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Broad sense heritability estimation, interrelationship and path coefficient analysis of yield and yield traits in Ethiopian mustard (*Brassica carinata* A. Braun) genotypes

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Abstract

This study was designed to assess genetic variability among randomly selected Ethiopian mustard (*Brassica carinata* A. Braun) genotypes from different agro ecology regions from Ethiopia. The objective of the studies were to estimate broad sense heritability and to determine nature of association of agronomic traits of 36 genotypes that were evaluated at Debre Tabor, Ethiopia. The experiment was laid out in simple lattice design with two replications. Broad sense heritability values for primary branches per plant, number of seeds per pod and 1000-seed weight were found to be low. High heritability was found coupled with high genetic advance for plant height, grain filling period, secondary branches per plant, number of pods per plant, biomass per plot , seed yield and oil yield. Phenotypic and genotypic path coefficient analysis of oil content showed that it is a dependent trait on day to maturity. Selection for day to maturity, therefore, can be very useful for seed yield improvement.

Keywords: Broad sense heritability, Correlation, Direct effect, Ethiopian mustards, Indirect effect, Path coefficient analysis.

Introduction

Ethiopian mustard (*Brassica carinata A. Braun*) is the six economically important species, namely, *Brassica rapa, B. oleracea, B. nigra, B. juncea, B. napus, and B. carinata* (Doweny and Röbbelen, 1989). Studies on the origin of *B. carinata* indicate that it has evolved as a natural cross between *B. nigra* (BB, n=8) and *B. oleracea* (CC, n=9). The elementary species include *B. rapa* (AA, 2n=20), *B. nigra* (BB, 2n=16) and *B. oleracea* (CC, 2n=18). The amphidiploids species include *B. carinata* (BBCC, 2n=34), *B. juncea* (AABB, 2n=36) and *B. napus* (AACC, 2n=38) (UN, 1935).

According to Falconer and Mackay (1996) heritability is the measure of the correspondence between breeding values and phenotypic values. Heritability estimates provide an indication of the expected response to selection in a segregating population. It is one of the main interest to the plant breeders, mainly as a measure of the value of selection for particular characters and as index of transmissibility.

Correlation is helpful in determining the component characters of a complex trait like yield. Such studies are useful in disclosing the magnitude and direction of the relationships between different characters and grain yield as well as characters among themselves (Falconer and Mackay, 1996). Generally, there are three types of correlations; phenotypic, genotypic and environmental correlations. The association between two characters that can be directly observed is the correlation of phenotypic values or phenotypic correlation. Genetic correlation is the association of breeding values (additive genetic variance) of the two characters. In early segregating generations, genetic correlation determines the degree of association between characters and how they would enhance selection.

Path coefficient analysis calculates the correlations between yield and its contributing components, taking account of the cross correlation, either positive or negative. It is useful to partition the total correlation into direct and indirect effects on different components (Tollenaar *et al*., 2004). In agriculture, plant breeders seek assistance in identifying traits that are useful as selection criteria to improve crop yield with help of path analysis. One component is being the path coefficient or standardized partial regression coefficient that measures the direct effect of a predicator variable upon its response variable and

the second component being the indirect effect(s) of a predictor variables. On the other hand, the above results very important to estimate broad sense heritability, and are useful for breeding quantitative traits in the most effective selection strategy to use in Ethiopian mustard breeding program. Breeding methods that use selection based on phenotype are effective when heritability is high for the trait of interest. Therefore, a high heritability would likely result in high response to selection to advance the population in the desired direction of the change. The present study, therefore, to assess genetic variability among randomly selected Ethiopian mustard (*Brassica Carinata A. Braun*) genotypes using agronomic traits. So, in order to assess broad sense heritability estimation, interrelationship and path coefficient analysis of yield and yield related traits within collected genotypes for further breeding works.

Material and Methods

Description of the experimental site: The experiment was conducted at Debre tabor, Ethiopia. The research station is located at 11º 89' N latitude and 39 º 09' E longitudes with an average elevation of about 2630 meter above sea level. The location is found in Amhara National Regional State, South Gondar Administrative Zone. The major portion of the total annual rainfall is received between June and October with an average rainfall of 1235.63 mm per annum. The average minimum and maximum temperature of the experimental plot are 9.71^{0}C and 21.82^{c}C, respectively, with average temperature of 12.11^{0}C. The most dominant soil type of the area is well-drained red brown (Tsige, 2002).

Experimental materials and procedures: A total of thirty six genotypes of Ethiopian mustard were used in the study. The genotypes were collected by Institute of Biodiversity and Conservation (IBC) from diverse agro-ecological areas of northern Ethiopia with an altitude range of 1600- 2700 meter above sea level, representing one of the major mustard production areas in the country. The genotypes and area of collection were described in Table (1).

Table (1): List of genotypes used in the study and their origin

Code	Acc.No.	Area of collection	Altitude (m)	Code	Acc.No.	Area of collection	Altitude (m)	Code	Acc.No.	Area of collection	Altitude (m)
1	PGRC/E 20052	Shewa/AdisAleam	2540	13	PGRC/E208 558	*	*	25	PGRC/E 21001	Shewa/Jibat	2350
2	"20059	Shewa/Chaliya	1630	14	"208559	*	*	26	"21057	Gojjam	*
3	"20068	Shewa/Ambo	2010	15	"208560	*	*	27	"21069	Bale	2450
4	"20080	*	*	16	"208565	*		28	"21162	Bedele	1920
5	"20163	East Tigray	2300	17	"208570	*	*	29	"21163	Wellega/Jima Arjo	1820
6	"20168	Gondar	2400	18	"208571	*	*	30	"21266	Wollo/Borena	2570
7	"20169	*	*	19	"208572	*	*	31	"21278	Welo/Desezuriya	*
8	"208507	*	*	20	"208576	*	*	32	"21369	Jimma	1720
9	"208524	*	*	21	"208584	*	*	33	"213168	Kefa	*
10	"208528	*	*	22	"208585	Shewa/Boset	1600	34	YD		
11	"208545	*	*	23	"208594	Hararghe	1750	35	Holetta-1	Released in 2005	
12	"208551	*	*	24	"208961	E. Wellega	2700	36	Local check	®	2240

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

The experiment was laid as 6 X 6 simple lattice designs using 5m x 1.8 m plots with two replications. Each row 5m long and spacing between plots, rows and replications were 0.6 m, 0.3 m and 2 m, respectively. The rates of fertilizer application was NPK kg/ha. Fertilizer were applied only at sowing and the seed rate was 10 kg/ha. Other cultural practices were followed as recommended for the area (Nigussie and Becker, 2002).

Data collection: The following data were collected from the central four rows.

1. Days to flowering (DF): It was recorded as number of days from planting to a stage when 50% of the plants in a plot produced flower.
2. Days to maturity (DM): The number of days from the date of sowing to a stage when 90% of plants have reached their physiological maturity.
3. Biomass (BM/P): The total above ground biological yield in grams obtained from each plot at

harvest.
4. Harvest index (HI/P): The fraction of dry seed in the above ground biological yield on a plot basis.
5. Thousand Seed weight (TSW): The weight in grams of 500 seeds sampled from each plot and multiplied by two.
6. Seed yield (SY/P): Seed yield per plot was measured in grams after moisture of the seed is adjusted to 7%.
7. Oil content (OC): The proportion of oil in the seed to the total oven dried seed weight as measured by Nuclear Magnetic Resonance Spectrometer (NMRS).
8. Oil yield (OY/P): The amount of oil in grams obtained by multiplying seed yield per plot by corresponding oil percentage.
The data for the following characters were recorded from ten randomly taken plants each experimental plot and the average were considered per plant basis.
1. Primary branches per plant (PB/PL): The average number of primary branches per plant.
2. Secondary branches per plant (SB/PL): The average number of secondary branches formed on primary branches per plant.
3. Number of pods per plant (PD/PL): The average number of pods counted from the same sample plants.
4. Silique (Pod) Length (SL): The main silique from the ten sampled plants were measured in cm and averaged to represent the pod length.
5. Number of seeds per pod (SD/PD): The average number of seeds per pod obtained from two randomly sampled pods of each of the 10 randomly taken plants.
6. Plant height (PH): The height of plants in each plot measured in centimeters from the ground surface to the top of the main stem at maturity.
Statistical Analysis:
Broad sense heritability: Broad sense heritability (H) expressed is as a percentage of the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) and was estimated on genotype mean base as described by (Allard, 1960) as: Heritability (H) = $H = \frac{s^2 g}{s^2 p} X\ 100$ Where: H = heritability in broad sense, $S^2 g$ = Genotypic variance, $S^2 p$ = Phenotypic variance = $S^2 g + S^2 e$ and $\sigma^2 e$ = environmental variance.
Estimation of phenotypic and genotypic correlations: Phenotypic and genotypic correlations between yield and yield related a trait was estimated using the method described by Miller *et al.* (1958).

$$rp_{xy} = \frac{Covp_{xy}}{\sqrt{Vp_x Vp_y}},$$

Where, r_{pxy} = phenotypic correlation coefficient between character x and y, Cov_{pxy} = Phenotypic covariance between character x and y ,Vp_x= Phenotypic variance for character x, Vp_y = Phenotypic variance for character y.

$$rg_{xy} = \frac{Covg_{xy}}{\sqrt{Vg_x Vg_y}},$$

Where, r_{gxy} = Genotypic correlation coefficient between character x and y
Cov_{gxy} = Genotypic covariance between character x and y, Vg_x= Genotypic variance for
character x, Vg_y = Genotypic variance for character y.
Path coefficient analysis: Path coefficient analysis was conducted as suggested by Wright (1921) and worked out by Dewey and Lu (1959) using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effects of yield components on seed yield based on the following relationship.

$$R_{ij} = P_{ij} + \sum r_{ik} P_{kj}$$

Where, Rij = Mutual association between the independent character (i) and dependent character, grain yield (j) as measured by the correlation coefficients. P_{ij} = Components of direct effects of the independent character (i) as measured by the path coefficients and $\sum$ Rik p_{kj} = summation of components of indirect effect of a given independent character (i) On a given dependent character (j) via all other independent characters (k). The contribution of the remaining unknown factor was measured as the residual factor (P_R), which is calculated as:

$$P_R = \sqrt{(1-\sum r_{ij} p_{ij})}$$

The magnitude of P_R indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary, 1999).

Results and Discussion

Heritability estimates: In this study estimate of heritability (in broad sense) values for the 16 characters ranged from 4.34% for primary branches per plant to 83.56% for oil yield per plot. According to Dabholkar's (1992) classification, days to maturity, days to flowering, grain-filling period, number of pods per plant, secondary branches per plant, plant height, biomass per plot, seed yield per plot and hectare, harvest index, oil yield per plot, and oil content exhibited high or very high heritability estimates in Ethiopian mustard. Hence, a good genetic progress can be made if some of

these traits are considered as selection criteria. High heritability estimates were also obtained for days to flowering, plant height and grain yield by Major and Singh (1996).

Estimates of expected genetic advance: Estimates of genetic advance as percent of mean at 5% selection intensity ranged from 2.63 for 1000-seed weight to 79.21 for secondary branches per plant. Moderately genetic advance values were observed for secondary branches per plant, harvest index, number of pods per plant, seed yield per plot and oil yield per plot. In the same way, estimates of genetic advance (as percent of the mean) for days to flowering, days to maturity, grain filling period, plant height, biomass per plot and seed yield per hectare were also considerably high. However, number of seeds per pods, pod length, oil content, and 1000-seed weight per plot and primary branches per plant showed less than 5%. A low GCV and low GAM observed for these characters indicated that the characters were under high environmental influence, and that selection based on these characters would be ineffective. De *et al.* (2000) reported high genetic advance as percent of the mean for plant height. Similarly, high genetic advance as percent of the mean was reported for number of pods per plant (Major and Singh, 1996) and number of seeds per pod (De *et al*., 2000). According to Johnson *et al.* (1955) high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The present study also showed high heritability coupled with high-expected genetic advance as percent of mean for secondary branches per plant harvest index, and seed yield per plot only. Therefore, these characters could be improved more easily than other characters measured in this study.

Table (2): Estimates of mean, range, variance components, and coefficients of variability, heritability and genetic advance of the 16 characters.

Characters	Range	Mean ± *Std.E*	σ2g	σ2e	σ2ph	GCV (%)	PCV (%)	h2b (%)	GA	GAM (%)
DF	51-106	77.8 ± 1.5	90	77.35	167.35	12.19	16.63	53.78	14.35	18.45
MD	134-192	159 ± 1.6	103.69	70.38	174.07	6.4	8.3	59.57	16.21	10.2
GFP	33-129	81.3 ± 2.2	188.3	173.88	362.18	16.87	23.39	51.99	20.41	25.09
PH	116-223	147.9± 2.9	394.92	202.28	597.21	13.44	16.53	66.13	33.34	22.55
PBP	8.0-24	15.4± 0.4	8.64	190.15	198.79	19.12	91.7	4.34	1.26	8.22
BP	4.0-45	20.9 ±1 .3	85.42	27.44	112.86	44.14	50.73	75.69	16.59	79.21
LP	3.0-6	4.4 ± 0.1	0.18	0.66	0.84	9.64	20.82	21.59	0.41	9.27
NPP	58-403	165.4 ± 9.5	4612.45	1913.34	6525.79	41.06	48.84	70.68	117.79	71.21
NSP	6.0-19	12.5 ± 0.3	0.56	6.86	7.42	5.97	21.72	7.55	0.42	3.38
BM (gm)	1.3-7.52	3.7 ± 0.2	0.74	0.81	1.55	23.1	33.43	47.65	1.22	32.86
BMh	2167-12533	6207±254.04	2045837	2246655.6	4292492.5	23.04	33.38	47.66	98.3226	32.82
HI	11286-879.28	339.5 ± 19.4	16614.01	10178.9	26792.91	37.97	48.21	62.01	209.39	61.68
TSW	2.3-6	3.8 ± 0.1	0.04	0.55	0.59	5.33	20.48	6.24	0.1	2.63
SY/P (gm)	940.47-2788.43	1613 ± 44.9	103050.3	43861.2	146911.5	18.64	34.11	70.14	554.65	49.36
SY (Ka/ha)	564.28-2185.74	1123.7 ± 48.3	51832.72	113554.77	165387.49	20.89	25.21	31.34	262.94	16.3
OC	36-46.3	41.8 ± 0.3	3.23	3.9	7.13	4.3	6.39	45.28	2.49	5.97
OY	37.65-118.41	67.7 ± 2.2	128.71	205.57	334.28	21.17	27	83.56	3151.76	46.55

Where: Std.E=standard error, σ^2_g=Genotypic variance, σ^2_{ph}=Phenotypic variance, σ^2_e =Environmental variance, GCV percentage=Genotypic coefficient of variation, PCV percentage=Phenotypic coefficient of variation, ECV percentage=Environmental coefficient of variation, h^2b =heritability in broad sense, GAM=Genetic advance in percent of mean at 5 %, GA=genetic advance.

Correlations of seed yield and yield related traits: In this study, seed yield per plot had positive genotypic associations with biomass per plot (r_g = 0.298), pod length (r_g = 0.149), number of seed per pod (r_g =0.002), oil yield per plot (r_g = 0.319), harvest index per plot (r_g = 0.209), 1000-seed weight (r_g = 0.059) and grain filling period (r_g = 0.037). On the other hand, day to flowering, secondary branches per plant, plant height, number of pod per plant, primary branches plant, oil content and days to maturity were negatively correlated with seed yield per plot. However, at phenotypic level, harvest index per plot oil yield per plot and biomass were observed to have positive and highly significant ($p<0.01$) correlations with seed yield per plot. Seed yield per plot had negative and highly significant genotypic correlation with oil content at both level. The present study is inconsistent with which was reported by Trehan *et al.* (1975) in which oil content had non-significant positive genotypic correlation with seed yield. Hence, it could be suggested as simultaneous improvement of oil and yield of seeds is difficult. Therefore, an independent breeding program has to be formulating for attaining the objective.

At genotypic level, seed yield per plot was positively associated with harvest index (r_g = 0.401) and biomass per plot (r_g =0.298). Similarly, it had positive and highly significant ($p<0.01$) correlations with harvest index per plot (r_{ph} = 0.378), biomass per plot (r_g =0.299) and oil yield per plot (r_g =0.319) at phenotypic level (Table 3). The genotypic correlations of harvest index per plot (r_g = 0.401) and biomass per plot (r_g =0.298) with seed yield per plot were highly significant ($p<0.01$). Oil content (r_{ph} =-0.306) had also significant ($p<0.01$) and negative phenotypic associations with seed yield per plot. Plant height were correlation with seed yield per plot (r_g =-0.198 and r_{ph} = -0.242) negatively significant ($p<0.05$) at both level.

Among the 16 characters studied, only oil content, days to flowering, plant height, number of primary and secondary branch per plant had negative phenotypic association with seed yield per plot. However, at genotypic level number of pods per plant, day to maturity, plant height, days to flowering oil content, primary and secondary branches per plant had negative association with seed yield per plot.

In short, positive and significant association of pairs of characters at phenotypic level, positive and high correlation genotypic level justified the possibility of correlated response to selection. The negative correlations prohibit the combined improvement of those traits in single breeding effort.

Correlation among yield related traits: Harvest index per plot was positively correlated with grain filling period (r_g = 0.292 and r_{ph} = 0.319), secondary branches per plant (r_g = 0.12 and r_{ph} = 0.126), number of pods per plant (rg = 0.118 and r_{ph} = 0.163), seed yield per plot (r_g = 0.298 and r_{ph} = 0.378), seed yield per hectare (r_g = 0.298 and r_{ph} = 0.133) and oil yield per plot (r_g = 0.378). However, its phenotypic and genotypic correlation with days to flowering (r_g = -0.447 and r_{ph} = -0.431), pod length (r_g = -0.061 and r_{ph} = -0.083) , number of seeds per pod (r_g = -0.234 and r_{ph} = -0.238), plant height, (r_g = -0.092 and r_{ph} = -0.11), primary branches per plant (r_g = 0.185 and r_{ph} = 0.179), biomass per plot (r_g =-0.67and r_{ph} = -0.685) and oil content (r_g = -0.025 and r_{ph} =-0.175) was negative and significant except pod length, plant height and oil content at phenotypic level .This implies improvements in these characters will lead to decrease in harvest index (Nigussie and Becker, 2002).

Biomass per plot was positively correlated with days to flowering (r_g = 0.301 and r_{ph} = 0.316), days to maturity (r_g = 0.002 and r_{ph} = 0.02), primary branches per plant (r_g = 0.163 and r_{ph} = 0.163), number of seeds per pod (r_g = 0.319 and r_{ph} =0.318), pod length (r_g = 0.071 and r_{ph} = 0.066) and 1000-seed weight, (r_g = 0.211 and r_{ph} = 0.207), seed yield per plot (r_g = 0.298 and r_{ph} = 0.299), seed yield per hectare (r_g = 0.071 and r_{ph} = 0.14) and oil yield per plot (r_g = 0.118 and r_{ph} = 0.142). On the other hand, it were negatively correlated with such characters as harvest index, oil content, plant height, secondary branch per plant and number of pod per plant at phenotypic and genotypic level. However, day to flowering and number of seeds per pod positively correlated with phenotypic and genotypic level and highly significant ($p<0.01$).

The genotypic correlation between number of pods per plant and number of seeds per pod was highly significant ($p<0.01$ and negative (r_g = -0.286 and r_{ph} =-0.293). Most of the characters had negatively genotypic correlations with number of pods per plant. Similarly , though low in magnitude, oil content (r_{ph} =-0.278), number of seed per pod (r_{ph} = -0.293) and harvest index per plot (r_{ph} = -0.238) showed negative phenotypic correlation with number of pods per plant.

Table (3): Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among 16 characters in 36 Ethiopian mustard genotypes

	DF	MD	GFP	PH	PBP	SBP	LP	NPP	NSP	BM	HI	TSW	SYh	SY	OC	OY
DF		-0.023	-0.705**	-0.094	0.274*	-0.09	0.074	-0.135	0.157	0.301**	-0.447**	0.076	0.041	-0.138	-0.09	0.029
MD	-0.11		0.722*	0.063	-0.193	0.134	-0.26*	0.396	-0.074**	0.002	-0.039	-0.144	0.064	-0.089	-0.079	0.049
GFP	-0.755**	0.733**		0.103	-0.324	0.161	-0.245	0.386	-0.171**	-0.212*	0.292**	0.292	0.029	0.037	-0.002	0.022
PH	-0.074	0.115	0.12		-0.018*	0.212*	-0.171	-0.034	0.06	-0.021	-0.092	0.123	-0.149	-0.198*	0.123	-0.116
PBP	0.28**	-0.208*	-0.326**	-0.018		-0.018	-0.024	-0.014	-0.004	0.163	-0.198*	0.029	0.065	-0.014	-0.032	0.074
SBP	-0.098	0.133	-0.326	0.217	-0.04*		-0.273*	0.098	-0.148	-0.116	0.12	-0.137	-0.086	-0.099	-0.021	-0.084
LP	0.105	-0.224*	-0.23*	-0.19	-0.024	-0.272*		-0.175	0.23*	0.071	-0.061	0.248*	0.06	0.149	0.29**	0.121
NPP	-0.197	0.333**	0.366**	-0.006	-0.014	0.093	-0.145		-0.286**	-0.2*	0.118	-0.062	0.144	-0.033	-0.276**	0.079
NSP	0.162	-0.075	-0.171	0.059	-0.004	-0.148	0.231*	-0.293**		0.319**	-0.234*	0.051	0.071	0.002	0.137	0.118
BM	0.316**	0.02	-0.208*	-0.026	0.163	-0.115	0.066	-0.196	0.318**		-0.67**	0.211*	0.298	0.298**	-0.025	0.133
HI	-0.431*	0.02	0.319**	-0.11	-0.201*	0.126	-0.083	0.163	-0.238*	-0.685**		0.267*	0.209*	0.401**	-0.169	0.152
TSW	0.116	-0.081	-0.141	0.105	0.029	-0.134	0.228*	0.163	0.05	0.207*	-0.302**		0.00	0.059	0.248*	0.055
SYh	0.007	-0.003	0.005	-0.133	0.066	-0.092	0.086	0.105	0.074	0.14	0.241*	0.032		0.392**	0.073	0.975**
SY	-0.086	0.028	0.081	-0.242*	-0.016	-0.094	0.113	0.046	0.00	0.299**	0.378**	0.005	0.47**		-0.284**	0.319**
OC	-0.086	0.028	0.002	0.121	-0.033	-0.02	0.289**	-0.278**	0.137	-0.027	-0.175	0.247*	0.079	-0.306**		0.276**
OY	-0.004	-0.017	0	-0.1	0.075	-0.091	0.148	0.038	0.121	0.142	0.181	0.089	0.974**	0.39**	0.285**	

*, ** = significant at 0.05 and 0.01level of probability DF = Days to flowering, DM = Days to maturity, GFP =Grain filling period, PH = Plant height, PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, LP= Length of pod, NPP = Number of pods per plant, NSP =Number of seeds per pod, BM = Biomass per plot, SY(gm) = Seed yield per plot, SYh = Seed yield per hectare, HI = Harvest index per plot, TSW =Thousand seed weight, OC = Oil content and OY = Oil yield per plot.

Number of seeds per pod were positively correlated with days to flowering (r_g = 0.157and r_{ph} = 0.162), 1000-seed weight (r_g = 0.051 and r_{ph} = 0.163), plant height (r_g = 0.06 and r_{ph} = 0.059), pod length(r_g = 0.23 and r_{ph} = 0.231), seed yield per plot (r_g = 0.002 and r_{ph} = 0.00), seed yield per hectare (r_g = 0.071 and r_{ph} = 0.074), oil content (r_g = 0.137and r_{ph} = 0.137) and oil yield per plot (r_g = 0.118 and r_{ph} = 0.121). However, it was negatively correlated with day to maturity (r_g = -0.074 and r_{ph} = -0.075), grain filling period (r_g = -0.171and r_{ph} = -0.171), primary branches per plant (r_g = -0.004and r_{ph} = -0.004) and secondary branches per plant (r_g = -0.148 and r_{ph} = -0.148) at both genotypic and phenotypic levels. Primary branches per plant was positively correlated with days to flowering (r_g = 0.274 and r_{ph} = 0.28), 1000-seed weight (r_g = 0.029and r_{ph} = 0.029), oil yield per plot (r_g = 0.074 and r_{ph} = 0.074) and seed yield per hectare (r_g = 0.065 and r_{ph} = 0.066). Conversely, primary branches had negative correlation with days to maturity (r_g = -0.193and r_{ph} = -0.208), grain filling period (r_g = -0.324 and r_{ph} = -0.326), plant height (r_g = -0.018 and r_{ph} = -0.018), secondary branches per plant (r_g = -0.018 and r_{ph} = -0.04), pod length (r_g = -0.245 and r_{ph} =-0.024) ,seed yield per plot(r_g = -0.014 6 and r_{ph} = -0.016) and oil content (r_g = -0.032 and r_{ph} = -0.033). Likewise, secondary branches per plant had negative phenotypic and genotypic correlation with day of maturity and plant height. Plant height had positive correlation with oil content (r_g = 0.123 and r_{ph} = 0.121). This implies, tall plants have a propensity to produce more oil (Getinet *et al.*, 1996). Seed yield, pod length, and oil yield per plot are negatively correlated at genotypic and phenotypic levels. Among the characters considered in the present

study, only oil content was positively correlated with oil yield (r_g = 0.276 and r_{ph} =0.285), seed yield per hectare (r_g = 0.073 and r_{ph} = 0.285) at both levels. The correlation between seed yield per plot and oil content was also negative, though significant ($p<0.01$) at genotypic and phenotypic level.

Path coefficient analysis for seed yield per plot: Seed yield per plot is the final product of components of several characters, since the simple correlation coefficients did not give clear information about the interrelationship between the causal and resultant variables; the correlation coefficient estimates were partitioned into direct and indirect effects to establish the intensity of effects of independent variables on dependent one. Path coefficient analysis provides important benefits in Ethiopian mustard breeding studies in the future. This technique is useful in determining the direct influence of one variable on another and separates the correlation coefficient into its components of direct and indirect effects (Rodriguez *et al*., 2001).

Seed yield and oil content were considered as resultant (dependable) variable while the rest of the variables that were positively correlated with the causal (independent) variables. Indirect selection through yield components has been proved more effective (Adefris, 2005).

Genotypic path analysis of seed yield with other characters: Primary branches per plant, secondary branches per plant and days to maturity had exerted positive direct effect on seed yield indicating that, with other variables kept constant, improvement of these characters will increase seed yield per plot. Number of pod per plant exerted favorable but weak direct influences on seed yield. whereas, day to flowering, grain filling period, plant height and oil content had showed negative direct effect on seed yield. Nigussie (1990) reported similar results and Singh *et al.* (1979) for number of pods and primary branches per plant, but opposite results was reported for plant height by and Nigussie (1990). Both authors deduced plant height and number of pods as the most important components contributing to seed yield (Table 4).

Primary branches per plant, secondary branches per plant and days to maturity, which showed positive genotypic correlation with seed yield, had exerted considerable direct effect on seed yield (Table 4). Day to flowering and grain-filling period contributed to seed yield mainly via their highest and positive indirect effect with primary branches per plant. The residual (0.11) indicates that characters, which are included in the genotypic path analysis, explained 89 % of the total variation in seed yield. Singh and Chaudhary (1999) reported that the residual value is small (for instance, nearly zero) the dependent character considered (seed yield) is fully explained by the variability in the independent characters.

Phenotypic path analysis of seed yield with other characters: The phenotypic path coefficient analysis also revealed that day to flowering, grain-filling period exerted high and favorable direct effects on seed yield. Primary branches per plant exerted favorable but weak influences on seed yield, whereas day to maturity, plant height and oil content had some negative influences at phenotypic level. The results of path coefficient analysis showed that, these correlations arose due to their high and favorable indirect effects via grain filling period (Table 5).

The magnitude of residual P_R indicates how best the causal factors account for the variability of the dependent factor (Singh & Chaudhary, 1999). That is, if P_R value is small (for instance, nearly zero) the dependent character considered (seed yield) is fully explained by the variability in the independent characters, whereas higher P_R value indicates that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent character (seed yield). In this study, the residual (P_R) value 0.171 this indicates that seed was fully explained by the variability in the independent characters (Table 5).

Genotypic path analysis of oil content with other characters: Days to maturity, number of pod per plant and primary braches per plant had exerted positive direct effect on oil content at genotypic level. However, day to flowering, grain filling period and seed yield per plot had exerted negative effect on oil content at genotypic level (Table 6).

On the other hand, day to flowering positive indirect effect on oil content *via* grain filling period at genotypic level. The residual (0.16) indicates that characters, which are included in the genotypic path analysis explained 84% of the total variation in oil content. Singh and Chaudhary (1999) reported that the residual value is small (for instance, nearly zero) while the dependent character considered (oil content) is fully explained by the variability in the independent characters.

Table (4): Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level for eight characters on seed yield per plot in Ethiopian mustard genotypes

	DF	DM	GFP	PH	PBP	SBP	NPP	OC	r_g
DF	-0.29	-0.007	0.21	0.003	0.057	-0.01	-0.002	0.046	-0.138
DM	0.032	0.064	-0.204	-0.004	-0.042	0.013	0.003	-0.015	-0.089
GFP	0.219	0.047	-0.278	-0.004	-0.066	-0.032	0.003	-0.001	0.037
PH	0.021	0.007	-0.033	-0.037	-0.004	0.021	-0.001	-0.063	-0.198
PBP	-0.081	-0.013	0.091	0.001	0.202	-0.004	0	0.017	-0.014
SBP	0.028	0.009	0.091	-0.008	-0.008	0.098	0.001	0.01	-0.099
NPP	0.057	0.021	-0.102	0	-0.003	0.009	0.009	0.144	-0.033
OC	0.026	0.002	-0.001	-0.004	-0.007	-0.002	-0.002	-0.52	-0.073

Residual = 0.11, r_g = *genotypic correlation with seed yield.*

Table (5): Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level for eight characters on seed yield/plot in Ethiopian mustard genotypes

	DF	DM	GFP	PH	PBP	SBP	NPP	OC	r_p
DF	0.339	0.014	-0.5661	0.0149	0.0049	0.0067	0.0194	0.0443	-0.086
DM	-0.0078	-0.607	0.5798	-0.01	-0.0035	-0.01	-0.057	0.0254	0.028
GFP	-0.24	-0.44	0.803	-0.0164	-0.006	-0.012	-0.056	0.0006	0.081
PH	-0.0319	-0.038	0.0827	-0.159	-0.0003	-0.0157	0.0049	-0.04	-0.242
PBP	0.093	0.1172	-0.2602	0.0029	0.018	0.003	0.002	0.0103	-0.016
SBP	-0.0305	-0.0813	0.1293	-0.0337	-0.0007	-0.074	-0.0141	0.0067	-0.094
NPP	-0.0458	-0.2404	0.31	0.0054	-0.0003	-0.0073	-0.144	0.0886	0.046
OC	-0.0468	0.0838	-0.0016	-0.0196	-0.0006	0.0016	0.0397	-0.321	-0.306

Residual = 0.171, r_p= *genotypic correlation with seed yield.*

Table (6): Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level for eight characters on oil content in 36 Ethiopian mustard genotypes

	DF	DM	GFP	PH	PBP	SBP	NPP	SY	r_g
DF	-4.113	-0.449	4.406	0.008	0.038	-0.006	-0.035	0.042	-0.09
DM	0.452	4.079	-4.278	-0.013	-0.028	0.009	0.06	-0.014	-0.079
GFP	3.106	2.99	-5.836	-0.014	-0.045	-0.021	0.066	-0.04	-0.002
PH	0.304	0.469	-0.7	-0.113	-0.002	0.014	-0.001	0.119	0.123
PBP	-1.152	-0.848	1.903	0.002	0.137	-0.003	-0.003	0.008	-0.032
SBP	0.403	0.543	1.903	-0.025	-0.005	0.064	0.017	0.046	-0.021
NPP	0.81	1.358	-2.136	0.001	-0.002	0.006	0.18	-0.023	-0.276
SY	0.354	0.114	-0.473	0.027	-0.002	-0.006	0.000	-0.492	-0.284

Residual = 0.16, r_g = *genotypic correlation with oil content*

Table (7): Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level for eight characters on oil content in 36 Ethiopian mustard genotypes

	DF	DM	GFP	PH	PBP	SBP	NPP	SY	r_p
DF	-0.777	-0.0145	0.6141	-0.0036	0.0027	0.0041	0.04037	0.04278	-0.086
DM	0.0179	0.63	-0.6724	0.0024	-0.0021	-0.006	-0.1184	0.1276	0.028
GFP	0.5478	0.4864	-0.871	0.0039	-0.0036	-0.0073	-0.1154	-0.0115	0.002
PH	0.07303	0.0397	-0.0897	0.038	-0.0002	-0.0095	0.0102	0.0614	0.121
PBP	-0.213	-0.122	0.20904	-0.0007	0.011	0.002	0.042	0.0434	-0.033
SBP	0.0699	0.08442	-0.1402	0.0081	-0.0004	-0.045	-0.0293	0.03069	-0.02
NPP	0.1049	0.2495	-0.3362	-0.0013	-0.0015	-0.0044	-0.299	0.01023	-0.278
SY	0.10072	-0.0561	-0.0322	-0.0075	-0.0015	0.0045	0.0099	-0.31	-0.306

Residual = 0.198 , r_p = *genotypic correlation with oil content.*

Phenotypic path analysis of oil content with other characters: Days to maturity, plant height and primary branches/plant had exerted positive direct effect on oil content at phenotypic level. However, day to flowering, grain filling period and seed yield had exerted negative direct on oil content.

Grain filling period showed positive indirect effect on oil content *via* day to maturity at phenotypic level (Table 7). The residual value (0.198) indicates that characters which are included in the genotypic path analysis, explained 80.2% of the total variation in oil content.

Conclusion

Path coefficient analysis provides more effective means of separating direct and indirect factors; permitting a critical examination of the specific forces acting to produce a given correlation and measuring the relative importance of the causal factors. The path coefficient analysis under such situations helps to determine the direct contribution of these characters and their indirect contributions via other characters. Generally, the tested genotypes were highly heritable. The characters showing wide range of broad sense heritability offer opportunities for genetic improvement through selection or selection. The significance of genotype difference indicates the presence of high heritability for each of the characters among the tested entries.

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