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Full Length Research Paper

Phenotypic Variability of Ethiopian Mustard (*Brassica Carinata A.Braun.*) Genotypes in South Gondar, Ethiopia

Tesfaye Walle Mekonnen

Wolkite University, P.O.Box 07, Wolkite, Ethiopia

E-mail: tesfaye.walle@gmail.com

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The appraisal of genetic variability is basic for the purpose of to identify the most important traits in Ethiopian mustard breeding program. The objective of the study was to estimate variability, heritability and genetic advance on thirty six morphological characters of Ethiopian mustard (Brassica carinata) genotypes were evaluated at Debre Tabor, Ethiopia. The experiment was laid out in simple lattice design. ANOVA of the experiment showed highly significant (p<0.01) for day of maturity, grain filling period, secondary branches per plant, harvest index, days of flowering, plant height, primary branches per plant, biomass per plot, number of seeds per pod, seed yield per plot, oil content and oil yield per plot showed highly significant (p<0.01) difference among the tested genotypes. However, characters like number of pods per plant, 1000-seed weight and length of pod was not significant. The magnitudes of all characters had high PCV values except days to maturity, days to flowering, plant height and oil content. PCV and GCV were high for seed yield per hectare, oil yield per plot, harvest index, number of pods per plant, biomass per plot and secondary branches per plant. High heritability was coupled with high genetic advance as percent of mean for plant height, grain filling period, secondary branches per plant, number of pods per plant biomass per plot, seed yield per plot and oil yield per plot.

Keywords: Ethiopian mustard, genetic advance, genetic variability, heritability.

INTRODUCTION

Ethiopian mustard (*Brassica carinata*) is one of six economically important species, Brassica carinata, commonly known as Ethiopian mustard, arose as a natural cross between B. nigra and B. oleracea in north-eastern Africa, in all probability in the Ethiopian plateau, where wild forms of B. nigra co-exist with cultivated forms of B. oleracea since ancient times (Tsunoda 1980). The species is only found under cultivation, mainly in Ethiopia and surrounding countries (Hanelt, 1986).

In Ethiopia, it is cultivated as an oilseed crop science ancient time and third in its production next to noug (Guizotia abyssinca Casa) and Linseed (Linum ustatismum L). 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, 2002).

The oil present in the embryo represent about 38-45% of the seed dry weight. The meal that is remaining after oil extraction is protein rich (30-45%) to be used either as high protein feed supplement provided that glucosinolate level is reduced or as organic fertilizer (Nigussie, 1999). The industrial value of its oil is indeed immense in: leather tanning, the manufacture of varnishes, diesel fuel, soap and lamps (Doweny, 1971; Bhan, 1979). Therefore, Ethiopian mustard can be an alternate choice by improving the oil and protein contents of an already adapted high yield giving oilseed varieties (Nigussie, 2001). Furthermore, adding Ethiopian mustard to everyday meal as a vegetable is advantageous. This is because; it has special nutritional components like vitamins, minerals, trace elements, dietary fiber and protein. It also gives zest and flavor of diets (Zemede, 1992; Tsige et al., 2005). Additional advantage of Ethiopian mustard is also immense in the farming systems, as a potential rotational-crop for

Table 1. List of genotypes considered in the study and their origin

Code	Acc.No.	Area of collection	Altitude(m)	Code	Acc.No.	Area of collection	Altitude(m)	Code	Acc.No.	Area of collection	Altitude(m)
1	PGRC/E 20052	AdisAlem	2540	13	PGRC/E208558	*	*	25	PGRC/E21001	Shewa/Jibat	2350
2	"20059	Shewa/Chaliya	1630	14	"208559	*	*	26	"21057	Gojjam	*
3	"20068	Shewa/Ambo	2010	15	"208560	*	*	27	"21069	Bale	2450
4	"20080	*	*	16	"208565	*		28	"21162	Bedele	1920
5	"20163	East Tigray	2300	17	"208570	*	*	29	"21163	Wellega/Jima Arjo	1820
6	"20168	Gondar	2400	18	"208571	*	*	30	"21266	Wollo/Borena	2570
7	"20169	*	*	19	"208572	*	*	31	"21278	Welo/Desezuriya	*
8	"208507	*	*	20	"208576	*	*	32	"21369	Jimma	1720
9	"208524	*	*	21	"208584	*	*	33	"213168	Kefa	*
10	"208528	*	*	22	"208585	Shewa/Boset	1600	34	YD	Released in 1986	
11	"208545	*	*	23	"208594	Hararghe	1750	35	Holetta-1	Released in 2005	
12	"208551	*	*	24	"208961	E. Wellega	2700	36	Local check	®	2240

*donated by foundation for agricultural plant breedingS.V.P.P.O.Box117 Wageningen, the Netherlands. - : Information not available. Code: Genotype by code. Acc. No: Genotype accession number.

cereals and pulses. Once seedling is established, broad statures of the leaves make canopy and suppress weeds, making the crop tolerant to weed infestation. It is known to improve soil structure and aeration due to the deep rooting nature of the crop (Doweny and Röbbelen, 1989). At earlier stages of development, the leaves and shoots of the crop are consumed as vegetable either by thinning or topping and seed can also be harvested from the plant for oil extraction and other traditional uses (Misteru and Yared, 2013; Adefris, 2005).

Understanding the pattern and extent of genetic diversity in a population is pivotal to the success of any crop improvement programme. It can provide valuable information for plant breeders who are interested in introgressing agronomically desirable traits into established cultivars or to select lines from the existing diversity. To this end, there had been efforts in Ethiopian mustard germplasm collection and characterization in the country. Ethiopia has a huge endowment of Ethiopian mustard genetic diversity. In fact activities to characterize, classify and identify the regional genetic wealth are minimal. Therefore, this research was undertaken to assess the genetic diversity, heritability and genetic gain of Ethiopian mustard genotypes from in different parts of Ethiopia.

MATERIAL AND METHODS

Description of the experimental site

The field experiment was conducted at Debre Tabor during the main rainy season in 2010. The research station is located at 11º 89' N latitude and 39 º 09' E longitudes with an average elevation of about 2630 meter above sea level (m.a.s.l). The location is found in Amhara National Regional State, **South Gondar** Administrative Zone. The major portion of the total annual rainfall received **between** June and October with an average rainfall of 1235.63 mm per annum, and the average minimum and maximum temperature of the study area are 9.71^0c and 21.82^0c, respectively, with average temperature of 12.11^0c. The most dominant soil type of the area is well-drained red brown (Tsige, 2002).

Experimental materials and procedures

A total of thirty six genotypes of Ethiopian mustard were used in the study. The genotypes were collected by Institute of Biodiversity and Conservation (IBC) from diverse agro-ecological areas of northern Ethiopia with an altitude range of 1600- 2700 meter above sea level, representing one of the major mustard production areas in the country. The genotypes and area of collection were described in Table 1.

The experiment was laid as 6x6 simple lattice designs using 5 m x 1.8 m plots with two replications. Single row plots, with each row 5m long and spacing between plots, rows and replications were 0.6 m, 0.3 m and 2 m, respectively. The rates of fertilizer application was 40.3 kg/ha and 150 kg/ha Urea and DAP respectively. Fertilizer were applied only at sowing and the seed rate

was 10 kg/ha. Other cultural practices were followed as recommended for the area (Nigussie, 2002).

Data collection

The following data were collected from the experiment both per plot and per plant basis.
The following data was recorded from the central four rows.
1. Days to flowering (DF): It was recorded as number of days from planting to a stage when 50% of the plants in a plot produced flower.
2. Days to maturity (DM): The number of days from the date of sowing to a stage when 90% of plants have reached their physiological maturity.
3. Biomass (BM/P): The total above ground biological yield in grams obtained from each plot at harvest.
4. Harvest index (HI/P): The fraction of dry seed in the above ground biological yield on a plot basis.
5. Thousand Seed weight (TSW): The weight in grams of 500 seeds sampled from each plot and multiplied by two.
6. Seed yield (SY/P): Seed yield per plot was measured in grams after moisture of the seed is adjusted to 7%.
7. Oil content (OC): The proportion of oil in the seed to the total oven dried seed weight as measured by Nuclear Magnetic Resonance Spectrometer (NMRS).
8. Oil yield (OY/P): The amount of oil in grams obtained by multiplying seed yield per plot by corresponding oil percentage.
The data for the following characters were recorded from ten randomly taken plants each experimental plot and the average were considered per plant basis.
1. Primary branches per plant (PB/PL): The average number of primary branches per plant.
2. Secondary branches per plant (SB/PL): The average number of secondary branches formed on primary branches per plant.
3. Number of pods per plant (PD/PL): The average number of pods counted from the same sample plants.
4. Silique (Pod) Length (SL): The main Silique from the ten sampled plants were measured in cm and averaged to represent the pod length.
5. Number of seeds per pod (SD/PD): The average number of seeds per pod obtained from two randomly sampled pods of each of the 10 randomly taken plants.
6. Plant height (PH): The height of plants in each plot measured in centimeters from the ground surface to the top of the main stem at maturity.

Statistical analysis

Data were subjected to analysis of variance using the procedures outlined by Steel and Torri, 1980); Gomez and Gomez, (1984). Least significant difference (LSD) was used to separate the means both 1 and 5% probability levels using SAS (2001). The Genotypic variance (σ^2_g) and phenotypic variance (σ^2_P) were estimated as suggested by Johnson *et al.* (1955), heritability (h^2) for all characters was computed as suggested by Falconer and Mackay (1996) Heritability (h^2) = $H = \frac{\sigma^2 g}{\sigma^2 p} X100$, expected Genetic advance (GA) for each character selection of superior at 5 % of the genotypes was computed in accordance with the methods illustrated by Johnson et al., (1955) and Allard (1960) as: $GA = K^* \sqrt{(\sigma^2 p)} * h^2$ Or $GA = K^* \sigma_P * h^2$ and genetic advance as percent of mean was calculated to compare the extent of predicted advance of different traits under selection, using the formula described by Comstock and Robinson (1952); $GAM = \frac{GA}{\bar{X}} X100$.

RESULT AND DISCUSSION

Analysis of Variance (ANOVA)

The analysis of variance for characters showed significant difference between genotypes (Table 2). Among 16 characters, 12 traits (day of maturity, grain filling period, secondary branch per plant, harvest index, day of flowering, plant height, primary branch per plant, biomass per plot, number of seeds per pod, seed yield per plot, oil content and oil yield per plot) showed highly significant ($p<0.01$) difference among the tested genotypes. However, characters like number of pods per plant, 1000-seed weight and length of pod was not significant.

Range and mean of different characters

The mean values of studied traits showed wide range of variability for most of the characters (Table 3). Days to flowering ranged from 51 to 106 with a mean of 77.8 days. Days to maturity ranged from134 to 192 with a mean of 159 days. The grain-filling period from 33 to 129, with the mean of 81.3 days.

Plant height varied from 116 cm to 223 cm with a mean height of 147.9cm. Number of pod per plant ranged from 58 to 403 with a mean of 165.4. Number of seed per pod varied from six to 19 with a mean of 12.5. Biomass yield ranged from 1300 gm per plot to 7520 gm per plot with a mean of yield of 3700 gm per plot. The range of harvest index ranged from 112.86 to 879.28 with a mean value of 339.51. Thousand seed weight ranged from 2.3 to 6 gm per plot with a mean value of 3.7 gm per plot, oil yield per plot ranged from 37.65 to118.41 with a mean value of 67.72 and there was a wide variation for the oil content it ranged from 36% to

Table 2: The mean squares, error and CV (%) for the 16 characters studied.

Characters	Replication (df=1)	Genotypes (35)	Error (71)	CV (%)
DF	1449.01	246.83*	139.41	17.50
MD	58.68	259.38**	78.34	6.19
GFP	924.50	600.88**	135.19	15.37
PH	3068.06	8443.00*	114.54	6.29
PBP	0.01	4.68*	2.33	11.41
SBP	4.01	485.21**	34.04	15.16
LP	2.72	0.40NS	0.29	13.89
NPP	11138.24	26.44NS	4826.97	26.44
NSP	9.78	4.41NS	4.28	15.87
BM(gm)	2.14	2.213*	1.18	24.98
BMh	5932098.80	6146428.60	3266225.70	24.98
HI	94955.69	43406.92**	29184.58	29.72
TSW	0.34	0.35NS	0.29	13.49
SY	58319.07	157404.78**	101594.99	15.46
SYh	58319.07	437235.51**	101594.99	15.46
OC	2.77	6.75**	1.96	3.42
OY	1122.03	496.24*	230.82	16.69

Where; Df = degrees of freedom, ns = not statistically significant; *, ** = significant at the 0.05 and 0.01 probability levels, respectively; and CV (%) = coefficient of variation, DF = Days to flowering, DM = Days to maturity, GFP =Grain filling period, PH = Plant height, PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, LP= Length of pod, NPP = Number of pods per plant, NSP =Number of seeds per pod, BM = Biomass per plot, BMh = Biomass/hectare(kg), SY(gm) = Seed yield per plot, SYh = Seed yield per hectare, HI/P = Harvest index per plot, TSW =Thousand seed weight, OC = Oil content and OY/P = Oil yield per plot.

46.3% with a mean value of 41.8%.

Seed yield per hectare ranged from 1160.57 kg/ha to 2613.89 kg/ha, which was really a wide variation with a mean value of 1613.03 kg/ha. The maximum yield was obtained from PGRC/E 208572 followed by PGRC/E 208524 and PGRC/E 208545 (Table 3). The high yielding genotype PGRC/E 208572 had a yield advantage of 47.2% and 62.3% over Yellow Dodolla and Holetta-1, respectively. Similarly, it had a yield advantage of 49% as compared with the local check.

Phenotypic and genotypic variations

The estimations of variance components, phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) of the characters studied were obtainable in Table 3. The genotypic variance took relatively much of the total variances for days to maturity, days to flowering, 1000-seed weight, plant height, number of pods per plant, biomass per plot, secondary branches per plant, seed yield per plot and oil content. These effects were also detected from high heritability estimates for these characters (Table 3). On the other hand, comparatively lower variances share of the total variance were observed for 1000-seed weight, primary braches per plant, number of seeds per pod and pod length oil yield per plot, indicating the greater share of environmental variance in the total variability.

The GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7% (Table 3). In most cases, the PCV values were greater than the GCV values for all characters studied. Comparatively high GCV estimates were observed for number of pods per plant, primary and secondary braches per plant, seed yield per plot, oil yield per plot, biomass per plot, harvest index and seed yield per hectar. Hence, there is a good opportunity for the improvement of these characters in the tested genotypes. Yadav and Hari (1996) 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, 1000-seed weight, plant height, pod length, number of seed per pod and the present findings are nearly similar with these results.

Table 3: estimates of mean, range, variance components, and coefficients of variability, heritability and genetic advance of the 16 characters studied.

Characters	Range	Mean±*Std.E*	σ^2_g	σ^2_e	σ^2_{ph}	GCV (%)	PCV (%)	h^2b (%)	GA	GAM (%)
DF	51-106	77.8 ± 1.5	90	77.35	167.35	12.19	16.63	53.78	14.35	18.45
MD	134-192	159 ± 1.6	103.69	70.38	174.07	6.4	8.3	59.57	16.21	10.2
GFP	33-129	81.3 ± 2.2	188.3	173.88	362.18	16.87	23.39	51.99	20.41	25.09
PH	116-223	147.9± 2.9	394.92	202.28	597.21	13.44	16.53	66.13	33.34	22.55
PBP	8.0-24	15.4± 0.4	8.64	190.15	198.79	19.12	91.7	4.34	1.26	8.22
SBP	4.0-45	20.9 ±1 .3	85.42	27.44	112.86	44.14	50.73	75.69	16.59	79.21
LP	3.0-6	4.4 ± 0.1	0.18	0.66	0.84	9.64	20.82	21.59	0.41	9.27
NPP	58-403	165.4 ± 9.5	4612.45	1913.34	6525.79	41.06	48.84	70.68	117.79	71.21
NSP	6.0-19	12.5 ± 0.3	0.56	6.86	7.42	5.97	21.72	7.55	0.42	3.38
BM (gm)	1.3-7.52	3.7 ± 0.2	0.74	0.81	1.55	23.1	33.43	47.65	1.22	32.86
BMh	2167-12533	6207±254.04	2045837	2246655.6	4292492.5	23.04	33.38	47.66	98.3226	32.82
HI	11286-879.28	339.5 ± 19.4	16614.01	10178.9	26792.91	37.97	48.21	62.01	209.39	61.68
TSW	2.3-6	3.8 ± 0.1	0.04	0.55	0.59	5.33	20.48	6.24	0.1	2.63
SY/P (gm)	940.47-2788.43	1613 ± 44.9	103050.3	43861.2	146911.5	18.64	34.11	70.14	554.65	49.36
SY (Ka/ha)	564.28-2185.74	1123.7 ± 48.3	51832.72	113554.77	165387.49	20.89	25.21	31.34	262.94	16.3
OC	36-46.3	41.8 ± 0.3	3.23	3.9	7.13	4.3	6.39	45.28	2.49	5.97
OY	37.65-118.41	67.7 ± 2.2	128.71	205.57	334.28	21.17	27	83.56	3151.76	46.55

Where: Std.E=standard error, σ^2_g=Genotypic variance, σ^2_{ph}=Phenotypic variance, σ^2_e =Environmental variance, GCV percentage=Genotypic coefficient of variation, PCV percentage=Phenotypic coefficient of variation, ECV percentage=Environmental coefficient of variation, h^2b =heritability in broad sense, GAM=Genetic advance in percent of mean at 5 %, GA=genetic advance. DF = Days to flowering, DM = Days to maturity, GFP =Grain filling period, PH = Plant height, PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, LP= Length of pod, NPP = Number of pods per plant, NSP =Number of seeds per pod, BM = Biomass per plot, BMh =SY(gm) = Biomass/ha (kg), Seed yield per plot, SYh = Seed yield per hectar, HI= Harvest index per plot, TSW =Thousand seed weight, OC = Oil content and OY = Oil yield per plot..

The range for PCV estimate was 8.3% for days to maturity to 91.7% for day to maturity primary branches per plant respectively. The PCV values were number of pods per plant, primary and secondary braches per plant, seed yield per plot, oil yield per plot, biomass per plot, harvest index and seed yield per hectare. The higher GCV and PCV for seed and oil yields, harvest index, biomass, number of pods per plant, primary and secondary branches provided better scope for improvement through selection. Generally, the GCV estimates nearly approached PCV estimates for days to flowering, days to maturity, plant height, oil content, oil yield per plot, seed yield per hectare, number of pod per plant, secondary branch per plant height and grain filling period indicating their sensitivity to environmental fluctuation and its influence of on these characters was high. However, there was a wide difference between PCV and GCV estimates primary branches per plant, pod length, number of seed per pod, harvest index, biomass per plot, 1000-seed weight and seed yield per plot, suggesting minimal influence of environment on the expression or their relative resistance to environmental alterations. Likewise, the PCV estimate was more than four-fold compared to the GCV estimate for 1000-seed weight and primary branches plant and nearly about three-fold for number of pod per plant. This indicates the presence of considerable influence of environmental factors on these characters.

Heritability estimates

In this study estimate of heritability (in broad sense) values for the 16 characters ranged from 4.34% primary

branches per plant to 83.56% for oil yield per plot. Based on Dabholkar's (1992) classification, days to maturity, days to flowering, grain-filling period, number of pods per plant, secondary branches per plant, plant height, biomass per plot, seed yield/plot and hectare, harvest index, oil yield per plot, and oil content exhibited high or very high heritability estimates. Hence, a good genetic progress can be made if some of these traits are considered as selection criteria. High heritability estimates were also obtained for days to flowering, plant height and grain yield by Major and Singh (1996). Similarly, high heritability estimates for days to flowering and maturity was reported by (Tewodros et al., 2013).

Estimates of expected genetic advance

The genetic advance as the percentage of the mean at 5% selection intensity showed in Table3. Estimates of genetic advance as percent of mean at 5% selection intensity ranged from 2.63 for 1000-seed weight to 79.21 for secondary branches per plant. Moderately highest genetic advance were observed for secondary branches per plant, harvest index, number of pods per plant, seed yield per plot and oil yield per plot. In the same way, estimates of genetic advance (as percent of the mean) for days to flowering, days to maturity, grain filling period, plant height, biomass per plot and seed yield per hectare were also considerably high. However, number of seeds per pods, pod length, oil content, and 1000-seed weight per plot and primary branches per plant showed less than 5%. A low GCV and low GAM observed for these characters indicated that the characters were under high environmental influence, and that selection based on these characters would be ineffective. Major and Singh (1996) reported high genetic advance as percent of the mean for plant height. Similarly, high genetic advance as percent of the mean was reported for number of pods per plant (Major and Singh, 1996; Shalini et al., 2000) and number of seeds per pod (De et al., 2000). According to Johnson *et al*. (1955) high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The present study also showed high heritability coupled with high-expected genetic advance as percent of mean for secondary branches per plant harvest index, and seed yield per plot only. Therefore, these characters could be improved more easily than other characters measured in this study.

CONCLUSION

In the present study, secondary branches per plant, number of pod per plant, harvest index and biomass per plot were high PCV and GCV values. Similarly, oil content and day to maturity were low value at both levels. The low GCV value of character suggests the difficulty of improving traits through simple selection. If the difference between PCV and GCV values were high indicating great roll of environment on the expression of characters and if it is low suggesting slight influence of environment on the expression of the characters and easy for improving these traits through simple selection.

High estimates of broad sense heritability were very low for 1000-seed weight, length of pod, number of seed per pod and primary branches per plant; but the characters were very high. Genetic advance as percent of the mean (GAM) was high for secondary branches per plant, number of pod per plant and harvest index whereas, number of seeds per pod, 100-seed weight and oil content showed low GAM. High heritability was coupled with high GAM for secondary branches per plant, number of pod per plant and harvest index and oil yield per plot, indicating the presence of additive gene effects for these characters.

Generally, the tested genotypes were highly variable. The characters showing wide range of variation offer opportunities for genetic improvement through selection or selection. The significance of genotype difference indicates the presence of variability for each of the characters among the tested entries.

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