Genetic Divergence and Correlation Study in Sesame *(Sesamum indicum L.)* Genotypes

A Thesis Submitted to the School of Graduate Studies of Addis Ababa University in Partial Fulfillment of the Requirement for the Degree of Master of Science in Biology (APPLLIED GENETICS)

BY

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SCHOOL OF GRADUATE STUDIES OF ADDIS ABABA UNIVERSITY

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Dedication

This piece of work is dedicated to my Beloved Family who gave me everything I have now

Acknowledgement

I would like first to praise the almighty, for helping me up to this stage. Next but not last I would like to extend my sincere gratitude to my major advisor, Dr. Adefris Teklewold for his professional, material support and utmost for his brotherly advices.

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Sileshi Andualem

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Abstract

A field experiment was designed at the research site of Werer Agricultural Research Center in the 2007/8 cropping season to assess genetic divergence and character associations among 13 agro-morphological traits of 100 local and exotic sesame (*Sesamum Indicum* L.) genotypes. The result indicated the existence of a wide variability among the genotypes for all the measured characters. The highest PCV and GCV estimates were observed for oil yield per plant (54.47%, 37.30%) followed by seed yield per plant (54.23%, 35.77%), number of primary branches (42.93%, 32.37%) and distance to the first pod (41.69%, 26.01%), respectively. More than half of the characters showed heritability (broad sense) values of greater than 50% and higher estimates of heritability values were recorded for days to flowering (62.45%) followed by number of primary branches (56.68%), 1000 seed weight (56%), capsule length(55%), days to maturity (54.865) and oil content (53.10%). Higher values of genetic advance that could be expected from selecting the top 5% genotypes, as percentage of mean was recorded for oil yield per plant (92.84%) followed by number of primary branches (50.31%) and seed yield per plant (48.64%). Higher estimates of broad sense heritability together with high genetic advance was observed for number of primary branches, number of capsules and seed yield and oil yield per plants, indicating the possible preponderance of additive gene action. Seed yield had shown significant and positive PCC and GCC with number of pods per plant (0.849, 0.967), thousand seed weight (0.744, 0.865), oil yield per plant (0.997, 0.998), plant height (0.326, 0.263) and oil percent (0.361, 0.551) while, it had significant but negative PCC and GCC values with number of seeds per pod (-0.281,-0.585) and days to flowering (-0.369, -0.454) respectively. Path analysis of seed yield revealed that number of pods per plant and number of primary branches had a positive direct effect on seed yield. Yield components 1000 seed weight, plant height and days to 50% flowering had negative values of direct effects although seed yield was counter balanced by higher positive indirect effects exerted through number of pods per plant, plant height and days to 50% flowering. Path analysis was also computed using oil yield as a dependant character and characters number of pods and seed yield per plants had positive direct effects on oil yield per plant. On the other hand negative direct effects were observed for 1000 seed weight and oil content, however these negative values were found to be counter balanced by positive indirect effects of the other component traits. The principal component analysis was performed and the first three principal components were found to explain 73% of the overall variability existing among the test entries. The major contributing factors for the total variability were found to be days to 50% flowering, days to maturity, distance to the first pod and number of primary branches in order of importance. Cluster analysis grouped 100 genotypes into eight diversity groups containing 39, 43, 3, 9, 3 genotypes in that order while, the remaining three clusters had single accession each signifying the fact that efficient germplasm management can be achieved through avoiding redundant accessions. Generally the study had shown the existence of high genetic diversity among the evaluated accessions that could be utilized for future breeding programs. Further investigations are needed to study the diversity of the crop at molecular levels to ascertain the finding of this study.

APPENDICES

Appendix 1. List of sesame genotypes tested at werer, 2007/08

No	Acceccession Number	Area of collection	Locality	Altitude mts. a.s.l
1	NS-065	North Shewa	Jejeba	1300
2	NS-0013	North Shewa	Jejeba	1260
3	NS-0047	North Shewa	Artumajelle	1290
4	NS-0025	North Shewa	Kewet	1210
5	NS-0074	North Shewa	Artumajelle	1460
6	NS-0022	North Shewa	Kewet	1360
7	NS-008	North Shewa	Korangoge	1250
8	NS-033	North Shewa	Senbete	1300
9	NS-004	North Shewa	Tarmaber	845
10	NS-006	North Shewa	Akake	1900
11	NS-034	North Shewa	Senbete	1200
12	NS-007	North Shewa	Majette	1200
13	BG-010(1)	Benshangul Gumuz	Mender 6	1050
14	BG-013	Benshangul Gumuz	Mandura	940
15	BG-002(2)	Benshangul Gumuz	Belojeganfo	1280
16	BG-006	Benshangul Gumuz	Dangur	910
17	BG-004	Benshangul Gumuz	Ipapo	1180
18	BG-008	Benshangul Gumuz	Danua	1020
19	BG-015	Benshangul Gumuz	Mandura	910
20	BG-010(3)	Benshangul Gumuz	Mender 5	1050
21	BG-019	Benshangul Gumuz	Mandura	965
22	BG-009	Benshangul Gumuz	Dangur	1250
23	BG-012(2)	Benshangul Gumuz	Mekane selam	1095
24	BG-007	Benshangul Gumuz	Dadush	1000
25	G-006	Gambella	Abobo	490
26	G-002(2)	Gambella	Cheba	500
27	G-004(1)	Gambella	Banga	480
28	G-003(2)	Gambella	Chebo	510
29	G-003(1)	Gambella	Chebo	500
30	G-004(2)	Gambella	Abobo	480
31	G-002(1)	Gambella	Bonga	510
32	G-005(1)	Gambella	Abobo	480
33	G-009(2)	Gambella	Merar	500
34	G-006(1)	Gambella	Bonga	465
35	G-001	Gambella	Jejeb	485
36	EW-008(1)	East Wollega	Diga	1325
37	EW-006	East Wollega	Gida Kiremu	1360
38	EW-020(1)	East Wollega	Diga	1390
39	EW-005	East Wollega	Abedunguru	1400
40	EW-020	East Wollega	Sasiga	1570
41	EW-015(1)	East Wollega	Abedunguru	1290
42	EW-013(5)	East Wollega	GidaKiremu	1300
43	WW-001(3)	West Wollega	Gimbi	1250
44	WW-002	West Wollega	Hawawelel	1090
45	WW-003(2)	West Wollega	Gimbi	1330
46	WW-003(1)	West Wollega	Goadale	1150
47	WW-003	West Wollega	Goadale	1190
48	WW-002(2)	West Wollega	Hawawelwel	1000
49	Acc-202-363	Wollo	Sirinka	1560
50	Acc-202-318	Wollo	Kalu	1400
51	Acc-202-355	Wollo	Artuma	1860

Appendix 1. Cont'd

No.	Accession Number	Area of collection	Locality	Altitude mts. a.s.l
52	Acc-202-293	Wollo	Ambasel	1460
53	Acc-202-343	Wollo	Harbu	1500
54	Acc-202-325	Wollo	Bati	1750
55	Acc-202-299	Wollo	Ambasel	1540
56	Acc-202-307	Wollo	Bati	1470
57	Acc-202-368	Wollo	Sirinka	1500
58	Acc-202-333	Wollo	Harbu	1450
59	HH-206-004	Humera	NA	600
60	HH-206-001	Humera	NA	600
61	HH-206-007	Humera	NA	600
62	HH-206-002	Humera	NA	600
63	HH-206-005	Humera	NA	600
64	Htn-206-002	Humera	NA	600
65	Htb-206-002	Humera	NA	600
66	Htb-206-001	Humera	NA	600
67	Htk-206-002	Humera	NA	600
68	Htk-206-004	Humera	NA	600
69	Hr-206-002	Humera	NA	600
70	Hr-206-003	Humera	NA	600
71	Hr-206-004	Humera	NA	600
72	Hr-206-001	Humera	NA	600
73	GoA-206-002	Humera	NA	700
74	GoA-206-004	Metema	NA	750
75	GoA-206-001	Metema	NA	750
76	GoA-206-003	Metema	NA	750
77	HN-206-003	Metema	NA	750
78	HN-206-004	Metema	NA	750
79	HN-206-005	Metema	NA	750
80	HN-206-002	Metema	NA	750
81	HN-206-001	Metema	NA	750
82	Hr-206-0010	Metema	NA	750
83	Hr-206-002(2)	Metema	NA	750
84	Hr-206-001(2)	Metema	NA	750
85	MT-206-001	Metema	NA	750
86	Acc-203-623	Zimbabwe	NA	NA
87	Localwhite-0034	Somalia	NA	NA
88	Giza-25	Egypt	NA	NA
89	Giza-32	Zimbabwe	NA	NA
90	Acc-203-505	Egypt	NA	NA
91	California-827	USA	NA	NA
92	Margo sel	Israel	NA	NA
93	T-6	India	NA	NA
94	K-60-383	Korea	NA	NA
95	Ying white	China	NA	NA
96	Instituto	Mexico	NA	NA
97	FAO-68-548	Venzuela	NA	NA
98	UCR-82-209	USA	NA	NA
99	Orotall	Israel	NA	NA
100	Etalokornia	Greece	NA	NA

Appendix 2. Mean values of 13 plant characters for 100 sesame genotypes

Trt	DTF	PHt	NP/Pl	NPB	IntL	CapL	DTM	NS/Pod	Yld/Pl	1000SW	OIL%	DTFP	OY/Pl
1	45.33	139.87	75.23	3.40	8.09	2.90	112.00	65.67	12.02	3.58	55.18	28.01	6.60
2	42.67	145.80	53.67	4.33	6.21	2.48	107.33	61.07	7.99	3.44	52.40	37.94	4.19
3	45.33	156.97	45.40	3.17	5.84	2.56	110.00	75.47	7.28	3.17	53.51	52.93	3.86
4	39.00	108.07	37.40	2.77	6.01	2.45	99.33	65.13	4.33	2.95	54.61	20.67	2.36
5	44.00	154.90	54.13	2.93	6.03	2.73	113.67	65.47	8.99	3.12	50.46	31.37	4.51
6	45.67	134.33	36.00	2.17	5.87	2.34	110.67	70.07	3.81	2.50	53.19	34.85	2.03
7	61.67	134.13	26.53	7.07	4.28	2.04	115.67	66.87	2.79	2.54	54.63	43.15	1.52
8	55.33	152.13	42.87	6.17	5.11	2.39	113.33	65.07	6.82	3.34	51.03	30.95	3.48
9	64.00	141.27	40.07	6.60	4.68	2.01	117.00	63.73	2.79	2.33	51.78	42.95	1.43
10	57.33	106.40	41.33	6.27	3.38	1.88	117.67	66.33	2.08	2.57	51.48	48.63	1.07
11	44.00	146.93	52.80	3.43	7.73	2.56	106.33	71.53	7.22	2.69	52.09	29.99	3.72
12	59.00	151.96	30.83	5.33	5.34	2.23	125.33	67.27	3.88	2.75	51.43	45.79	2.02
13	49.67	155.23	32.97	3.10	5.75	2.33	115.00	72.13	3.75	2.43	50.83	29.34	1.92
14	49.33	155.30	31.67	2.63	6.50	2.31	115.00	73.67	3.29	2.16	51.27	23.33	1.69
15	48.67	131.10	26.17	1.90	6.55	2.26	116.33	72.27	2.82	2.19	51.70	19.81	1.46
16	48.00	143.83	32.47	3.00	5.05	2.25	115.33	73.47	3.53	3.05	50.36	29.29	1.78
17	49.00	148.03	40.23	3.23	5.72	2.25	115.00	67.93	3.43	2.12	50.04	23.83	1.70
18	49.67	146.07	30.90	2.50	5.21	2.29	115.67	65.67	3.12	2.16	50.94	23.25	1.58
19	63.67	120.93	25.80	4.23	5.09	2.47	125.67	63.67	2.41	1.99	49.46	25.99	1.15
20	46.33	130.20	46.23	3.47	5.14	2.37	116.33	70.13	5.69	2.45	52.50	22.97	2.96
21	49.33	157.57	43.23	3.83	8.23	2.31	115.67	71.07	4.95	2.30	51.68	26.37	2.55
22	49.33	167.87	47.20	4.10	5.34	2.39	115.00	69.40	4.73	2.17	52.08	33.95	2.46
23	48.00	157.37	45.27	3.10	6.79	2.36	112.33	72.13	4.55	2.26	51.07	27.19	2.33
24	46.67	155.67	40.90	2.43	6.36	2.46	112.33	74.27	5.17	2.45	51.27	27.77	2.65
25	42.00	151.57	52.70	2.37	7.30	2.51	111.00	69.87	8.29	2.90	52.89	21.17	4.38
26	42.67	102.27	23.40	1.63	7.51	2.99	97.00	70.80	1.61	2.43	47.46	14.03	0.76
27	43.00	119.80	29.93	2.17	5.30	2.52	98.33	69.33	3.22	2.40	50.50	16.93	1.62
28	40.33	128.70	56.97	3.00	5.19	2.92	102.00	67.47	10.52	3.73	54.84	22.18	5.76
29	41.33	120.17	34.47	2.23	5.97	2.84	99.33	74.80	4.15	2.73	50.77	14.24	2.11
30	43.33	129.57	34.80	2.73	5.34	2.65	102.00	65.33	4.23	2.84	52.17	18.94	2.22
31	45.67	156.87	59.70	3.40	7.61	2.66	114.00	74.73	7.70	2.63	51.34	28.58	3.98
32	46.00	146.80	46.77	3.10	6.29	2.73	103.00	74.07	8.17	2.39	49.99	21.41	4.02
33	47.00	164.57	44.73	3.70	5.23	2.39	114.00	74.80	4.63	2.26	51.29	33.40	2.39
34	42.00	133.77	32.23	2.43	7.97	2.68	102.67	75.00	4.26	2.71	52.09	21.91	2.23
35	44.00	148.57	48.33	3.03	5.99	2.43	104.00	64.60	7.32	2.90	52.07	26.08	3.87
36	45.33	148.57	36.67	2.60	6.02	2.21	112.67	67.73	4.80	2.54	51.68	27.53	2.46
37	45.67	134.80	43.40	2.77	6.81	2.37	112.00	70.73	4.98	2.59	51.12	21.55	2.52
38	47.67	144.77	39.60	2.73	5.17	2.32	117.00	73.20	3.80	2.19	52.13	28.72	1.97
39	46.00	134.93	32.33	2.27	5.52	2.39	108.33	67.00	2.92	2.36	51.00	27.77	1.48
40	46.33	133.13	47.73	3.27	6.03	2.33	116.00	73.33	7.44	2.60	52.56	22.26	3.88
41	48.33	157.23	41.40	2.83	6.37	2.45	114.00	72.87	4.38	2.20	51.17	27.23	2.24
42	49.67	157.10	39.63	2.83	6.75	2.31	114.67	72.27	4.63	1.93	51.16	32.07	2.38

Appendix 2. cont'd

Trt	DTF	PHt	NP/Pl	NPB	IntL	CapL	DTM	NS/Pod	Yld/Pl	1000SW	OIL%	DTFP	OY/Pl
43	47.67	156.50	42.07	3.20	6.81	2.45	113.33	69.73	5.96	2.40	51.43	29.84	3.05
44	48.00	160.37	33.53	2.57	5.65	2.33	111.00	67.07	3.50	2.02	51.28	24.39	1.79
45	47.00	148.67	34.40	2.87	5.73	2.41	116.00	74.27	3.86	2.18	52.39	25.33	2.02
46	49.00	146.23	42.40	2.87	5.15	2.29	117.33	71.67	3.96	1.99	51.68	28.25	2.06
47	47.67	152.17	40.33	2.63	5.36	2.31	118.33	75.47	4.97	2.31	51.27	25.17	2.52
48	50.00	132.77	25.37	2.33	5.15	2.07	117.67	70.87	3.51	2.16	51.99	30.90	1.84
49	58.00	156.90	40.27	7.27	6.00	2.03	122.67	67.73	4.45	2.79	53.21	51.98	2.36
50	43.33	132.07	55.27	2.70	5.23	2.32	114.33	70.60	6.30	2.59	53.07	27.17	3.35
51	53.33	155.50	39.60	5.30	4.89	2.07	116.67	64.80	4.77	2.54	52.46	45.44	2.53
52	48.33	159.10	43.83	4.17	5.45	2.41	115.67	69.20	7.39	2.96	52.38	31.37	3.87
53	41.67	138.23	43.20	2.93	6.23	2.58	101.00	65.27	6.62	3.28	54.00	27.92	3.57
54	48.33	220.30	42.87	3.40	5.86	2.20	117.67	61.53	6.28	2.93	51.33	35.25	3.24
55	58.00	161.40	28.90	6.67	3.77	1.85	123.33	65.93	4.71	2.71	53.08	59.93	2.50
56	58.33	164.20	35.30	5.13	6.37	2.27	121.33	67.53	4.61	2.86	52.93	44.36	2.45
57	46.33	172.83	80.17	3.10	5.57	2.31	117.67	69.27	7.55	3.10	52.17	28.85	3.92
58	42.67	133.27	31.40	2.30	5.90	2.22	109.33	61.27	4.63	3.19	54.58	24.67	2.53
59	44.00	120.97	33.27	2.93	6.53	2.50	107.00	65.47	5.26	2.81	52.59	25.29	2.76
60	48.67	124.53	36.63	2.77	5.11	2.22	109.67	69.13	4.02	2.81	53.52	26.10	2.16
61	42.33	148.07	53.67	2.97	7.75	2.72	104.00	66.60	8.37	2.84	52.17	25.91	4.37
62	41.67	135.20	46.87	2.53	6.45	2.66	96.33	63.87	6.98	2.74	54.74	16.21	3.83
63	38.67	132.27	37.03	3.07	6.37	2.90	95.33	66.67	5.73	2.79	52.13	25.09	3.00
64	44.33	122.03	28.13	2.03	6.97	3.00	96.33	74.40	2.41	2.52	48.59	18.96	1.17
65	45.67	122.40	18.03	1.77	6.13	2.46	99.00	70.13	1.58	2.41	48.93	21.03	0.77
66	46.33	127.30	29.00	1.97	5.46	2.49	102.33	70.53	2.39	2.55	48.57	25.50	1.16
67	44.33	118.27	31.37	2.23	6.00	2.93	100.00	74.93	4.55	2.73	51.54	16.79	2.36
68	42.67	130.67	53.67	2.33	5.79	2.85	98.67	69.47	2.90	2.29	50.09	17.84	1.44
69	40.00	118.43	36.50	2.00	5.90	2.72	103.00	61.33	6.22	3.30	53.53	19.37	3.30
70	45.00	128.77	59.10	2.53	6.01	2.83	104.00	68.20	9.75	2.79	53.84	16.80	5.24
71	45.00	129.37	27.57	3.10	6.38	2.24	103.33	65.93	3.84	2.71	54.99	27.58	2.11
72	44.33	148.23	45.93	3.27	6.45	3.22	96.67	66.93	6.28	2.85	53.29	32.70	3.35
73	46.33	123.17	26.67	3.10	7.79	2.99	112.00	67.07	2.70	2.63	54.17	25.53	1.47
74	45.67	129.40	40.10	3.17	6.63	2.79	98.33	78.07	3.98	2.27	52.87	23.43	2.13
75	50.33	119.70	18.13	1.77	7.82	3.41	105.33	74.87	1.50	1.81	53.98	18.43	0.81
76	49.00	131.37	24.50	1.83	6.80	3.43	108.00	72.80	1.87	1.89	54.19	20.09	1.01
77	43.67	124.50	33.27	2.57	4.81	2.72	105.33	67.53	4.25	2.56	54.62	27.10	2.35
78	45.00	124.73	30.37	1.97	5.57	2.63	100.67	67.20	3.36	2.52	54.18	19.28	1.83
79	43.00	129.70	31.33	2.33	5.78	2.57	101.33	67.67	4.66	2.92	54.39	26.70	2.52
80	45.33	114.33	39.07	2.43	6.47	2.37	102.67	68.07	4.50	2.80	53.71	19.69	2.41
81	41.00	142.43	56.67	3.13	5.87	2.77	103.33	62.40	7.42	2.92	52.21	27.43	3.88
82	41.00	131.43	49.30	3.40	6.63	2.83	94.67	66.07	7.78	2.95	53.08	22.57	4.12
83	42.67	143.43	44.10	2.97	6.47	3.02	97.67	73.93	8.01	2.95	55.77	22.63	4.46
84	42.67	142.40	43.47	2.60	8.04	2.91	100.00	70.00	7.53	2.97	54.37	24.07	4.09
85	44.00	120.20	30.90	2.00	6.60	2.97	98.00	74.07	1.80	2.20	48.36	19.64	0.87
86	44.67	160.20	53.20	3.40	6.01	2.81	107.67	69.53	7.02	3.08	54.30	33.00	3.82

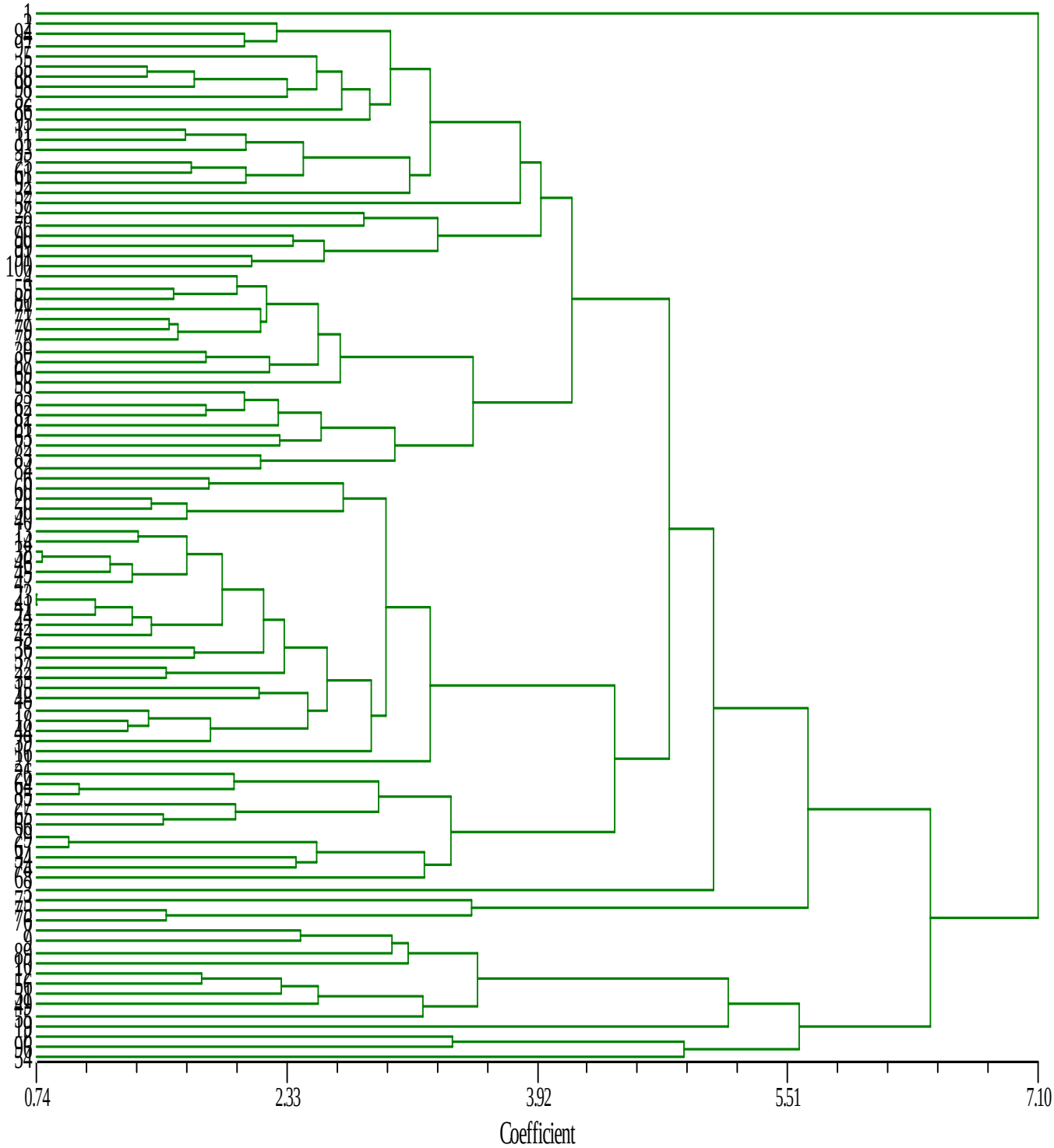
Appendix 2. cont'd

Trt	DTF	PHt	NP/Pl	NPB	IntL	CapL	DTM	NS/Pod	Yld/Pl	1000SW	OIL%	DTFP	OY/Pl
87	38.33	114.20	40.90	2.40	4.92	2.57	101.33	65.27	5.23	2.97	52.99	14.88	2.77
88	44.00	143.27	51.10	2.63	6.22	2.35	111.33	66.93	7.18	3.17	52.00	24.59	3.72
89	56.00	139.00	36.20	5.17	3.35	1.97	124.00	65.20	3.71	2.81	53.61	41.17	1.99
90	45.33	135.37	59.47	2.80	4.83	2.57	105.33	60.33	9.52	3.42	54.53	23.99	5.15
91	45.00	126.13	50.77	3.57	5.76	2.29	110.33	61.73	8.21	3.37	52.96	26.09	4.28
92	41.33	144.93	58.60	3.00	6.57	2.43	106.67	68.33	8.54	3.03	54.59	19.54	4.66
93	47.00	149.47	59.30	3.50	7.01	2.37	111.33	72.27	9.18	3.01	52.60	26.53	4.80
94	45.33	149.60	54.17	3.40	7.67	2.39	110.67	64.87	8.89	3.43	52.88	33.68	4.67
95	45.33	181.53	43.50	3.33	6.25	2.57	108.33	62.40	6.46	3.06	50.88	29.88	3.27
96	47.33	158.57	51.70	4.40	4.92	2.35	115.33	62.40	9.53	3.18	48.77	41.13	4.56
97	44.67	147.53	63.23	3.20	6.13	2.37	114.67	63.13	10.07	3.48	52.71	31.15	5.29
98	48.00	148.63	44.30	2.73	6.23	2.30	115.33	66.20	6.83	3.05	53.30	25.31	3.62
99	41.67	133.30	50.97	2.97	5.03	2.38	100.33	65.40	8.19	3.14	54.98	15.20	4.48
100	47.67	117.30	52.23	3.27	4.54	2.19	111.67	62.53	8.07	3.30	53.43	13.74	4.22
C.V.	**7.74**	**12.01**	**31.81**	**28.20**	**23.11**	**9.60**	**5.62**	**7.29**	**24.76**	**12.30**	**2.67**	**32.58**	**14.76**

- NA= not available

Appendix 3.

Dendrogram of the 100 sesame genotypes using Average Linkage (Between Groups)



INTRODUCTION

Sesame is probably the most ancient oil crop used by man and its domestication is lost in the mists of antiquity (Weiss, 2000). Sesame (*Sesamum indicum* L. syn *Sesamum orientale* L.; 2n = 26) is a popular oil seed crop cultivated for its quality edible oil, high protein, vitamin contents and balanced amino acid profile. Sesame oil contains anti-oxidative constituents such as sesaminol, sesamolin and tocopherol which impart it a longer shelf life with minimal rancidity (Ashri, 1989). Beside the oil, sesame seed finds its use in various culinary preparations. The oil cake is also a rich source of protein, carbohydrates and minerals, which makes it a nutritious feed for livestock (Venkataramana *et al*., 1999).

Sesame is an international crop grown in tropical and temperate zones of the world, between 40^0N and 40^0S latitude (Ashri, 1989). In Ethiopia, sesame shows wider adaptation and is cultivated in areas with an altitude range of 500-1250 meters above sea level, receiving 500-700 mm rainfall with a mean temperature range of 23-28° C (Getinet *et al*., 1997). The Humera and Metema areas of North Western Ethiopia containing most of the large scale sesame farms can be considered as sesame belt. Sesame is a crop of major economic and cultural importance in Ethiopia. Due to its importance as a major export commodity, the area coverage and volume of production of sesame has been increasing since 1996 (Ethiopian Export Promotion Agency, 2000). In 2005, sesame cultivation occupied 136,220 hectares (ha) of land, producing 115,364 tons (CSA, 2005).

Despite the high nutritional value and economic, historic and cultural importance of the crop, the global research on sesame has been scarce. Unlike most international crops, no CGIAR (Consultative Group on International Agricultural Research) center is mandated to sesame (Laurentin and Karlovisky, 2006). Although in Ethiopia research on sesame dates back to the late 1960s (Tadele, 2005) the status and strength of the research is not to the desired level and has been of limited significance in generating information, knowledge and technologies relevant to sesame development. To this effect, sesame production in Ethiopia is still largely traditional.

As an important and fast growing export oilseed crop of Ethiopia, the futurity of the crop and sesame farmers of Ethiopia, however, depend on the availability of superior varieties along with their agro techniques. Hence, the genetic improvement and enhancement of superior varieties will remain to be the core component of sesame research and development in Ethiopia. As a result, sesame improvement program in Ethiopia is geared towards developing varieties which are high yielding, widely adaptable, tolerant to biotic and abiotic stresses and good quality edible oil which meets the current standards set for the international market. Resistance to shattering and lodging along with determinate or semi-determinate growth habit are also essential plant characters in the development of superior varieties.

Plant breeding is essentially a selection process. In the development of superior varieties the response to selection depends on the intensity of selection, existing genetic variation and the reliability with which the genetic values of a genotype can be determined (Diepenbrock and Becker, 1992; Singh 1990).

Progress in breeding for economic characters often depends on the availability of a large germplasm representing a diverse genetic variation (Hawks, 1983). Describing and measuring the magnitude of variability present in a crop species is therefore of utmost importance as it allows effective selection. The amount of variability observed in a specific crop or related crop plants are described by statistical parameters like mean, range, standard deviation, variance, etc. Observed variability could be due to phenotypic or genotypic factors or combination of both. The genotypic component being heritable is the base for selection and is usually the concern of the plant breeders (Fayan *et al.*, 1991; Adugna, 2002).

Technically, selection can be direct or indirect. Direct selection is based on direct experimental estimation of yield, while indirect selection is based on information on a related secondary character that has a reasonably high genetic correlation with yield. Hence, understanding the interdependence that exists between the different characters of a crop plant and yield and among themselves is essential in formulating efficient multiple trait selection scheme.

A useful quantification of similarity of the population is provided by genetic distance between components of the population. Genetic diversity denotes the variability in the genetic characteristics of organisms that could belong to the same or different classification levels (Allard, 1988; Hawks, 1983). Genetic diversity measures individual variation within a population and reflects the frequency of different types in the population (Frankel *et al*., 1995). Quantifying genetic diversity and studying the eco-geographic patterns of the variability are of prime importance in plant breeding and germplasm conservation as well as for basic studies in crop evolution (Jain, 1977; Arunachalam, 1981; Souza and Sorrells, 1989; Smith and Smith, 1989; Martin *et al*., 1991; Messmer *et al*., 1993; Barrett and Kidwell, 1998; Mohammadi and Prasanna, 2003). It is particularly useful in characterizing individual accessions and cultivars, to detect duplications of genetic materials in germplasm collections, and as a general guide in selecting parents for crossing in breeding programs and in developing informative mapping populations for genome mapping (Harlan 1975; Jain et al. 1975; Jain, 1977; Arunachalam 1981; Souza and Sorrells, 1989; Smith and Smith, 1989; Mohammadi, 2003). In heterosis breeding, analysis of genetic diversity helps to select inbred parents or tester for maximizing heterotic response (Thormann and Osborn, 1992).

Diversity is derived from wild progenitors (Moll *et al.*, 1965) and is a product of interplay of biotic factors, physical environment, domestication, artificial selection and plant characters such as size, mating system, mutation, migration and dispersal (Allard, 1988; Frankel *et al*., 1995, Falconor and Macky, 1996; Hartl and Clark, 1997; Hedrick, 2000). The pattern and the level of genetic diversity in a given crop gene pool can be measured in terms of genetic distances and/or genetic similarity. Genetic distance is the extent of gene differences between individuals as measured by allelic frequencies at a sample of loci and quantifies the average genetic divergence between individuals or populations (Souza and Sorrells, 1989). Genetic distances are means for data reduction and a simple technique for pair-wise comparisons. Genetic distances also enable to extrapolate the period of time, which has passed since the diversification of the objects

from a common ancestor. This is particularly the case in the reconstruction of phylogenetic trees.

So far, substantial amount of sesame landraces from major sesame growing areas of Ethiopia have been collected and many introductions are made available by the National Lowland Oil Crops Research Project at Werer Agricultural Research Center in collaboration with the Institute of Biodiversity Conservation. But the magnitude of variability existing in the germplasm and other important genetic parameters decisive for the genetic improvement of the crop have not been systematically investigated and interpreted in the way that can be useful for sesame researchers/breeders. Similarly, no detailed information on the extent and nature of interrelationships among plant characters is worked out. Genetic variability studies carried out so far in the country were based on few morphological characters and the data was described using few descriptive statistics of central tendencies and dispersion such as mean, range and standard deviations. Realizing the limitations of the previous works on sesame germplasm variability and recognizing the need for such investigation, this research project has been initiated with the objective of assessing the existing genetic variability and interrelationships existing among some morpho-agronomic characters for future breeding programs.

2. LITERATURE REVIEW

2.1 Production and Importance of the Crop

Sesame is an important and ancient oil yielding annual crop cultivated extensively from the tropical to the temperate zones; Africa, the Mediterranean, Central Asia, India and the Indies, Indo-china, China and Central and South America (Bedigan 1980; Kbayashi, 1981; Weiss, 2000). The area covered by sesame in the year 2005 touches over seven million hectares worldwide producing almost three million tons of seed. India, Sudan, Myanmar, Ethiopia, Uganda and China are the major sesame producers, covering 75% of world production (FAO, 2006).

Sesame has got multifarious purposes as a source of superior quality oil which is about 50% in its seed nearly matching olive oil in quality. Besides, it contains about 22% protein of which 90% is assimilable, and its cake contains about 22% ash which is rich in phosphorous (Khan *et al*, 2001). Sesame seed is also used as a raw material in the preparation of confectionaries, sweets, bakery products, margarine, soap, perfume, carbon papers and type writer ribbons (Weiss, 2000; Khan *et al*, 2001).

Sesame, called selit in Amharic and Tigrigna, and sallet in Afan Oromo, is one of the 15 cultivated oil crops in Ethiopia (Seegeler, 1983), grown primarily as a cash crop. The crop is widely grown in the low lying areas of Ethiopia bordering Sudan and Somalia; particularly in Amhara (Gonder and Wello), Tigray (Setit-Humera), Benshangule (Pawe, Assosa and Beles), Oromya (Wellega and Harar) and Gambella regions. Recently, with the increase in sesame price both in the domestic and international markets, large areas of the Gibe Valley, Jinka plain, lower and middle Awash Valley and lowlands of northern Omo have been covered with sesame (Wijnands *et al.*, 2007; Weiss, 2000). In 2008 sesame price reached the highest of its history, 28 Birr/kg (white sesame) in Ethiopia; quite comparable to the country's most dependable export crop, coffee.

According to the Ethiopian Central Statistics Agency (CSA), the area under production of sesame is estimated to be 91,527 ha, 136,220 ha and 205,153 ha in the 2003/4, 2004/5, 2005/6 cropping seasons, respectively (CSA, 2007). Sesame is the leading export oil crop

in Ethiopia. About 90% of the total production is destined to export market (Ethiopian Export Promotion Agency, 2003).

Though Ethiopia has a great potential for sesame production as depicted by the recent increase in area and volume of production, the national average yield remains very low, 5.2 quintals/ha (CSA, 2007) due to various production constraints. Lack of sufficient infrastructures in most production areas, efficient marketing system, and strong research extension system are among the major bottlenecks for the expansion of sesame production. Moreover, shortages of improved varieties adapted to the diverse agro-ecologies remain among the major limitations to exploit the production potential of the crop in the country.

2.2 Taxonomy and Origin

2.2.1 Taxonomy

Sesame belongs to the division Spermatophyta, subdivision Angiospermae, class Dicotyledoneae, order Tubiflorae, family Pedaliaceae and genus *Sesamum*. The genus *Sesamum* contains about 36 species of which 19 are indigenous to Africa including the major cultivated species *Sesamum indicum* L. (Weiss, 2000). The species S*esamum indicum* L. (2n=26) is one of the most popular edible oil seed crops which has hundreds of varieties and strains with considerable variation in plant size, form, and growth pattern, color of flower, seed size, seed color and composition (Zhang, 1990; IPGRI and NBPGR, 2004; Akpan *et al.*, 2005;).

2.2.2 Origin and Distribution of Sesame

The center of origin of sesame has long been a debatable issue and different authors do have different views on the subject. The greatest weight of evidence indicates the Ethiopian area as the origin of cultivated sesame although there is a considerable argument in favor of the Afghan/Persian region, with subsidiary centers in Indo-Malaya and China (Weiss, 1971). Vavilov (1926) noted the Abyssinian region including Somalia as the basic center of the species; the Indian region including Assam and Burma

excluding North West India as the basic center of the cultivated varieties; and the Chinese region, distinguished by dwarf forms, as a secondary center.

Hildebrandt (1932), relaying on morphological, biochemical and physiological differences between groups of sesame, identified distinct morpho-geographic units and concluded that the primary center is Africa, where more primitive types and the majority of wild *Sesamum* species can be found. Seegler (1983) also argued that the Abyssinian reion is rich in the diversity of both the cultivated and wild forms of sesame. Similarly, while comparing the diversity of the Indian and African *Sesamum*, Rheenen (1980) found out that in Africa there is narrow variation for cultivated sesame but wide variation for other species of the genus *Sesamum*. The opposite holds true for India. According to Weiss (2000) Africa is the center of origin to sesame and later the crop spread to India and China during the first dynasty of Ura about 2130-2000 B.C. and it was also an important crop in the Persian region; where under cultivation the main center of distribution of sesame arose (Weiss, 2000). Based on evidences from reciprocal crosses and cytological studies, however, Bedigan (2004) suggests that sesame is first domesticated in India and was taken to Mesopotamia during the Early Bronze Age.

2.3 Genetic Variability, Heritability and Genetic Advance

2.3.1 Genetic Variability

Crop improvement among other things depends on the magnitude of genetic variability existing in the germplasm, genetic architecture and the extent to which the desired characters are heritable. Genetic variation can be assembled and utilized through hybridization to create new favorable gene combinations and crosses between genetically divergent parents which are expected to result with large genetic variance among progenies in subsequent selfing generations that can be exploited as line cultivar than crosses from closely related parents (Adefris, 2005). The variability present among genotypes can be assessed in three ways: employing ANOVA, by simple measurements like range, mean, standard error, phenotypic and genotypic coefficients of variation and through estimation of genetic diversity (Singh, 1990).

There are a lot of studies on the assessment of genetic variability in sesame, some of which are reviewed below.

Kandamasay and his colleagues (1991) conducted a study on variability of six characters in 26 sesame genotypes and found higher genotypic coefficient of variation for characters: number of primary branches, number of capsules and seed yield.

Studying the amount of genetic variation of 36 released varieties of sesame and their parents with respect to six plant characters, Fayan *et al*. (1991) reported high genetic variation for number of capsules per plant, length of fruiting sections and seed yield per plant but lower variation was reported for plant height and 1000 seed weight.

Genetic variability on some physiological traits was studied in a population of thirty genotypes of sesame and high phenotypic and genotypic coefficients of variability was revealed for leaf area index, days to flowering and oil yield per plant while it was moderate for days to maturity and low for oil content (Banerjee, 2006).

Study on 45 M_3 high yielding and disease resistant sesame mutants revealed higher genotypic and phenotypic variances for capsule/plant followed by plant height and biomass per plant (Sarwar *et al.,* 2006). Maximum genotypic coefficient of variation was observed for seed yield per plant followed by biomass and branches per plant. Seed yield also showed maximum phenotypic coefficient of variation.

The genetic variability of some agronomically important traits were determined in a set of 21 genotypes of sesame and it was found that the differences between phenotypic and genotypic coefficients of variation (PCV and GCV) were very low for all characters studied indicating minimal environmental effects in the developments of these parameters. The highest GCV was recorded for number of branches per plant followed by seed yield per plant, number of capsules per plant, plant height, 1000 seed weight and number of seeds per capsule (Khan *et al*., 2001).

2.3.2 Heritability and genetic advance

The magnitude of variability expressed by a genotype or group of genotypes in any species can be due to genotypic or phenotypic factors or the combination of both (Allard, 1988). Hence, it can be partitioned to genotypic and/or phenotypic component. The genotypic component being the heritable portion of the total variability, its magnitude for yield and its components, influences strategies to be followed by the breeder. Heritability (broad sense) is, therefore, a quantitative measure which provides information about the proportion of genotypic variance to phenotypic variance. Heritability is expressed in percentage (Dabholkar, 1999; Diepenbrock and Becker, 1992). High heritability estimates indicate a character is controlled by those genes which are less influenced by the environment and vice versa and it also give a useful indication of the relative values of selection based on the phenotypic expression (Gangadhara, 2005).

However, heritability *per se* is not enough in predicting the effectiveness and outcome of selection unless it is considered together with genetic advance (Johnson *et al*., 1955; Allard, 1999). Genetic advance is the rate of improvement in the performance of the resultant population over the original population after one generation of selection. Hence, genetic advance under selection measures the difference between the mean genotypic value of the selected population over the mean genotypic value of the original population (Allard, 1999). The genetic advance that can be expected for a particular trait through selection is the product of heritability, phenotypic standard deviation and selection differential (Sharma, 1998).

High heritability combined with high genetic advance for a particular character is an indicator that character is governed by additive types of gene action, while high heritability combined with low genetic advance shows the character is mainly under the control of non-additive types of gene action i.e. epistasis and/or dominance action(Sarwar *et al*., 2004, Saravanan *et al*., 2003).

Different researchers carried out heritability and genetic advance studies on different morpho-agronomic parameters of sesame and some are reviewed as follows.

Seventy two sesame genotypes were evaluated to determine the heritability and genetic advances of some selected characters by Gahandra (2005), and high heritability combined with high genetic advance was observed in plant height, number of capsules and 1000 seed weight, indicating simple selection may be beneficial for the improvement of these particular characters. On the other hand, high heritability with low genetic advance was observed for days to 50% flowering, days to maturity, number of branches and seed yield which shows selecting superior lines and conducting biparental crosses followed by recurrent selection in the succeeding generations to be effective for the improvement of these characters.

According to Fayan and his co-workers (1991) plant height and 1000 seed weight had the highest heritability values of 89.4 and 77.9 % respectively together with relatively higher relative genetic advance, while capsules per plant, length of fruit bearing zone and seed yield per plant had moderate heritability and genetic advance. They also found that seeds per capsule had the smallest heritability value among six characters considered in the study.

Banerjee (2006) studied the broad sense heritability and genetic advance on some plant characters in thirty sesame genotypes. They observed high to moderate estimates of heritability accompanied with high to moderate genetic advance for leaf area index, days to flowering and oil yield per plant, indicating the predominance of additive gene action for the expression of these characters.

In a different study, low heritability with medium genetic advance was reported for number of capsules and seed yield, suggesting that these characters are influenced highly by the environment, while high heritability value was found for days to maturity and plant height (Kandasamay *et al.*, 1991). Gupta and Chopra (1984) observed very high value of genetic advance as percentage of mean in number of primary branches and low for days to 50% flowering and plant height.

Sarwal and his co-workers (2006), while studying heritability and genetic advances in 32 mutant sesame genotypes, noted maximum heritability estimate for plant height followed by seed yield, seed per capsule and branches per plant. Genetic advance as percent of mean was highest for seed per capsule followed by capsule length and seed yield per plant.

Khan *et al*. (2001) found out higher heritability estimate for seed yield per plant, 1000-seed weight and number of branches per plant. The same authors reported higher genetic advance as percent mean for seed yield per plant, number of capsules per plant, 1000 seed weight and plant height signaling that these characters can apparently be under the control of additive genes.

2.4 Correlation and Path Coefficient Analysis

In crop improvement, two types of selection have to be distinguished: direct and indirect selections. Direct selection is selection based on direct experimental estimate of the character in question and indirect selection is selection based on information on a correlated character (Diepenbrock and Becker, 1992). Seed yield is a complex character conditioned by the interaction of various growth and physiological processes throughout the life cycle of the plant (Ercan *et al*., 2002). A selection for growth and physiological process is an indirect selection, since the ultimate goal is not some growth and physiological process in itself but a high and stable yield. The ultimate drawback with a direct selection for yield is that the expression of the genetic yield potential is largely influenced by environmental factors. To overcome such problem an indirect selection for yield can be done through selection for other trait that are easy to select and less influenced by environmental factors (Singh, 1990). A prerequisite for indirect selection is a reasonably high correlation between secondary trait and the primary trait of interest, in most cases yield (Diepenbrock and Becker, 1992). The correlation coefficient analysis helps to determine the nature and degree of association between any two measurable characters, although it does not consider the dependence of one variable on the other (Sharma, 1998). The nature of association between grain yield and its components

determine the appropriate traits to be considered in indirect selection seeking crop improvement (Sofi and Rather, 2004).

However, correlation coefficient *per se* does not give a complete picture of the causal basis of association existing between the different characters. Hence, selection based on simple correlation coefficient without taking into consideration the interaction between the component traits can be misleading. Path coefficient analysis is a statistical procedure used to partition correlation coefficients in to direct and indirect effects, effects exerted through other variables (Sofi and Rather, 2004). Path analysis is basically a standardized partial regression analysis and deals with a closed system of variables that are linearly related (Wright, 1921). Unlike correlation analysis such information provides a realistic basis for the allocation of appropriate weight to the various yield components.

In sesame, Khan and his co-workers (2001) reported that correlation coefficient for number of capsules per plant with seed yield was highly significant followed by plant height, 1000 seed weight and number of branches per plant. They also noted that number of capsules per plant directly contributed the maximum towards seed yield per plant followed by 1000 seed weight, number of seed per capsule and plant height. Moreover, number of capsules per plant contributed indirectly via all other parameters studied except plant height. Seed yield per plant and 1000 seed weight imparted significant effect on seed yield via number of capsules per plant and plant height.

Ercan *et al.* (2002) characterizing Turkish sesame landraces for the different agronomical and morphological variables, reported that plant height was positively and significantly correlated with height to the first capsule (r=0.776**), number of capsules on the main stem (r=0.78**) and time to flowering (r=0.579**). And height to the first capsule was also positively and significantly correlated with number of capsules on the main stem (r=0.991**) and time to flowering (r=0.591**). Total number of capsules per plant was positively correlated with number of seeds per capsule (r=0.681**) but negatively with time to flowering (r=-0.316*).

In other studies targeted to determine different genetic parameters of some important plant characters, seed yield per plant of sesame was positively and significantly correlated with plant height, length of pod bearing section, number of primary branches, days to 50% flowering and number of capsules per plant but negatively associated with days to maturity (Fayan *et al*., 1991; Kandasamay *et. al*., 1991).

Bisht *et al*. (1998) observed a negative correlation for days to flowering with plant height, capsules per plant, seeds per capsule and 1000 seed weight but a highly significant positive correlation with days to maturity. The same researchers reported a positive and significant correlation for plant height with capsules per plant, seeds per capsule, 1000 seed weight and seed yield.

Wongyai and Juttupornpong (1992) reported that genotypic correlation coefficient between capsule size and seed weight was positive and highly significant and recommended indirect selection for seed weight through capsule size to be effective.

2.5 Genetic Divergence

Genetic divergence refers to the variation among alleles of genes in different individuals of populations of a species (IPGRI, 1993). While the ultimate source of genetic diversity is gene mutation, it is molded and shaped by selection, recombination, genetic drift and migration in the face of heterogeneous environment in space and time enabling populations to survive, evolve and adapt (Falconer and Mackay, 1996). Information on the extent of genetic diversity amongst the breeding materials is very important in that crosses between groups with maximum genetic divergence would be more responsive to improvement since they are likely to produce desirable recombination and segregation in their progenies after hybridization (Reddy, 1988). Generally, genetic diversity is an important tool of plant breeding in developing high yielding varieties and maintaining the productivity of such varieties by incorporating genes for resistance of biotic as well as abiotic stresses (Kobayashi, 1990; Allard, 1999).

Information on the degree of genetic relatedness among genotypes has been obtained using various approaches since long time ago. This information is usually obtained

indirectly from eco-geographic information about the genotypes, their pedigree and heterosis data and directly from plant characteristics data such as morphological traits, biochemical traits and more recently from biochemical/molecular data (isozymes, storage proteins, DNA markers, fats and fatty acid profiles), parentage analysis, and heterosis record (Adugna, 2002).

In morphological analysis of genetic diversity, genotypes are grown on the field or glass house condition and estimates of relationship are based on the range of expression of various traits among genotypes (Adugna, 2002). When phenotypic estimates are used to represent the degree of genetic relationship between two lines or populations, it is assumed that similarity in phenotype accurately reflects similarity in genotype (Sharma, 1998). This approach has been extensively used in genetic diversity studies and morphological traits continue to be the first useful step in the studies of genetic relationships in most of the breeding programmes. This is because the existing data base on germplasm collection or breeding stocks can often be used for genetic analysis; Statistical procedures for morphological trait analysis are readily available, morphological information is useful in understanding the ideotype performance relationships; and explanation of hetrosis may be enhanced if morphological measures of distance included as independent variable (Adugna, 2002).

Multivariate analysis based on morphological characters provides genetic information that will allow the breeder to improve his population by selecting from specific regions (Ercan *et al*., 2002). Moreover, multivariate methods are useful for characterization and classification of genotypes when a large number of accessions are to be assessed for many characters. The application of the method for handling morphological variation in the germplasm collections have been demonstrated in many crop plants (Ayana and Bekele, 1999).

So far, different pieces of works have been done on multivariate analysis of sesame genotypes and are reviewed as follows.

Ercan and his co-workers (2002) evaluated 52 Turkish sesame populations collected from different geographical locations for 13 morpho-agronomical characters. They reduced the data set into six principal components and use these six PCs to cluster the populations using hierarchical cluster analysis into four groups where the numbers of genotypes included in the clusters were 2, 4, 1 and 45, respectively. The genetic distance among the populations was found to be narrow ranging between 0.18-6.38percent.

A study was conducted to analyze the genetic diversity of Indian sesame collections (100 accessions) representing all eco-geographical regions of the country using multivariate analysis for a range of morphological and agronomical characters and the accessions were classified into seven discrete clusters and the PCA generally confirmed the groupings obtained through cluster analysis (Bisht *et al*., 1998).

An experiment conducted to study the genetic diversity of 100 sesame genotypes including 11 exotic ones (5 from Bulgaria, 2 from Korea, 2 from Bangladesh and 1 each from USA and Japan) using multivariate analysis (D^2 statistic) revealed that oil content (%) and days to 50% flowering had the highest contribution to the divergence followed by 1000 seed weight, seed yield, plant height, number of capsules per plant, days to maturity and number of branches per plant. The exotic genotypes did not show much diversity among themselves and fall in three clusters of very low cluster distance (Ranghuwanshi and Duhoon, 2005).

An assessment made to determine the level of genetic diversity in relation to geographical origins and morphological characteristics on a total of 96 accessions collected from different parts of the world using AFLP markers revealed that the genotypes fall into two major groups and the relatedness, geographical origin and their morphological characteristics were reflected to the similarity of AFLP pattern (Ghulam *et al*., 2006).

Fifty eight accessions of sesame (36 from different states of India and 22 exotic accessions from 21 sesame growing countries in the world) were analyzed using RAPD technique by Venkataramaan *et al*. (1999). The results indicated the presence of high

level of genetic diversity but the extent of diversity was greater in the collections from Indian sub-continent as compared to the exotics, indicating the nativity of the crop. In the same study, the phenetic analysis grouped 48 of the 58 accessions in to six clusters and the remaining highly diverse accessions were placed outside these close-knit clusters.

2.6 Measures of Genetic Distance

The pattern and level of genetic diversity in a given gene pool can be measured in terms of genetic distances. Genetic distance is measured from the average genetic divergence between cultivars or populations and is defined as genetic divergence of two varieties as a function of their ancestry, geographic separation and adaptation at different environments. According to Nie (1987), cited by (Adugna, 2002) genetic distance is the extent of gene differences between cultivars, as measured by allelic frequencies at a sample locus.

3. OBJECTIVES

3.1 General Objective

- To assess and analyze the magnitude and pattern of genetic diversity existing in the genotypes and interrelationships between some agronomically important characters

3.2 Specific Objectives

- To estimate the phenotypic and genotypic coefficients of variation, heritability and genetic advance of some agronomically important characters;
- To assess interrelationship existing among yield and some important components to set selection criteria and partitioning the association of the characters in to direct and indirect effects using path coefficient analysis;
- To assess the magnitude of genetic diversity and classify genotypes into different clusters based on Mahalobnosis D^2 statistic; and
- To determine the combination of variables that displays the large amount of variation (principal component analysis)

4. MATERIALS AND METHODS

A field experiment was carried out at the research site of Werer Agricultural Research Center (WARC) of the Ethiopian Agricultural Research Institute in the 2007/8 cropping season under irrigation. One hundred sesame genotypes comprising local landraces collected from different sesame growing areas of the country and introduced accessions obtained from the National Lowland Oil Crops research Project were evaluated for their genetic variability potential and correlation existing among some morpho-agronomic characters.

4.1 Description of the Experimental Site

The center is situated at about 278 km North East of Addis Ababa at 9”16'N latitude, 40”9'longitude and at an altitude of 740 m.a.s.l. It is among the lowland areas of the country considered as potential irrigated sesame production corridor. According to some authors, studies on genetic variability should be conducted under favorable environmental conditions to facilitate the fullest expression of different traits (Somayajulu *et al*., 1970; Upadhyay and Murty, 1970). Thus, it was expected that the test genotypes could express their full genetic potentials for the traits under consideration.

The soil is classified as an alluvial vertisol. The area is characterized by dry hot arid climatic condition with mean maximum and mean minimum temperature of 34.1^{o}C and 19.2^{o}C, respectively according to Werer Meteorological Station. The mean annual rainfall of the area ranges from 410 mm – 591 mm.

4.2 Experimental Design

The experiment was laid out using a 10x10 triple lattice design. The plots consisted three rows of 3 m long and 30 cm inter row spacing. The position of each block as well as each of the accessions within a block was randomized following the procedures described by Gomez and Gomez (1984). The two outer rows were planted by a standard variety (Adi) to provide uniform competition. The seeds were drilled by hand and the seedlings were thinned 15 days after sowing to maintain an intra-row spacing of 10 cm. Other cultural

practices including land preparation, weed control and irrigation schedule were done as per the research recommendations by Werer Agricultural Research center.

4.3 Planting Materials

More than 1,000 locally collected and introduced germplasm accessions have been maintained at WARC. The materials have been obtained from local collections and introductions. Among them, 100 accessions were systematically selected and used in this study. Eighty five of the tested genotypes were local collections which represent low to mid altitude areas of sesame production in Ethiopia. The remaining 15 genotypes were foreign introductions three accessions from each sub-continent America, Europe, Asia, Latin America and Africa. The details of the tested materials are attached in the appendix (Appendix 2).

4.4 Characters Scored

The following observations were recorded as per IPGRI and NBPGR (2004) sesame descriptor lists either on plot basis or from ten randomly selected competent plants at different growth stages.

4.4.1 Characters measured on plot basis

i. **Days to 50% flowering**: The actual count of the number of days from sowing until 50% of the plants with in a plot bear at least one flower;
ii. **Days to 75% physiological maturity**: The actual count of the number of days taken by each accession from sowing measured until 75% of the plants with in a plot reached physiological maturity (2/3 of the lower leaves turned to yellow/ yellowish brown);

4.4.2 Characters measured from sample plants

i. **Plant height (cm):** the average length of the main stem at harvest from the soil surface to the tip of the stem of 10 plants;
ii. **Internode length (cm):** the average distance between successive leaf axils, measured at the middle of the main stem (three measures taken from 10 sample plants);
iii. **Number of primary branches:** number of branches that developed from the main stem;
iv. **Distance from the base to the first capsule (cm):** mean distance from the soil surface to the first pod bearing site of 10 sample plants;
v. **Number of capsules per plant:** the mean number of capsules counted from 10 sample plants in each accession;
vi. **Capsule length (cm):** the length of three individual capsules taken from each of the 10 sample plants;
vii. **Number of seeds per capsule:** mean number of seeds obtained from 3 individual capsules taken from each of the 10 sample plants.
viii. **Seed yield per plant:** mean weight of seeds harvested from 10 sample plants;
ix. **Oil content (percentage):** proportion of fat in the whole seed determined from 22 gram of oven dried ($130\ ^{0}$ C) clean seeds of each accession using Nuclear Magnetic Resonance Spectrometer (Madson 1976);
x. **Oil yield per plant (gm):** seed oil content (percentage) multiplied by seed yield per plant;
xi. **1000 seed weight (gm):** mean weight of 1000 seeds determined from the bulked seeds of the 10 sample plants.

4.5 Statistical Analysis

All measured characters considered in this study were subjected to statistical analysis. The data were analyzed using different statistical computer soft wares (SAS, SPSS, Spar-1, and NTSY-1) to analyze variance components, covariance, genetic and phenotypic coefficients of correlations, path coefficients, principal components and clustering. Detail accounts are given under the following subsection.

4.5.1 Analysis of Variance

The data was first subjected to MSTAT-C computer software to see the relative blocking efficiency of using lattice square design over RCBD. Because the relative efficiency of lattice design over randomized complete block design (RCBD) was less than or equal to 110% (Table 3), all statistical analysis were done following RCBD (Cochran and Cox, 1957) for the sake of simplicity. Accordingly, analysis of variance was conducted using SAS 8.8 (SAS Institute, 1988) computer software, following PROC ANOVA procedure. Considering genotypes as random variables the formulas used to partition the total variance into the different components and to calculate the expected mean squares are given in Table 1 (Gomez and Gomez, 1984).

Table 1. RCBD ANOVA and expected mean squares.

Source of variation	D.f.	Mean Squares	Expected Mean Square
Replications	(r -1)	MS_r	$\sigma^2_e + g\sigma^2r$
Genotypes	g-1	MS_g	$\sigma^2_e + r\sigma^2g$
Error	(r-1)(g-1)	MS_e	σ^2_e
Total	rg-1		

Df =degrees of freedom, r = number of replication, and g = number of genotypes MSr = mean square of replication, MSg = mean square of genotypes, MSe = mean square of error

The ANOVA had been computed using the following model.

$Y_{ij} = \mu + r_j + g_i + e_{ij}$

Where, Y_{ij} = the observation of the i^{th} genotype in the j^{th} replication;

μ = the grand mean of trait Y; rj = the effect of $_j^{th}$ replication;

g_i = the effect of the i^{th} genotype; e_{ij} = experimental error of observation ij

The significance of the variability existing between each test material and the precision of measuring the different data were tested using the least significant difference (LSD) and coefficient of variation (C.V. %) respectively.

4.5.2 Genetic Parameters

4.5.2.1 Estimation of Variance Components

The variance components were estimated by equating the mean squares from the ANOVA table with their expectation using the random model where all the genotypes were considered as random variables (Table 1). Accordingly, the variance components, namely genotypic variance (σ^2_g), environmental variance (σ^2_e) and phenotypic variance ($\sigma_p{}^2$) were estimated according to Falconer *et al*. (1996) as described below:

$$\sigma_g^2 = \frac{MSS_g - MSS_e}{r}$$

Where: $\sigma_g{}^2$= genotypic variance, MSS_g = genotypic mean square, MSS_e = error mean square, r = the number of replications.

$$\sigma_p^2 = \sigma^2_g + \sigma^2_e$$

Where: ($\sigma_p{}^2$) = phenotypic variance, $\sigma_e{}^2$ = MSS_e = error mean square i.e., environmental variance on genotype mean basis.

4.5.2.2 Estimation of Variability Measures

The degree of variation among the 100 genotypes with respect to the 13 characters studied was determined by computing both simple statistics such as range, standard error, and other measures of dispersion such as phenotypic and genotypic variances and

coefficients of variation. The phenotypic and genotypic coefficients of variation expressed as percent of their respective means were calculated following the method suggested by Sharma (1998) as:

$$GCV = \left(\frac{\sqrt{\sigma^2_g}}{\bar{Y}...} \right) X100$$

$$PCV = \left(\frac{\sqrt{\sigma^2_p}}{\bar{Y}...} \right) X100$$

Where**:** GCV and PCV are genotypic and phenotypic coefficients of variance respectively, $\bar{Y}$ is the grand mean of a particular character

Heritability (h^2): heritability in broad sense was computed for all characters as suggested by Allard (1999):

$$\mathbf{H^2 = \sigma^2_g / \sigma^2_p \ x\ 100}$$

Where: H^2= broad sense heritability: σ_g^2= genotypic variance and (σ_p^2) = phenotypic variance

Genetic Advance (GA): Genetic advance as percent of mean was calculated for each character using the formula given by Johnson *et al*. (1955):

$$\mathbf{GA = \frac{h^2 x\ k \sigma_p}{\bar{Y}}\ x\ 100}$$

Where: h^2 is the heritability estimate, k is the selection differential (2.06) at 5% selection intensity and σ_p is the phenotypic standard deviation, $\bar{Y}$ is mean of the trait.

4.5.2.3 Association of Characters

Correlation Coefficient

Phenotypic and genotypic coefficients of correlation between any two characters were computed using genotypic and phenotypic variance and covariance components as (Sharma, 1998). Phenotypic (σ^2_{pxy}) and genotypic ($\sigma^2_{gxy)}$ co-variances were computed from the table of covariance analysis in a similar manner to that of the analysis of variance (Table 2). After the co-variance analysis is conducted, the mean cross products (MSCP) were equated with their expectations to solve for the covariance components using the formula described below.

$$\textbf{Genotypic covariance } (\sigma^2_{gXY}) = \frac{MSCPgxy - MSCPexy}{r}$$

$$\textbf{Phenotypic covariance } (\sigma^2_{p}XY) = \sigma^2_{g}XY + \sigma^2_{e}XY$$

Where: σ^2_{g} xy = genotypic covariance of traits x and y,

σ^2_{p} xy = phenotypic covariance of traits x and y

σ^2_{e} xy (environmental covariance between trait x and y) $= \frac{MSCPexy}{r}$

$MSCP_g xy$ = mean sum of cross product of genotype for traits x and

$MSCP_e xy$ = mean sum of cross product of environment for trait x and y

r = number of replications

Table 2. Analysis of covariance

Source of variation	D.f.	MSCP	Expected MSCP
Replication	r -1	MSCPrxy	
Genotype	g-1	MSCPgxy	$\sigma^2_{exy} + r\sigma^2_{gxy}$
Error	(r-1)(g-1)	MSCPexy	σ^2_{exy}

*df= degrees of freedom, r= number of replications, g= number of genotypes, MSCPrxy = mean sum of cross product of replication for traits x and y, MSCPgxy= mean sum of cross product of genotype for traits x and y, MSCPexy= mean sum of cross product of environment for trait x and y, σ^2_{exy} = environment covariance between traits x and y. σ^2_{gxy} =genotypic covariance of traits x and y.

Phenotypic correlation coefficient, the degree of association between two variables, which includes both genotypic and environmental components, was also estimated using the formula suggested by Sharma (1998) as:

$$r_{gxy} = \sigma^2_{gxy} / [(\sigma^2_{gx})(\sigma^2_{gy})]^{1/2}$$

$$r_{pxy} = \sigma^2_{pxy} / [(\sigma^2_{px})(\sigma^2_{py})]^{1/2}$$

Where: rp(XY) is phenotypic correlation coefficient and rg (XY) is genotypic correlation coefficient between characters x and y; σ2p (XY) and σ2g (XY) are phenotypic covariance and genotypic covariance between characters x and y, respectively.

The coefficients of correlation at phenotypic level were tested for their significances using (g-2) degrees of freedom (Gomez and Gomez, 1984) using simple t- table, with observed t as;

$$t = \frac{r_{px}\sqrt{g-2}}{\sqrt{1-r_{pxy}^2}}$$

The calculated 't' value was compared with the tabulated 't' value at (g-2) degrees of freedom. The correlation coefficient at genotypic level was tested with the following formula forwarded by Sharma (1998):

$$t = r_g XY / r_g XY$$

Where: $r_g XY$ = genotypic correlation coefficient, SEr_{gxy} = Standard error of genotypic correlation coefficient calculated as:

$$\mathbf{SEr_g\ XY} = \sqrt{(1-r^2gxy)^2 / 2h^2xh^2y}$$

Where: h^2_x and h^2_y are heritability for character x and y. The calculated t value for each genotypic correlation was tested against tabulated t at (g-2) degrees of freedom.

4.5.3 Path Coefficient Analysis

Path analysis was performed to find out whether the component traits (independent variables) do have a direct or an indirect effect on the dependant variables in a positive or negative direction. Path coefficient analysis was calculated using SPAR-1 computer software. Two characters namely, seed yield and oil yield per plant were selected as resultant (dependent) variables and the rest of the characters as the causal (independent) variables. Each of the two dependant variables were also considered as causal variable, while conducting path analysis of the other dependant variable exclusively. The direct and indirect effects of the different characters on the resultant variables were estimated by simultaneous solution of the equation following the general formula suggested by Dewy and Lu (1959):

$$\mathbf{r_{ij} = p_{ij} + \sum r_{ik}p_{kj}}$$

Where: rij is mutual association between the independent traits (i) and dependent variable (j) as measured by the correlation coefficient,

p_{ij} is component of direct effects of the independent trait (i) on the dependent variable (j); and

$\sum r_{ik}p_{kj}$ is the summation of components of indirect effect of a given independent trait i on the dependent variable j via all other independent traits k.

The residual effect (U) which was not addressed by the independent variables considered was calculated following the formula of Dewey and LU (1959) as:

$$\mathbf{U} = \sqrt{1 - R^2}$$

Where: $R^2 = \sum r_{ik} p_{kj,}$

4.5.4 Cluster Analysis

The data was first standardized to a mean of zero and a standard deviation of one to avoid the effect of scale differences. Mahalabnobis's Generalized Distance (D^2) statistics was calculated using PROC FASCLUS procedure of SAS computer software (SAS Institute, 1988) for assessing the divergence between the genotypes based on 13 quantitative traits This procedure is preferable for clustering a large number of accessions. The generalized squared distance between any two populations can be defined as:

$$\mathbf{D^2_{ij} = (Xi - Xj)\, S^{-1}\, (Xi - Xj)}$$

Where: D^2ij = is the distance between any two groups i and j;

Xi and Xj are the vector mean of the traits for the i^{th} and j^{th} groups respectively,

S^{-1} = the inverse of the pooled covariant matrix.

A dendrogram was constructed using NTSYS computer software to asses the similarity levels of the different genotypes. The tree was cut at a similarity level of $3.92<d<5.51$ to produce the same eight clusters using Ward's method.

4.6 Principal Component Analysis

Principal component analysis was performed using the correlation matrix as an input to define the patterns of variation between the accessions. This was done by reducing the variables into a closed system of linearly uncorrelated system which can explain most of the variation existing between the variables. The analysis was done using PROC PRIN procedure of SAS statistical computer software (SAS Institute, 1988).

5. RESULTS

5.1 Genetic Variability

5.1.1 Analysis of variance

The results of analysis of variance for all of the 13 quantitative traits considered in this study are summarized in Table 3. As can be seen from the table, there was a highly significant difference ($P<0.01$) among the genotypes for all the traits indicating the existence of substantial variability. Higher values of total variance were recorded for plant height followed by number of capsules per plant, distance to the first capsule, days to maturity, and days to flowering signifying that the test genotypes were highly variable with regard to these traits. Seed and oil yields had higher coefficients of variation followed by distance to the first capsule, number of capsules per plant and number of primary branches per plant. The higher coefficients of seed yield and oil yield per plant were expected because they are characters which are sensitive to environmental variation. The mean performance of all the genotypes is presented in (Appendix 2).

5.1.2 Estimation of variability parameters

Variability present in the germplasm was estimated by computing range, phenotypic and genotypic coefficients of variation, heritability and genetic advance for each of the characters evaluated in this study and the results are presented below (Table 4).

Table 3. Mean sum of squares for 13 characters of 100 sesame genotypes grown at Werer 2007/08

Source of variation	Df	DTF	PHt	NP/Plt	NPB	IntL
Replication	99	101.45	12445.20	1583.01	6.05	8.21
Genotype (adj.)	2	78.29**	925.52**	388.63**	3.99**	2.85**
Error	198	13.07	286.01	174.90	0.81	1.92
LSD (P>0.05)		5.82	27.23	21.29	1.45	2.23
(p>0.01)		7.67	35.97	28.11	1.85	2.71
CV (%)		7.74	12.01	31.81	28.20	23.11
Block efficiency		100.61	100.02	100.13	106.46	118.15

Table 3. cont'd

Source of variation	CapL	DTM	NS/P	Yld/Plt	1000SWt	Oil%	DTFP	OYld/Plt
Replication	0.60	373.61	125.37	29.51	0.27	120.29	1345.07	29.51
Genotype (adj.)	0.28**	175.32**	50.55**	16.27**	0.53**	8.53**	231.89**	16.27**
Error	0.06	37.73	24.97	4.91	0.11	1.94	79.62	4.91
LSD (P>0.05)	0.39	9.89	8.05	3.57	0.53	2.24	14.37	3.57
(p>0.01)	0.49	12.70	10.51	4.70	0.71	2.78	18.95	2.40
CV (%)	9.60	5.62	7.29	40.76	12.30	2.67	32.58	40.76
Block efficiency	106.52	105.91	102.36	100.00	100.00	113.21	100.00	100.00

** = significant at 1% probability, df. =degrees of freedom, DTF=days to flowering, PHt=plant height, NP/Plt. =number of capsules per plant, NPB=number of primary branches, IntL. =Internode length, CapL. =Capsule length, DTM=days to maturity, NS/P=number of seeds per capsule , Yld/Plt. =Seed yield per plant, 1000SWt. = Thousand seed weight, Oil%= Seed oil content, DTFP. =Distance from the ground to the first podding site, OYld/Plt. =Oil yield per plant

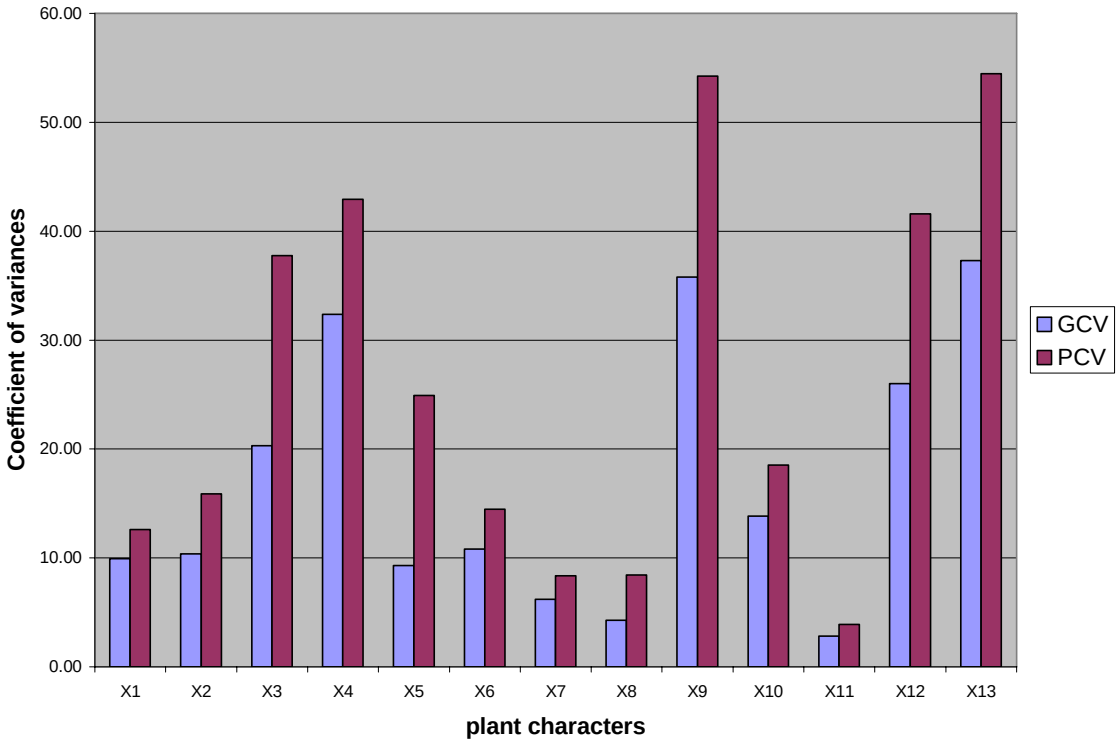


Figure 1. Phenotypic and genotypic coefficients of variation among sesame genotypes for 13 quantitative traits

X1 = days to flowering, X2 = plant height, X3 = number of pods per plant, X4 = number of primary branches, X5 = internode length, X6 = capsule length, X7 = days to maturity, X8 =number of seeds per pod, X9 =seed yield per plant, X10 = thousand seed weight, X11 = seed oil content, X12 = distance from the ground to the first podding site, X13 = oil yield per plant

A wide range of variation was observed for plant height (74.4 cm-325.3 cm) with a mean value of 140.78±16.91 cm followed by number of capsules per plant (7.9-139), distance to the first pod (6.24 cm-79.08 cm), days to maturity (92-132 days) and number of seeds per capsule (53.2-88.8).

The PCV ranged between 3.89% and 54.23 %, while the GCV ranged between 2.83% and 37.30 %. The highest PCV and GCV estimates were observed for oil yield per plant (54.47%, 37.30%) followed by seed yield per plant (54.23%, 35.77%), number of primary branches (42.93%, 32.37%) and distance to the first pod (41.69%, 26.01%) respectively (Figure 1).

The broad sense heritability values were computed for all the traits under consideration and showed a wide range of variation ranging from 13.9% for inter node length to 62.45% for days to flowering. Genetic advance as percentage of mean was also computed for each trait and showed a wide range of variation in magnitude. Higher values of genetic advance as percentage of mean were recorded for oil yield per plant (92.845%) followed by number of primary branches per plant (50.31%). The estimates of broad sense heritability along with genetic advances for the respective traits are presented graphically (Figure 2) and described as follows.

Days to flowering

The range for days to flowering lied between 37 to 71 days with an overall mean of 46.6±3.62 days. Both the PCV (12.6%) and GCV (9.93%) values are found to be lower but it has got the highest heritability value (62.45%) together with low genetic advance (16.26) as percentage of mean.

Plant height

Mean plant height was found to be 140.78±16.91 cm and ranged between 74.4 cm and 325.3 cm. Lower values of PCV (15.87%) and GCV (10.34%) with a moderate value of heritability estimate (42.7%) and lower genetic advance as percent of mean (13.96%) were observed for this character.

Number of capsules per plant

Number of capsules per plant ranged from 7.90 to 139.00 with a mean value of 41.57±13.23. A moderate value of PCV (37.4%) and a relatively high GCV (20.30%) were observed for the same trait. A broad sense heritability estimate of 28.94% and genetic advance of 22.5 was recorded for the character.

Number of primary branches

This character ranged between 0.5 and 9.60 with a mean value of 3.18±0.89. This trait has got relatively higher values of PCV (42.93%) and GCV (32.37%) values. Moreover high value of broad sense heritability (56.68%) together with high genetic advance as percentage of mean was recorded for the trait.

Inter node length

The range observed for this trait was between 2.5 cm and 12.18 cm with a mean value of 6.00±1.39 cm. A moderate PCV (24.91%) and low GCV (9.30%) were recorded for the same character. Lower heritability (broad sense) estimate (13.90%) together with low genetic advance as percentage of mean (7.11%) was recorded.

Capsule length

Mean capsule length was found to be 2.49 ± 0.24 cm and ranged between 1.54 cm and 4.2 cm. Lower PCV (14.46%) and GCV (10.81%) were recorded for the character. Nevertheless, a high heritability estimate (55%) was recorded together with moderate genetic advance (16.38).

Days to maturity

Days to maturity ranged between 92 and 132 days with a mean value of 109.31±6.14days. This character showed lower values of PCV (8.36%) and GCV (6.20%). But higher heritability estimate (55%) was recorded with lower genetic advance (16.38%) value as percentage of mean for the trait.

Number of seeds per capsule

The average number of seeds per capsule ranges between 53.2 and 88.8 seeds with a mean value of 68.59±4.99. The character was also found to have lower PCV (8.44%) and GCV (4.26%) values with moderate heritability (25.46%) and lower genetic advance as percentage of mean (4.43%).

Seed yield per plant

This character has shown a wide range of variation which falls between 0.23 g and16.95 g with a mean value of 5.44±2.22. The character showed higher values of PCV (54.23 %) and GCV (35.77 %) together with higher values of heritability estimates (43.54 %) and genetic advance (48.64 %) as percentage of means.

1000 seed weight

This character ranged between 1.17 g and 4.49 g with a mean value of 2.70±0.33. The character also showed higher value of heritability estimate (56%) together with low genetic advance a percentage of mean (21.36%).

Oil content (%)

Oil percentage has showed values ranging between 46% and 58.73% with a mean value 52.29±1.39. It showed the lowest PCV (3.89%) and GCV (2.83%) values among all the traits considered but recorded higher heritability percentage (53.1%) accompanied with lower genetic advance as percentage of mean (4.25%).

Distance to the first capsule

Distance to the first capsule ranged between 6.24 cm and 79.8 cm with a mean value of 27.39±.92 cm. The character showed high value of PCV (41.89) and GCV (26.01) while the heritability estimate was found to be 38.93% accompanied with moderate genetic advance as percentage of mean (33.44%).

Oil yield per plant

Oil yield per plant ranged between 0.12 g and 8.2 g with a mean value of 2.85±1.13 g. The character showed the highest PCV (54.47%) and GCV (37.30%) values among all the characters studied. Moreover higher heritability estimate (46.54%) together with the highest genetic advance (37.30%) values were recorded for this character.

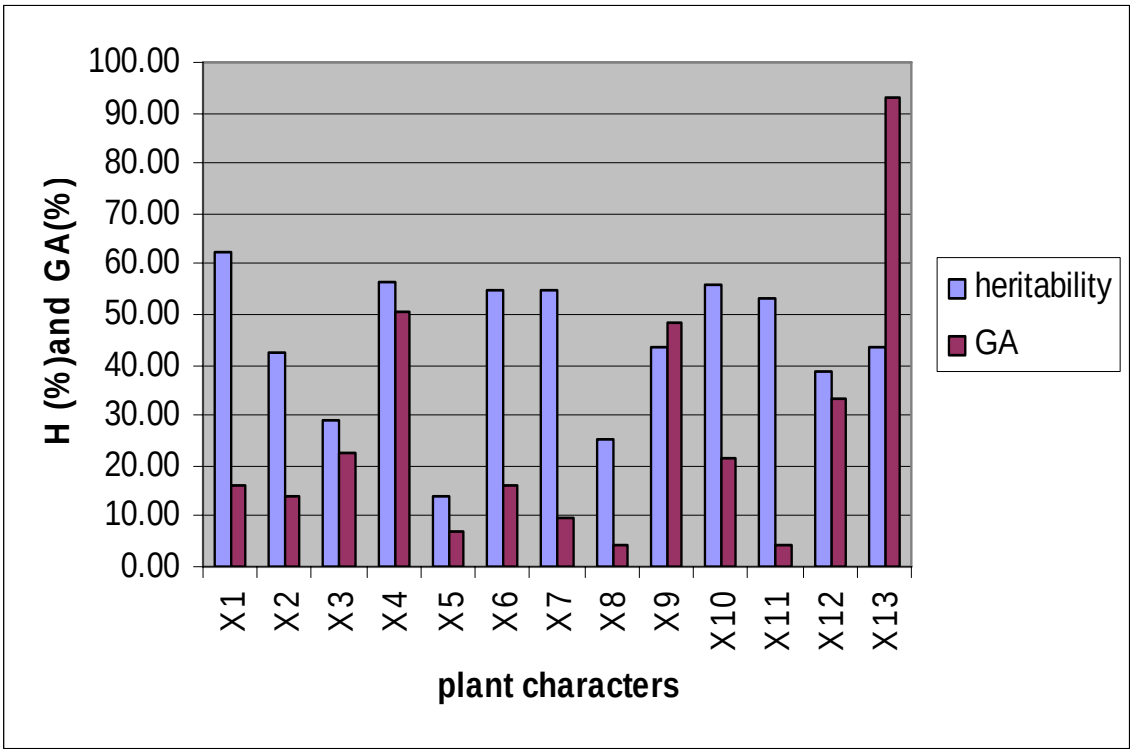


Figure 2. Heritability and genetic advance as percent of means among sesame genotypes for 13 quantitative traits

X1 = days to flowering, X2 = plant height, X3 = number of pods per plant, X4 = number of primary branches, X5 = internode length, X6 = capsule length, X7 = days to maturity, X8 =number of seeds per pod, X9 = seed yield per plant, X10 = thousand seed weight, X11 = seed oil content, X12 = distance from the ground to the first podding site, X13 = oil yield per plant

Table 4. Range, mean, phenotypic and genotypic coefficient of variability, heritability and genetic advance for the tested 100 sesame genotypes

Characters	Range			Mean ±SE	Coefficient of variability (%)		Heritability (Broad sense)	Genetic advance as % of mean
	Minimum	Maximum	Unit		Phenotypic	Genotypic		
Days to flowering	37.00	71.00	34.00	46.69±3.62	12.60	9.93	62.45	16.26
Plant height	74.40	325.30	250.90	140.78±16.91	15.87	10.37	42.70	13.96
No. of capsules per plant	7.90	139.00	131.1	41.57±13.23	37.74	20.30	28.94	22.50
No. primary branches	0.50	9.60	9.10	3.18±0.89	42.93	32.37	56.68	50.31
Inter node length	2.50	12.18	9.68	6.00±1.39	24.91	9.30	13.90	7.11
Capsule length	1.54	4.20	2.66	2.49±0.24	14.46	10.81	55.00	16.38
Days to maturity	92.00	132	40.00	109.31±6.14	8.36	6.20	54.86	9.45
No. of seeds per capsule	53.20	88.80	35.60	68.59±4.99	8.44	4.26	25.46	4.43
Yield per plant	0.23	16.95	16.72	5.44±2.22	54.23	35.77	43.54	48.64
1000 seed weight	1.17	4.49	3.32	2.70±0.33	18.51	13.83	56.00	21.36
Oil content (%)	46.00	58.73	12.73	52.29±1.39	3.89	2.83	53.10	4.25
Dist. to the first capsule	6.24	79.08	72.84	27.39±8.92	41.69	26.01	38.93	33.44
Oil yield per plant	0.12	8.20	8.08	2.85±1.13	54.47	37.30	46.54	92.84

5.2 Character Association Studies

The results of the inter-character associations among the 13 quantitative characters computed at both phenotypic (r_p) and genotypic (r_g) levels are presented in Tables 5 and 6. Among the 78 pairs of characters for which genotypic and phenotypic correlations were determined, 41phenotypic and 49 genotypic coefficients of correlation (PCC and GCC) were found to be significantly different from zero at P<0.01and P<0.05 levels of significance regardless of their directions. Of these 16 phenotypic and 21 genotypic coefficients of correlation were found to be negative while, 25 phenotypic and 28 genotypic correlation coefficients were found to be positive.

5.2.1 Correlation between seed yield and other characters

Seed yield per plant had significant and positive PCC and GCC with number of pods per plant (0.849 and 0.967), thousand seed weight (0.744 and 0.960), oil yield per plant (0.997 and 0.866), plant height (0.326 and 0.420) and oil percent (0.361 and 0.513) while, it had significant but negative PCC and GCC values with number of seeds per pod (-0.281and -0.583) and days to flowering (-0.369 and-0.454). The phenotypic and genotypic correlation coefficients between seed yield and the other 12 characters are presented graphically (Figure 3).

5.2.2 Correlation between oil yield and other characters

A significant and positive PCC and GCC were found between oil yield and number of pods per plant (0.847 and 0.721), 1000 seed weight (0.755and 0.844), oil % (0.420 and 0.593) and plant height (0.34 and 0.236), respectively. Oil yield per plant was found to be correlated significantly in a negative direction with days to flowering (-0.378 and -0.454) and number of seeds per pod (-0.309 and -0.290). The phenotypic and genotypic correlation coefficients existing between oil yield per plant and the other 12 characters are presented graphically (Figure 4).

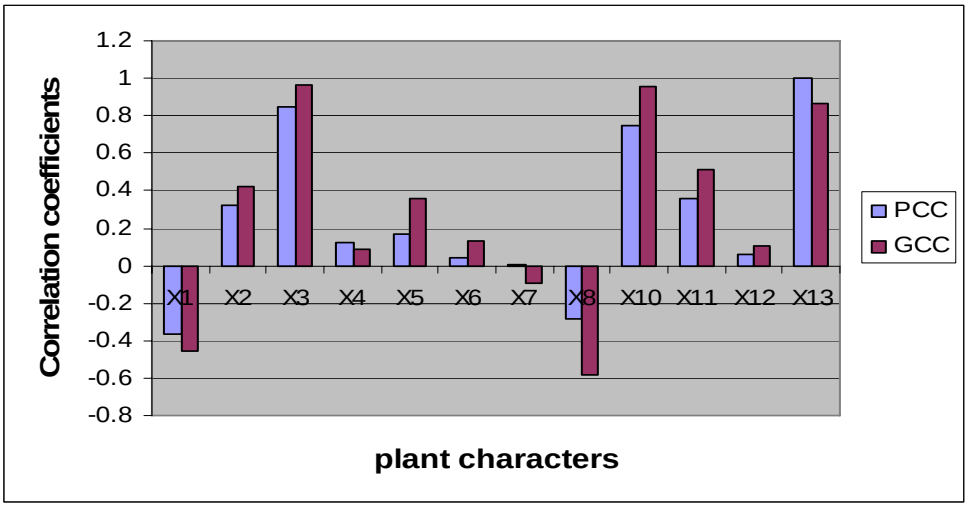


Figure 3. Phenotypic and genotypic correlation coefficients between seed yield and 12 quantitative traits of sesame genotypes

X1 = days to flowering, X2 = plant height, X3 = number of capsule per plant, X4 = number of primary branches, X5 = Internode length, X6 = Capsule length, X7 = days to maturity, X8 =number of seeds per capsule, X10 = Thousand seed weight, X11 = Seed oil content, X12 = Distance from the ground to the first podding site, X13 = Oil yield per plant

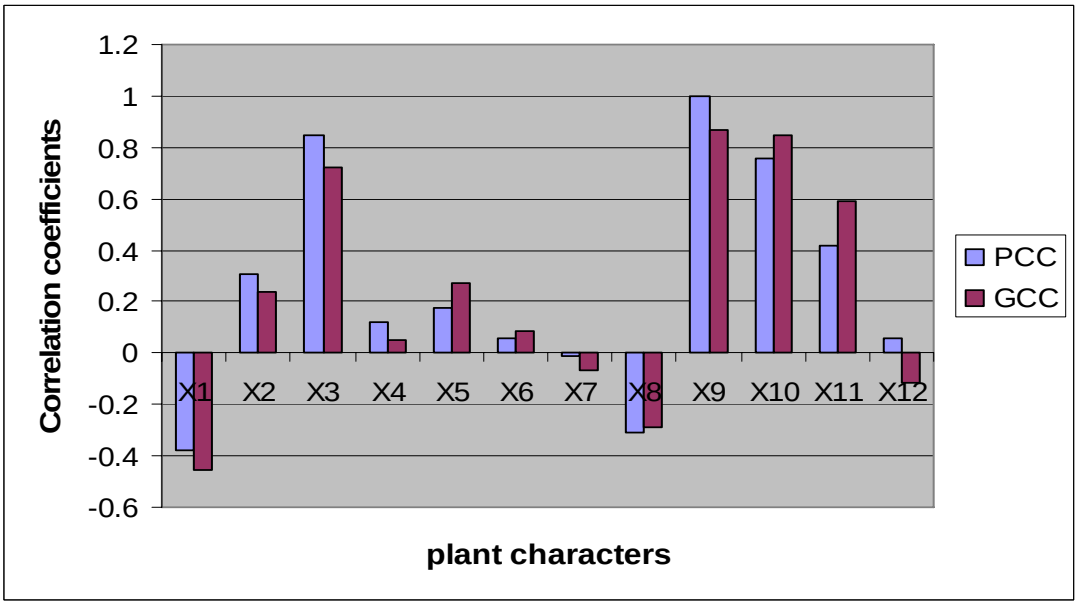


Figure 4. Phenotypic and genotypic correlation coefficients between oil yield and 12 quantitative traits of sesame genotypes

X1 = days to flowering, X2 = plant height, X3 = number of capsules per plant, X4 = number of primary branches, X5 = Internode length, X6 = Capsule length, X7 = days to maturity, X8 =number of seeds per capsule, X9 =Seed yield per plant, X10 = Thousand seed weight, X11 = Seed oil content, X12 = Distance from the ground to the first podding site

5.2.3 Correlation among other characters

Days to flowering

Days to 50% flowering was found to have a significant positive correlation with plant height (0.234 and 0.310), number of primary branch (0.721 and 0.791) and distance to the first pod (0.624 and 0.813) at phenotypic and genotypic levels, respectively. Negative and significant phenotypic and genotypic correlations were also found between days to flowering and internode length (-0.403 and -0.698), number of pods per plant (-0.288 and -0.435), capsule length (-0.539 and -0.623), yield per plant (-0.369 and -0.454), 1000 seed weight (-0.343 and -0.410), and oil yield per plant (-0.378 and -0.454).

Plant height

Plant height showed a significant positive PCC and GCC with distance to the first pod (0.485 and 0.710), days to maturity (0.482 and 0.660), number of pods per plant (0.353 and 0.540) and number of primary branches (0.309 and 0.410). On the other hand, it was found to be significantly correlated with capsule length in the negative direction (-0.325 and -0.421) at phenotypic (-0.35) and genotypic levels (-0.421), respectively.

Number of capsules per plant

A highly significant positive correlation was observed between number of pods per plant and yield per plant (0.849 and 0.967), oil yield per plant (0.847 and 0.721), 1000 seed weight (0.561 and 0.830) and oil % (0.205 and 0.482) at phenotypic and genotypic levels respectively. It had significant but negative correlation with number of seeds per pod (-0.485) at genotypic level. However, there was no association between number of pods per plant and number of seed per pod at phenotypic level.

Number of primary branches

A positive and significant correlation was observed between number of primary branches and days to maturity (0.569 and 0.689) and distance from the first pod (0.773 and 0.936) at phenotypic and genotypic levels, respectively but significant negative

correlation was observed with internode length (-0.420 and 0 -0.780), capsule length (-0.543 and -0.629) and number of seeds per pod (-0.358 and -0.476).

Inter node length

Internode length was found to be significantly and positively correlated with capsule length (0.612, 0.991), number of seeds per pod (0.335, 0.730), yield per plant (0.371, 0.360) at phenotypic and genotypic level, respectively while a significant correlation in the negative direction was observed with days to maturity (-0.366, -0.660) and distance to the first pod (-0.364, -0.730).

Capsule length

A positive and significant correlation was observed between capsule length and number of seeds per pod (0.310, 0.328). But capsule length was negatively correlated with days to maturity (-0.695, -0.806) and distance to the first pod (-0.537, -0.710) at phenotypic and genotypic levels respectively.

Table 5. Phenotypic coefficients of correlation among the 13 characters of the 100 sesame genotypes grown at Werer in 2007/08

Characters	DTF	PHt	NP/Plt	NPB	IntL	CapL	DTM	NS/Pod	Yld/Plt	1000Swt	Oil%	DTFP	OYld/Plt
DTF	1	0.234*	-0.288*	0.721**	-0.403**	-0.539**	0.751**	-0.106	-0.369*	-0.343*	-0.179	0.624**	-0.378**
PHt		1	0.353**	0.309*	-0.053	-0.325*	0.482**	-0.045	0.326**	0.068	-0.070	0.485**	0.304**
NP/Plt			1	0.145	0.106	-0.020	0.083	-0.193	0.849**	0.561**	0.205*	0.068	0.847**
NPB				1	-0.420**	-0.543**	0.569**	-0.358**	0.124	0.218*	0.157	0.773**	0.122
IntL					1	0.612**	-0.366**	0.335**	0.371**	-0.022	-0.005	-0.364*	0.172
CapL						1	-0.695**	0.310*	0.046	-0.046	0.010	-0.537**	0.056
DTM							1	-0.126	0.008	-0.094	-0.021	0.630**	-0.009
NS/Pod								1	-0.281*	-0.516**	-0.200	-0.236*	-0.309*
Yld/Plt									1	0.744**	0.361**	0.064	0.997**
1000Swt										1	0.367**	0.166	0.755**
Oil%											1	0.109	0.420**
DTFP												1	0.059
OYld/Plt													1

Table 6. Genotypic coefficients of correlation among the 13 characters of the 100 sesame genotypes grown at Werer in 2007/08

Characters	DTF	PHt	NP/Plt	NPB	IntL	CapL	DTM	NS/Pod	Yld/Plt	1000Swt	Oil%	DTFP	OYld/Plt
DTF	1	0.310*	-0.435**	0.791**	-0.698**	-0.623**	0.881**	-0.052	-0.454**	-0.36**	-0.160	0.813**	-0.454**
PHt		1	0.329**	0.353**	0.094	-0.421**	0.595**	-0.086	0.263*	0.028	-0.071	0.536**	0.236*
NP/Plt			1	0.054	0.216*	0.095	0.056	-0.485**	0.967**	0.778**	0.482**	-0.066	0.721**
NPB				1	-0.646**	-0.629**	0.684**	-0.476**	0.002	0.167	0.154	0.936**	0.005
IntL					1	0.991**	-0.559**	0.73**	0.271*	-0.078	0.027	-0.709**	0.510**
CapL						1	-0.806**	0.328*	0.098	0.035	0.135	-0.687**	0.113
DTM							1	-0.173	-0.126	-0.182	-0.078	0.766**	-0.139
NS/Pod								1	-0.585**	-0.805**	-0.313**	-0.323*	-0.573**
Yld/Plt									1	0.865**	0.551**	0.120	0.998**
1000Swt										1	0.511**	0.103	0.866**
Oil%											1	0.145	0.593**
DTFP												1	-0.113
OYld/Plt													1

5.3 Path Analysis

In this study, some component characters were selected based on their genotypic coefficients of correlation with the dependant variables (seed yield per plant and oil yield per plant) and the genotypic correlation coefficients were partitioned into direct and indirect effects through path coefficient analysis.

5.3.1 Path analysis for seed yield

Here, seed yield was considered as a dependant variable influenced by eight independent variables which were considered to be the causes. The independent variables were selected based on the magnitude (significance) of their GCC with the dependent variable. They are days to 50% flowering, plant height, number of capsules per plant, inter node length, number of seeds per capsule, 1000 seed weight, oil percentage and oil yield per plant. The direct (the main diagonal of the table) and indirect effects of the respective independent variables are presented in Table 7.

5.3.1.1 Direct effects

Path analysis revealed that the component characters days to flowering (-0.213), plant height (-0.270), number of seeds per pod (-0.600), 1000 seed weight (-2.760) and oil yield per plant (-0.815) do have negative direct effects. However, number of capsule per plant has a higher positive direct effect (0.950) on seed yield followed by inter node length (0.014) and oil % (0.005).

5.3.1.2 Indirect effects

The character 1000 seed weight, despite its negative direct effect on seed yield, has exerted higher positive indirect effects on seed yield through number of primary branches (0.739) and days to 50% flowering (0.766). On the other hand, number of pods per plant exerted a higher and positive indirect effect on seed yield through days to 50% flowering (0.919) and a significant negative indirect effect on seed yield through oil yield per plant (-0.922). Plant height through number of pods/plant (0.313) and days to 50% flowering

through number of primary branches (90.483) exerted moderate indirect effects on seed yield.

5.3.2 Path analysis for oil yield

In separate analysis, oil yield per plant was considered as a dependant variable influenced by eight independent variables. The independent variables were selected based on their highly significant positive genotypic correlation with the dependent variable (oil yield per plant). They were days to 50% flowering, plant height, number of primary branches per plant, number of pods per plant, inter node length, 1000 seed weight seed yield per plant and oil percentage. The direct and indirect effects of the respective independent variables are presented in Table 8.

Table 7. Direct and indirect effects of some yield components on seed yield of 100 sesame genotypes grown at Werer in 2007/08

Characters	DTF	PHt	NP/Pl	NPB	IntL	CapL	DTM	NS/Pod	1000SW	OIL%	DTFP	OY/Plt	Correlation coefficient
DTF	**-2.113**	-0.081	-0.413	0.483	-0.010	-0.695	1.540	0.032	0.100	-0.001	0.334	0.370	-0.454
PHt	-0.638	**-0.270**	0.313	0.215	0.001	-0.469	1.040	0.052	-0.008	0.00	0.220	-0.193	0.263
NP/Pl	0.919	-0.089	**0.950**	0.033	0.003	-0.106	0.098	0.291	-0.215	0.002	-0.027	-0.922	0.967
Int.L	1.474	-0.025	0.191	-0.394	**0.014**	1.104	-0.978	-0.625	0.021	0.000	-0.292	-0.219	0.271
NS/Pod	0.111	0.023	-0.460	-0.290	0.014	0.364	-0.302	**-0.600**	0.222	-0.002	-0.133	0.468	0.583
1000SW	0.766	-0.008	0.739	0.101	-0.001	0.039	-0.318	0.483	**-0.276**	0.003	0.042	-0.706	0.865
Oil %	0.339	0.019	0.458	0.094	0.000	0.151	-0.137	0.188	-0.141	**0.005**	0.060	-0.483	0.551
OY/Plt	0.959	-0.064	0.968	0.002	0.004	0.126	-0.243	0.344	-0.239	0.003	-0.047	**-0.815**	0.998

*Bolded numbers are direct effects, R = -0.0105

Table 8. Direct and indirect effects of some yield components on oil yield of 100 sesame genotypes grown at Werer in 2007/08

Characters	DTF	PHt	NP/Pl	NPB	IntL	CapL	DTM	NS/Pod	Yld/Plt	1000SW	OIL%	DTFP	Correlation coefficient
DTF	**-0.755**	-0.031	-0.134	0.175	-0.011	-0.235	0.553	0.010	-0.152	0.024	-0.008	0.110	-0.454
PHt	-0.228	**-0.104**	0.102	0.078	0.001	-0.159	0.373	0.017	0.088	-0.002	-0.003	0.072	0.236
NP/Pl	0.228	-0.034	**0.308**	0.012	0.003	-0.036	0.035	0.095	0.147	-0.051	0.023	-0.009	0.721
Int.L	0.526	-0.010	0.062	-0.143	**-0.015**	-0.374	-0.351	-0.204	0.091	0.005	-0.001	-0.096	0.510
NS/Pod	0.040	0.009	-0.149	-0.105	0.016	0.123	-0.109	**-0.196**	-0.196	0.053	-0.015	-0.044	-0.573
Yld/Plt	0.343	-0.027	0.317	0.001	0.004	0.037	-0.079	0.115	**0.335**	-0.057	0.027	-0.016	0.998
1000SW	0.273	-0.003	0.240	0.037	-0.001	0.013	-0.114	0.157	0.290	**-0.065**	0.025	0.014	0.866
Oil %	0.121	0.007	0.149	0.034	0.000	0.051	-0.049	0.061	0.185	-0.033	**0.048**	0.020	0.593

*Bolded numbers are direct effects, R = -0.0105

5.3.2.1 Direct effects

The characters number of pods per plant (0.308), seed yield per plant (0.335) and oil percentage(0.048) were found to exert positive direct effects on the dependant variable (oil yield per plant). On the other hand, the rest of the characters (1000 seed weight and oil content) were found to exert negative direct effects of -0.065 and -0.033 which implicates that the high association of these characters with oil yield was attributed to the interaction of other component traits. Thus it can be emphasized that the ideal plant type should have higher values of number of pods per plant and seed yield per plant which exert positive direct effects on oil yield.

5.3.2.2 Indirect effects

Number of pods per plant, seed yield per plant and 1000 seed weight were found to exert a positive indirect contributions for the dependant variable, oil yield, through seed yield per plant (0.344), number of pods per plant (0.317), number of pods per plant (0.240) and seed yield per plant (0.290), respectively as shown in Table 8.

5.4 Principal Component Analysis

Principal component analysis is one of the most frequently used multivariate techniques which are used to transform the data from one set of coordinate axes to another. After inter-correlations among all quantitative traits were evaluated by correlation analysis, the resulting 13X13 correlation matrix was used as input for the PCA to remove the effects of scale. The first three principal components with eigen values of greater than unity explained about 73 % of the total variation (Table 9). The first principal component alone explained about 32% of the entire variability among the 100 genotypes. The second and third principal components explained about 30% and 11% of the entire variability among the 100 genotypes, respectively.

Table 9. Principal component analysis of 100 sesame genotypes grown at werer, 2007/08

	PC1	PC2	PC3
Eigen value	4.177	3.93211	1.411
IVE	32.10	30.25	10.85
CVE	0.321	0.624	0.732
Characters		**Eigenvectors**	
DTF	0.439	-0.001	0.035
PHt	0.163	0.229	0.536
NP/Plt	-0.162	0.394	0.231
NPB	0.347	0.238	-0.072
IntL	-0.265	-0.123	0.442
CapL	-0.367	-0.153	0.104
DTM	0.391	0.147	0.202
NS/Pod	-0.026	-0.265	0.511
Yld/Plt	-0.216	0.431	0.129
1000Swt	-0.177	0.385	-0.249
Oil%	-0.123	0.204	-0.215
DTFP	0.359	0.206	0.087
OYld/Plt	-0.224	0.431	0.107

* IVE= individual variability explained, CVE= cumulative variability explained, character abbreviations follows the same trait and order as the other tables

Although there is no clear guideline to determine the significance of a trait coefficient (eigen vector), one rule of thumb is to regard a coefficient that is greater than half divided by the square root of the standard deviation of the eigen vectors of the respective principal components as significant or important (John and Wichern, 1988). The criterion was used by the present study to decide the importance of the characters in the three principal components. Accordingly, days to 50% flowering, days to maturity, number of primary branches and distance to the first pod were the most important traits contributing to the first , seed yield, oil yield, 1000 seed weight and number of pods per plant for the second and plant height, number of seed per pod and internode length for the third principal components, respectively.

5.5 Cluster Analysis

Multivariate distance analysis was carried out to classify the 100 sesame genotypes into different diversity groups yielded eight major cluster groups. The list of genotypes which belong to each cluster along with their origins and altitudinal classes are presented in Table 10. The first cluster comprising 39 accessions (39% of the genotypes) contain dominantly white-seeded genotypes originated mostly from Benshangul gumuz, Gambella and Wollega areas. Cluster two comprised 43 genotypes is the largest cluster of all and most of the accessions which have exotic origins were found to be included in this cluster together with those which were mainly collected from the Northern parts of the country (North Shewa, Wollo, Metema and Humera areas). The remaining six clusters had one to nine genotypes (three clusters with one genotype each.

The clustering enabled to mark genotypes that excel in one or another way or vise versa (Brown, 1991). No single cluster contained genotypes with all desirable plant characters. Seed yield per plant, oil content, oil yield per plant, number of pods per plant and 1000 seed weight were highest for Cluster VIII that contained only a single genotype (Tables 12 and 13). Cluster II contained the earliest flowering and maturing, while Cluter VI contained the latest flowering and maturing sesame genotype. Cluster VI also include the shortest genotype, while Cluster V included the tallest. Cluster IV included genotypes with the highest mean for number of primary branches. Cluster III included genotypes with the longest internode length and capsule length. The single genotype grouped under Cluster VI had the highest number of seeds per plant and the longest distance from the base to the first pod.

Pair wise generalized squared distance (D^2) between the eight clusters were computed using SAS computer software version 8.0 (SAS Institute, 1988) and are presented in Table 11. The maximum distance was found between clusters VI and VII, followed by those between clusters VI and VIII, and III and VII. The minimum distance was also found between clusters I and II, followed by between clusters II and V, and clusters I and V. The D^2 values among the eight clusters ranged from 14.55 (between Cluster I and II) to 215.88 (between Clusters VI and VII).

The intra (within) cluster pair wise generalized squared distance D^2 values of the eight clusters were also computed using the same software and ranged from 1.69 (cluster I) to 9.21 (Clusters VI, VII and VIII). Genotypes in clusters VI, VII and VIII were genetically more distant among themselves as well as from the other clusters so they formed the most divergent single genotyped clusters.

The dendrogram of the 100 genotypes was done using NTSYS computer soft ware version 2.1 (Appendix 3) summarized the number of clusters in different ranges of average Euclidean distance coefficients in order of decreasing width of the range.

Table 10. Accession number, seed color, origin and altitude of collection site of the 100 sesame genotypes grown at Werer in 2007/08

Cluster	No. of genotypes	Accession no./name	Original source	Seed Color	Altitude
I	39	NS-0022	North Shewa	light grey	1360
		BG-010(1)	Benshangul Gumuz	dirty white	1050
		BG-013	Benshangul Gumuz	white	940
		BG-002(2)	Benshangul Gumuz	white	1280
		BG-006	Benshangul Gumuz	mixed(dominantly white)	910
		BG-004	Benshangul Gumuz	dirty white	1180
		BG-008	Benshangul Gumuz	white	1020
		BG-010(3)	Benshangul Gumuz	white	1050
		BG-019	Benshangul Gumuz	pure white	965
		BG-009	Benshangul Gumuz	white	1250
		BG-012(2)	Benshangul Gumuz	dirty white	1095
		BG-007	Benshangul Gumuz	mixed	1000
		G-002(2)	Gambella	dirty white	500
		G-004(1)	Gambella	white	480
		G-003(1)	Gambella	dirty white	500
		G-009(2)	Gambella	yellowish white	500
		G-006(1)	Gambella	dirty white	465
		EW-008(1)	East Wollega	white	1325
		EW-006	East Wollega	dirty white	1360
		EW-020(1)	East Wollega	dirty white	1390
		EW-005	East Wollega	white	1400
		EW-020	East Wollega	dirty white	1570
		EW-015(1)	East Wollega	yellowish white	1290
		EW-013(5)	East Wollega	white	1300
		WW-001(3)	West Wollega	white	1250
		WW-002	West Wollega	white	1090
		WW-003(2)	West Wollega	white	1330
		WW-003(1)	West Wollega	yellowish white	1150
		WW-003	West Wollega	white	1190
		WW-002(2)	West Wollega	white	1000
		Acc-202-318	Wollo	mixed	1400
		HH-206-001	Humera	pure white	600
		Htn-206-002	Humera	pure white	600
		Htb-206-002	Humera	grey	600
		Htb-206-001	Humera	grey	600
		Htk-206-002	Humera	greenish white	600
		Htk-206-004	Humera	greenish white	600
		GoA-206-004	Metema	pure white	750
		MT-206-001	Metema	dirty white	750

Table 10. Cont'd

Cluster	No. genotypes	Accession no./name	Original source	Seed color	Altitude
II	43	NS-0013	North Shewa	dirty white	1260
		NS-0025	North Shewa	mixed	1210
		NS-0074	North Shewa	mixed(dominantly grey)	1460
		NS-034	North Shewa	mixed(grey,white and black)	1200
		G-006	Gambella	mixed	490
		G-003(2)	Gambella	pure white	510
		G-004(2)	Gambella	dirty white	480
		G-002(1)	Gambella	mixed(grey and white)	510
		G-005(1)	Gambella	dirty white	480
		G-001	Gambella	dirty white	485
		Acc-202-293	Wollo	mixed dominantly grey	1460
		Acc-202-343	Wollo	mixed (deep grey, white)	1500
		Acc-202-368	Wollo	grey	1500
		Acc-202-333	Wollo	mixed (grey and white)	1450
		HH-206-004	Humera	pure white	600
		HH-206-007	Humera	pure white	600
		HH-206-002	Humera	pure white	600
		HH-206-005	Humera	pure white	600
		Hr-206-002	Humera	pure white	600
		Hr-206-003	Humera	white	600
		Hr-206-004	Humera	dirty white	600
		Hr-206-001	Humera	dirty white	600
		HN-206-003	Metema	pure white	750
		HN-206-004	Metema	pure white	750
		HN-206-005	Metema	pure white	750
		HN-206-002	Metema	pure white	750
		HN-206-001	Metema	pure white	750
		Hr-206-0010	Metema	pure white	750
		Hr-206-002(2)	Metema	pure white	750
		Hr-206-001(2)	Metema	pure white	750
		Acc-203-623	Zimbabwe	mixed (grey and white)	-
		Localwhite-0034	Somalia	mixed (light, white, black)	-
		Giza-25	Egypt	light green	-
		Acc-203-505	Egypt	mixed	-
		California-827	USA	mixed(dominantly deep grey)	-
		Margo sel	Israel	dirty white	-
		T-6	India	light green	-
		K-60-383	Korea	light green	-
		Ying white	China	greenish white	-
		FAO-68-548	Venzuela	yellowish white	-
		UCR-82-209	USA	mixed (dominantly light grey)	-
		Orotall	Israel	white	-
		Etalokornia	Greece	mixed	-

Table 10. Cont'd

Cluster	No. genotypes	Accession no./name	Original source	Seed color	Altitude
III	3	GoA-206-002	Humera	pure white	700
		GoA-206-001	Metema	pure white	750
		GoA-206-003	Metema	pure white	750
IV	9	NS-008	North Shewa	deep grey	1250
		NS-004	North Shewa	deep grey	845
		NS-006	North Shewa	pure white	1900
		NS-007	North Shewa	yellowish white	1200
		Acc-202-363	Wollo	deep grey	1560
		Acc-202-355	Wollo	mixed dominantly grey	1860
		Acc-202-299	Wollo	deep grey	1540
		Acc-202-307	Wollo	mixxed (dominantly light grey	1470
		Giza-32	Zimbabwe	deep grey	-
V	3	NS-033	North Shewa	deep grey	1300
		Acc-202-325	Wollo	deep grey	1750
		Instituto	Mexico	deep grey	-
VI	1	BG-015	Benshangul Gumuz	pure white	910
VII	1	NS-0047	North Shewa	dirty white	1290
VIII	1	NS-065	North Shewa	mixed (dominantly pure white)	1300
		GoA-206-002	Humera	pure white	700

Table 11. Intra (main diagonal) and inter-cluster generalized D^2values for eight clusters formed by 100 sesame accessions

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**(1.88)**	14.55	78.43	61.94	45.72	108.98	66.50	93.82
II	14.55	**(1.69)**	79.68	70.89	30.81	129.61	63.68	63.65
III	78.43	79.68	**(7.01)**	124.23	126.16	90.19	152.00	102.59
IV	61.94	70.89	124.23	**(4.81)**	57.88	69.91	91.36	136.55
V	45.72	30.81	126.16	57.88	**(7.01)**	121.88	95.31	131.07
VI	108.98	129.61	90.19	69.91	121.88	**(9.21)**	215.88	152.06
VII	66.50	63.68	152.00	91.36	95.31	215.88	**(9.21)**	121.63
VIII	93.82	63.65	102.59	136.55	131.07	152.06	121.63	**(9.21**)

Table 12. The nearest and distant clusters from each cluster based on D^2 value

Cluster No.	No. of genotypes grouped	Nearest two clusters	Farthest two clusters
I	39	II, V	VI, VIII
II	43	II, V	III, VI
III	3	I, II	V, VII
IV	9	I, V	III, VIII
V	3	I, II	III, VIII
VI	1	III, IV	VII, VIII
VII	1	I, II	III, VI
VIII	1	I, II	IV, VI

Table 13. Cluster mean values for the 13 quantitative characters of the 100 sesame genotypes

Cluster .	DTF	PHt	NP/Plt	NPB	IntL	CapL	DTM	NS/Pod	Yld/Plt	1000 Swt	Oil%	DTFP	OY/Plt
I	46.67	139.90	36.87	2.69	6.06	2.45	109.75	71.59	3.98	2.37	51.30	24.87	2.05
II	43.60	139.23	47.62	3.00	6.10	2.58	105.46	66.61	7.08	3.00	53.12	24.82	3.75
III	48.47	124.73	23.15	2.23	7.92	3.27	108.65	71.42	2.02	2.11	54.10	21.35	1.10
IV	58.19	145.71	35.40	5.96	4.75	2.04	121.11	66.19	3.75	2.66	52.60	47.04	1.99
V	50.21	177.02	45.72	4.56	5.33	2.30	115.98	62.62	7.54	3.15	50.28	35.78	3.76
VI	63.93	120.87	25.73	4.27	5.37	2.45	125.75	62.99	2.41	1.99	49.73	25.99	1.15
VII	45.00	157.04	45.51	3.01	5.54	2.60	111.16	75.98	7.28	3.17	53.37	52.93	3.86
VIII	44.90	140.19	75.17	3.08	7.78	2.93	114.88	66.51	12.02	3.58	55.02	28.01	6.60

6. DISCUSSION

Development of plant breeding strategy mainly hinges on the support provided by genetic information on the inheritance and behavior of major quantitative traits associated with yield, quality or any economic trait of concern to the breeder. To derive such genetic information, it is necessary to conceive a genetic model in relation to the material that is to be utilized.

Success in plant breeding activities aimed to improve the architecture of a given crop is heavily dependant on the existence of genetic variability in the germplasm pool of a given species. It is therefore, pertinent to study the extent and pattern of genetic diversity of the crop species that can be exploited through selection. Though some findings from the Indian scientists suggested India as the center of origin for sesame (*Sesamum indicum* L.), Vavilov and recent reports on the existence of wild relatives of the crop in Ethiopia indicates occurrence of great diversity in the country as well (FAO, 2005).

In this study, 100 sesame genotypes collected from the different regions of Ethiopia and abroad were evaluated for their genetic variability, diversity and character associations. The results of the study are discussed below in detail.

The analysis of variance for 13 agro-morphological characters considered showed significant variation among the 100 genotypes for all characters. The range of variation was also found to be higher for plant height, followed by number of capsules per plant, distance to the first pod and days to maturity. The existence of this significant variation among the entries offers a great opportunity in the genetic improvement of the crop through selection and hybridization. Similar results except for seed yield per plant have been reported by Bisht and his co-workers (Bisht *et al*., 1998). The finding of Khan and his colleagues was also in agreement with this study for most of the traits except for number of seeds per capsule (Khan *et al*., 2001) and the report of Sarwal and Haq (2006) that totally agrees with the result of this study.

The wide ranges of values for the various traits also offer great flexibility and scope for the development of improved crop varieties adapted for the diverse agro-ecological setup of the country.

The total variance (phenotypic variance) of the genotypes was computed and partitioned into genetic and non-genetic components to estimate the true breeding value of each genotype. The phenotypic and genotypic coefficients of variation were used to compare the magnitude of variability since the means of the different characters were different. The PCV and GCV were higher for oil yield per plant, followed by seed yield per plant and number of primary branches. Thus selection to improve these characters can be practiced effectively. In this study the GCV was found to be less than its corresponding estimates of PCV for all traits, indicating the involvement of the environment in the expression of these traits. However, the difference between PCV and GCV values was small for most of the studied characters, signifying minimal environmental effects in the development of these parameters. This finding is in line with what has been reported by Khan and his colleagues (Khan *et al.*, 2001). This suggests that selection can be effective for these traits even at phenotypic level. This finding is in line with the report of Sarwar *et al.* (2006). Moderate PCV and GCV were recorded for days to flowering (12.60% and 9.93%) and lower estimates for oil content (3.89%) and this finding is in line with the works of other authors (Banerjee and Kole, 2006; Solanki and Gupta, 2001).

It has been emphasized that these genetic parameters (PCV and GCV) need to be studied together with the estimates of broad sense heritability and expected genetic advance to get the best prediction of genetic advance expected from selection (Adugna, 2002). Higher heritability estimates give a useful indication of the relative values of selection based on phenotypic expression (Johnson *et al.*, 1955).

Accordingly, the estimated broad sense heritability values were computed for the 13 traits under consideration and they showed a wide range of variation, ranging from 13.9% for inter node length to 62.45% for days to flowering. Moreover, half of the plant characters showed heritability (broad sense) values of greater than 50%, indicating

higher observed variability attributed to genetic difference. Higher estimates of heritability values were recorded for days to flowering, followed by number of primary branches, 1000 seed weight, capsule length, days to maturity and oil percent.

Genetic advance that could be expected from selecting the top 5% genotypes, as percentage of mean was also computed and ranged from 4.25% to 92.85% for oil content and oil yield per plant. In the same way, higher genetic advance as percentage of mean were observed for oil yield per plant, followed by number of primary branches and seed yield per plant. This shows the expected genetic gain of these characters in the subsequent selective breeding efforts would be greater.

Plant height showed moderate heritability value (42.7) with lower genetic advance as percentage of mean (13.96). However, Rao (2005) reported high heritability estimate along with high genetic advance as percent of mean for plant height, capsules per plant and 1000 seed weight. This may be due to the differences in genetic make up of the studied materials (Rao, 2005)

Higher estimates of broad sense heritability together with high genetic advance was observed for number of primary branches, number of capsules, seed yield per plant and oil yield per plant, indicating the possible preponderance of additive gene action. This finding is in line with the report of Sarwar and Haq (2006). Seed yield showed higher values of heritability estimates (43.54) and genetic advance as percentage of means. Genetic advance as percent of the mean was highest in the case of seed yield per plant, capsule number and number of branches per plant (Sarwar *et al*., 2006; Akpan *et al.*, 2005). On the other hand, Kandasamy (1991) argued that the lower heritability of seed yield and number of capsules suggested that these traits were highly influenced by the environment. Generally, higher values of broad sense heritability combined with expected genetic advance indicates bright future of selection of better genotypes (Johanson, 1955). However, the worth of heritability and genetic advance values could also be related to the economic importance of the trait under consideration. For instance a unit improvement in days to flowering may not be as worthy as a unit improvement in oil yield or seed yield (Gemechu, 1996).

On the other hand days to 50% flowering and days to maturity were observed to have higher heritability values (62.45% and 55%) together with low genetic advance as percentage of mean (16.26% and 16.38%) in the given order. This result is in agreement with other works (Kandaswamy *et al.*, 1991; Rao, 2005 and Padmavathi, 2007) indicating non additive gene action (dominance and/or epistasis). Oil percent has also showed higher heritability percentage (53.1) accompanied with lower genetic advance as percentage of mean (4.25%). In a similar way, higher heritability values for days to flowering and maturity and high heritability estimates but with low genetic advance for oil content (Banerjee, 2006).

Understanding the magnitude and direction of associations existing among all the plant characters is of major importance for the improvement of a particular target character through indirect selection. Correlation could be through pleiotropic action of genes, linkage, natural and/or artificial selection and correlation coefficient measures the magnitude and direction of association among characters (Johnson and wichern, 1988). Genotypic relationships among traits affecting seed yield elucidate true association of characters as they exclude environmental influences. Though comparable in magnitude, the value of GCC for all traits except for seed yield per plant and oil yield per plant was found higher in magnitude than their corresponding PCC, indicating a strong inherent relationship among the studied characters. The lower PCC could result from the modifying effect of the environment (Gemechu, 1996; Izge *et.al*., 2006).

Seed yield had shown significant and positive PCC and GCC with number of pods per plant, thousand seed weight, yield per plant, plant height and oil percent, while it had significant but negative PCC and GCC values with number of seeds per pod and days to flowering. This finding is some how in line with the results reported by the authors who observed a positive and significant correlation coefficient between seed yield and capsule number per plant, plant height and number of branches per plant at both phenotypic and genotypic level (Kandasamy *et al*., 1991; Fayan, 1991; Khan *et al*., 2001; Akpan *et al*., 2005; Sarwar, 2006; Sarwar and Haq, 2006). This suggests that improvement in seed yield can be achieved through selecting plants having larger number of capsules,

branches and taller plant height. On the contrary, Akpan *et al*. (2005) reported high and positive relationship between seed yield and days to 50% flowering.

Seed yield is a complex character influenced by other component characters which are interrelated to each other and with seed yield. Therefore, a rapid improvement in yield is expected to result if selection is practiced for component characters (indirect selection) with differential emphasis based on their degree of influence. Each component has two action paths, namely, direct effect by itself and indirect effect through other component traits by virtue of the association it has with them. The degree and pattern of influence of component characters can be expressed in quantitative terms using path analysis through partitioning the correlation coefficient. Hence path analysis can provide a measure of the relative importance of each independent variable (characters) to the prediction of changes in the dependant variable.

Path analysis of seed yield revealed that the characters number of pods per plant and number of primary branches had a positive direct effect on seed yield. However, these positive direct effects were counter balanced by some negative indirect effects by 1000 seed weight and days to flowering. Yield components 1000 seed weight, plant height and days to 50% flowering had got negative values of direct effects although seed yield was counter balanced by higher positive indirect effects exerted through number of pods per plant, plant height and days to 50% flowering. On another report significant and positive direct effect of plant height and number of capsules per plant was reported on seed yield (Sarwar and Haq 2006; Khan *et al.*, 2001).

Path analysis was also computed using oil yield as a dependant character and number of pods per plant and seed yield per plant were found to exert positive direct effects on oil yield per plant. On the other hand negative direct effects were observed for 1000 seed weight and oil content, however these negative values were found to be counter balanced by positive indirect effects of the other component traits.

The principal component analysis performed on the 13 quantitative variables revealed the existence of significant divergence among the tested accessions of sesame. The

overall diversity (almost 99%) was explained by10 components. The first three principal components with eigen value of greater than unity were found to explain 73% of the overall variability existing among the test entries. The major contributing factors for the total variability were found to be days to 50% flowering, days to maturity, distance to the first pod and number of primary branches in this order of importance. Research reports on principal component analysis performed to select Korean core collections revealed that the first two principal components explained 65% of the overall variability and the first PC is mostly related to agronomic characters such as plant height, capsule number and date of flowering, while the second principal component (PC) is strongly related with capsule length, height of capsule bearing stem and number of branches and seed yield per plant (Kang *et al*., 2006). Principal component analysis performed on linseed collections from Ethiopia and abroad grouped 11 characters of 60 linseed accessions in to 10 components which explained 90% of the total variability (Adugna, 2002). In this study the first 5 eigen vectors were responsible for about 66.4% of the gross variability and this variability was due to days to flowering, plant height, bolls per plant branches per plant and seed yield per plant.

Cluster analysis was also conducted on the 100 sesame genotypes based on 13 characters and they were grouped into eight clusters. The first five clusters contain 39, 43, 3, 9 and 3 genotypes in that order, while the remaining three clusters had single accession each indicating their wide variability. Reports made by Venkatamarana and his colleagues (1999) on the phenetic analysis of 144 Indian sesame accessions were comparable with this finding. They reported that the 144 sesame accessions were grouped into six clusters among which 4 accessions were found highly diverse and placed outside these close-knit clusters.

Moreover, the clustering pattern showed that there is a certain pattern of relation between the genetic diversity and geographical diversity (collection localities) to some extent. About 75% of the genotypes constituting cluster I were from adjoining regions (Gambella Benshangul and Wollega) while cluster II was found to be constituted by genotypes from the northern part (50%) of the country (Wollo, North shewa, Humera and Metema). In this respect, geographic range can be used to predict the level of variation in sesame. The

high rate of out-crossing percentage (5-60%) reported by Ashri (1988) could also be a potent source of genetic variability (Venkatamarana *et al.*, 1999).

On the other hand, a considerable amount of sesame accessions of similar geographic origins are found distributed among the eight clusters this could be due to exchange of breeding materials and genetic drift due to selection in the different agro-ecologies. This result is in line with the report of Ghulam *et al.*, (2007); he found a close genetic relation between sesame accessions as determined by geographical origin using AFLP markers. The first cluster comprising proportional number of accessions from Benshangul-Gumuz, Gambella, Wollega and Humera, are early maturing varieties which most probably be taken from the Humera and Metema plains during the settlement programs of the 1970's. The second cluster contains accessions largely from Metema and Humera, Gambella, Wello and North Shewa which are nearer in genetic distance to the above cluster. Besides, almost all of the introduced materials from Africa (Somalia and Zimbabwe), Asia (India, Korea, China, Venezuela), America (USA) and Europe (Israel) belonged to this cluster, indicating their close similarity in their genetic make up. The third cluster is occupied with accessions from Metema region characterized by higher seed oil content. Cluster number four contains accessions from North shewa and Wollo which are neighboring regions with similar agro-ecological conditions, where gene flow can take place in a pronounced manner. The accessions were characterized by highly branched growth habit with longer growing period. The same trend like cluster IV holds true for cluster V. The rest three clusters were made up of single genotypes. These accessions are a bit distinct in type compared to accessions in the remaining clusters.

7. CONCLUSION AND RECOMMENDATIONS

The study revealed that, there was a great wealth of sesame genetic resource in the country which could be exploited in the future sesame improvement programs through selection and hybridization. The finding of this work also questions the authors who are in favor of the idea that the Indian region as the primary center of origin of cultivated sesame and the Abyssinian region as rich only in wild type sesame. However, further intensive works are needed involving more germplasm materials collected from all sesame growing regions and considering other crucial morphological, physiological and molecular characters. The usefulness of parental selection based on genetic divergence as source of desirable recombination that yield useful segregants up on hybridization need to be assessed for future breeding. The study also calls for further investigation using more reliable tools like DNA markers to substantiate the current argument.

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APPENDICES

Appendix 1. Local and exotic Collections of Sesame land races

No	Acceccession Number	Area of collection	Locality	Altitude mts. a.s.l
1	NS-065	North Shewa	Jejeba	1300
2	NS-0013	North Shewa	Jejeba	1260
3	NS-0047	North Shewa	Artumajelle	1290
4	NS-0025	North Shewa	Kewet	1210
5	NS-0074	North Shewa	Artumajelle	1460
6	NS-0022	North Shewa	Kewet	1360
7	NS-008	North Shewa	Korangoge	1250
8	NS-033	North Shewa	Senbete	1300

9	NS-004	North Shewa	Tarmaber	845
10	NS-006	North Shewa	Akake	1900
11	NS-034	North Shewa	Senbete	1200
12	NS-007	North Shewa	Majette	1200
13	BG-010(1)	Benshangul Gumuz	Mender 6	1050
14	BG-013	Benshangul Gumuz	Mandura	940
15	BG-002(2)	Benshangul Gumuz	Belojeganfo	1280
16	BG-006	Benshangul Gumuz	Dangur	910
17	BG-004	Benshangul Gumuz	Ipapo	1180
18	BG-008	Benshangul Gumuz	Danua	1020
19	BG-015	Benshangul Gumuz	Mandura	910
20	BG-010(3)	Benshangul Gumuz	Mender 5	1050
21	BG-019	Benshangul Gumuz	Mandura	965
22	BG-009	Benshangul Gumuz	Dangur	1250
23	BG-012(2)	Benshangul Gumuz	Mekane selam	1095
24	BG-007	Benshangul Gumuz	Dadush	1000
25	G-006	Gambella	Abobo	490
26	G-002(2)	Gambella	Cheba	500
27	G-004(1)	Gambella	Banga	480
28	G-003(2)	Gambella	Chebo	510
29	G-003(1)	Gambella	Chebo	500
30	G-004(2)	Gambella	Abobo	480
31	G-002(1)	Gambella	Bonga	510
32	G-005(1)	Gambella	Abobo	480
33	G-009(2)	Gambella	Merar	500
34	G-006(1)	Gambella	Bonga	465
35	G-001	Gambella	Jejeb	485
36	EW-008(1)	East Wollega	Diga	1325
37	EW-006	East Wollega	Gida Kiremu	1360
38	EW-020(1)	East Wollega	Diga	1390
39	EW-005	East Wollega	Abedunguru	1400
40	EW-020	East Wollega	Sasiga	1570
41	EW-015(1)	East Wollega	Abedunguru	1290
42	EW-013(5)	East Wollega	GidaKiremu	1300
43	WW-001(3)	West Wollega	Gimbi	1250
44	WW-002	West Wollega	Hawawelel	1090
45	WW-003(2)	West Wollega	Gimbi	1330
46	WW-003(1)	West Wollega	Goadale	1150
47	WW-003	West Wollega	Goadale	1190
48	WW-002(2)	West Wollega	Hawawelwel	1000
49	Acc-202-363	Wollo	Sirinka	1560
50	Acc-202-318	Wollo	Kalu	1400
51	Acc-202-355	Wollo	Artuma	1860

Appendix 1. Cont'd

No.	Accession Number	Area of collection	Locality	Altitude mts. a.s.l
52	Acc-202-293	Wollo	Ambasel	1460
53	Acc-202-343	Wollo	Harbu	1500
54	Acc-202-325	Wollo	Bati	1750
55	Acc-202-299	Wollo	Ambasel	1540
56	Acc-202-307	Wollo	Bati	1470
57	Acc-202-368	Wollo	Sirinka	1500
58	Acc-202-333	Wollo	Harbu	1450
59	HH-206-004	Humera	NA	600
60	HH-206-001	Humera	NA	600
61	HH-206-007	Humera	NA	600

62	HH-206-002	Humera	NA	600
63	HH-206-005	Humera	NA	600
64	Htn-206-002	Humera	NA	600
65	Htb-206-002	Humera	NA	600
66	Htb-206-001	Humera	NA	600
67	Htk-206-002	Humera	NA	600
68	Htk-206-004	Humera	NA	600
69	Hr-206-002	Humera	NA	600
70	Hr-206-003	Humera	NA	600
71	Hr-206-004	Humera	NA	600
72	Hr-206-001	Humera	NA	600
73	GoA-206-002	Humera	NA	700
74	GoA-206-004	Metema	NA	750
75	GoA-206-001	Metema	NA	750
76	GoA-206-003	Metema	NA	750
77	HN-206-003	Metema	NA	750
78	HN-206-004	Metema	NA	750
79	HN-206-005	Metema	NA	750
80	HN-206-002	Metema	NA	750
81	HN-206-001	Metema	NA	750
82	Hr-206-0010	Metema	NA	750
83	Hr-206-002(2)	Metema	NA	750
84	Hr-206-001(2)	Metema	NA	750
85	MT-206-001	Metema	NA	750
86	Acc-203-623	Zimbabwe	NA	NA
87	Localwhite-0034	Somalia	NA	NA
88	Giza-25	Egypt	NA	NA
89	Giza-32	Zimbabwe	NA	NA
90	Acc-203-505	Egypt	NA	NA
91	California-827	USA	NA	NA
92	Margo sel	Israel	NA	NA
93	T-6	India	NA	NA
94	K-60-383	Korea	NA	NA
95	Ying white	China	NA	NA
96	Instituto	Mexico	NA	NA
97	FAO-68-548	Venzuela	NA	NA
98	UCR-82-209	USA	NA	NA
99	Orotall	Israel	NA	NA
100	Etalokornia	Greece	NA	NA

Appendix 2. Mean values of 13 plant characters for 100 sesame genotypes

Trt	DTF	PHt	NP/Pl	NPB	IntL	CapL	DTM	NS/Pod	Yld/Pl	1000SW	OIL%	DTFP	OY/Pl
1	45.33	139.87	75.23	3.40	8.09	2.90	112.00	65.67	12.02	3.58	55.18	28.01	6.60
2	42.67	145.80	53.67	4.33	6.21	2.48	107.33	61.07	7.99	3.44	52.40	37.94	4.19
3	45.33	156.97	45.40	3.17	5.84	2.56	110.00	75.47	7.28	3.17	53.51	52.93	3.86
4	39.00	108.07	37.40	2.77	6.01	2.45	99.33	65.13	4.33	2.95	54.61	20.67	2.36
5	44.00	154.90	54.13	2.93	6.03	2.73	113.67	65.47	8.99	3.12	50.46	31.37	4.51
6	45.67	134.33	36.00	2.17	5.87	2.34	110.67	70.07	3.81	2.50	53.19	34.85	2.03
7	61.67	134.13	26.53	7.07	4.28	2.04	115.67	66.87	2.79	2.54	54.63	43.15	1.52
8	55.33	152.13	42.87	6.17	5.11	2.39	113.33	65.07	6.82	3.34	51.03	30.95	3.48

9	64.00	141.27	40.07	6.60	4.68	2.01	117.00	63.73	2.79	2.33	51.78	42.95	1.43
10	57.33	106.40	41.33	6.27	3.38	1.88	117.67	66.33	2.08	2.57	51.48	48.63	1.07
11	44.00	146.93	52.80	3.43	7.73	2.56	106.33	71.53	7.22	2.69	52.09	29.99	3.72
12	59.00	151.96	30.83	5.33	5.34	2.23	125.33	67.27	3.88	2.75	51.43	45.79	2.02
13	49.67	155.23	32.97	3.10	5.75	2.33	115.00	72.13	3.75	2.43	50.83	29.34	1.92
14	49.33	155.30	31.67	2.63	6.50	2.31	115.00	73.67	3.29	2.16	51.27	23.33	1.69
15	48.67	131.10	26.17	1.90	6.55	2.26	116.33	72.27	2.82	2.19	51.70	19.81	1.46
16	48.00	143.83	32.47	3.00	5.05	2.25	115.33	73.47	3.53	3.05	50.36	29.29	1.78
17	49.00	148.03	40.23	3.23	5.72	2.25	115.00	67.93	3.43	2.12	50.04	23.83	1.70
18	49.67	146.07	30.90	2.50	5.21	2.29	115.67	65.67	3.12	2.16	50.94	23.25	1.58
19	63.67	120.93	25.80	4.23	5.09	2.47	125.67	63.67	2.41	1.99	49.46	25.99	1.15
20	46.33	130.20	46.23	3.47	5.14	2.37	116.33	70.13	5.69	2.45	52.50	22.97	2.96
21	49.33	157.57	43.23	3.83	8.23	2.31	115.67	71.07	4.95	2.30	51.68	26.37	2.55
22	49.33	167.87	47.20	4.10	5.34	2.39	115.00	69.40	4.73	2.17	52.08	33.95	2.46
23	48.00	157.37	45.27	3.10	6.79	2.36	112.33	72.13	4.55	2.26	51.07	27.19	2.33
24	46.67	155.67	40.90	2.43	6.36	2.46	112.33	74.27	5.17	2.45	51.27	27.77	2.65
25	42.00	151.57	52.70	2.37	7.30	2.51	111.00	69.87	8.29	2.90	52.89	21.17	4.38
26	42.67	102.27	23.40	1.63	7.51	2.99	97.00	70.80	1.61	2.43	47.46	14.03	0.76
27	43.00	119.80	29.93	2.17	5.30	2.52	98.33	69.33	3.22	2.40	50.50	16.93	1.62
28	40.33	128.70	56.97	3.00	5.19	2.92	102.00	67.47	10.52	3.73	54.84	22.18	5.76
29	41.33	120.17	34.47	2.23	5.97	2.84	99.33	74.80	4.15	2.73	50.77	14.24	2.11
30	43.33	129.57	34.80	2.73	5.34	2.65	102.00	65.33	4.23	2.84	52.17	18.94	2.22
31	45.67	156.87	59.70	3.40	7.61	2.66	114.00	74.73	7.70	2.63	51.34	28.58	3.98
32	46.00	146.80	46.77	3.10	6.29	2.73	103.00	74.07	8.17	2.39	49.99	21.41	4.02
33	47.00	164.57	44.73	3.70	5.23	2.39	114.00	74.80	4.63	2.26	51.29	33.40	2.39
34	42.00	133.77	32.23	2.43	7.97	2.68	102.67	75.00	4.26	2.71	52.09	21.91	2.23
35	44.00	148.57	48.33	3.03	5.99	2.43	104.00	64.60	7.32	2.90	52.07	26.08	3.87
36	45.33	148.57	36.67	2.60	6.02	2.21	112.67	67.73	4.80	2.54	51.68	27.53	2.46
37	45.67	134.80	43.40	2.77	6.81	2.37	112.00	70.73	4.98	2.59	51.12	21.55	2.52
38	47.67	144.77	39.60	2.73	5.17	2.32	117.00	73.20	3.80	2.19	52.13	28.72	1.97
39	46.00	134.93	32.33	2.27	5.52	2.39	108.33	67.00	2.92	2.36	51.00	27.77	1.48
40	46.33	133.13	47.73	3.27	6.03	2.33	116.00	73.33	7.44	2.60	52.56	22.26	3.88
41	48.33	157.23	41.40	2.83	6.37	2.45	114.00	72.87	4.38	2.20	51.17	27.23	2.24
42	49.67	157.10	39.63	2.83	6.75	2.31	114.67	72.27	4.63	1.93	51.16	32.07	2.38

Appendix 2. cont'd

Trt	DTF	PHt	NP/Pl	NPB	IntL	CapL	DTM	NS/Pod	Yld/Pl	1000SW	OIL%	DTFP	OY/Pl
43	47.67	156.50	42.07	3.20	6.81	2.45	113.33	69.73	5.96	2.40	51.43	29.84	3.05
44	48.00	160.37	33.53	2.57	5.65	2.33	111.00	67.07	3.50	2.02	51.28	24.39	1.79
45	47.00	148.67	34.40	2.87	5.73	2.41	116.00	74.27	3.86	2.18	52.39	25.33	2.02
46	49.00	146.23	42.40	2.87	5.15	2.29	117.33	71.67	3.96	1.99	51.68	28.25	2.06
47	47.67	152.17	40.33	2.63	5.36	2.31	118.33	75.47	4.97	2.31	51.27	25.17	2.52
48	50.00	132.77	25.37	2.33	5.15	2.07	117.67	70.87	3.51	2.16	51.99	30.90	1.84
49	58.00	156.90	40.27	7.27	6.00	2.03	122.67	67.73	4.45	2.79	53.21	51.98	2.36
50	43.33	132.07	55.27	2.70	5.23	2.32	114.33	70.60	6.30	2.59	53.07	27.17	3.35

51	53.33	155.50	39.60	5.30	4.89	2.07	116.67	64.80	4.77	2.54	52.46	45.44	2.53
52	48.33	159.10	43.83	4.17	5.45	2.41	115.67	69.20	7.39	2.96	52.38	31.37	3.87
53	41.67	138.23	43.20	2.93	6.23	2.58	101.00	65.27	6.62	3.28	54.00	27.92	3.57
54	48.33	220.30	42.87	3.40	5.86	2.20	117.67	61.53	6.28	2.93	51.33	35.25	3.24
55	58.00	161.40	28.90	6.67	3.77	1.85	123.33	65.93	4.71	2.71	53.08	59.93	2.50
56	58.33	164.20	35.30	5.13	6.37	2.27	121.33	67.53	4.61	2.86	52.93	44.36	2.45
57	46.33	172.83	80.17	3.10	5.57	2.31	117.67	69.27	7.55	3.10	52.17	28.85	3.92
58	42.67	133.27	31.40	2.30	5.90	2.22	109.33	61.27	4.63	3.19	54.58	24.67	2.53
59	44.00	120.97	33.27	2.93	6.53	2.50	107.00	65.47	5.26	2.81	52.59	25.29	2.76
60	48.67	124.53	36.63	2.77	5.11	2.22	109.67	69.13	4.02	2.81	53.52	26.10	2.16
61	42.33	148.07	53.67	2.97	7.75	2.72	104.00	66.60	8.37	2.84	52.17	25.91	4.37
62	41.67	135.20	46.87	2.53	6.45	2.66	96.33	63.87	6.98	2.74	54.74	16.21	3.83
63	38.67	132.27	37.03	3.07	6.37	2.90	95.33	66.67	5.73	2.79	52.13	25.09	3.00
64	44.33	122.03	28.13	2.03	6.97	3.00	96.33	74.40	2.41	2.52	48.59	18.96	1.17
65	45.67	122.40	18.03	1.77	6.13	2.46	99.00	70.13	1.58	2.41	48.93	21.03	0.77
66	46.33	127.30	29.00	1.97	5.46	2.49	102.33	70.53	2.39	2.55	48.57	25.50	1.16
67	44.33	118.27	31.37	2.23	6.00	2.93	100.00	74.93	4.55	2.73	51.54	16.79	2.36
68	42.67	130.67	53.67	2.33	5.79	2.85	98.67	69.47	2.90	2.29	50.09	17.84	1.44
69	40.00	118.43	36.50	2.00	5.90	2.72	103.00	61.33	6.22	3.30	53.53	19.37	3.30
70	45.00	128.77	59.10	2.53	6.01	2.83	104.00	68.20	9.75	2.79	53.84	16.80	5.24
71	45.00	129.37	27.57	3.10	6.38	2.24	103.33	65.93	3.84	2.71	54.99	27.58	2.11
72	44.33	148.23	45.93	3.27	6.45	3.22	96.67	66.93	6.28	2.85	53.29	32.70	3.35
73	46.33	123.17	26.67	3.10	7.79	2.99	112.00	67.07	2.70	2.63	54.17	25.53	1.47
74	45.67	129.40	40.10	3.17	6.63	2.79	98.33	78.07	3.98	2.27	52.87	23.43	2.13
75	50.33	119.70	18.13	1.77	7.82	3.41	105.33	74.87	1.50	1.81	53.98	18.43	0.81
76	49.00	131.37	24.50	1.83	6.80	3.43	108.00	72.80	1.87	1.89	54.19	20.09	1.01
77	43.67	124.50	33.27	2.57	4.81	2.72	105.33	67.53	4.25	2.56	54.62	27.10	2.35
78	45.00	124.73	30.37	1.97	5.57	2.63	100.67	67.20	3.36	2.52	54.18	19.28	1.83
79	43.00	129.70	31.33	2.33	5.78	2.57	101.33	67.67	4.66	2.92	54.39	26.70	2.52
80	45.33	114.33	39.07	2.43	6.47	2.37	102.67	68.07	4.50	2.80	53.71	19.69	2.41
81	41.00	142.43	56.67	3.13	5.87	2.77	103.33	62.40	7.42	2.92	52.21	27.43	3.88
82	41.00	131.43	49.30	3.40	6.63	2.83	94.67	66.07	7.78	2.95	53.08	22.57	4.12
83	42.67	143.43	44.10	2.97	6.47	3.02	97.67	73.93	8.01	2.95	55.77	22.63	4.46
84	42.67	142.40	43.47	2.60	8.04	2.91	100.00	70.00	7.53	2.97	54.37	24.07	4.09
85	44.00	120.20	30.90	2.00	6.60	2.97	98.00	74.07	1.80	2.20	48.36	19.64	0.87
86	44.67	160.20	53.20	3.40	6.01	2.81	107.67	69.53	7.02	3.08	54.30	33.00	3.82

Appendix 2. cont'd

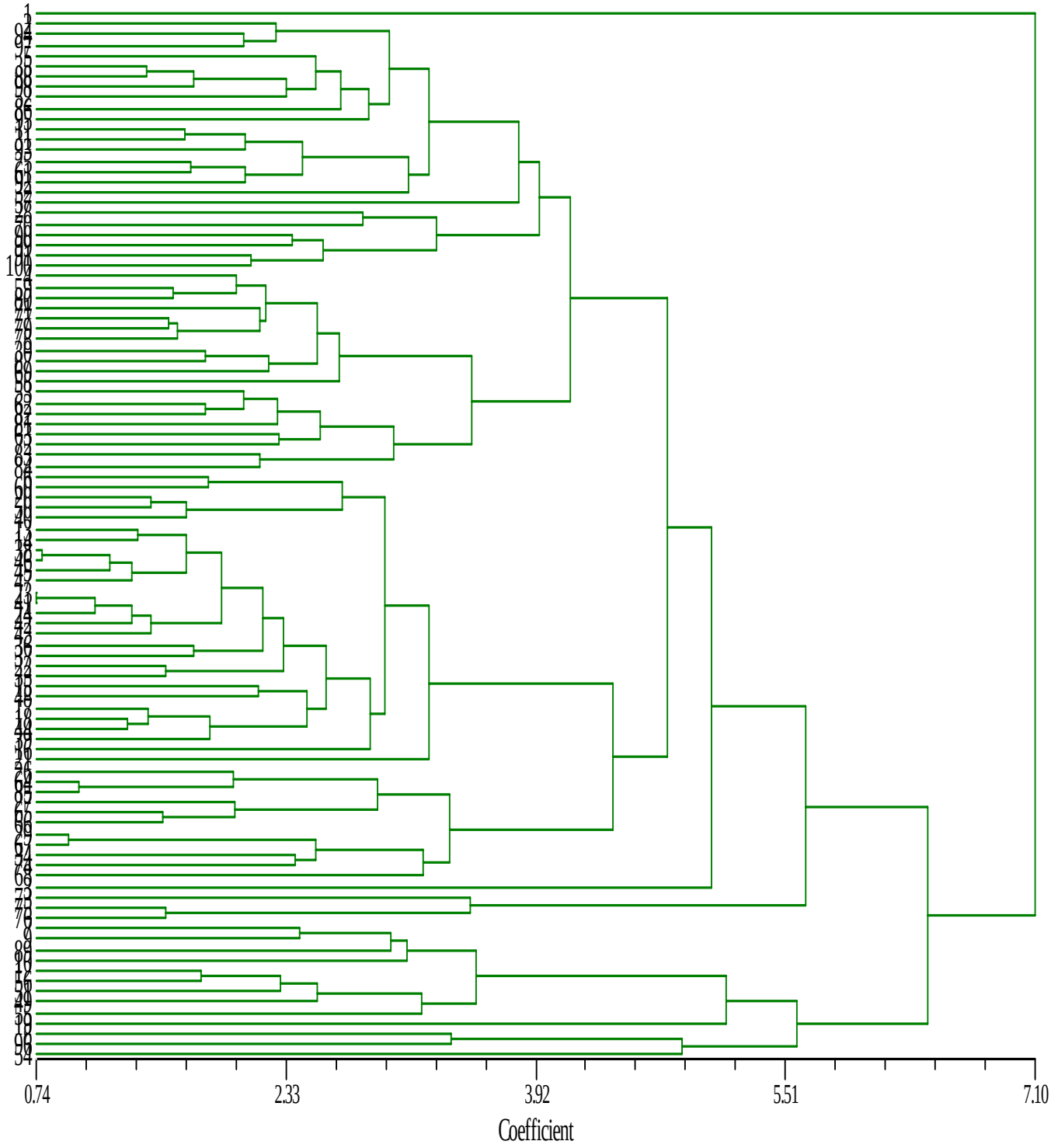
Trt	DTF	PHt	NP/Pl	NPB	IntL	CapL	DTM	NS/Pod	Yld/Pl	1000SW	OIL%	DTFP	OY/Pl
87	38.33	114.20	40.90	2.40	4.92	2.57	101.33	65.27	5.23	2.97	52.99	14.88	2.77
88	44.00	143.27	51.10	2.63	6.22	2.35	111.33	66.93	7.18	3.17	52.00	24.59	3.72
89	56.00	139.00	36.20	5.17	3.35	1.97	124.00	65.20	3.71	2.81	53.61	41.17	1.99
90	45.33	135.37	59.47	2.80	4.83	2.57	105.33	60.33	9.52	3.42	54.53	23.99	5.15
91	45.00	126.13	50.77	3.57	5.76	2.29	110.33	61.73	8.21	3.37	52.96	26.09	4.28
92	41.33	144.93	58.60	3.00	6.57	2.43	106.67	68.33	8.54	3.03	54.59	19.54	4.66
93	47.00	149.47	59.30	3.50	7.01	2.37	111.33	72.27	9.18	3.01	52.60	26.53	4.80
94	45.33	149.60	54.17	3.40	7.67	2.39	110.67	64.87	8.89	3.43	52.88	33.68	4.67

95	45.33	181.53	43.50	3.33	6.25	2.57	108.33	62.40	6.46	3.06	50.88	29.88	3.27
96	47.33	158.57	51.70	4.40	4.92	2.35	115.33	62.40	9.53	3.18	48.77	41.13	4.56
97	44.67	147.53	63.23	3.20	6.13	2.37	114.67	63.13	10.07	3.48	52.71	31.15	5.29
98	48.00	148.63	44.30	2.73	6.23	2.30	115.33	66.20	6.83	3.05	53.30	25.31	3.62
99	41.67	133.30	50.97	2.97	5.03	2.38	100.33	65.40	8.19	3.14	54.98	15.20	4.48
100	47.67	117.30	52.23	3.27	4.54	2.19	111.67	62.53	8.07	3.30	53.43	13.74	4.22
C.V.	**7.74**	**12.01**	**31.81**	**28.20**	**23.11**	**9.60**	**5.62**	**7.29**	**24.76**	**12.30**	**2.67**	**32.58**	**14.76**

- NA= not available

Appendix 3.

Dendrogram of the 100 sesame genotypes using Average Linkage (Between Groups)



* The numbers correspond to the treatment numbers listed under appendix 1.

Declaration

I, the undersigned, declared that this is my original work, has not been presented for a degree in this or any other University, and that all sources of materials used for the thesis have been duly acknowledged.

Name: Sileshi Andualem Mekuriaw

Signature: ----------

Place: Addis Ababa

Date of Submission:

This thesis has been submitted for examination with my approval as University Advisor.

Name: _____

Signature: ----------

Name: _____

Signature: ----------

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