characters in the tested genotype. Nigussie (2001) also evaluated 36 accessions of Ethiopian mustard, for several characters at three locations and reported existence of enormous amount of genetic variability.

The variation due to replication was highly significant ($p \leq 0.01$) for plant height (82.521), secondary branch per plant (52.727), biomass per plant (106.723), biomass per plot (478780.5), seed yield per plot (27782.43) and also variance due replication is significant ($p \leq 0.05$) for days to flowering (5.508), primary branch per plant (1.463) and seed yield per plant (6.147) but non-significant for, harvest index per plant (0.001), harvest index per plot (0.001) and thousand seed weight (0.035). The present study somewhat related to the report of IAR (1992) who reported the variation due to replication was non-significant for most of the characters but significant for days to flowering, primary branches per plant, seed yield per plant, number of pod per plant and number of pod per plot.

Range and Mean Values

The range, mean and standard errors of the studied characters are presented in Table 4. Wide ranges were recorded for biomass per plot, biomass per plant, seed yield per plot, plant height, days to flowering and seed yield per plant. This result was in harmony with the reports of IAR (1992) that noted wide range of variation for plant height seed yield per plot secondary branches and 1000- seed weight in Ethiopian mustard genotypes.

The mean value of plant height for all genotype was high (178.3cm), but five genotypes are of short stature. Among the studied genotypes there are also accessions that are not sated fruit which leads to absence of harvest index per plot and harvest index per plant. This implies

that among the tested genotypes they do not perform well under experimental environment (Appendix I). Mean value for Primary branches and Secondary branches for genotypes were 13.3, 30.5 respectively as shown in Table 4. Mean seed yield for the genotype was 642.7g on plot bases and 9.6g on plant bases (Table 4). Mean above ground biomass per plot was 3119.4g and biomass per plant was 47.8g. The mean value of 1000-weight were 3.1.

In general, 1000-seed weight and seed yield in the present experiment were low for the tested genotypes. This is mainly due to the terminal moisture stresses which become not ideal for tested genotype and that prevailed during seed filling stage of Ethiopian mustard genotype (Appendix I). Yet, the finding suggests that there is the scope of improving seed, biomass and harvest index in the tested genotype.

Early flowering Variety that is suitable for moisture stress areas and variety with short stature can also be obtained if selection is carried out among the tested genotypes. The present study closely agrees with that of Belete *et al.,* (2012) who observed influence of environment on the expression of genes controlling seed yield and plant height.

Phenotypic and Genotypic Variation

The amount of phenotypic and genotypic variation that exists in species is essential in developing better varieties and initiating a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population Nigussie (2001). The estimation of variability is a prerequisite for breeding programs aimed at crop improvement. According to (Deshmukh and Chavan, 1990) PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. The presence of narrow gap between PCV and GCV for most characters studied suggested that the influence of environment on the character is low. Estimated variance components, phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) of a character studied are presented in Table 4.

In the present study, the genotypic variance took relatively the highest genotypic variances were found for days to flowering, 1000-seed weight, seed yield per plot, plant height, biomass per plot and seed yield per plot. These effects were also detected from high heritability estimates for these character (Table 4).On the other hand, relatively lower variances share of the total variance were observed for seed yield per plant, biomass per plot, secondary branches per plant, indicating the greater share of environmental variance in total variability.

The GCV ranged from 6.9% for plant height to 31.03% seed yield per plot and PCV ranges from 7.5% for days to flowering to 39.4% seed yield per plot. In general, the PCV value was greater than the GCV value for the characters studied. Relatively high PCV value was recorded for biomass per plant, harvest index per plot and harvest index per plant, seed yield per plant and secondary branches per plant. Hence, there is a good opportunity for the improvement of these characters in the tested genotypes. Yadava *et al.,* (2011) also reported wide genetic variations for secondary branches and seed yield by evaluating newly evolving and released varieties of Indian mustard under dry land conditions. On the other hand, Yadav and Hari (1996) reported low genetic variations for days to flowering, plant height, 1000-seed weight and harvest index and the present finding are nearly similar with these results.

The PCV values were high for seed yield per plot, biomass per plot, secondary branches per plant, seed yield per plant, biomass per plant, harvest index per plot and harvest index per plant. The higher GCV and PCV for seed yields, biomass and secondary branches provided better scope for improvement through selection. Generally, the GCV estimate nearly approached PCV estimate for days to flowering, plant height, and biomass per plot, seed yield per plot, 1000-seed weight, and primary branches per plant. However, there was wide difference between PCV and GCV estimates for the remaining characters. It indicates the influence of environment than genetics for all these traits under study. Likewise, the PCV estimate was more than three–fold compared to the GCV estimate for the biomass per plant and seed yield per plant. This indicates the presence of considerable environmental influence/factor on these characters.

The phenotypic and genotypic coefficients of variation for seed yield per plot were high (39.4) and (31.03) respectively and for days to maturity were low estimate of PCV (7.5) for days to flowering and GCV (6.9) for plant height was observed.

The characters, like secondary branches per plant and biomass per plot also recorded moderate values of phenotypic and genotypic coefficient of variation

respectively. This suggests that these characters are majority under the influence of genetic control. Hence, simple selection can be relied upon and practiced for further improvement of these characters. These results are in consonance with Yadava *et al.,* (2011).

Heritability Estimates

The estimated heritability for the studied characters is also presented in Table 4. The heritability values for the characters ranged from 8.2% for seed yield per plant to 87.9% for days to flowering. Dabholker (1992) generally classified heritability estimates as low (5-10%), medium (10-30%) and high (30-60%). Based on this classification, days to flowering, 1000-seed weight, plant height, biomass per plot, seed yield per plot and primary branches per plant exhibited high or very high heritability estimates.

Hence, a good progress can be made if some of these traits are considered as selection criteria. High heritability estimate were also obtained for days to flowering, 1000-seed weight, plant height, and seed yield per plot by Malik *et al.,* (2000) who reported similar results for days to flowering, 1000-seed weight, plant height, primary branches per plant and seed yield per plot.

On the other hand, seed yield per plant and biomass per plant exhibited low heritability estimates. In contrast to the present investigation, Jeromel *et al.,* (2007) reported that in Brassica species, seed yield exhibited very high heritability estimates with plant height. The heritable portion of the overall observed variation can be obtained by studying the components of variation such as coefficients of genotypic and phenotypic variability, heritability and predicted genetic advance.

Generally, heritability estimates were high for all the characters studied, except seed yield per plant biomass per plant. This suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programmea as the genetic variance is mostly due to additive gene action. These results are in accordance with the findings of (Krishnaiah *et al.,* 2002).

Estimates of Expected Genetic Advance

The genetic advance as the percentage of the mean at 5% selection intensity is presented in Table 4. Estimates of genetic advance as percent of mean at 5% selection intensity ranged from 4.5 for seed yield per plant to 50.4 for seed yield per plot. Relatively high genetic advance was observed for seed yield per plot and biomass per plot. Likewise, estimates of genetic advance as percent of the mean for 1000-seed weight, days to flowering, plant height, primary branches per plant and secondary branches per plant were also considerably high (Table4). However, seed yield per plant and biomass per plant showed less than 5%. A low EGA and GAM observed for these characters indicated that the characters were under high environmental influence, and that selection based on these characters would be ineffective. Contrary to the present investigation, Afrin *et al.,* (2011) reported high heritability with high genetic advance as percent of the mean for plant height, primary branch and secondary branch per plant and recommended that phenotypic selection for seed yield per plant would be valuable.

Character Associations

The phenotypic and genotypic correlation coefficients were worked out for 11 characters and the data were presented in Tables 5. Improvement for a target character can be achieved by indirect selection via other characters that are more heritable and easy to select. This selection strategy requires understanding the interrelationships of the characters among themselves and with the target characters.

Correlations of seed yield and yield related traits

Knowledge of association between yield and its components is useful to make simultaneous selection for more than one character. The correlation analysis helps in determining the direction and number of characters to be considered in improving the yield.

Genotypic and phenotypic correlations among the characters are presented in Table 5. Seed yield per plot had high and positive genotypic associations with biomass per plot (r_g = 0.967), harvest index per plot (r_g = 0.591), plant height (r_g=0.576), and harvest index per plant (r_g = 0.488). At phenotypic level, biomass per plot, harvest index per plant, harvest index per plot, plant height and seed yield per plant were observed to have positive and high significant ($p \leq 0.01$) correlation with seed yield per plot. Though low, 1000-seed weight and biomass per plant had positive association with seed yield per plot, at phenotypic level. On the other hand, seed yield per plot was negatively correlated with day to flowering (r_g= -0.738), primary branches per plant (r_g = -

0.684), and secondary branches per plant (r_g = -0.520). It also had highly significant ($p < 0.01$) and negative phenotypic correlation with days to flowering (r_p = -0.485). The phenotypic correlations of primary branches per plant with seed yield per plot were significant ($p < 0.05$) and negative.

Generally, seed yield per plot was positively correlated with biomass per plot, harvest index per plot, plant height, harvest index per plant, and seed yield per plant at both genotypic and phenotypic levels. However, it was negatively correlated with days to flowering and primary branches per plant at both level and, with secondary branches per plant and biomass per plant at genotypic level. Hence, making simultaneous increase for these characters with seed yield per plot is difficult. The present result is in line with that reported by Nigussie (1990) with regard to the correlations between seed yield per plot, plant height and primary branches per plant.

At genotypic level, seed yield per plant was positively associated with harvest index per plant (r_g = 0.595), 1000-seed weight (r_g = 0.541), biomass per plant (rg = 0.379). Similarly, it had positive and highly significant ($p < 0.01$) correlations with biomass per plant, secondary branches per plant and harvest index per plant at phenotypic levels (Table 5). It also had low and negative genotypic associations with primary branches per plant and plant height. Hence, compromise should be made to improve these characters simultaneously.

Seed yield per plant had positive correlations with harvest index per plant, biomass per plant and 1000-seed weight at both genotypic and phenotypic level, and with secondary branches per plant at phenotypic level only. This indicates that these characters are merits to improve seed yield per plant. Among the 11 characters studied, there are no characters that had negative phenotypic association with seed yield per plant, though very low. However, at genotypic level primary branches per plant and plant height had low and negative association with seed yield per plant.

Plant height exhibited highly significant positive association with seed yield per plot both at phenotypic and genotypic levels suggesting that selection would be effective. Such significant association of plant height with seed yield per plot has also been observed by Nigussie (1990).

Negative association between primary branches per plant and seed yield per plot at both phenotypic and genotypic levels in the present investigation is in confirmation with the results of Singh, H. and Singh, V. P. (1998). Thus, it would be desirable to select the plants with more number of primary branches to improve seed yield.

High correlation of biomass per plot and seed yield per plot at both the levels indicates that biomass per plot is a reliable yield indicator. Similar results were reported by Nigussie Alemayhu, Adefris Teklewold and Tadele Zerihun (1996). This clearly indicates that increased biomass plot were increase seed yield. Hence, more emphasis should be given to this character while making selection for yield.

Days to flowering had negative association with the seed yield per plot and significant at phenotypic level but non-significant at genotypic level. 1000-seed weight exhibited significant positive correlation with seed yield per plot. Similar observations were reported by Erena Aka. (2001) for days to flowering and for 1000-seed weight.

Correlation among yield related traits

Many interesting associations were observed among yield related traits (Table 5). The genotypic and phenotypic association between harvest index per plot and harvest index per plant were strong and positive (r_g = 0.999) and (r_p = 0.661). However, for harvest index per plant its phenotypic correlation with day to flowering (r_p = -0.323) was negative and significant ($p < 0.05$). This indicates that breeding for early flowering type might result in high harvest index. Although non-significant, harvest index per plant was also negatively correlated with plant height (r_p = -0.187) and primary branches per plant (r_p = -0.160) at phenotypic level.

Harvest index per plot had significant ($p < 0.01$) and negative association with days to flowering (r_g = -0.805 and r_p = - 0.406). Its phenotypic associations with plant height and primary branches per plant were also negative but non-significant. This implies increasing these characters will lead to increase in harvest index per plot.

Biomass per plot was strongly and positively correlated with plant height (r_g = 0.736 and r_p = 0.513). Its phenotypic correlation with 1000-seed weight (r_p = 0.273) was also positive and significant. On the other

hand, it was negatively correlated with day to flowering (r_g = -0.608 and r_p = -0.402).

Considering the correlation of biomass per plant, it had positive associations with day to flowering, primary branches per plant, secondary branches per plant, and 1000-seed weight. None of the characters exhibited negative and significant phenotypic association with biomass per plant.

Primary branches per plant was strongly and positively correlated with days to flowering (r_g = 0.728 and r_p = 0.497) and secondary branch per plant (r_g = 0.748 and r_p = 0.602). However, none of the characters depicted significant and negative association with secondary branches per plant at phenotypic level. The phenotypic and genotypic correlation between days to flowering and 1000-seed weight was strong and positive (r_g = 0.340 and r_p = 0.275).

Plant height had also strong and positive correlations with seed yield per plot (r_g = 0.576 and r_p = 0.385). This implies, tall plant produce more seed yield. However, none of the character depicted significant and negative association with 1000-seed weight at phenotypic level.

Generally seed yield per plant was positively correlated with day to flowering (r_g = 0.163 and r_{ph} = 0.127), secondary branch per plant (r_g = 0.198 and r_p = 0.729), seed yield per plot (r_g = 0.323 and r_p = 0.347), harvest index per plant (r_g = 0.595 and r_p = 0.454), biomass per plot (r_g = 0.173 and r_p = 0.267), biomass per plant (r_g = 0.379 and r_p = 0.831), harvest index per plot (r_g = 0.588 and r_p = 0.350) and 1000-seed weight (r_g = 0.541 and r_p = 0.258). The results in this present investigation clearly indicate all these characters as highly correlated with seed yield and this clearly indicates that increasing these character were increase seed yield.

Hence, more emphasis should be given to this character while making selection for yield.

From the present investigation, it indicted that characters like day to flowering, secondary branch per plant, seed yield per plot, harvest index per plant, biomass per plot, biomass per plant, harvest index per plot and 1000-seed weight, are highly and positively correlated with seed yield per plant and needs to be considered for selection.

Path Coefficient Analysis

Path coefficient analysis provide more effective means of direct and indirect factors, permitting a crucial examination of the specific force acting to produce a given correlation and measuring the relative importance of the causal factors. Therefore, path coefficient analysis was carried out to partition correlation coefficients into direct and indirect effects.

Path coefficient analysis for seed yield per plot

Path coefficient analysis was carried out both at phenotypic and genotypic levels considering seed yield as dependent character and yield attributes as independent characters.

Each component has two path action; direct effect on seed yield and indirect effect through components, which are not revealed by correlation studies. The correlations were partitioned into direct and indirect effects on seed yield per plant and the data is presented in Tables 6 and 7, respectively. In this study, it was assumed that seed yield per plot was the end product of the days to flowering, plant height, primary branches per plant and secondary branches per plant. Moreover, biomass per plot, harvest index per plot and 1000-seed weight were considered as yield components.

Based on genotypic path coefficient analysis, the highest and favorable direct effect was exerted on seed yield by biomass per plot (0.468), followed by harvest index per plot (0.263), plant height (0.252) and secondary branches per plant (0.149). Except secondary branches per plant, these characters were also correlated strongly and positively with seed yield per plot. Hence, these three characters could be considered in the improvement of seed yield per plot.

In other words, favorable direct effect of biomass per plot, harvest index per plot and plant height on seed yield indicate that, with the other variables kept constant, improvement of these characters will increase seed yield per plot. 1000-seed weight exerted favorable but weak direct influence on seed yield, whereas days to flowering (-0.159), and primary branches per plant (-0.162) had negative direct influence. These three characters also exhibited strong and negative genotypic correlation with seed yield. Similar results were reported by Nigussie (1990) for plant height, primary branches. The authors deduced plant height is the most important components contributing to seed yield.

Table 6 indicated some considerable indirect effects on seed yield per plot at genotypic level, which were observed in the correlation analysis. Plant height (0.344),

harvest index per plot (0.171) and 1000-seed weight (0.169) exhibited positive genotypic indirect effect via biomass per plot, which suggests merits of biomass per plot for improving seed yield per plot. These indirect effects had considerable contribution to their total correlation. The genotypic path coefficient analysis also revealed that biomass per plot (0.185) and 1000-seed weight (0.154) had positive indirect effect on seed yield through plant height.

Similarly, direct and indirect effects revealed the importance of biomass per plot, harvest index per plot and harvest index per plant height for improvement of seed yield per plot. Biomass per plot and plant height had positive in direct effects through most of the characters. However, days to flowering, primary branches per plant and secondary branches per plant had negative indirect effects via several characters considered in the study. The genotypic indirect effects of these characters were important component of genotypic correlations among these characters and seed yield per plot.

The phenotypic path coefficient analysis revealed that biomass per plant (0.879) and harvest index per plant (0.258) exerted high and favorable direct effects on seed yield per plot. Harvest index per plot also exerted positive indirect effects on seed yield via biomass per plot (Table7). Days to flowering and 1000-seed weight exerted favorable but weak influence on seed yield, whereas plant height (-0.041), primary branches per plant (-0.017) and secondary branches per plant (-0.028) had some negative direct influence. The favorable direct effects of biomass and harvest index on seed yield indicates that, with other variables kept constant, improvement of these characters will increase seed yield. The direct effects of biomass (0.879) had the greatest contribution to positive and highly significant correlation between biomass and seed yield (r_{ph} = 0.952). However, its indirect effects through other characters were low (Table 7).

Plant height (0.451), 1000-seed weight (0.240) and harvest index (0.237) exhibited considerably positive indirect effects on seed yield via biomass. Therefore, these situations further confirm the crucial role of biomass in improving seed yield. It is also logical to select for plant height and 1000-seed weight to improve seed yield. Days to flowering exerted negative indirect effect via several characters considered. Similarly, day to flowering (-0.353) had considerable negative indirect effects via biomass. Hence, it could not be used for indirect selection for improving seed yield.

Path coefficient analysis for seed yield per plant

The genotypic direct and indirect effects of seven yield related traits on seed yield per plant are show in Table 8 and the phenotypic direct and indirect effects are shown in Table 9. The highest positive genotypic direct and indirect effects were detected for biomass per plant (1.252) and the second highest direct effect was for harvest index per plant (0.840). In the case of this study, the two important phenotypic direct effects on seed yield were that of biomass (0.813) and harvest index (0.479). Biomass and harvest index had also relatively strong and positive associations with seed yield at genotypic level (Table 8), and positive and highly significant associations at phenotypic level (Table 9). Phenotypic path coefficient analysis also revealed that the correlation of biomass and harvest index with seed yield per plant were largely the effect of these direct effects. These direct effects, therefore, indicates the merits of biomass and harvest index for improving seed yield.

At genotypic level, day to flowering (0.208), exhibit positive direct effects on seed yield per plant, though relatively low. Likewise, it had high positive association with seed yield per plant (r_g = 0.797). On the other hand, plant height (-0.216) exerted substantial negative direct effect on seed yield. Moreover, primary branches (-0.059), secondary branches (-0.042) and 1000-seed weight (-0.099) had some negative direct influence. Except 1000-seed weight these traits also exhibited weak associations with seed yield (Table 8).

As it can be seen from Table 8 and 9, the genotypic and phenotypic direct effect of primary branches, secondary branches and 1000-seed weight on seed yield were low. However, these characters contributed indirectly and favorably to seed yield through biomass as shown in (Table 8). Hence, it is logical to consider biomass for improving seed yield.

On the other hand, at genotypic level except harvest index all characters considered in this analysis had positive indirect effects on seed yield via biomass (Table 8). Similarly, at phenotypic level, except harvest index the remaining characters exerted positive indirect effects on seed yield through biomass (Table 9). These situations farther confirm the importance of biomass for improving seed yield.

Table.1 Lists of the 25 Ethiopian mustard genotypes used in the study.

No	Accession code number	Area of collection	Altitude
1	PGRC/E 21025	Arsi/Abomsa	2520
2	PGRC/E 20005	Arsi/Dodota	2550
3	PGRC/E 20067	Arsi/Shirka	1910
4	PGRC/E 20110	Gojam/Inemay	2550
5	PGRC/E 200017	Bale/Adaba	2500
6	PGRC/E 20001	Gojam/Dangla	1950
7	PGRC/E 20004	Gojam/Macha	2050
8	PGRC/E 200011	Gonder/Dembiya	1850
9	PGRC/E 20006	Hararghe/Ciro	2260
10	PGRC/E 20112	Hararghe/Kombolcha	2100
11	PGRC/E 20066	Hadiya/Hangacha	2180
12	PGRC/E 20106	Illubabor/chora	2180
13	PGRC/E 20132	Illubabor/Gomay	1820
14	Yellow Dodolla	Released in 1986	NA
15	S-67	Released in 1976	NA
16	Holetta-1	Released in 2005	NA
17	PGRC/E 201017	Shawa/Addis Alem	2540
18	PGRC/E 21008	Shewa/Ambo	2010
19	PGRC/E 21029	Shewa/Boset	1600
20	PGRC/E 20069	Shewa/Merhabete	1800
21	PGRC/E 20002	Shewa/Minjar	2755
22	PGRC/E 20165	Welayita/Sodozuriya	1820
23	PGRC/E 20003	Wollega/Arjo	2340
24	PGRC/E 20163	Wellega/Horo	1980
25	PGRC/E 20166	Shewa/Fitche	2016

Source: HARC
NA: Not available

Table.2 Analysis of variance

Source of variation	df	Mean square	EMS
Replication	r-1	ms_r	$\sigma^2e + g\,\sigma^2r$
genotypes	g-1	ms_g	$\sigma^2e + r\,\sigma^2g$
Error	(r-1) (g-1)	ms_e	σ^2e
Total	gr-1		

Where, r = number of replications; ms_r = mean square due to replications; g = number of genotypes, ms_g = mean square due to genotypes, ms_e = mean square of error; σ^2g, σ^2r and σ^2e are variances due to genotype, replication and error, respectively.

Table.3 The mean squares for different source of variation and the corresponding CV (%) for the characters studied.

Characters	Replication(1)	Genotype (24)	Error(24)	CV	SE	LSD 5%
DF	8.672	125.258**	5.508	2.6	0.30	3.80
PH	199.606	529.660**	81.521	5.09	1.17	14.6
PB/PL	2.094	4.892**	1.463	9.06	0.16	1.96
SB/PL	54.116	88.949**	52.727	23.8	0.94	11.74
BM/PL	127.926	144.057**	106.723	21.66	1.33	16.02
BM/P	1299387	3028892.429**	478780.5	20.69	89.3	1119
SY/PL	0.207	7.799**	6.147	25.26	0.37	4.01
SY/ P	61319.59	164861.548**	27782.43	24.2	21.5	269.5
HI/PL	0.003	0.002**	0.001	13.26	0.004	0.051
HI/ P	0.001	0.002**	0.001	11.78	0.003	0.051
TSW	0.044	0.235**	0.035	6.06	0.024	0.30

** Indicates significance at 0.01 probabilities: figure in parenthesis refers to degrees of freedom.
DF= Days to flowering, PH=Plant height, PB/PL=Primary branches per plant, SB/P= Secondary branches per plant, BM/P= Biomass per plot, BM/PL= Biomass per plant, SD/PL= Seed yield per plant, SD/P= Seed yield per plot, HI/P= Harvest index per plot, HI/PL= Harvest index per plant, TSW= Thousand seed weight. CV= Coefficient of variation, SE=standard error, LSD 5%=List significance difference

Table.4 Estimates of mean, range, variance components, and coefficient of variability, heritability and genetic advance of the characters studied.

Character	Mean	Range	σ^2_g	σ^2_e	σ^2_p	GCV	PCV	h^2b	EGA K=5%	GAM K=5%
DF	90.8	75-108	39.9	5.5	45.4	7.0	7.5	87.9	12.2	13.5
PH	178.3	149-198	149.4	81.5	230.9	6.9	8.6	64.7	20.3	11.4
PB/PL	13.3	10-17	1.1	1.5	2.6	8.0	12.1	43.9	1.5	10.9
SB/PL	30.5	21-41	12.1	52.7	64.8	11.4	26.4	18.6	3.1	10.1
BM/PL	47.8	31-62	12.4	106.7	119.2	7.4	22.9	10.4	2.4	4.9
BM/P	3119.4	868-5950	850037.3	478780.5	1328818	27.6	34.5	63.9	1519.0	45.4
SY/PL	9.6	0.00-13	0.6	6.2	6.7	7.5	26.4	8.2	0.4	4.5
SY/P	642.7	0.00-1305	45693.04	27782.4	73475.5	31.03	39.4	62.2	347.3	50.4
HI/PL	0.2	0.00-0.3	0.0003	0.001	0.0013	8.7	17.4	23.1	0.02	8.2
HI/P	0.3	0.00-0.7	0.0003	0.001	0.0013	8.9	17.7	23.1	0.02	8.4
TSW	3.1	0.00-0.4	0.07	0.04	0.102	8.5	10.4	65.7	0.4	14.1

DF= Days to flowering, PH=Plant height, PB/PL=Primary branches per plant, SB/P= Secondary branches per plant, BM/P= Biomass per plot, BM/PL= Biomass per plant, SY/PL= Seed yield per plant, SY/P= Seed yield per plot, HI/P= Harvest index per plot, HI/PL= Harvest index per plant, TSW= Thousand seed weight

σ^2g = Genotypic coefficient of Variance, σ^2e = Error Variance, σ^2p = Phenotypic Variance, GCV = Genotypic Coefficient of Variance, PCV = Phenotypic Coefficient of Variance, h^2b = Heritability in broad sense, EGA = Expected genetic advance, GAM = Genetic advance as percent of mean, and K = Selection intensity

Table.5 Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among characters in 25 Ethiopian mustard genotypes studied.

	DF	PH	PB/PL	SB/PL	BM/PL	SY/PL	HI/PL	BM/P	SY/P	HI/P	TSW
DF		-0.073	0.728	0.652	1.030	0.163	-0.729	-0.608	-0.738	0.805	0.340
PH	-0.127		-0.279	-0.582	0.307	-0.139	-0.532	0.736	0.576	-0.248	0.610
PB/PL	0.497**	-0.172		0.748	0.374	-0.152	-0.461	-0.630	-0.684	-0.515	0.127
SB/PL	0.345**	-0.175	0.602**		0.300	0.198	-0.02	-0.570	-0.520	-0.093	0.079
BM/PL	0.384**	0.128	0.426**	0.677**		0.379	-0.502	-0.185	-0.275	-0.497	0.920
SY/PL	0.127	0.027	0.253	0.729**	0.831**		0.595	0.171	0.323	0.588	0.541
HI/PL	-0.323*	-0.187	-0.160	0.268*	-0.093	0.454**		0.255	0.488	0.999	-0.328
BM/P	-0.402**	0.513**	-0.216	0.008	0.146	0.267*	0.186		0.967	0.366	0.361
SY/P	-0.485**	0.385**	-0.266*	0.052	0.132	0.347**	0.355**	0.952**		0.591	0.233
HI/P	-0.406**	-0.128	-0.217	0.187	-0.008	0.350**	0.661**	0.270*	0.524**		-0.352
TSW	0.275*	0.430**	0.072	0.127	0.280*	0.258*	0.041	0.273*	0.225	-0.033	

*, ** Indicate significance at 0.05 and 0.01probability levels.

DF= Days to flowering, PH=Plant height, PB/PL=Primary branches per plant, SB/P= Secondary branches per plant, BM/P= Biomass per plot, BM/PL= Biomass per plant, SY/PL= Seed yield per plant, SY/P= Seed yield per plot, HI/P= Harvest index per plot, HI/PL= Harvest index per plant, TSW= Thousand seed weight

Table.6 Genotypic direct (bold diagonal) and indirect (off diagonal) effects of the characters on seed yield per plot.

	DF	PH	PB/PL	SB/PL	BM/P	HI/P	TSW	r_g
DF	**-0.159**	-0.018	-0.118	0.097	-0.284	-0.211	0.025	-0.738
PH	0.012	**0.252**	0.045	-0.087	0.344	-0.065	0.044	0.576
PB/PL	-0.116	-0.070	**-0.162**	0.112	-0.295	-0.135	0.009	-0.684
SB/PL	-0.104	-0.147	-0.121	**0.149**	-0.267	-0.025	0.006	-0.520
BM/P	0.097	0.185	0.102	-0.085	**0.468**	0.096	0.026	0.967
HI/P	0.128	-0.062	0.083	-0.014	0.171	**0.263**	-0.026	0.591
TSW	-0.054	0.154	-0.021	0.012	0.169	-0.093	**0.073**	0.233

DF= Days to flowering, PH=Plant height, PB/PL=Primary branches per plant, SB/P= Secondary branches per plant, BM/P= Biomass per plot, HI/P= Harvest index per plot, TSW= Thousand seed weight, r_g = Genotypic correlation.

Table.7 Phenotypic direct (bold diagonal) and indirect (off diagonal) effects of the characters on seed yield per plot.

	DF	PH	PB/PL	SB/PL	BM/P	HI/P	TSW	r_{ph}
DF	**0.041**	0.005	-0.008	-0.010	-0.353	-0.105	0.011	-0.485**
PH	-0.005	**-0.041**	0.003	0.005	0.451	-0.033	0.018	-0.382**
PB/PL	0.021	0.007	**-0.017**	-0.017	-0.190	-0.056	0.003	-0.266*
SB/PL	0.014	0.007	-0.01	**-0.028**	0.007	0.048	0.005	0.052
BM/P	-0.017	-0.021	0.004	0.000	**0.879**	0.07	0.011	0.952**
HI/P	-0.017	0.005	0.004	-0.005	0.237	**0.258**	-0.001	0.524**
TSW	0.011	-0.018	-0.001	-0.004	0.240	-0.009	**0.041**	0.225

*, ** Indicates significance at 0.05 and 0.01 probability level, respectively.
DF= Days to flowering, PH=Plant height, PB/PL=Primary branches per plant, SB/P= Secondary branches per plant, BM/P= Biomass per plot, HI/P= Harvest index per plot, TSW= Thousand seed weight, r_{ph} = phenotypic correlation.

Table.8 Genotypic direct (bold diagonal) and indirect (off diagonal) effects of the characters on seed yield per plant.

	DF	PH	PB/PL	SB/PL	BM/PL	HI/PL	TSW	rg
DF	**0.208**	0.016	-0.043	-0.027	1.29	-0.612	-0.034	0.797
PH	-0.015	**-0.216**	0.017	0.024	0.384	-0.446	-0.061	-0.313
PB/PL	0.151	0.06	**-0.059**	-0.031	0.469	-0.387	-0.013	-0.191
SB/PL	0.136	0.126	-0.044	**-0.042**	0.375	-0.017	-0.008	0.526
BM/PL	0.214	-0.066	-0.022	-0.013	**1.252**	-0.421	-0.091	0.846
HI/PL	-0.152	0.115	0.027	0.001	-0.628	**0.84**	0.033	0.227
TSW	0.071	-0.132	-0.008	-0.003	1.152	-0.275	**-0.099**	0.715

DF= Days to flowering, PH=Plant height, PB/PL=Primary branches per plant, SB/PL= Secondary branches per plant, BM/PL= Biomass per plant HI/PL= Harvest index per plant, TSW= Thousand seed weight, r_g = Genotypic correlation.

Table.9 Phenotypic direct (bold diagonal) and indirect (off diagonal) effects of the characters on seed yield per plant.

	DF	PH	PB/PL	SB/PL	BM/PL	HI/PL	TSW	r_{ph}
DF	**0.002**	-0.002	-0.015	-0.010	0.312	-0.154	0.008	0.127
PH	0.0002	**0.012**	0.005	0.005	0.104	-0.090	0.012	0.027
PB/PL	0.000	-0.002	**-0.030**	-0.017	0.347	-0.076	0.002	0.253
SB/PL	0.000	-0.002	-0.018	**-0.028**	0.551	0.128	0.004	0.729**
BM/PL	0.001	0.002	-0.013	-0.019	**0.813**	-0.045	0.008	0.831**
HI/PL	0.000	0.002	0.005	-0.008	-0.076	**0.479**	0.001	0.454**
TSW	0.001	0.005	-0.002	-0.004	0.228	0.020	**0.029**	0.258**

** Indicates significance at 0.01 probability level.
DF= Days to flowering, PH=Plant height, PB/PL=Primary branches per plant, SB/PL= Secondary branches per plant, BM/PL= Biomass per plant HI/PL= Harvest index per plant, TSW= Thousand seed weight, r_{ph} = phenotypic correlation

The phenotypic path coefficient analysis also revealed that biomass and harvest index exerted high and favorable direct effects on seed yield. They had also positive and highly significant correlation with seed yield (Table 9). Day to flowering, plant height, and 1000-seed weight exerted favorable but weak influences on seed yield, whereas primary branches (-0.030) and secondary branches (-0.028) had some negative influences at phenotypic level. Although secondary branches and 1000-seed weight had positive and significant correlation with seed yield, their direct effects on seed yield was low in magnitude. The results of path coefficient analysis showed that, these correlations arose due to; their high and favorable direct effects on seed yield.

Day to flowering exerted positive indirect effect on seed yield through biomass per plant and negative indirect effects via harvest index at both levels. On the other hand, only secondary branches exerted positive indirect effects on seed yield via harvest index at phenotypic and genotypic level, respectively. Likewise, 1000-seed weight exerted favorable indirect effect (0.228) on seed yield through biomass, this was main contributor of its correlation with seed yield (r_{ph} = 0.258).

At phenotypic level, plant height exerted negligible indirect effects via all traits. It had also low positive direct effect and correlation with seed yield. On the other hand, secondary branches exerted high and positive indirect effects on seed yield via biomass and harvest index. These indirect effects were the major components of the positive and highly significant correlations with seed yield (Table 9). Primary branches exhibited high and positive indirect effects on seed yield through biomass. Therefore, the results of genotypic and phenotypic path coefficient analysis revealed advantage of biomass and harvest index for indirect improvement of seed yield.

In this study, 25 Ethiopian mustard genotypes acquired from diverse zones/regions of Ethiopia was evaluated using randomized complete block design at Haramaya campus, Rare site, East Hararge Zone, with the objectives of assessing the extent and pattern of genetic variability of Ethiopian mustard; to estimate heritability and genetic advance and to estimate association among seed yield and yield related traits and partition the genetic correlation into direct and indirect effects.

The analysis of variance showed the presence of highly significant difference among the tested genotypes for all characters considered, indicating the existence of variability among the tested genotype for these characters. High phenotypic coefficient of variation (PCV) was recorded for seed yield per plot, biomass per plot and seed yield per plant. But low PCV was detected for days to flowering and plant height. Generally, the magnitudes of PCV and genotypic coefficient of variation (GCV) were high for seed yield per plot, biomass per plot and secondary branches per plant.

Heritability estimates were very high for days to flowering, 1000-seed weight, and biomass per plot, plant height and seed yield per plot. Similarly, the heritability values of primary branches were also high. Genetic advance as percent of mean (GAM) was high for seed yield per plot and biomass per plot. Whereas, seed yield per plant and biomass per plant showed low GAM. High heritability was coupled with high GAM for biomass per plot and seed yield per plot indicating the possibility of the additive gene effects for these characters.

Seed yield per plot was positively correlated with biomass per plot, harvest index per plot, plant height, harvest index per plant and seed yield per plant at both genotypic and phenotypic levels. On the other hand, it was negatively correlated with days to flowering, and primary branches per plant at both levels and, with secondary branches per plant, biomass per plant at genotypic level.

There were positive correlations among seed yield per plant and harvest index per plant, 1000- seed weight and biomass per plant at genotypic and phenotypic levels. On the other hand, primary branches per plant and plant height had low and negative genotypic associations with seed yield per plant. However, none of the characters depicted negative and significant phenotypic associations with seed yield per plant.

Path coefficient analysis of seed yield per plot revealed that biomass per plot and harvest index per plot were major contributors of seed yield. Plant height, harvest index per plot and 1000-seed weight added indirectly to seed yield per plot via biomass per plot at genotypic level.

Similarly, plant height, harvest index per plot and 1000-seed weight had favorable indirect effects on seed yield per plot at phenotypic level. Hence, biomass and harvest index per plot were the major determinants of seed yield per plot, while plant height and 1000-seed weight were the second important characters for the improvement of seed yield in Ethiopian mustard genotype.

Similarly, biomass and harvest index per plant contributed directly to seed yield per plant at phenotypic levels. On the other hand, 1000-seed weight and plant height exerted negative direct effects on seed yield per plant at genotypic level. Nevertheless, days to flowering exerted positive indirect effects on seed yield per plant via biomass per plant and negative indirect effects via harvest index per plant at both levels.

The present study revealed that the presence of considerable variability for all the 11 characters studied. Seed yield per plot, seed yield per plant, plant height and 1000-seed weight showed high heritability coupled with high genetic advance as percent of mean. These conditions indicate that there is good opportunity these characters using the tested genotypes.

Based on correlation and path coefficient analysis, seed yield per plot was determined by biomass per plot, harvest index per plot, plant height and 1000-seed weight. Seed yield per plant was also determined by seed yield per plant and harvest index per plant.

Summing up the results, biomass per plot, harvest index per plot, plant height and 1000-seed weight could be useful for indirect selection criteria for the improvement of seed yield.

Recommendation

Based on the findings of this study, the following recommendations may be drown:

1. Varieties like, Yellow Dodola and S-67 could be used as commercial variety in Haramaya area and areas with similar agro-ecology in eastern Ethiopia.
2. PH, PB, BM/plant, BM/plot, TWS and HI could be used as a selection criteria and/or index to improve seed yield of Ethiopian mustard.
3. Accessions PGRC/E 21025, PGRC/E 20005 and PGRC/E 200017 may be used in future breeding activities to develop improved varieties.

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Appendix Table-I Mean values and range of the studied 25 genotypes for characters tested.

Entry	DF	PH	PB/PL	SB/PL	BM/PL	SY/PL	HI/PL	BM/P	SY/P	HI/P	TSW
PGRC/E 21025	81	177	16.6	34.8	47.3	8.4	0.17	2650	497	0.19	3.6
PGRC/E 20005	86	179	14.6	30	46.7	12.4	0.21	4110	806	0.21	3.4
PGRC/E 20067	90	184	13.3	25.1	49.7	9.5	0.22	3631	740	0.20	3.4
PGRC/E 20110	86	196	14.9	36.1	58.8	10.4	0.21	3793	822	0.21	3.2
PGRC/E 200017	94	188	11.9	24.2	38.7	7.7	0.22	1970	389	0.52	2.6
PGRC/E 20001	100	189	12.7	34.1	46.3	11.9	0.24	2253	596	0.26	3.3
PGRC/E 20004	108	158	11.6	25.5	46.8	6	0.19	1620	302	0.18	2.5
PGRC/E 200011	99	187	13.1	26.3	43	9.4	0.22	3510	745	0.21	3.4
PGRC/E 20006	92	162	14.3	31.5	49.7	12.5	0.22	1430	277	0.22	3.2
PGRC/E 20112	101	198	10.3	29.6	43.8	12.4	0.23	4630	1099	0.24	3.3
PGRC/E 20066	85	194	11.9	32.2	43.7	7.6	0.18	3183	519	0.35	3.4
PGRC/E 20106	91	150	12.9	27.9	31.2	9.1	0.18	867	151	0.16	3.3
PGRC/E 20132	93	181	15.2	30.4	45.7	10.5	0.25	1600	363	0.24	3.5
PGRC/E 21017	101	174	15.5	43.7	49	8.6	0.19	3620	756	0.21	3.3
PGRC/E 21008	76	157	14.1	40.5	54.8	9	0.19	4431	891	0.20	3.2
PGRC/E 21029	85	179	13.4	23.3	45	12.5	0.25	4550	1021	0.22	3.2
PGRC/E 20069	100	180	15.1	26.2	48.7	10.4	0.26	3110	754	0.67	2.9
S-67	84	191	12.8	27.9	43.8	8.8	0.23	4610	914	0.61	3.5
PGRC/E 20002	75	155	11.8	31.8	49.3	9.2	0.19	2870	534	0.18	3.1
PGRC/E 20165	90	198	12.7	32.1	55.7	11	0.25	2660	462	0.18	2.9
Yellow Dodola	86	188	14.9	36.1	41	8.5	0.22	3513	685	0.21	3.3
PGRC/E 20003	103	189	13	23.2	62.3	0.00	0.00	1430	0.00	0.00	0.0
Holeta 1	83	180	13.8	38.5	58.2	13.3	0.23	5950	1305	0.22	3.6
PGRC/E 20163	84	149	11.2	21.7	42.2	12.3	0.22	3430	784	0.22	2.9
PGRC/E 20166	98	185	11.3	29.9	52.3	8.9	0.17	2543	656	0.25	2.8

(Continued)

Mean	**90.8**	**178.3**	**13.3**	**30.5**	**47.8**	**9.6**	**0.2**	**3119.4**	**642.7**	**0.3**	**3.1**
Range	75-108	149-98	10.3-17	21-41	31.2-62	0.00-13	0.00-0.3	868-5950	0.00-1305	0.00-0.7	0.00-4
CV	2.60	5.09	9.06	23.80	21.66	25.26	13.26	20.69	24.20	11.78	6.06
LSD5%	3.8	14.6	1.96	11.74	16.02	4.01	0.051	1119	269.5	0.051	0.30
LSD 1%	5.02	19.3	2.59	15.52	22.0	5.30	0.068	1479	356.3	0.068	0.40

DF= Days to flowering, PH=Plant height, PB/PL=Primary branches per plant, SB/P= Secondary branches per plant, BM/P= Biomass per plot, BM/PL= Biomass per plant, SD/PL= Seed yield per plant, SD/P= Seed yield per plot, HI/P= Harvest index per plot, HI/PL= Harvest index per plant, TSW= Thousand seed weigh

Appendix Table of Figures used in future breeding activities to develop improved varieties

Figure.1

Yellow Dodola

Figure.2

S-67

Figure.3

PGRC/E 21025

Figure.4

PGRC/E 200017

Figure.5

PRRC/E 20005