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Abstract: The experiment was carried to assess traits of leaf variability in their different plant parts for Ethiopian mustard land races in relation to high quantity and quality of leaf production at Holetta Agricultural research Center, Ethiopia. Therefore forty nine genotypes of Ethiopian mustard land races collected from different agro ecologies were evaluated to assess the traits of leaf variability in their different parts of bottom, middle and top of plant parts for Ethiopian mustard land races in relation to high quantity and quality of leaf production. The experiment was carried out in a simple lattice design. Univariate analysis of variance showed that there were significant differences among genotypes for all leaf parameter in their bottom, middle and top different plant parts of genetic variability reflection in genetic effects of leaf variability traits among the accessions which is important for improvement of these traits. The present study revealed the presence of considerable variability among genotypes for all of leaf traits except leaf width and leaf area from top plant area from top plant parts assessed in their different plant parts. The significant difference of results indicates that the presence of good opportunity to improve these leaf traits of Ethiopian mustard land races suing the tested genotypes.

Keywords: Ethiopian mustard, leaf production, variability traits, plant parts

1. INTRODUCTION

Ethiopian mustard is believed to be originated in the highlands of the Ethiopian plateau and the adjoining portion of East Africa and the Mediterranean coast (Gomez-Campo and Prakash, 1999).It evolved as a natural cross between B. nigra (BB) (n=8) and B. oleracea (CC) (n=9) and underwent further chromosomal doubling (2n=34; UN, 1935). It is partially amphidiploids. It is cultivated primarily as leafy vegetable and for oil in the seeds, annual, and grows up to 150 and 200 cm, branched, glabrous to slightly hairy at stem and petiole bases, leaves are alternate and simple. It can adapt to highland areas (2600 msl), with cool climate 0-5 degree centigrade. Cool weather followed by high temperature induces flowering, but decrease leaf production. The crop is traditionally used for many purposes, such as greasing traditional bread-baking clay pan, curing certain diseases and as a source of vegetable relish (Nigussie, 2001). It is the only highland oil seed vegetable crop able to consume by defoliating its leaves or sold to generate income after month of sowing in most near big city parts of the country. In characterization of Ethiopian mustard for vegetative agro-morphological traits Jane Muthoni, (2010) reported as great variation was seen in leaf number per plant, leaf bloom and leaf blade blistering. Crop improvement through plant breeding, thus, occurs through selection operating on genetic variability. Genetic variability is therefore essential for crop improvement. Breeding of mustard crop has emphasized its improvement mostly as an oilseed crop. No major breeding program to improve the leaf vegetable of mustard is known. Identifying leaf variability traits of Ethiopian mustard that is heritable to be reflected as effects on quantity and quality for the mass leaf production is crucial for further investigation of improvement program of the crop. Therefore the present study was, executed with the objective of assessing traits of leaf variability for Ethiopian mustard land races in different plant parts with relation to high quantity and quality of leaf production traits.

2. MATERIALS AND METHODS

2.1. Experimental Site

The experiment was conducted at Holetta Agricultural Research Center in 2013/2014 cropping season from June to December 2013. Holetta (West Shewa Zone of Oromia Region) is located at latitude 9° N

and longitude 38° E, altitude of 2400 m a.s.l situated 30km West of Addis Ababa. It is one of the representatives of oil seed *Brassica* growing areas in the central highlands of Ethiopia (Nigussie and Mesfin, 1994). The area has a mean annual rainfall of 1059 mm and temperatures of 23°C (maximum) and 8°C (minimum). The soil type is Nitisols with soil ph in the range of 6.0 -7.5(Nigussie and Mesfin, 1994).

2.2. Description of Test Materials

A total of forty-nine mustard land races that include one local check and one standard check were used in this study. The majority of the accessions represent the national collection from different major mustard growing regions of the country and that are maintained at Holetta agricultural research Center. The accessions were obtained kindly from Holetta agricultural research center of highland oil crops improvement program. The details of the accessions used in the experiment are given in Table 1.

No.	Accession number	Area of collection	Altitude(m)
1	PGRC/E 20001	West Wollega/Arjo	2420
2	" 20002	Bale Zone/Kitu	2500
3	" 20004	South Gonder/Liba	1980
4	" 20005	SouthGonder/Debretabor	1830
5	" 20006	South Gonder/Debretabor	1980
6	" 20007	North Gonder/Woger/Dabat	2500
7	" 20017	West Gojiam /Awi /Dangila	1980
8	" 20056	West Shewa/Jibatenamecha	2200
9	" 20065	West Shewa/Jibatena mecha	2200
10	" 20066	West Shewa/Ambo	1950
11	" 20067	West Shewa/Ambo	2010
12	" 20076	SNNP/Wenago	1853
13	" 20077	South East Tigray/Inderta	2000
14	" 20112	West Gojam/JabiTehnan	1980
15	" 20117	West Shewa/Jibatnamecha	2050
16	" 20127	West Shewa/chelia	1700
17	" 20133	West Shewa/Menagesha	2600
18	" 20134	West Shewa/Jibat	2200
19	" 20146	West Gojam/Bahirdarzuria	1980
20	" 20165	West Gojiam/Awi/Dangila	1980
21	" 20166	West Gojiam/Awi/Dangila	1980
22	" 21008	Arsi/Gedeb	2380
23	" 21012	West shewa/Dendi	2900
24	" 21017	West Shewa/Gendbert	2470
25	" 21026	West Gojiam Awi/Dangila	2000
26	" 21035	West Gojam/Sekela	2540
27	" 21037	West Gojiam/Awi/Dangila	2165
28	" 21068	Bale/Adaba	2500
29	" 21157	SNNP /South omo	2830
30	" 21225	East Gojam/Enemay	2000
31	" 208411	West Gonder/Debretabor	2150
32	" 229665	West Gojam/Burie	2050
33	" 237048	Arsie-Robe	2350
34	" 241907	South Gonder/Fogera	1825
35	" 241910	South Gonder/Farta	2289

Table1. List of 49 Ethiopian mustard genotypes used in the study and their origin

36	" 242856	Arsi zone /Sherka	2360
37	" 242858	Arsi zone /Sherka	2360
38	" 243738	South Wollo/Desiezuria	2928
39	" 243739	South Wollo/Tenta	2950
40	" 21256	West Gojam/Bahirdarzuria	1940
41	" 243750	Wollo/kalu	2020
42	" 2243756	South Gonder/ Debark	3115
43	" 243761	Gonder Zuria	2050
44	" 243763	South Gonder/Kemkem	2070
45	" 208556	West Shewa/Adis Alem	2200
46	" 208585	East Shewa/yerer	1600
47	Yellow dodolla	Bale/Dodolla	2500
48	(ZemX Yellow Dodolla)	Cross	2400
49	Local check	Holetta area	2400

Source: Holetta highland oil crops research program

2.3. Experimental Design, Management and Season

The experiment was executed from June 2013 to December 2013. The experiment was laid out in simple lattice design with two replications. A plot of four central rows each three-meter long and 30cm spacing between rows were used for data collection. Each replication had seven blocks and each block was represented by seven plots. The path between blocks was 2 m and the spacing between plots with in sub-blocks was also 0.6 m. Each entry was manually drilled a rate of 10 kg/ha and urea and phosphorous fertilizers were applied at the rates of 46/69 kg/ha N/P₂O₅ respectively following the national recommendations. All other recommended agronomic and cultural practices were carried out following practices described by Adefris (2005).

2.4. Data Collected

Data on plant was collected from five plants randomly selected from the central rows of each plot and averaged for statistical analysis.

1. Date of 50% flowering: total days from sowing to 50% date of flowering observed.

2. Seeds yield per plot(SYP): Seed yield per plot measured in grams after moisture of the seed was adjusted to 7 percent.

3. Plant height (PHT): The average height of five randomly selected plants was measured in centimeters from the ground surface to the top of the main stem at maturity.

4. Petiole length: Measurements of the petiole length of three leafs of petiole from bottom, middle and top of five plants of leaves excluding leaves.

5. Leaf length (cm): measurements of the leaf length of three leafs length from bottom, middle and top of five plants. From each leaf starting from the base to the apex of leaf blade excluding petiole was measured at full vegetative stage.

6. Leaf width (cm): An actual measurement of width of leafs across the widest portion/section of the same leaf from bottom, middle and top of five plants was measured at full vegetative stage.

7. Leaf area: was measured using leaf area meter from bottom, middle and top of five plants for three leaf blade.

3. RESULTS AND DISCUSSION

3.1. Mean Values of Ethiopian mustard Leaf Traits from Bottom, Middle and Top Parts of Plants

Average mean values of the leaf traits from bottom, middle and top parts of plants and its related traits of the Ethiopian mustard were recorded for date of flowering, seed yield per plot, plant height, petiole length of leaf from bottom, middle and top of plant parts, leaf length from bottom, middle, and top of plant parts, leaf area from bottom middle and

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top of plant parts are presented in Table 2. Means of date of flowering was greater than 100 days for ten genotypes (PGRC/E20056, PGRC/E20065, PGRC/E20117, PGRC/E20127, PGRC/E 20134, PGRC/E21012, PGRC/E21017, PGRC/E21035, PGRC/E237048 and PGRC/E243756). Mean values of seed vield per plot was highest for the genotype vellow dodola (3297kg/ha) and the least was recorded for the genotypes PGRC/E20065 (904kg/ha). The highest mean values of petiole length of the tested genotypes from bottom, middle and top of plant parts was recorded for the genotypes PGRC/E20134, PGRC/E243756 and PGRCE/E2006 (14.4, 14.4, 7.5, 13. 2, 13. 2, 10. 7, 12.9, 12.9, and 9.2 cm) respectively. Similarly the highest average mean values of leaf length of the tested genotypes from bottom, middle and top of plant parts was recorded for the genotypes PGRC/E243756, PGRC/E20134 and PGRCE/E20065(12.4,12.2,9.9,13.2,11.3,8.8,11.1,10.1 and 9.6 cm) respectively. In addition to highest leaf length the wider leaf width of mean value was recorded from bottom, middle and top of genotype PGRC/E20134, PGRC/E229665 for the and PGRCE/E21035 plant parts (10.5,8.6,5.2,10.3,8.5,5.8,9.6,8.9,6.8cm) respectively. On the other hand the highest and best of all genotypes tested average mean value of leaf area of genotypes from bottom, middle and top of plant recorded for the genotypes PGRC/E20134. PGRC/E20117 parts was and PGRC/E237048(83.8,72.1,37.5,76.8,58.5,24.0,76.6,51.8,47.0 cm) respectively.

Table2. Mean values of the studied 49 genotypes for 15 leaf traits of Ethiopian mustard tested at Holetta, 2013/14

 Value 2012/14

					Petiol	e length	from	Leaf I	ength	from	Leaf w	vidth fro	m pla	nt Lea	f area	from
					plant	parts of	2	plant j	plant parts of			of	1	plant parts of		of
Ν	Treatmen	D	SY	Р	bott	Mid	То	Bott	mid	То	Bott	mid	То	botto	mid	ton
0	ts	F	Р	Н	om	dle	n	om	dle	n	om	dle	n	m	dle	top
1		95	20	15	11.6	11.6	4.5	12.3	10.1	9.1	8.7	6.3	2.9	42.8	28.8	9.5
-	PGRC/E	10	45	8	1110	1110		12.0	1011	<i>,</i> ,,,	017	0.0	>	.2.10	20.0	2.0
	20001		_	_												
2	"	81	13	15	4.4	4.4	3.6	5.3	5.5	5.7	4.0	3.3	2.6	13.4	5.9	8.1
	20002		34	3												
3	"	90	13	17	5.1	5.1	4.6	7.8	91	77	4.6	54	3.8	21.3	15.9	14
5	20004	70	90	2	5.1	5.1	4.0	7.0	7.1	/./	4.0	5.4	5.0	21.5	15.7	3
-	20004	0.6	10	- 17	6.0	6.0	1.6	7.4	67	6.2	5.6	1.0	2.5	20.0	25.0	10
4	20005	86	18	1/	6.8	6.8	4.6	7.4	6.7	6.3	5.6	4.8	3.5	29.9	25.0	19.
5	20005	00	17	ð 10	11.5	11.5	4.2	111	0.2	62	0.2	75	27	50.5	12.2	8 16
5	20006	99	33	19	11.5	11.5	4.2	11.1	9.2	0.2	9.2	1.5	2.1	59.5	45.5	10. 5
	20000		55	1									• •		.	5
6	20007	90	19	20	7.7	7.7	3.5	9.1	8.2	7.1	6.7	5.3	2.9	34.3	29.4	11.
	20007		/5	3												/
7	"	94	18	19	9.0	9.0	4.9	10.4	10.1	8.4	8.0	6.6	4.1	41.4	44.8	19.
	20017		66	0												5
8	"	10	12	15	9.8	9.8	6.4	8.5	7.3	6.5	6.8	5.7	5.6	38.5	30.3	20.
	20056	2	26	9												3
9	"	11	90	11	12.9	12.9	92	111	10.1	9.6	79	74	5.1	48.7	55.7	29
	20065	3	4	5	12.7	12.7	1.2	11.1	10.1	7.0	1.5	7.4	5.1	-0.7	55.7	1
	20000	0.1		10	10.0	10.0	0.5	11.5	10.6	0.0	0.0	0.1		(0.0	64.0	-
1		91	13	18	12.2	12.2	8.5	11.5	10.6	9.3	9.2	8.4	6.5	68.3	64.0	31.
0	20066		/5	4												0
1		89	25	19	6.7	6.7	4.6	7.4	8.1	7.5	5.1	5.7	3.4	20.7	20.5	14.
1	20067		34	8												4
1		94	25	17	10.5	10.5	4.5	11.0	9.4	7.8	7.9	6.1	2.9	47.4	26.6	8.8
2	20076		80	3											10.0	0.1
1		85	18	17	7.7	7.7	4.2	9.1	7.1	7.0	6.1	3.7	2.4	22.3	10.9	8.1
3	20077	00	83	4	0.2	0.2	47	8.0	0.7	7.0	0.1	76	5.0	50.2	52.2	26
	20112	98	24	19	8.5	8.5	4./	8.9	9./	7.9	8.1	7.6	5.2	50.2	55.2	20. 7
4	20112	10	20	17	11.8	11.8	57	11.0	0.7	73	88	77	4.5	76.8	585	24
5	20117	10	80	0	11.0	11.0	5.1	11.9	7.1	1.5	0.0	1.1	4.3	70.0	58.5	24. 0
1	20117	10	18	17	12.3	12.3	77	11.9	10.6	92	9.0	78	54	58.1	52.7	38
6	20127	7	46	3	12.5	12.5		11.7	10.0	1.2	2.0	7.0	5.4	50.1	52.7	0
1	"	85	99	15	4.4	4.4	2.6	6.2	6.4	4.9	4.1	3.5	1.9	14.3	9.3	7.2
7	20133		9	4												

1 8	" 20134	10 2	24 73	20 9	14.4	14.4	7.5	13.2	11.3	8.8	10.5	8.6	5.2	83.8	72.1	37. 5
1	20146	92	23 60	18 1	7.8	7.8	3.5	9.9	9.2	7.4	7.6	6.1	3.9	36.6	32.3	16. 9
2	20165	97	24 65	21 9	10.4	10.4	5.6	11.8	10.5	8.6	8.9	7.7	4.8	68.5	43.6	29. 7
2	20166	94	23	21	8.8	8.8	4.0	10.1	9.5	6.4	7.3	6.7	3.3	36.4	36.8	13. 3
$\frac{1}{2}$	21008	82	16	15	5.7	5.7	2.6	6.8	6.2	4.7	4.5	3.1	2.2	15.4	14.4	5.4
2	21008	10	21	9 14 7	9.7	9.7	5.9	9.5	8.5	7.3	7.6	6.7	4.8	43.2	39.9	21.
2	21012	2 10	22	17	11.8	11.8	6.9	10.6	10.0	7.6	8.7	7.3	4.7	47.6	57.7	/ 19.
4 2	21017	- 5 - 99	40 30	9	8.4	8.4	5.2	9.5	9.5	8.1	7.8	7.2	5.1	51.2	55.8	1 29.
2	21026	10	54 16	3 19	12.8	12.8	10.	12.3	11.6	8.8	9.6	8.9	6.8	50.9	57.7	9 47.
2	21035	6 94	43 26	4 22	11.1	11.1	3 7.9	11.4	10.2	8.2	8.9	7.2	5.3	66.3	48.5	1 28.
2	21037	79	39 18	4	3.2	3.2	2.3	4.8	4.6	4.4	2.3	2.5	1.6	5.8	6.0	3
8	21068	90	04 13	14	12.6	12.6	7.2	12.4	10.9	8.0	9.3	8.1	5.5	69.8	65.8	27.
9	21157	79	42 19	4	3.4	3.4	2.6	5.4	6.3	6.2	2.9	2.6	2.2	9.0	10.4	5 8.1
3	21225	10	28 15	0 17	8.7	8.7	4.7	9.3	7.9	7.0	6.9	5.3	3.7	37.4	29.9	18.
1	208411	0	86 19	9 19	11.1	11.1	5.7	13.0	10.9	9.3	10.3	8.5	5.8	59.0	63.7	3 34.
2	229665	0	04	4	11.6	11.6	0.0	11.6	10.5	10	8.0	0.1	7.4	76.6	51.0	2
3 3	237048	9	88	1	11.0	11.0	9.9	11.0	10.5	10. 4	8.9	0.1	7.4	/0.0	51.8	47. 0
3 4	" 241907	93	19 88	19 5	7.5	7.5	4.8	8.2	8.9	7.3	6.6	6.2	4.3	44.4	26.7	19. 4
3 5	" 241910	93	25 66	18 7	8.7	8.7	4.7	8.5	8.4	7.1	6.9	6.2	3.4	29.0	31.5	11. 4
3	"	90	21	17	8.0	8.0	3.9	8.8	7.8	6.5	6.1	4.6	2.7	32.1	21.5	10.
3	"	97	20	20	12.4	12.4	7.6	11.0	9.4	8.0	7.8	6.8	4.1	48.7	42.6	8 25.
7	242858	88	19 20	4	5.8	5.8	2.9	7.7	6.9	5.7	5.0	3.9	2.1	22.9	15.5	1
8	243738	0.0	22	8	5.6	5.0			5.1		4.0	2.6	2.1	44.5	44.6	22
3 9	243739	86	31	8	5.4	5.4	3.9	6.3	5.1	5.6	4.2	3.6	2.4	44.5	44.6	23. 9
4 0	" 21256	98	22 91	22 1	11.0	11.0	8.8	12.4	11.9	9.0	8.4	9.1	6.9	23.4	29.9	30. 5
4 1	" 243750	85	21 42	19 3	7.1	7.1	3.4	8.4	7.2	6.5	5.8	4.1	3.2	27.0	22.0	13. 6
4 2	" 243756	10 8	18 59	18 6	13.2	13.2	10. 3	12.4	11.2	9.9	9.9	8.9	7.7	63.3	63.1	42. 0
4	" 243761	88	19 31	16 3	12.5	12.5	5.6	11.5	8.2	7.0	8.9	6.6	4.4	52.0	37.8	16. 2
4	"	95	13	16	9.6	9.6	4.0	9.1	8.1	5.5	7.2	6.3	2.8	36.6	28.2	12.
4	"	86	18	17	6.7	6.7	5.6	7.7	7.6	7.0	5.8	5.0	4.4	26.4	17.6	19.
5	208556	94	79 21	2 20	11.9	11.9	7.1	10.9	11.0	8.0	9.7	8.0	5.7	48.1	42.6	3 16.
6	208585	05	42	8	67	67	20	7.0	7.2	62	55	A 4	2.0	167	11.2	4
4	dodolla	85	32 97	$\begin{bmatrix} 1 \\ 7 \end{bmatrix}$	0.0	0.0	3.8	1.2	1.2	0.3	5.5	4.4	5.2	10./	11.2	11. 8

4	(ZemXY	80	26	20	6.4	6.4	3.4	8.8	6.9	6.1	5.9	3.7	3.0	28.2	13.7	10.
8	D)		03	3												2
4	Local	85	22	15	4.9	4.9	3.2	6.0	5.9	6.1	4.1	3.4	2.7	10.6	9.0	7.5
9	check		12	5												
	Mean	93	19	18	8.9	7.4	5.3	9.5	8.7	7.3	7.11	6.01	4.0	40.77	35.0	19.
			99	1			3						7		7	85
	CV(0)	3.	24.	7.	20.3	22.6	37.	18.2	18.3	24.	20.7	22.8	42.	39.96	46.4	71.
	CV (%)	38	08	18	0	7	99	2	9	31	8	6	62		9	96
	LSD	6.		29	3.7	3.4	4.1	3.5	3.2	3.6	2.9	2.7	3.5	32.7	34.9	28.
	(0.05)	34		.1												7

The analysis of variance for the 15 leaf traits studied is given in Table 3. The analysis of variance showed that there were significant differences among genotypes for all leaf parameter in their bottom, middle and top different plant parts of leaf traits except leaf width and leaf area from top plant parts compared. Among analyzed leaf traits highly and significantly differences were observed in date of 50% flowering, plant height, petiole length from bottom plant parts, petiole length from middle plant parts , petiole length from top plant parts, leaf length from bottom parts of plants , leaf length from middle parts of plants , leaf length from top parts of plants , leaf width from bottom parts of plants, leaf width from middle parts of plants, leaf area from bottom parts of plants, leaf width from middle parts of plants, leaf area from bottom parts of plants, leaf area from middle parts of plants traits. The significant difference indicates the existence of genetic variability among the accessions that is important for selection and breeding. Rabbani *et al.* studied 52 mustard accessions for various both agronomic and physiological interests. Revilla and Tracy found considerable level of diversity among their executed experiment.

no		Genotype(48)	Block(12)	Replication(1)	Intra Block
	Character			-	error(36)
1	Date of flowering	141.98**	6.39	0.91	9.96
2	Seed yield per plot	503441*	15.9527	88.2551	9.6692
3	Plant height	1004.12**	1102.13	2812.50	1004.12
4	Petiole length from bottom of plant parts	17.0989**	3.3784	53.6352	3.3339
5	Petiole length from middle of plant parts	12.1198**	3.2264	32.5740	2.7985
6	Petiole length from top of plant parts	9.0237**	2.3248	15.4409	4.1043
7	Leaf length from bottom of plant parts	10.0723**	2.4737	20.2066	3.0007
8	Leaf length from middle of plant parts	6.8706**	1.8345	18.5180	2.5594
9	Leaf length from top of plant parts	3.8865**	2.6045	28.1250	3.1752
10	leaf width from bottom of plant parts	8.2355**	1.6135	22.6368	2.1843
11	Leaf width from middle of plant parts	6.9200**	2.7802	20.6633	1.9212
12	Leaf width from top plant parts	4.6029ns	2.1734	23.0230	3.0136
13	leaf area from Bottom of plant parts	5.1346**	323.22	565.44	265.54
14	leaf area from middle parts of plants	5.1571**	494.55	229.59	265.95
15	leaf area from top parts of plants	2.76692ns	293.30	729.07	204.20

Table3. Mean squares for different sources of variations for 15 leaf traits of 49 Ethiopian mustard genotypes

3.2. Analysis of Variance

The data collected for traits of leaf on different parts of plants were subjected to analysis of variance (ANOVA) for simple lattice design. Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.2, (SAS Institute, 2008). Analysis of variance (Table 4) for the considered traits was done using the model for lattice design as follows:

Yil(j) = u + ti + rj + (b/r)l(j) + eil(j)

Where, Yil(j) is the observation of the treatment $i(i = 1,...V, k^2)$, in the block l(l = 1,...k) of the replication j(j = 1,...,m);

 μ is a constant common to all observations;

 t_i is the effect of the treatment i;

rj is the effect of the replication j;

 $(b|r)_{1(j)}$ is the effect of the block l of the replication j;

 $e_{il(j)}$ is the error associated to the observation $Y_{il(j)}$, where $e_{il(j)} \sim N(0,s)$ independent.

Table4. Simple Lattice analysis of variance and expected mean squares

Source of variation	Df	SS	MS	F-value
Replication(r)	r-1	SSr	MSr	MSr/MSe
Genotype(g)	g-1	SSg	MSg	MSg/MSe
Block within replication	r(b-1)	SSb	MSb	MSb/MSe
Intra-block error	(b-1)(rb-b-1)	SSe	MSe	
Total	rb2-1	SST		

Where, Df = degree of freedom, SS sum of squares; MS: mean of squares, SSr and MSr sum of squares and mean of replication, respectively: SSg and MSg are sum of squares and mean of genotypes, respectively: SSb and MSb are sum of squares and mean of blocks within replication respectively. SSe and MSe are sum of squares and mean of intera-block error.

3.3. Estimation of Phenotypic and Genotypic Variability

The variability present in the population was estimated by simple measures, namely range, mean, standard error, and phenotypic and genotypic variances and coefficients of variations. The phenotypic and genotypic variance and coefficients of variation was also estimated as per the procedure suggested by Burton and De Vane (1953) as follows:

$$\delta^{2} p = \delta^{2} g + \delta^{2} e$$
$$\delta^{2} g = \frac{MSg - MSe}{MSg - MSe}$$

Where, $\delta^2 g$ =Genotypic variance

 $\delta^2 P$ = Phenotypic variance

 $\delta^2 e$ = Environmental (error) variance or Error mean square

MSg = mean sum square due to genotypes (accessions)

MSe =mean sum square of error (environmental variance)

r = number of replications

$$PCV = \frac{\sqrt{\delta^2 p}}{x} x100$$

Phenotypic Coefficient of Variation (PCV),

$$GCV = \frac{\sqrt{\delta^2 g}}{\frac{1}{x}} x100$$

Genotypic coefficient of Variation (GCV),

 \mathcal{X} = Population mean of the character being evaluated

3.4. Heritability (in broad sense)

Heritability in the broad sense for quantitative characters was computed using the formula suggested by Singh and Chaudhary (1985):

$$H = \frac{\delta^2 g}{\delta^2 p} x 100$$

Where, H= heritability in the broad sense.

$$(\delta^2 g)_{=\text{Genotypic variance and}}$$

 $(\delta^2 p)_{=\text{Phenotypic variance}}$

3.5. Expected genetic advance (GA)

The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard (1999) as:

$$GA = K * \delta_P * H$$

Where, GA = expected genetic advance, δ_p^P =phenotypic standard deviation on mean basis, H= Heritability in broad sense, K =selection differential (k=2.06 at 5% selection intensity)

Genetic advance (as percent of mean) (GA) was computed to compare the extent of predicted genetic advance of different traits under selection using the formula:

$$GAM = \frac{GA}{\overline{X}} * 100$$

Where, x =population mean of the quantitative character, GAM =genetic advance as percent of mean.

3.6. Analysis of Genetic Parameters

Genotypic and Phenotypic Coefficient of Variation

Estimates of genotypic and phenotypic variances, genotypic coefficient of variation (GCV), phenotypic coefficients of variation (PCV), heritability in broad sense, expected genetic advances and genetic advances as percent mean are given in Table5. Estimated genetic variance ranged from 0.3557% for leaf length from top of plant parts to 135887 for seed yield per plot (Table5). Likewise phenotypic variance ranged from 7.0617% for leaf length from top of plant parts to 735108kg/ha for seed yield per plot. Phenotypic coefficients of variation ranged from 13.254% for date of 50% flowering to 68.995% leaf width from top parts of plants. Genotypic coefficients of variation ranged from 8.169% for leaf length of top of plants to 30.90% for petiole length from top parts of plants. seed yield per plot(735108, 135887),Plant height (1173.58, 417.33), leaf area from bottom parts of plants (1025.39, 247.16),date of 50% flowering(151.945,66.01) petiole length from bottom parts of plants (20.43,6.883), petiole length from middle parts of plants (14.92,4.661) and leaf length of from bottom of plant parts (13.07,3.536) showed high phenotypic and genotypic variances, respectively indicating that the genotypes could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these traits.

Low genotypic variance as compared to environmental variance was recorded for traits such as leaf length from top parts of plants (0.356) and leaf area from top parts of plants (0.658), leaf length from middle parts of plants (2.1556) and petiole length from top parts of plants (2.6821). However, high genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were shown

in traits such as petiole length of from top of plant parts(30.900, 67.195), petiole length of from middle of plant parts(29.477, 52.195), leaf width from middle of plant parts(26.05,49.474), leaf width from top of plant parts (22.286,68.995), leaf area from middle parts of plants (24.908,45.257) and leaf area from bottom parts of plants (22.192,42.022) respectively, which means selection of these traits based on phenotype characteristics may be useful for assessment of leaf variability in different parts of plant for improvement leaf traits.

Heritability in the broad sense

Breeders can make rapid progress where heritability is high by using selection methods that are dependent solely on phenotypic characteristics (e.g. mass selection). However, where heritability is low methods of selection based on families and progeny testing are more effective and efficient. Heritability estimated using the total genetic variance is called broad sense heritability. Heritability in the broad sense of the traits is presented in Table 5. In this study, heritability values were found to be sufficiently high for most important yield component characters. Dabholkar (1992) generally classified heritability estimates as low (5-10%), medium (10-30%) and high (30-60%). Based on this classification, date of 50 % flowering (43.442%), plant height (35.560), petiole length from bottom of plant parts(33.684%), petiole length from middle of plant parts(31.241%), leaf width from bottom of plant parts(30.134%) and leaf width from middle of plant parts(30.291%) exhibited high heritability estimates. On the other hand leaf width from middle of plant parts(28.270%), leaf area from bottom of plant parts(27.889%),leaf length from bottom of plant parts(27.047%),leaf length from middle of plant parts(22.859), seed yield per plot (18.485), leaf area from top of plants(15.59%) and leaf width from top of plants(10.433%) exhibited medium heritability estimates while only leaf length from top of plant parts(5.036%) exhibited low heritability estimates. Date of 50% flowering was found to be the most heritable trait in the genotype, with heritability of 43.442%, followed by plant height (35.56%), petiole length from bottom of plant parts 33.684%. Except only leaf length from top of plant parts all leaf traits showed high and medium heritability estimates. This indicates that selection for these traits in the genotype would be most effective for the expression of these traits in the succeeding generations.

Therefore, good improvement can be made if some of these traits are considered as selection criteria in future leaf traits improvement program. Similar findings had been reported by Jane Muthoni (2010) for leaf number/plant, leaf bloom and leaf blade blistering, flowering time, plant height, and seed yield per plant. High heritability value for thousand seed weight and seed yield per plot recorded in the current study was also recorded by Yared (2010) and Abebe (2006).According to Singh (1993), if the heritability of a character is high, selection for such character is fairly easy as selected character will be transmitted to its progeny. This is because there would be a close correspondence between the genotype and phenotype due to a relatively similar contribution of the environment to the genotype.

Genetic advance

Concerning the genetic advance at 5% intensity the highest genetic gain was predicted for seed yield per plot (326.490%) ,plant height(25.095%) followed date of 50% flowering (11.031%) and while the lowest genetic advance was predicted for leaf length from top plant parts(0.276%). Genetic advance as a percent mean ranged from 3.77% for leaf length from top of plant parts to 35.242% for petiole length from bottom of plant parts (Table 5). Within this range, a relatively high genetic advance as a percent mean was observed for petiole length from bottom of plant parts (35.242%) and petiole length from middle of plan parts (33.591%)followed by petiole leaf length from top of plant parts(29.272). On the other side high genetic advance with medium heritability was shown for seed yield per plot 326.490% which may be because of the presence of both additive and non-additive gene action (Liang *et al.*, 1972). On the other hand, the lowest genetic gain as percent of means was observed for leaf length from top of plant parts 3.777% and date of 50% date of flowering 11.861%.. Low genetic advance as percent means observations in this study indicates that characters probably were under environmental influence than the genotypic expression and that selection based on these traits would be ineffective.

Table5. Components of variance, coefficients of variability, heritability and genetic advance and Genetic advanceas percent of mean of studied traits

			-					GA	GA/Grand
Character	Mean	$\delta^2 g$	$\delta^2 e$	δ²ph	GCV	PCV	h²b	k = 5%	mean
									*100 k 5%

Date of	93								
flowering	20	66.01	85.93	151.94	8736	13.254	43.442	11.031	11.86
Seed yield per	1999								
plot		135887	59921	735108	18.441	42.891	18.485	326.49	16.33
Plant height	181	417.33	756.25	1173.58	11.28	18.927	35.56	25.09	13.86
Petiole length	8.9								
from bottom of									
plant parts		6.8825	13.55	20.4328	29.14	50.789	33.68	3.13	35.242
Petiole length	7.4								
from middle of									
plant parts		4.6607	10.26	14.9183	29.57	52.195	31.24	2.48	33.591
Petiole length	5.3								
from top of									
plant parts		2.6821	10.00	12.6832	50.15	67.195	21.15	1.55	29.272
Leaf length	9.5								
from bottom of									
plant parts		3.5358	9.54	13.073	18.8	38.06	27.05	2.01	21.205
Leaf length	8.7								
from middle of									
plant parts		2.1556	7.27	9.43	16.31	35.297	22.86	1.44	16.621
Leaf length	7.3								
from top of									
plant parts		0.3557	6.71	7.0617	8.52	36.403	5.036	0.56	3.777
leaf width	7.1								
from bottom of									
plant parts		3.097	7.18	10.2771	25.14	45.152	30.13	1.98	28.029
Leaf width from	6.01								
middle of plant									
parts		2.4994	6.34	8.8412	28.09	49.474	28.27	1.73	28.812
Leaf width	4								
from top plant									
parts		0.7947	6.82	7.61652	22.28	68.995	10.43	0.59	14.829
leaf area from	6.1								
Bottom of plant									
parts		1.839	4.751	6.59	22.192	42.022	27.889	1.4275	24.142
leaf area from	5.6								
middle parts of									
plants									
		1 9/6	1 171	6.42	24 008	15 257	30 201	1 581	28 240
leaf area from	4.2	1.940	4.4/4	0.42	24.700	+5.251	50.271	1.501	20.240
ton parts of	4.2								
nlants									
Plants									
		0.658	3.562	4.22	19,495	49.372	15,591	0.660	15.857
L	I	0.050	5.502		17.175	17.514	10.071	0.000	10.001

variance, $\delta^2 e = Error$ variance, $\delta^2 ph = Phenotypic$ variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, h2b = Broad sense heritability, GA = Genetic advance and K = Selection intensity

4. CONCLUSION

In this study, 49 Ethiopian mustard genotypes acquired from diverse zones/regions of Ethiopia were evaluated in simple lattice design with two replications at Holetta Agricultural Research Center, West Shewa zone, with the objective of assessing traits of leaf variability in their different plant parts of Ethiopian mustard land races in relation to high quantity and quality of leaf production traits. The analysis of variance showed the presence of significant differences among genotypes for all leaf parameter in their bottom, middle and top different plant parts of leaf traits except leaf width and leaf area from top plant parts compared. The significant difference indicates the existence of genetic variability among the accessions which is important for leaf traits improvement. Likewise phenotypic variance ranged from 4.22 % for leaf area from top of plant parts to 735108 % for seed yield per plot. Phenotypic coefficients of variation ranged from 13.254 % for date of 50 % flowering to 68.995 % leaf

width from top parts of plants. Genotypic coefficients of variation ranged from 8.169 % for leaf length from top of plant parts to 30.900 % for petiole leaf length from top parts of plants.

High phenotypic coefficient of variation (PCV) was recorded for leaf width from top parts of plant 68.995 %, petiole leaf length from top parts of plant 67.195% and leaf length from middle parts of plants 52.195%.. But low PCV was detected for date of 50 % flowering and plant height. Generally, the magnitudes of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high for leaf width from top of plants, petiole leaf length from top of plant parts and petiole length from middle of plant parts. Heritability in broad sense estimates was high for date of 50 % flowering, plant height, petiole length from bottom of plant parts, petiole length from middle of plant parts, leaf width from middle of plant parts. On the other hand leaf width from middle of plant parts, leaf area from bottom of plant parts, leaf length from bottom of plant parts, leaf length from middle of plant parts, seed yield per plot, leaf area from top of plants and leaf width from top of plants exhibited medium heritability estimates while only leaf length from top of plant parts exhibited low heritability estimates .Genetic advance as percent of the mean (GAM) was high for petiole length from bottom of plant parts petiole length from middle of plant parts, petiole length from top of plant parts and while the lowest genetic advance was predicted for leaf length from top plant parts (0.276%). Genetic advance as a percent mean ranged from 3.777% for leaf length from top of plant parts to 35.242% for petiole length from bottom of plant parts (Table 5). Within this range, a relatively high genetic advance as a percent mean was observed for petiole length from bottom of plant parts(35.242%) and petiole leaf length from middle of plan parts (33.591%) followed by leaf width from middle of plant parts(28.812). On the other side high genetic advance with medium heritability was shown for seed yield per plot and plant height which may be because of the presence of both additive and non-additive gene action. These results indicate that there is good opportunity to improve leaf variability traits using the tested genotypes.

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