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ANALYSIS OF GENETIC PARAMETERS ON ETHIOPIAN MUSTARD (*BRASSICA CARINATA* A. BRAUN*)* GENOTYPES IN NORTHWESTERN ETHIOPIA

ABSTRACT

This study was carried out with the objective to estimate the genotypic variability and other yield related traits of Ethiopian mustard in North West Ethiopia. A total of 36 genotypes of Ethiopian mustard were considered for this study. Analysis of variance was computed to contrast the variability within the collected genotypes based on yield and other yield related traits. The results revealed highly significant values($p<0.01$) for days to 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 ($p<0.05$) were noted for days to flowering, plant height, primary branch per plant, biomass per plot, oil yield per plot differences among the genotypes. Genotypic coefficient of variation (GCV %) was lower than phenotypic coefficient of variation (PCV %) for all the traits studied. High genetic advance with heritability was observed in the following characters; plant height, biomass of the plant, number of secondary branch per plant and grain filling period. There are variations in the extent of genetic variability, heritability and genetic advance of traits which can facilitate selection for further improvement of important traits of Ethiopian mustard. Therefore, it can be concluded that the variability within Ethiopian mustard genotypes collected from different areas of northern Ethiopia is high and vital for better crop improvement.

Key words: Ethiopian mustard, genotype, heritability, phenotype, variability.

INTRODUCTION

Ethiopian mustard (*Brassica carinata A. Braun*) is one of the most economically important crop in Ethiopia. *Brassica carinata*, commonly known as Ethiopian mustard, arose naturally from a cross between *B. nigra* and

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B. oleracea in the horn of Africa (Nigussie, 1990). The species is only found under cultivation, mainly in Ethiopia and surrounding countries (Hanelt, 1986; Tsunoda 1980). It is cultivated as leaf vegetable and oilseed crop next from noug (*Guizotia abyssinca* Casa) and Linseed (*Linum ustatismum* L) in the country. The oil content of mustard varies, ranging from 38-45% depending on the variety. Apart from vegetable and oil, it is also used as raw materials in industries, where its oil is indeed of immense importance in: leather tanning, manufacture of varnishes, diesel fuel, soap and lamps (Nigussie, 1999; Tesfaye *et al.*, 2011).

In Ethiopia, although reliable statistical information on the distribution and production of mustard is lacking, the crop has been cultivated widely in many areas of the country with low amount of yield (Tesfaye *et al.*, 2011). This might be due to the fact that mustard has been widely neglected by research and development programs (Jianchu *et al.*, 2001) and its genetic resources are being eroded by physical and bio-physical factors (Tewodros and Biruk, 2012). As a result, the country frequently faces a considerable amount of genetic erosion for the last decades (Adefris, 2005; Tewodros and Getachew, 2013). Therefore, collection and evaluation of Ethiopian mustard genotypes is the best means of obtaining genetic variability for further improvement of this crop (Nigussie, 2002; Adefris, 2006). Genetic variability is found to be the principal raw materials of any breeding programme (Zemede, 1992; Tsige *et al.*, 2005). Determining the level of variation and identifying the variants within the collected species is invaluable for genetic improvement and conservation of the crop (Tewodros and Biruk, 2012; IPGRI/IITA, 1997). However in Ethiopia, where mustard is becoming an important vegetable and oil crop, there has been little effort so far with regard to the estimation of the level and magnitude of genetic variation among the collected genotype of this crop. Therefore, the present study intended to estimate the nature and extent of genetic variability of collected Ethiopian mustard in North West parts of Ethiopia.

MATERIAL AND METHODS

Description of the study area

The field experiment was conducted at Adet Agricultural Research Center which is located at a latitude of 11°16´N and longitude 37°29´E at an altitude of 2240 meter above sea level (m.a.s.l). The area receives mean annual rainfall of 1230 mm with maximum and minimum temperature of 26.1°C and of 13.50°C, respectively. The soil is sandy loam with pH 5.90.

Table1

List of genotypes considered in the study and their origin

Code	Accession Number.	Area of collection	Altitude [m]
1	PGRC/E 20052	Shewa/AdisAlem	2540
2	"20059	Shewa/Chaliya	1630
3	"20068	Shewa/Ambo	2010
4	"20080	*	*
5	"20163	East Tigray	2300
6	"20168	Gondar	2400
7	"20169	*	*
8	"208507	*	*
9	"208524	*	*
10	"208528	*	*
11	"208545	*	*
12	"208551	*	*
13	PGRC/E208558	*	*
14	"208559	*	*
15	"208560	*	*
16	"208565	*	
17	"208570	*	*
18	"208571	*	*
19	"208572	*	*
20	"208576	*	*
21	"208584	*	*
22	"208585	Shewa/Boset	1600
23	"208594	Hararghe	1750
24	"208961	E. Wellega	2700
25	PGRC/E 21001	Shewa/Jibat	2350
26	"21057	Gojjam	*
27	"21069	Bale	2450
28	"21162	Bedele	1920
29	"21163	Wellega/Jima Arjo	1820
30	"21266	Wollo/Borena	2570
31	"21278	Welo/Desezuriya	*
32	"21369	Jimma	1720
33	"213168	Kefa	*
34	YD	Released in 1986	
35	Holetta-1	Released in 2005	
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

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 m.a.s.l, 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 5m x 1.8m 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).

Statistical Analysis

The phenotypic and genotypic coefficients of variation were calculated by (Burton *et.al*., 1953) considering genotypes as random effects using SAS statistical packages (SAS, 1999).

Genotypic variance component

$$\sigma_g^2 = \frac{(MS_g - MS_e)}{r}$$

where MS_g is genotypic mean square, MS_e is error mean square and r is replication

Environmental variance component (on genotypic mean basis)

$$\sigma_g^2 = \frac{MS_e}{r}$$

Phenotypic variance component

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 + \sigma_{ge}^2$$

Genotypic and phenotypic coefficients of variation were calculated according to the method suggested (SAS, 1999). As: Genotypic coefficients of variation (*GCV*)

$$GCV = \frac{\sqrt{\sigma_g^2}}{X} \times 100$$

Phenotypic coefficients of variation (PCV)

$$PCV = \frac{\sqrt{\sigma_g^2}}{X} \times 100$$

where X is the grand mean value of the trait

Broad sense heritability (h^2) in percents was estimated in each character using variance components as described by (Allard, 1960).

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The expected gain or genetic advance with one cycle of selection, assuming the selection intensity of 5%, was predicted as suggested by (Johanson, 1955).

$$G_A = k \times \sigma_p \times h^2$$

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).

$$GAM = \frac{GA}{X} \times 100$$

RESULT AND DISCUSSION

Analysis of Variance

The analysis of variance for characters showed significant differences between genotypes (Table 2). The analyzed data indicated the existence of variability within the collected genotypes this provides for selection from genotypes and the genetic improvement of this crop. Among 16 characters, seven (i.e. days to maturity, grain filling period, secondary branches /plant, harvest index, seed yield/plot, seed yield/hectare and oil content) showed highly significant ($p<0.01$) difference among the tested genotypes.

Table 2

The mean squares, genotypes, 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	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

*, ** = significant at the 0.05 and 0.01 probability level,
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

Similarly, day of flowering, plant height, number of pod/plot, primary branch/plant, biomass/plot, oil yield /plot revealed significance difference at ($p<0.05$) among tested genotypes. Base on the Table 2, the tested genotypes with associated were showed wide range of variation, the results providing that there is an opportunities for genetic improvement through selection or cross breeding of the Ethiopian mustard.

Phenotypic and Genotypic variations

Phenotypic and genotypic variances, heritability, genetic advance and genetic advance of mean of the characters were shown in table 2. Higher

variances were observed for plant height (cm), days to flowering, grain filling period, biomass/plot (g × plot^{-1}) and harvesting index/plot. Grain yield being a quantitative trait is known to be controlled by many genes, which are highly influenced by environmental factors (biotic and abiotic factors). Variability is the addition of total hereditary effects from alarmed genes as well as the environment (Tewodros and Getachew, 2013). Therefore, the variability is grouped into heritable and non-heritable components with suitable genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA). These genetic parameters help breeders in selection of suitable genotypes for genetic improvement of this crop.

Phenotypic coefficient of variation (PCV %) was found superior to the genotypic coefficient of variation (GCV %) for all the characters. High GCV along with high heritability and high genetic advance will give good information than each parameter (Saha, 1990; Tewodros and Biruk, 2012; Tewodros and Getachew, 2013). Thus, in this study, plant height (37.96), number of secondary branches/plant (39.02), grain filling period (20.17) and biomass yield/plot (16.58) showed high genotypic coefficients of variation, high heritability together with high genetic advance as percent of means. This suggests the occurrence of additive gene action with low environmental influence for the determination of these traits and could be valuable in phenotypic selection of Ethiopian mustard.

Heritability Estimates

Heritability estimates varied from 1.44% for number of seed/plot to 99.98% for biomass yield/ plot (Table 3). The maximum heritability was obtained for biomass yield/plot, plant height, number of secondary branches/plant, grain filling period and days to maturity. It was observed that the maximum genotypic coefficients of variation were supported by high estimates of heritability. Moreover, number of seeds/pod, number of pods/plant, thousand seed weight/g, seed yield g/plot and seed yield kg/ha have comparatively low heritability estimates (Table 3). Genetic advance indicates the degree of gain in a character obtained under a particular selection and helps the breeder to predict the degree of improvement that can be achieved in different characters.

High heritability together with high genetic advance is vital tool for selection of the best individuals and for successful genetic improvement (Tewodros and Getachew, 2013). Estimates of genetic advance ranged from 0.06 for number of primary branches and number of seeds/plot to 1369.5 for biomass yield/plot (Table 3). The value of genetic advance as percentage of means varied from 0.46% for number of seed/plot to 77.25% for plant height. It was observed that plant height with high heritability (77.25%) had the highest genetic advance (131.33), while grain filling

period and days to maturity showed similar trend in heritability and genetic advance. The genetic advance as percentage of means was also higher for plant height/plant (77.25%) and grain filling period (33.1%), and this in line with their respective heritability (Table 3). This indicates that selection for traits like plant height and grain filling period is easier than selection for other characters. Moderate genetic advance together with high heritability for harvest index, days to flowering and days to maturity suggest the presence of intra and inter allelic interactions in the appearances of these characters.

Table 3

Estimates of means, ranges, variance components, and coefficients of variability, heritability and genetic advance of the sixteen characters studied.

Character	Mean ± Std.	Range	s^2_G	s^2_P	GCV [%]	PCV [%]	h2b [%]	GA	GAM [%]
DF	67.32±1.71	46-100	53.71	193.12	10.89	20.64	27.81	7.97	11.84
MD	142.96±1.52	126-179	90.52	168.86	6.64	9.07	53.61	14.37	10.03
GFP	75.64±2.29	34-122	232.84	368.03	20.17	25.36	63.27	25.04	33.1
PH	170±1.74	134-198	4164.23	4278.77	37.96	38.48	97.32	131.33	77.25
PBP	13.3686±0.22	10-17.1	1.17	3.5	2.8	4.83	33.55	1.3	3.34
SBP	38.49±1.89	15-82	225.59	259.63	39.02	0.22	86.89	28.88	0.40
LP	4.39±0.08	3-6	0.05	0.35	0.16	0.41	15.7	0.19	0.13
NPP	141.75±11.42	24-514	0.06	4.34	1.92	15.98	1.45	0.06	0.48
NSP	13.04±0.25	9-18	0.06	4.34	1.88	15.58	1.44	0.06	0.46
BM (gm)	4341.67±153.68	1400-8000	1105.91	1107.09	0.76	0.76	99.89	68.57	1.58
BMh	7236±256.14	2333-13333	1440101.45	4706327.15	16.58	29.98	30.60	1369.50	18.93
HI	540.38±29.62	182-1390	7111.17	36295.75	15.42	34.83	19.59	77.00	14.08
TSW	4±0.07	3-6	0.03	0.32	4.19	14.11	8.72	0.10	2.54
SY/P(gm)	1237.2±36.5	654.41-1890.66	6041.49	42615.69	6.28	25.17	14.18	91.08	12.92
SY (kg/ha)	2062±60.83	1090.69-3151.1	16782.03	118377.02	6.28	25.15	14.18	151.81	32.32
OC	40.96±.25	37-45	2.39	4.35	3.78	5.09	54.99	2.37	5.78
OY	91.0383±2.28	45.7-145.19	132.71	363.53	12.64	20.92	36.51	14.36	15.75

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/ha (kg)SY(gm)=seed yield per plot, Seed yield per plot, SYh = Seed yield per hectare, HI= Harvest index per plot, TSW =Thousand seed weight, OC = Oil content and OY = Oil yield per plot

CONCLUSION

The analysis of variance showed the presence of highly significant differences among the tested genotypes for day of maturity, grain filling period, ,secondary branches per plant, harvest index, seed yield per plot and oil content were showed highly significant ($p<0.01$) difference among the tested genotypes at both locations. Nevertheless, length of pod, number of and seed per pod showed non- significance among tested genotypes at both locations. Similarly day of flowering, plant height, primary branch per plant, biomass per plot, oil yield per plot showed significance difference at ($p<0.05$). The PCV and GCV were high for grain filling period, plant height and number of secondary branches per plant. Similarly, harvest index had high GCV value. The PCV was low length of pod, number of pod per plant, number of seed per pod and biomass per plot. The GCV was low biomass, length of pod, primary branches per plant and oil content. 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. Plant height and secondary branches per plant only had high Genetic advance as percent of the mean (GAM) values whereas, number of seeds per pod, number of pod per plant and length of pod showed low GAM.

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