ISSN: 2637-7721



Journal of Plant Biology and Crop Research

Open Access | Research Article

Correlation Coefficient and Path Coefficient Analysis for Seed Yield and Yield Related Traits of Rapeseed (*Brassica Napus*) Genotypes

Mohammed Abu*; Birhanu Mengistu

Ethiopian Institute of Agricultural Research, Holeta Agricultural Research Center, P.O.Box, 31, Holeta, Ethiopia.

*Corresponding Author(s): Mohammed Abu

Ethiopian Institute of Agricultural Research, Holeta Agricultural Research Center. P.O.Box, 31, Holeta, Ethiopia. Email: moabu1440@gmail.com

Received: Oct 20, 2023 Accepted: Dec 04, 2023 Published Online: Dec 11, 2023 Journal: Journal of Plant Biology and Crop Research Publisher: MedDocs Publishers LLC Online edition: http://meddocsonline.org/ Copyright: © Abu M (2023). This Article is distributed under the terms of Creative Commons Attribution 4.0 International License

Keywords: Direct effect; Indirect effect; Brassica napus; Interrelationship; Yield components.

Abstract

Background and objective: The study was conducted with twelve rapeseeds (Brassica napus) genotypes to estimate the correlation and path coefficient analysis among eleven quantitative traits and their association with seed yield at 12 locations in 2020/2021 and 2021/2022.

Materials and methods: A randomized complete block design with four replications was used. Data were recorded for eleven quantitative traits based on plot and plant bases. The recorded data were subjected to analysis using a combination of software. Analysis of variance showed significant differences among treatments.

Results: The correlation coefficient analysis revealed that the genotypic correlation coefficient for most of the traits was higher than the phenotypic correlation coefficient indicating that their inter-relationship was largely due to genetic reason. Positive significant phenotypic correlation was observed for seed yield with all traits except days to flowering, thousand seed weight and number of seeds per pod. A Positive significant genotypic correlation was observed for seed yield with days to maturity, oil content, plant height, oil yield and number of seeds per pod indicating that these traits can be used as selection criteria for seed yield improvement in rape seed. Days to flowering, thousand seed weight, number of primary branches, number of secondary branches and number of pods per plant showed negative genotypic correlation with seed yield.

Conclusion: Oil yield exerted the highest positive phenotypic direct effect on seed yield whereas the highest positive genotypic direct effect on seed yield was observed for a number of secondary branches.



Cite this article: Mohammed A, Mengistu B. Correlation Coefficient and Path Coefficient Analysis for Seed Yield and Yield Related traits of Rapeseed (*Brassica napus*) Genotypes. Plant Biol Crop Res. 2023; 6(2): 1093.

Introduction

Rapeseed (Brassica napus,) 2n=38 is one of the most important oil seed crops in the world [1]. It is an amphidiploids believed to be arisen from the inter-specific hybridization between Brassicarapa L (2n=20) and Brassica oleracae L (2n=18). It is across-pollinated crop of the brassicae family widely grown in northern Europe, Canada, and China. Brassica napus is one of the main sources of high quality vegetable oil with a low quantity of saturated fatty acid and medium level of polysaturated fatty acids [2]. It is a good source of oil, protein and also used for biodiesel production being an important source of bio-renewable energy [3]. Several breeding strategies for rapeseed deal with developing new varieties with high seed yield improved oil content and low glucosinolate and erucic acid [4]. Production of rapeseed in Ethiopia is very low compared to its potential. This low production is attributed to disease susceptibility of the varieties (black leg) and lack of improved released varieties.

To improve rape seed crops for seed yield and release better varieties for cultivation; designing and improving the breeding programs is found to be important. Yield is a polygenic trait that is influenced by genetic, environmental and interaction of both [5]. Estimation of the inter relationship between the dependent and independent trait is important for rapeseed breeders to determine the direct and indirect contribution of yield related traits for high yield in rapeseed breeding [6]. Therefore, to improve seed yield study of trait association/ direct and indirect effects of yield components on seed yield provides the basis for a successful breeding program. Various researchers studied the direct and indirect effects of yield components on seed yield to determine selection criteria in rapeseed improvement programs. Understanding the direct and indirect effects of yield-related traits on seed yield is important in plant breeding for the improvement of seed yield. The current study aim was to increase the seed yield of brassica napus knowledge of the interrelationship among various traits of the crop will help us in proper planning of our breeding programme.

Hence this experiment was conducted to estimate the relationship between seed yield and yield-related traits and to determine the extent of their direct and indirect effects on contributing characters to seed yield in the studied rapeseed genotypes.

Table 1: Genotypes used to study the association of traits inRapeseed.

| Genotype name | Genotype code | Status | Source |
|---------------|---------------|--------|--------|
| Dodger Sel.7 | 1 | NVT | HARC |
| Sunder sel-3 | 2 | NVT | HARC |
| Sunder sel-5 | 3 | NVT | HARC |
| Sunder Sel-8 | 4 | NVT | HARC |
| Axana Sel-1 | 5 | NVT | HARC |
| Axana Sel-3 | 6 | NVT | HARC |
| Belinda sel-7 | 7 | NVT | HARC |
| Bulder sel-9 | 8 | NVT | HARC |
| Pura sel-19 | 9 | NVT | HARC |
| Pura sel-25 | 10 | NVT | HARC |
| Axana | 11 | NVT | HARC |
| Swifter | 12 | NVT | HARC |

Materials and Methods

Study area: The study was conducted at multiple locations namely; Holeta, Kulumsa, Bekoji, Adet, Sirinka, and Worabe for two consecutive years using the following genotypes.

Study materials: Twelve rapeseed genotypes obtained from the Holeta agricultural research center were evaluated at multiple locations (**Table 1**).

Experimental procedures and trial management

The data used for the study were generated from 10 field experiments conducted during the 2020/2021 and 2021/2022 main cropping seasons. The experiment was laid out using a randomized complete block design with four replications. The total plot size used was 5.4 m² (6 rows at 30 cm spacing with 3 m row length). All the recommended packages were followed as per national recommendation. Ten plants were selected randomly in each plot for recording the observation on days to flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of pods per plant and number of seeds per pod. Observation on seed yield per hectare and thousand seed weight were computed as standard procedures (measured using digital balance). Oil content was analyzed using a Nuclear Magnetic Resonance Machine (NMRS) instruments (Agilent Technologies[®], Palo Alto, CA, USA) and oil yield was computed from seed yield and oil content.

Statistical analysis

Data analysis was done using SAS software version 9.3 [7]. Correlation coefficients among traits were used for the formation of symmetric correlation matrix. The correlation coefficient was calculated by using the formula suggested by Singh and Chaudhary [8] and Path analysis was done following Dewey and Lu [9] to partition the correlation coefficient into direct and indirect effects using Excel software, 2010.

Results and discussion

Phenotypic and genotypic correlation coefficient analysis

Correlation coefficients were computed among the eleven traits and the result indicated that there are significant associations between the studied characters. Seed yield showed positive and significant phenotypic correlation with days to maturity (0.043*), plant height (0.66**), oil content (0.388*), oil yield per hectare (0.991**), NPBRA (0.071*), NSBRA (0.056*), NPODPL (0.129*) (**Table 2**). Significant negative phenotypic correlation with seed yield was observed for days to flowering (-0.180*) thousand seed weight and number of seeds per pod (**Table2**).

Higher values of the correlation coefficient at the genotypic level show the heritable association of the characters [10]. Significant and strong genotypic correlation coefficients were recorded for seed yield with days to maturity (0.573*), plant height (0.904**), oil content (0.735**), oil yield (0.999**) and NSPPOD (0.759**) (**Table 3**). The significant and positive genotypic correlation indicates that the simultaneous selection of these traits will result in significant seed yield improvement in rapeseed. Significant negative genotypic correlation was observed for NPBRA (-0.932**), NSBRA (-0.241*) and NPODPL (-0.496*) (**Table 3**). This implies that even if those traits were desirable; they may cause yield penalty by consuming more assimilates which could be allocated to seed yield by affecting seed filling percentage. Another significant negative genotypic

| Variable | DF | DM | РН | TSW | YLD | ос | OYLD | NPBRA | NSBRA | NPODPL | NSPPOD |
|----------|--------|--------|--------|--------|---------|--------|--------|--------|--------|--------|--------|
| DF | 1 | 0.599 | -0.393 | 0.000 | -0.180* | 0.384 | -0.117 | -0.206 | -0.183 | 0.164 | 0.266 |
| DM | 0.599 | 1 | -0.209 | -0.029 | 0.043* | 0.552 | 0.118 | -0.141 | -0.082 | 0.525 | -0.268 |
| PH | -0.393 | -0.209 | 1 | -0.046 | 0.660* | 0.326 | 0.662 | 0.103 | 0.043 | 0.021 | -0.070 |
| TSW | 0.000 | -0.029 | -0.046 | 1 | -0.041* | -0.054 | -0.043 | -0.017 | -0.035 | -0.040 | -0.039 |
| YLD | -0.180 | 0.043 | 0.660 | -0.041 | 1 | 0.388 | 0.991 | 0.071 | 0.056 | 0.129 | -0.046 |
| ос | 0.384 | 0.552 | 0.326 | -0.054 | 0.388* | 1 | 0.500 | -0.160 | -0.215 | 0.259 | -0.139 |
| OYLD | -0.117 | 0.118 | 0.662 | -0.043 | 0.991** | 0.500 | 1 | 0.043 | 0.020 | 0.157 | -0.069 |
| NPBRA | -0.206 | -0.141 | 0.103 | -0.017 | 0.071* | -0.160 | 0.043 | 1 | 0.279 | 0.168 | -0.055 |
| NSBRA | -0.183 | -0.082 | 0.043 | -0.035 | 0.056* | -0.215 | 0.020 | 0.279 | 1 | 0.313 | 0.080 |
| NPODPL | 0.164 | 0.525 | 0.021 | -0.040 | 0.129* | 0.259 | 0.157 | 0.168 | 0.313 | 1 | -0.401 |
| NSPPOD | 0.266 | -0.268 | -0.070 | -0.039 | -0.046* | -0.139 | -0.069 | -0.055 | 0.080 | -0.401 | 1 |

Table 2: Phenotypic correlation among eleven quantitative traits in rapeseed genotypes.

Whereas; *: Significant At 0.05; **: Significant At 0.01; DF: Days To Flowering; DM: Days To Maturity; PH: Plant Height (cm); YLD: Seed Yield(kg)/ ha, TSW: Thousand Seed Weight (g); OC: Oil Content (%); OYLD: Oil Yield (kg/ha); NPBRA: Number Of Primary Branch; NSBRA: Number of Secondary Branch; NPODPL: Number of Pod Per Plant; NSPPOD: Number of Seed Per Pod.

| Table 3 | Table 3: Genotypic correlation among eleven quantitative traits in rapeseed genotypes. | | | | | | | | | | |
|----------|--|--------|--------|--------|---------|--------|--------|--------|--------|--------|--------|
| Variable | DF | DM | PH | TSW | YLD | ос | OYLD | NPBRA | NSBRA | NPODPL | NSPPOD |
| DF | 1 | -0.692 | 0.231 | -0.682 | -0.206* | -0.489 | -0.219 | 0.363 | -0.892 | -0.661 | 0.326 |
| DM | -0.692 | 1 | 0.247 | 0.656 | 0.573* | 0.958 | 0.600 | -0.818 | 0.500 | 0.391 | -0.097 |
| РН | 0.231 | 0.247 | 1 | -0.558 | 0.904** | 0.496 | 0.897 | -0.757 | -0.633 | -0.795 | 0.912 |
| TSW | -0.682 | 0.656 | -0.558 | 1 | -0.239* | 0.444 | -0.208 | -0.104 | 0.856 | 0.938 | -0.813 |
| YLD | -0.206 | 0.573 | 0.904 | -0.239 | 1 | 0.735 | 0.999 | -0.932 | -0.241 | -0.496 | 0.759 |

0.735**

0.999**

-0.932**

-0.241*

-0.496*

0.759**

0.444

-0.208

-0.104

0.856

0.938

-0.813

Whereas; *: Significant at 0.05; **: Significant at 0.01; DF: Days to Flowering; DM: Days to Maturity; PH: Plant Height (cm); YLD: Seed Yield (kg/ ha; TSW: Thousand Seed Weight (g); OC: Oil Content (%); OYLD: Oil Yield (Kg/Ha); NPBRA: Number of Primary Branch; NSBRA: Number of Secondary Branch; NPODPL: Number of Pod Per Plant; NSPPOD: Number of Seed Per Pod.

1

0.759

-0.930

0.230

0.127

0.140

0.759

1

-0.945

-0.224

-0.473

0.738

-0.930

-0.945

1

0.016

0.206

-0.488

0.230

-0.224

0.016

1

0.919

-0.712

0.127

-0.473

0.206

0.919

1 -0.923 0.140

0.738

-0.488

-0.712

-0.923

1

correlation of seed yield was observed for days to flowering, this may affect the seed yield by consuming more time for vegetative growth and allocating less time for the seed filling period. Singh *et al* [11]. Reported a negative non-significant correlation of seed yield with a number of primary branches per plant and a positive and significant correlation of seed yield with days to flowering.

Path coefficient analysis

-0.489

-0.219

0.363

-0.892

-0.661

0.326

0.958

0.600

-0.818

0.500

0.391

-0.097

0.496

0.897

-0.757

-0.633

-0.795

0.912

ос

OYLD

NPBRA

NSBRA

NPODPL

NSPPOD

Path coefficient analysis is used in partitioning the correlation coefficient into direct and indirect effects to determine the relative contribution of each component trait to the seed yield. The direct effect refers to the portion of the correlation coefficient contributed by the trait under consideration alone whereas, the indirect effect refers to the portion of the correlation coefficient contributed by a given trait through others due to their interrelationship. Phenotypic and genotypic path coefficient analyses were done to identify the most important traits that influence the end product (seed yield) in rapeseed genotypes. The phenotypic and genotypic direct and indirect effects of different traits on seed yield were presented in **Table 4** and **Table 5** respectively. The highest phenotypic direct effect was recorded by oil yield kg/ha (1.059) followed by NSPPOD (0.009) (**Table 4**). Its negative indirect effects were exerted through days to flowering, thousand seed weight and NSPPOD.

NSBRA exerted the highest positive genotypic direct effect (1.377) on seed yield followed by plant height (1.232). Its negative indirect effect was observed through days to flowering, plant height, oil yield and NSPPOD. The negative indirect effect for plant height was observed through TSW, NPBRA, NPODPL and NSBRA. Another significant genotypic direct effect was recorded by days to flowering (0.684), thousand seed weight (0.444) and oil yield (0.412). The negative indirect effect through days to flowering was recorded for all traits except NSPPOD at the genotypic level. The direct effect of NSBRA (1.337) was greater than its correlation coefficient (0.0682) with seed yield (Table 5) and this is attributed to negative indirect effects through it. Similarly, the direct effects of days to flowering, thousand seed weight and NSBRA were greater than their correlation coefficient. Such higher direct effects also indicate the importance of those traits in influencing seed yield. Pradan et al [12]. Reported the positive direct effect of thousand seed

weights on seed yield. The positive direct effect of days to fifty percent flowering and a number of primary branches on seed yield was reported by [11].

Table 4: Phenotypic Path coefficient analysis of the direct (diagonal) and indirect (off-diagonal) effects of other traits on seed yield in rapeseed genotypes.

| | 1 | 1 | | | | | | | 1 | |
|----------|---------|---------|---------|--------|---------|---------|-----------|---------|---------|---------|
| Variable | DF | DM | PH | TSW | ос | OYLD | NPBRA | NSBRA | NPODPL | NSPPOD |
| DF | -0.0029 | 0.0004 | -0.0016 | 0.0000 | -0.0540 | -0.1238 | -0.0004 | -0.0004 | 0.0002 | 0.0024 |
| DM | -0.0018 | 0.001 | -0.0008 | 0.0001 | -0.0777 | 0.1252 | -0.000296 | -0.0002 | 0.0006 | -0.0025 |
| РН | 0.0012 | -0.0001 | 0.004 | 0.0001 | -0.0459 | 0.7010 | 0.0002 | 0.0001 | 0.0000 | -0.0006 |
| TSW | 0.0000 | 0.0000 | -0.0002 | -0.002 | 0.0077 | -0.0456 | 0.0000 | -0.0001 | 0.0000 | -0.0004 |
| ос | -0.0011 | 0.0004 | 0.0013 | 0.0001 | -0.141 | 0.5298 | -0.0003 | -0.0005 | 0.0003 | -0.0013 |
| OYLD | 0.0003 | 0.0001 | 0.0027 | 0.0001 | -0.0704 | 1.059 | 0.0001 | 0.0000 | 0.0002 | -0.0006 |
| NPBRA | 0.0006 | -0.0001 | 0.0004 | 0.0000 | 0.0225 | 0.0450 | 0.002 | 0.0006 | 0.0002 | -0.0005 |
| NSBRA | 0.0005 | -0.0001 | 0.0002 | 0.0001 | 0.0303 | 0.0214 | 0.0006 | 0.002 | 0.0004 | 0.0007 |
| NPODPL | -0.0005 | 0.0003 | 0.0001 | 0.0001 | -0.0364 | 0.1664 | 0.0004 | 0.0007 | 0.001 | -0.0037 |
| NSPPOD | -0.0008 | -0.0002 | -0.0003 | 0.0001 | 0.0196 | -0.0735 | -0.0001 | 0.0002 | -0.0005 | 0.009 |

Whereas; DF: Days to Flowering; DM: Days to Maturity; PH: Plant Height (Cm); YLD: Seed Yield (Kg)/Ha; TSW: Thousand Seed Weight (G); OC: Oil Content (%); OYLD: Oil Yield (Kg/Ha); NPBRA: Number of Primary Branch; NSBRA: Number of Secondary Branch; NPODPL: Number of Pod per Plant; NSPPOD: Number of Seed Per Pod.

 Table 5: Genotypic Path coefficient analysis of the direct (diagonal) and indirect (off-diagonal) effects of other traits on seed yield in rapeseed genotypes.

| Variable | DF | DM | РН | TSW | ос | OYLD | NPBRA | NSBRA | NPODPL | NSPPOD |
|----------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| DF | 0.684 | 0.8846 | 0.2839 | -0.3028 | 0.1626 | -0.0902 | -0.4612 | -1.2279 | -0.1085 | -0.0312 |
| DM | -0.4737 | -1.278 | 0.3038 | 0.2912 | -0.3183 | 0.2473 | 1.0391 | 0.6881 | 0.0642 | 0.0093 |
| РН | 0.1577 | -0.3152 | 1.232 | -0.2475 | -0.1647 | 0.3697 | 0.9614 | -0.8713 | -0.1305 | -0.0874 |
| TSW | -0.4669 | -0.8385 | -0.6871 | 0.444 | -0.1475 | -0.0859 | 0.1316 | 1.1795 | 0.1540 | 0.0779 |
| ос | -0.3347 | -1.2238 | 0.6105 | 0.1970 | -0.332 | 0.3129 | 1.1820 | 0.3161 | 0.0208 | -0.0134 |
| OYLD | -0.1497 | -0.7663 | 1.1042 | -0.0924 | -0.2522 | 0.412 | 1.2004 | -0.3086 | -0.0776 | -0.0707 |
| NPBRA | 0.2484 | 1.0451 | -0.9320 | -0.0460 | 0.3092 | -0.3896 | -1.271 | 0.0226 | 0.0338 | 0.0467 |
| NSBRA | -0.6101 | -0.6385 | -0.7792 | 0.3800 | -0.0763 | -0.0924 | -0.0208 | 1.377 | 0.1508 | 0.0682 |
| NPODPL | -0.4522 | -0.5002 | -0.9794 | 0.4163 | -0.0422 | -0.1950 | -0.2617 | 1.2655 | 0.164 | 0.0885 |
| NSPPOD | 0.2229 | 0.1239 | 1.1238 | -0.3608 | -0.0466 | 0.3044 | 0.6197 | -0.9804 | -0.1516 | -0.096 |

Whereas; DF: Days to Flowering; DM: Days to Maturity; PH: Plant Height (Cm); YLD: Seed Yield (Kg)/Ha; TSW: Thousand Seed Weight (G); OC: Oil Content (%); OYLD: Oil Yield (Kg/Ha); NPBRA: Number of Primary Branch; NSBRA: Number of Secondary Branch; NPODPL: Number of Pod per Plant; NSPPOD: Number of Seed per Pod.

Conclusion

The study from this experiment reflects that seed yield was positively and significantly correlated with all traits except with days to flowering, thousand seed weight and number of seeds per pod at the phenotypic level. A positive and significant correlation of seed yield at the genotypic level was observed with days to maturity, plant height, oil content, number of seeds per pod and oil yield per hectare. Whereas negative and significance was observed with days to flowering, thousand seed weight, number of primary branches, number of secondary branches and number of pod per plant. The results from path coefficient analysis showed that all traits had a positive phenotypic direct effect on seed yield except days to flowering and thousand seed weight. All traits showed a positive genotypic direct effect on seed yields except days to maturity, number of secondary branches and number of seeds per pod. Hence results can recommend that direct selection of these traits can help to improve seed yields in the genotypes included in this study.

References

- 1. Biabani A, Foroughi A, Karizaki AR., Rassam GA, Hashemi M, et al. Physiological traits, yield, and yield components relationship in winter and spring canola. J. Sci. Food Agric. 2020; 101: 3518–3528.
- E Hasan, HSB Mustafa, T Bibi, M Mahmood. Genetic variability, correlation and path analysis in advanced lines of rapeseed (Brassica napus L.) for yield components. Cercetari Agronomicein Moldova. 2014; 47: 71–79.
- JI Wattoo, AS Khan, Z Ali, M Babar, M Naeem, et al. Study of correlation among yield related traits and path coefficient analysis in rice (Oryza sativa L.). African Journal of Biotechnology. 2010; 9: 7853-7856.
- Shivendra Kumar, Ramdeo Seepaul, Michael J. Mulvaney, Blaire Colvin, et al. Brassica carinata genotypes demonstrate potential as a winter biofuel crop in South East United States, Industrial Crops and Products. 2020; 150: 0926-6690. https://doi. org/10.1016/j.indcrop.

- Khayat M, Rahnama A, Lorzadeh S, Lack S, et al. Physiological indices, phenological characteristics and trait evaluation of canola genotypes response to different planting dates. Proc. Natl. Acad. Sci., India, Sect. B Biol. Sci. 2018; 88: 153–163.
- Adel Abdelrazek Abdelazim Mohdaly, Mohamed Fawzy Ramadan, Characteristics. composition and functional properties of seeds, seed cake and seed oil from different Brassica carinata genotypes, Food Bioscience. 2022; 48: 2212-4292. https://doi. org/10.1016/j.fbio.
- 7. SAS, Statistical Analysis System, Version 9.3. SAS Institute Inc. Cary, NC, USA. 2014.
- Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis. Kalayani Publisher, New Delhi (India) 2940b, 1985.
- D Dewey, K Lu, A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production. Agronomy Journal. 1959; 51: 515.

- Johnson HW, HF Robinson, RI Comstock. Estimates of genetic and environmental variability in soybeans. Agron J. 1995; 47: 314-318.
- Singh VK, Singh D, Singh AK. Genetic divergence for important economic and quality traits in Indian mustard (Brassica juncea L. Czern and Coss), Pantnagar Journal of Research. 2011; 9:183-188
- Pradhan AM, Choudhury MR, Sawarkar A, Das S. Genetic Analysis of Some Genotypes of Indian Mustard (Brassica juncea L.) for Yield and Yield Attributing Traits. Current Journal of Applied Science and Technology. 2021; 51–60.
- 13. Rout S, Kerkhi SA, Chauhan C. Character association and path analysis among yield components in Indian mustard [Brassica juncea (L.) Czern and Coss]. International Journal of Current Microbiology and Applied Science. 2018; 7: 50-55.