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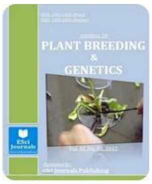

GENOTYPIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN ETHIOPIAN MUSTARD (*BRASSICA CARINATA* A.BRAUN.) GENOTYPES AT NORTHWESTERN ETHIOPIA

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ABSTRACT

The assessment of genetic variability is fundamental 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 Adet Agricultural Research Center, 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, number of pod per plot, secondary branches per plant, harvest index, seed yield per plot, seed yield per hectare and oil content. Significant differences ($p<0.01$) were noted for day of flowering, plant height, primary branch per plant, biomass per plot, oil yield per plot. High phenotypic coefficient of variation (PCV) was recorded for days to flowering, grain filling period, plant height, secondary branches per plant, harvest index, oil yield per plot, seed yield per plot and hectare. The magnitudes of PCV and genotypic coefficient of variation (GCV) were high for grain filling period, plant height and secondary branches per plant. Heritability estimates were high for days to maturity, grain-filling period, days to flowering, plant height, biomass per plot, secondary branches per plant, primary branches per plant, oil content and oil yield per plot. High heritability was coupled with high genetic advance as percent of mean for plant height, grain filling period, secondary branches per plant were recorded. The study showed that there are variation in the extent of genetic variability, heritability and genetic advance in traits under study which can facilitate selection for further improvement of important traits of Ethiopian mustard.

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). The crop is used both as a leaf vegetable as well as an oil crop. 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* L), is the main commercial product (Nigussie, 2001). 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, 1990). 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).

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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 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 (Nigussie, 2001; 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.

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 MATHEDS

Description of the experimental site: The field experiment was conducted at Adet Agricultural Research Center which is located at 37°29 ´E and 11°16 ´N in the Amhara National Regional State, Ethiopia. Adet is found 45km from Bahir Dar along the main road that runs from Bahir Dar to Addis Ababa through Motta. It is located at 2240 meter above sea level (m.a.s.l) and receives an average annual rain fall of 1230 mm.

Experimental materials and Procedures: Thirty six genotypes of Ethiopian mustard including the standard check (Holetta-1and Yellow Dodolla) were used in the study. The genotypes were collected by Institute of Biodiversity and Conservation (IBC) from diverse geographical region of the country. The genotypes by origin are described in Table 1.

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	Shewa/Adis Alem	2540	13	PGRC/E208558	*	*	25	PGRC/E 21001	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	LC	®	2240

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

The experiment was carried out using 6x6 simple lattice designs with two replications. Each genotype was planted in a plot size of 9 m^2 (6 rows, 5 m row length x 1.8m width). The distances 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. Fertilizers were applied in one times at sowing; the seed rate was 10 kg/ha. Seed and fertilizer were drilled uniformly by hand. Other cultural practices were followed as recommended for the area (Nigussie, 2001).

Statistical Analysis: Data was 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 statistical software. 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;

$$GA = K * \sqrt{(\sigma^2 p)} * h^2 \text{ Or } GA = K * {}_{\sigma P} * h^2$$

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); $GAM = \frac{GA}{\bar{X}} X100$.

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA): Among 16 characters, eight (day of maturity, grain filling period, number of pod per plot, secondary branches per plant, harvest index, seed yield per plot, seed yield per hectare and oil content) showed highly significant ($p<0.01$) difference among the tested genotypes. Similarly, day of flowering, plant height, primary branch per plant, biomass per plot, oil yield per plot revealed significance difference at ($p<0.05$) among tested genotypes.

Generally, the tested genotypes were highly variable. The characters showed wide range of variation, providing opportunities for genetic improvement through selection or cross breeding of the Ethiopian mustard.

Range and mean of different characters: The estimated range and mean of the characters studied were presented in Table 3. Wide ranges of variability were recorded for number of pods per plant, harvest index, grain-filling period, seed yield per hectare and seed yield and oil yield per plot. This result was in concord with report of Ahmed *et al*. (2002) who noted wide range of variations in days to maturity, plant height, seeds per pod, secondary branches and 1000-seed weight in Ethiopian mustard genotypes.

More than half of the tested genotypes (25) had mean maturity period below the overall mean of the genotypes (Table 3). Twenty-two and 26 genotypes were earlier maturing than the released varieties (Yellow Dodolla and Holetta-1), respectively.

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

Character	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

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.

Hence, there is an opportunity to find genotypes, among the tested entries, that perform better than the existing varieties in moisture stressed areas and/or to use them as parents for hybridization programs. However, nine genotypes matured later than the nationally released varieties (Yellow Dodolla). The mean value of plant height for all the genotypes was high (170 cm) and 26 genotypes had shorter statures. Mean values for primary branches per plant, secondary branches and number of pods per plant for the genotypes were 13.37, 38.76 and 145.19, respectively as shown in Table 3. More than half of the genotypes (19) were observed to have mean number of pods per plant had less than the grand mean. Biomass yield ranged from 2333 kg/ha to 13333 kg/ha with a mean of yield of 7236 kg/ha. Plant height varied from 134 cm to 198 cm with a mean height of 170 cm. The range of harvest index ranged from 1400 gm/plot to 8000 gm/plot, with a mean value of 4341.67gm/plot. Thousand seed weight ranged from 2.3 to 4.75 gm, with a mean value of 3.75 gm, and there was a wide variation for the oil content, which ranged from 37% to 45.4%, with a mean value of 40.97 %. Seed yield per hectare ranged from 1090.69 kg/ha to 3151.10 kg/ha, with the mean value of 2063.63 kg/ha, which was really a wide variation with a mean value of 2060.42 kg/ha. The maximum yield was obtained from PGRC/E-20052 followed, by PGRC/E-208572 and PGRC/E- 208524 (Table 3). The high yielding genotype PGRC/E-20052 had a yield advantage of 47.2% and 62.3%, respectively compared with that of the standard checks (Yellow Dodolla and Holetta- 1).

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

Character	Mean±Std. E	Range	σ2g	σ2e	σ2ph	GCV (%)	PCV (%)	h2b (%)	GA	GAM %
DF	67.32±1.71	46-100	53.71	139.41	193.12	10.89	20.64	27.81	7.97	11.84
MD	142.96±1.52	126-179	90.52	78.34	168.86	6.64	9.07	53.61	14.37	10.03
GFP	75.64±2.29	34-122	232.84	135.19	368.03	20.17	25.36	63.27	25.04	33.1
PH	170±1.74	134-198	4164.23	114.54	4278.77	37.96	38.48	97.32	131.33	77.25
PBP	13.3686±0.22	10-17.1	1.17	2.33	3.5	2.8	4.83	33.55	1.3	3.34
SBP	38.49±1.89	15-82	225.59	34.04	259.63	39.02	0.22	86.89	28.88	0.40
LP	4.39±0.08	3-6	0.05	0.29	0.35	0.16	0.41	15.7	0.19	0.13
NPP	141.75±11.42	24-514	0.06	4.28	4.34	1.92	15.98	1.45	0.06	0.48
NSP	13.04±0.25	9-18	0.06	4.28	4.34	1.88	15.58	1.44	0.06	0.46
BM (gm)	4341.67±153.68	1400-8000	1105.91	1.18	1107.09	0.76	0.76	99.89	68.57	1.58
BMh	7236±256.14	2333-13333	1440101.45	3266225.70	4706327.15	16.58	29.98	30.60	1369.50	18.93
HI	540.38±29.62	182-1390	7111.17	29184.58	36295.75	15.42	34.83	19.59	77	14.08
TSW	4±0.07	3-6	0.03	0.29	0.32	4.19	14.11	8.72	0.1	2.54
SY/P(gm)	1237.2±36.5	654.41-1890.66	6041.49	36574.2	42615.69	6.28	25.17	14.18	91.08	12.92
SY (kg/ha)	2062±60.83	1090.69-3151.1	16782.03	101594.99	118377.02	6.28	25.15	14.18	151.81	32.32
OC	40.96±.25	37-45	2.39	1.96	4.35	3.78	5.09	54.99	2.37	5.78
OY	91.0383±2.28	45.7-145.19	132.71	230.82	363.53	12.64	20.92	36.51	14.36	15.75

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.

Phenotypic and Genotypic variations: According to Deshmukh *et al.* (1986) PCV and GCV values greater than 20% were regarded as high, whereas values less than 10% are considered low and values in between 10% and 20% to be medium. Based on this description, secondary branches per plant, days to flowering, grain-filling period, harvest index, seed yield per hectare and oil yield per plot had high coefficient of variation (PCV) values. The PCV values for 1000-seed weight, seeds/pod and number of pods per plant were medium. However, numbers of days to maturity, primary braches per plant, biomass yield/hectare, pod length and oil content had low PCV values, which was as low as 0.22 for secondary branches/plant. Phenotypic coefficient variation was generally higher than GCV values in all characters in this study (Table 3) this could be due to high environmental influence. Genotypic coefficient of variability (GCV) values were recorded high for primary branches per plant, days to maturity, seed yield per plot, seed yield per hectare, 1000-seed weight, number of seed per pod ,number of pods per plant, oil content and biomass yield/hectare; had high GCV value. The high GCV values of these characters suggest that the possibility of improving these trait through selection.

The difference between PCV and GCV values was estimate high for seed yield per hectare, number of seeds per pod, number of pods per plant, secondary branches per plant, harvest index, number of pods per plant, oil yield, days to flowering and grain filling period; which indicated a large extent of the environment influences on these characters. However, this difference was low for days to maturity, plant height, 1000 - seed weight, oil content, primary braches per plant, pod length, biomass yield per hectare; suggesting minimal influence of environment on the expression of the characters so that it is easy to improve these characters in the improvement programs.

Heritability Estimates: The estimated heritability for the studied characters was present in Table 3. These estimated values for the 16 characters were ranged from 1.44% for seeds per plant to 99.89% for biomass per plot. According to Dabholkar (1992) generally classified heritability estimates as low (5-10%), medium (10-30%) and high (30-60%). Based on this classification, days to maturity, grain-filling period, primary branches per plant, secondary branches per plant, plant height, biomass per plot, oil yield per plot, and oil content exhibited high or very high heritability estimates. Hence, a good progress can be made if some of these traits were considered as selection criteria. High heritability estimates were also obtained for plant height and grain yield by Major and Singh (1996). Similarly, high heritability estimates for days to flowering and maturity reported by Dhagate *et al*., (1972).

Understanding of heritability of a trait guides a plant breeder to predict performance of succeeding generations and helps to predict the response to selection (Larik *et al*., 1989). On the other hand, number of pods per plant, number of seed per plot and 1000 seed weight exhibited low heritability estimates. Then again, days to flowering, pod length, harvest index, seed yield per plot, seed yield per hectare, exhibited medium heritability estimates; Dabholkar (1992) explained that heritability of a character refers to a particular population under particular environmental conditions where the experiment was conducted. Moderate heritability estimates suggest that selection should be late to more advance generations for this character.

Estimates of Expected Genetic Advance: The genetic advance as the percentage of the mean at 5% selection intensity was presented in Table 3. Estimates of genetic advance as percent of mean at 5% selection intensity ranged from 0.13 for pod length to 77.25 for plant height. Moderately highest genetic advance was observed for secondary branches per plant, harvest index, seed yield per plot and seed yield per hectare. In the same way, estimates of genetic advance (as percent of the mean) for grain filling period, plant height, and seed yield per hectare were also considerably high (Table 3). However, day to maturity, number of per plant, number of seed per pods, pod length, biomass per plot, oil content, and 1000-seed weight per plot and primary branches per plant, seed yield per plot and hectare 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 less effective. Major and Singh (1996) and De *et al*. (2000) reported high genetic advance as percent of the mean for plant height. As opposed to the present investigation, high genetic advance as percent of the mean was reported for seed yield per hectare (Major and Singh, 1996; Shalini *et al*., 2000).

According to Johnson *et al*. (1995) high heritability estimates along with the high genetic advance is usually more helpful in predicting increase under selection than heritability estimates alone. The present study showed that high heritability coupled with high expected genetic advance as percent of mean for plant height, grain filling period and secondary branches per plant plot only. Therefore, these characters could be improved more easily than other characters measured in this study. At the present most of the characters in these genotypes had shown high heritability and very low genetic advance as percent of the mean, this makes the improvement program of important traits or characters of Ethiopian mustard makes complicated.

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