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Mean Performance Evaluation and Variability Estimation in Ethiopian Mustard (Brassica Carinata A Braun) Genotypes

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Abstract: Study of genetic variability is crucial in plant breeding to find traits of interest in genetic resources for any crop improvement. The present study was carried out using 36 genotypes including two checks to evaluate the mean performance of the genotypes, to examine the genetic variability, heritability, expected genetic advance and genetic advance as percent of mean. All the thirty six genotypes were tested using simple lattice design at Holeta Agricultural Research Center during 2018/2019. Observations were recorded on plot basis for days to flowering (days), days to maturity (days), yield per plot (g), yield per hectare(kg), oil yield (kg), oil content (%) and thousand seed weight (g) and on plot basis for plant height (cm). Analysis of variance revealed the significant differences among the tested genotypes for all traits considered. The phenotypic coefficient of variation observed in this study was higher than the genotypic coefficient of variation for all traits considered implying that high influence of environment on those traits. High phenotypic coefficient of variation was observed for all traits and moderate genotypic coefficients of variation recorded by seed yield per hectare, seed yield per plot and oil yield per plot. Low genotypic coefficient of variation was recorded by days to flowering, days to maturity, oil content, thousand seed weight and plant height. The study of genetic advance in this experiment showed high genetic advance for all traits except thousand seed weight which recorded low genetic advance.

Keywords: Genetic Variability, Heritability, Genetic Advance, Oilseed Brassica

1. Introduction

Ethiopian mustard (Brassica carinata A. Braun) 2n=34, BBCC is thought to be originated from the highlands of Ethiopia [1]. It is an amphidiploids species evolved from the natural cross of two brassica species namely Brassica nigra L, (BB, 2n=16) and Brassica Oleracea L. (CC, 2n=18). It has been being cultivated for different purpose. Its leaves are used for human consumption as vegetables, its seeds are used in the production of edible oil, and defeated proteins are used for animal feed [2]. It is also used as bioenergy crop as its oil is also used in the production of biofuel because of its high erucic and linoleic content with less saturated fatty acids [3].It can tolerate the harsh environments and can be cultivated on the marginal land [4]. It requires low inputs like pesticides and fertilizers and can withstand biotic and a biotic stresses [5]. These agronomically desirable traits make the crop to be cultivated across different agro ecologies. Since it has the ability to tolerate and resist stresses it can be used as sources of desirable genes for the improvement of other brassica species.

Ethiopian mustard has been widely grown in different parts of the country and abuduntly in Arsi, Bale, Shewa, Gojam, Gondar, Wollo, Sidamo and Wellega [6]. Study of Genetic variability is important in estimating the degree of dissimilarity and the level of variability for the traits of interest in available germplasm for further genetic improvement and conservation of crop genetic resources [7]. Studies on brassica carinata for agro morphological and quality traits by different scholars reported the presence of variability among genetic materias for different traits. Ousman *et al* [8] reported significant variability for leaf vegetables among Ethiopian mustard genotypes. Variability studied in Ethiopian mustard is high for yield and yield related traits [9]. Despite its various use, wide distribution and stress tolerance ability the crop is challenged from lack of attention from research initiatives, lack of lab facility for its improvement for traits like erucic acid, glucosinolate and genetic depletion of available genetic resources. Thus study of genetic variability is suggested as ameans to provide information about germplasms for conservation and improvement of genetic resource of the crop.

Hence, this study was conducted to estimate the extent of genetic variability, heritability and genetic advance in selection of better genotypes for genetic improvement of Ethiopian mustard.

2. Materials and Methods

Study area description and experimental procedures

The study was conducted at Holetta and Kulumsa agricultural research center during the main cropping season of 2018/2019. Holetta agricultural Research center is located at 09°04' N latitude and 38°29' E longitude with the altitude of 2400m a.s.l. wheras Kulumsa is located at 08°01' N latitude and 39°09' E longitude with the altitude of 2200m a.s.l. 36 genotypes including local and standard checks obtained from Holetta agricultural research center (Table 1) were included in the study using simple lattice design (6x6) at both locations. The plot size used in the arrangement of treatment was 3m long with six rows (30cm between rows and 60cm between plots).All agronomic practices were applied as per national recommendation.

Table 1. *Genotypes used for mean performance evaluation and variability studies at Holetta and Kulumsa during 2018/2019.*

No	Pedigree	No	Pedigree	Source
1	yellow Dodolla/ sps/2/4	19	S67xBAR-1030/79-328/2001/4/1/6/2/9/2	HARC
2	S-67xHoletta-1-9/2/18/2/41/1	20	Y.D.xBAR-1030/79-328/2001/8/2/13/1/22/2	HARC
3	Y.D.xBAR-1030/79-436/2001/6/1/10/2/16/1	21	S-67xHoletta-1-7/1/13/2/26/2	HARC
4	S-67xY.D.3/1/5/1/9/4	22	S-67xHoletta-1-8/2/16/2/30/3	HARC
5	S-67xHoletta-1-9/2/18/2/37/4	23	S-67xHoletta-1-9/2/18/2/41/1	HARC
6	S-67xHoletta-1-7/1/13/1/25/3	24	Y.D.xBAR-1029/79-436/2002/9/2/15/1/28/1	HARC
7	Y.D.xBAR-1030/79-436/2001/6/2/11/1/18/3	25	S-67x34477 Pakistan 5/2/9/2/14/3	HARC
8	S-67xHoletta-1-7/1/13/2/26/2	26	S-67xHoletta-1-9/2/18/2/41/4	HARC
9	S-67xY.D.2/2/4/1/7/3	27	S-67xHoletta-1-6/2/12/2/24/2	HARC
10	Y.D.xBAR-1030/79-436/2001/6/1/10/1/15/3	28	Y.D.xBAR-1030/79-328/2001/8/2/13/1/22/4	HARC
11	Y.D.xBAR-1029/79-436/2002/9/2/15/1/26/1	29	S-67xHoletta-1-9/2/18/2/33/1	HARC
12	S-67xHoletta-1-9/2/18/2/45/3	30	Y.D.xBAR-1030/79-436/2001/6/2/11/1/18/2	HARC
13	S-67xHoletta-1-5/2/10/2/20/4	31	Holetta-1-SPS/3/2	HARC
14	S-67xHoletta-1-9/2/18/2/37/3	32	S-67xHoletta-1-9/2/18/2/37/4	HARC
15	yellow Dodolla SPS/1/5	33	Y.D.xBAR-1029/79-436/2002/9/2/15/1/28/1	HARC
16	S 67xBAR-1030/79-436/2001/2/1/2/1/3/1	34	yellow Dodolla SPS/2/6	HARC
17	S 67xBAR-1030/79-328/2002/3/2/5/1/7/2	35	Holetta-1	HARC
18	Y.D.xBAR-1029/79-328/2002/9/2/15/1/26/2	36	Local Check	HARC

Whereas; HARC= Holetta agricultural research center

Data collected

Data were collected on plot basis for days to fifty percent flowering, days to maturity, seed yield per plot, seed yield per hectare, oil content, oil yield and thousand seed weight whereas plant height was measured by taking ten plants per plot randomly.

Statistical Data Analysis

Statistical data analysis was done using a combination of soft wares and following different biometricians. Analysis of variance was done using SAS 9.3 [10].

Phenotypic and genotypic coefficient of variation

The phenotypic and genotypic variances were calculated following the formula suggested by Burton and Devane [11].

$$\text{Genotypic Varience}(\sigma^2 g) = \frac{\text{MSS due to treatment(Mt)} - \text{MSS due to error(Me)}}{\text{Number of replications(r)}}$$

$$phenotypicvarience(\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

σ^2 e = error variance

The genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were also computed using the formula suggested by Burton and Devane [11] and classified following Sivasubramanian and menon [12] who classified, phenotypic coefficients of variance (PCV) and genotypic coefficients of variance (GCV) Values more than 20%, less than 10% and between 10% and 20% are regarded as high, low and medium respectively.

$$\text{Phenotypic cofficient of variation(PCV)} = \frac{\sigma^2 P}{\bar{X}} \times 100$$

$$\text{Genotypic coefficient of variatio(GCV)} = \frac{\sigma^2 g}{\bar{X}} \times 100$$

Heritability and Genetic advance

Heritability in the broad sense (H^2) was estimated following the formula of Falconer and Mackay [13] and Classified following Johnson *et al* [14] as low (below 30%), medium (30-60%) and high (above 60%).

$$H^2 = \left[\sigma^2 g / \sigma^2 p \right] \times 100$$

Where, H² =heritability in broad sense, σ2g = Genotypic variance and σ2p= Phenotypic variance

GA was calculated as per the formula recommended by Singh and Chaudhary [15].

$$GA = K * H^2\sqrt{\sigma^2 ph}$$

Where, H^2 = Heritability in broad sense, σph= Phenotypic standard deviation (phenotypic standard deviation=square root of phenotypic variance), GA= Expected genetic advance k = the standardized selection differential at 5% selection intensity (2.06).

The genetic advance as percentage population mean (GAM) was estimated following the methods described by Singh and Chaudhary [15] and classified as low (<10%), moderate (10-20%) and high (>20%).

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

Where, GA=Genetic advance under selection and x̄=Grand Mean of the trait.

3. Results and Discussion

Mean and Range

The mean values for the 36 gomenzer genotypes studied at Holeta are presented in Table2. Seed yield per hectare ranged from 1294.929 to 3676.184.the highest seed yield per hectare was recorded by yellow Dodolla followed by Y.D.xBAR-1030/79-436/2001/6/2/11/1/18/3 and S-67xHoletta-1-6/2/12/2/24/2 while the lowest was observed for S-67xHoletta-1-9/2/18/2/37/3. 58 percent of the genotypes gave yield above the grand mean (2569.18). 33 percent of genotypes out yielded the standard check. Variability observed for seed yield in this study was due to genetic variation among the tested genotypes. Oil content ranged from 40.763 to 49.436. The highest oil content was obtained from yellow Dodolla/ sps/ followed by Y.D.xBAR-1030/79-436/2001/6/1/10/2/16/1and S-67xHoletta-1-9/2/18/2/37/4 while the minimum was recorded by S-67xHoletta-1-9/2/18/2/33/1.days to flowering ranged from 57 to78. The maximum days to flowering were observed for S-67xHoletta-1-6/2/12/2/24/2 and the minimum was recorded for S-67xHoletta-1-9/2/18/2/41/1.days to maturity ranged from 145 to 158. Genotype S-67xHoletta-1-7/1/13/2/26/2 was the early maturing genotype with shortest days to maturity as compared to others. Plant height ranged from 130.487cm to 190.546cm. S 67xBAR-1030/79-328/2001/4/1/6/2/9/2 was the tallest genotype with the maximum plant height of 190.546cm followed by S-67xHoletta-1-6/2/12/2/24/2 while Y.D.xBAR-1030/79-436/2001/6/1/10/1/15/3 was the shortest genotype with130.487cm plant height. Oil yield ranged from 584.949 for S-67xHoletta-1-9/2/18/2/37/3 to 1693.272 for Y.D.xBAR-1030/79-436/2001/6/2/11/1/18/3. Thousand seed weight showed the highest value (5.544) for S-67xHoletta-1-6/2/12/2/24/2 followed by S 67xBAR-1030/79-328/2001/4/1/6/2/9/2 and S-67xHoletta-1-5/2/10/2/20/4 while the lowest thousand seed weight(3.566) was obtained from yellow Dodolla/ sps/2/4.

Table 2. *Mean performance evaluation of 36 genotypes studied at Holetta and Kulumsa during 2018/2019.*

Genotypes	FD	MD	PH	PYLD	YLDKPH	OC	OYLD	TSW
yellow Dodolla/ sps/	71	155	179.927	328.686	1833.254	49.436	858.432	3.566
S-67xHoletta-1-9/2/18/2/41/1	69	150	150.779	425.132	2366.737	49.237	1178.839	5.022
Y.D.xBAR-1030/79-436/2001/6/1/10/2/16/1	72	153	191.876	234.804	1309.899	44.434	587.707	4.412
S-67xY.D.3/1/5/1/9/4	75	158	172.221	262.989	1467.187	45.668	700.878	3.890
S-67xHoletta-1-9/2/18/2/37/4	67	150	158.449	533.225	2968.981	45.835	1342.865	5.000
S-67xHoletta-1-7/1/13/1/25/3	66	150	161.909	601.370	3346.518	48.165	1592.091	5.022
Y.D.xBAR-1030/79-436/2001/6/2/11/1/18/3	72	151	175.992	655.857	3646.611	47.098	1693.272	4.566
S-67xHoletta-1-7/1/13/2/26/2	67	145	161.546	386.307	2154.034	41.269	892.798	4.566
S-67xY.D.2/2/4/1/7/3	66	149	158.642	468.979	2612.196	45.465	1178.666	4.456
Y.D.xBAR-1030/79-436/2001/6/1/10/1/15/3	62	148	130.487	568.164	3162.484	45.199	1436.337	4.434
Y.D.xBAR-1029/79-436/2002/9/2/15/1/26/1	71	150	172.366	372.207	2074.799	45.370	935.542	4.022
S-67xHoletta-1-9/2/18/2/45/3	68	151	165.386	375.831	2092.791	46.766	955.159	4.088
S-67xHoletta-1-5/2/10/2/20/4	63	150	140.825	329.852	1838.336	44.699	816.768	5.044
S-67xHoletta-1-9/2/18/2/37/3	72	151	167.409	232.339	1294.929	44.633	584.949	4.088
yellow Dodolla	66	146	137.462	387.789	2160.852	45.804	997.475	4.588
S 67xBAR-1030/79-436/2001/2/1/2/1/3/1	70	149	173.559	456.460	2542.014	48.500	1243.843	3.978
S 67xBAR-1030/79-328/2002/3/2/5/1/7/2	71	152	156.403	421.145	2346.802	43.734	1027.514	3.956
Y.D.xBAR-1029/79-328/2002/9/2/15/1/26/2	71	151	154.086	574.550	3197.806	43.902	1392.087	4.934
S 67xBAR-1030/79-328/2001/4/1/6/2/9/2	74	156	190.546	381.696	2126.843	46.731	981.813	5.456
Y.D.xBAR-1030/79-328/2001/8/2/13/1/22/2	70	150	154.629	472.682	2630.935	46.665	1234.994	4.500
S-67xHoletta-1-7/1/13/2/26/2	69	151	170.183	474.132	2638.358	46.835	1244.020	4.000
S-67xHoletta-1-8/2/16/2/30/3	68	147	159.279	485.304	2700.020	46.532	1252.388	4.890
S-67xHoletta-1-9/2/18/2/41/1	57	147	152.970	398.818	2220.384	42.699	942.340	5.132
Y.D.xBAR-1029/79-436/2002/9/2/15/1/28/1	71	153	161.624	513.489	2856.808	46.266	1335.559	4.368
S-67x34477 Pakistan 5/2/9/2/14/3	66	151	145.159	585.730	3258.539	47.633	1535.827	4.478
S-67xHoletta-1-9/2/18/2/41/4	72	153	171.619	491.876	2737.076	47.462	1278.054	4.500
S-67xHoletta-1-6/2/12/2/24/2	78	153	188.702	604.862	3366.669	45.396	1514.735	5.544
Y.D.xBAR-1030/79-328/2001/8/2/13/1/22/4	73	154	177.756	572.312	3187.092	44.566	1415.761	4.544
S-67xHoletta-1-9/2/18/2/33/1	72	155	162.853	457.984	2549.254	40.763	1014.628	4.434

Genotypes	FD	MD	PH	PYLD	YLDKPH	OC	OYLD	TSW
Y.D.xBAR-1030/79-436/2001/6/2/11/1/18/2	73	157	182.197	539.169	2998.542	44.997	1346.299	3.912
Holetta-1	69	149	159.023	462.768	2578.306	48.370	1212.866	5.132
S-67xHoletta-1-9/2/18/2/37/4	67	150	164.120	414.439	2308.968	48.566	1091.734	4.522
Y.D.xBAR-1029/79-436/2002/9/2/15/1/28/1	58	147	133.465	470.625	2620.256	40.801	1069.405	5.500
yellow Dodolla	74	160	176.183	661.050	3676.184	43.804	1631.406	4.956
Holetta-1	60	146	150.142	490.695	2729.221	46.133	1268.133	4.478
Local Check	59	147	153.726	519.682	2890.814	45.566	1323.314	5.022
Grand Mean	68	151	162.88	461.47	2569.18	45.69	1169.68	4.58
CV	3.30	1.37	5.12	24.06	24.00	2.39	23.62	13.27
LSD	4.35	4.08	16.98	145.62	807.94	2.35	392.62	0.58

Estimates of variance components

Phenotypic coefficient of variation from 23.963 for days to maturity to 226.359 for oil yield per hectare while genotypic coefficient of variation ranged from 2.191 for days to maturity to 15.279 for oil yield per hectare (Table 3). The phenotypic coefficient of variability observed in this study was higher than the genotypic coefficient of variability for all traits considered. Phenotypic coefficient of variation greater than 20 are high, between 10 and 20 moderate and below 10 are high [12]. According to this classification phenotypic coefficient of variation was high for all traits. Genotypic coefficients of variation values are moderate for seed yield per hectare, seed yield per plot and oil yield per hectare while its low values were observed for days to maturity, oil content, days to flowering, thousand seed weight and plant height (Table 2).The difference between PCV and GCV values was high for all traits indicating the high influence of environment in the expression of these traits. Heritability values greater than 60% (high), less than 30% (low) and between 30% and 60 % are high Johnson et al [14]. According to this classification heritability values observed in this study were low for all considered traits.

Estimation of expected genetic advance and genetic advance as percent of mean

Expected genetic advance ranged from 2.155 for thousand seed weight to 4485.624 for seed yield per hectare while genetic advance as percent of mean ranged from 41.273 for days to maturity to 212.442 oil yield per hectare. According to Johnson *et al*. [14]. Genetic advance as percentage population mean (GAM) was classified as low (<10%), moderate (10-20%) and high (>20%). Based on this bench mark high genetic advance was observed for all traits except thousand seed weight wich exhibited low genetic advance (Table 2). Estimates of genetic advance as percent of mean at 5% selection intensity was high for all traits considered in this study implying that these traits were less influenced by the environment and selection based on these traits is effective in brassica carinata improvement. But heritability along with genetic advance is more important in predicting gain in crop improvement Johnson *et al* [14]. In this study no high heritability with high genetic advance was observed. All traits showed low heritability with high genetic advance and it is possible to get other breeding approaches than making attempts to improve those traits through selection.

Table 3. *Estimation of genetic variability, heritability and genetic advance for 36 genotypes studied at Holetta and Kulumsa during2018/219.*

Traits	Mean	PV	GV	EV	PCV%	GCV%	H%	GA	GAM
Days to flowering (days)	68.347	2394.028	21.392	5.096	71.589	6.767	0.894	90.065	131.775
Days to maturity (days)	150.917	1307.802	10.935	4.287	23.963	2.191	0.836	62.288	41.273
Plant height(cm)	162.875	22838.12	193.636	69.491	92.785	8.544	0.848	263.951	162.057
yield per plot(g)	461.472	1011702	3954.878	12324.29	217.962	13.628	0.391	809.979	175.521
yield per hectare (kg)	2569.181	31175470	121580	380349.4	217.326	13.572	0.390	4485.624	174.594
Oil content (%)	45.694	469.5936	4.098	1.196	47.424	4.430	0.873	38.954	85.249
Oil yield (kg/ha)	1169.681	7010220	31937.92	76328.55	226.359	15.279	0.456	2484.895	212.442
Thousand seed weight (g)	4.583	23.57143	0.0508	0.3698	105.928	4.917	0.215	2.155	47.022

4. Conclusion

The success of any breeding program relies on the variability present in the available genetic resources. The Ethiopian mustard genotypes included in this study showed significant variability for all traits considered. The highest phenotypic coefficient of variation was observed for all traits whereas moderate genotypic coefficient of variation was recorded by all traits under study except thousand seed weight wich showed low genotypic coefficient of variability. Mean performance evaluation of the studied genotypes showed 33% genotypes were found to be having the highest seed yield per hectare than the standard check. Among the genotypes studied 42% of studied genotypes showed high all content over the standard check.

Conflicts of Interest

The authors declare no conflicts of interest.

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