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Cluster analysis of morphological and yield attributing trait of *Brassica napus* genotypes

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Abstract: Significant variations were noted in 15 Brassica napus. genotypes in respect of morphological and chemical characters. The analysis of variance showed significant differences for plant height, primary branches, secondary branches, number of seeds in a silique, seed yield of a plant, 1000 seed weight, oil contents, protein contents, oleic acid contents, linolenic acid and erucic acid contents. Cluster analysis grouped the genotypes into five clusters. Cluster 1, 4 and 5 were most diverse while clusters 2 and 3 were least diverse. Cluster centroids showed that silique per plant had maximum and positive value followed by plant height. So, these traits showed high level of diversity and these traits could be used for selection criteria in these genotypes.

Keywords: *Brassica napus,* cluster analysis, oilseed

1.   Introduction

Brassica belongs to Cruciferae family with large number of species. Roots, seeds condiments, stems, leaves and buds are produced by the brassica species. These species may be used as oilseed as well as forage crops. Rapeseed is one of the major oilseed crops after canola and sunflower in oil extraction. It is listed as second number in oil extraction after cotton in Pakistan. Rapeseed (Brassica napus L.), is cultivated for seeds. It has 35-45 % oil which is basically used for edible purpose. Its seeds are used for the extraction of oil by different methods. Plant oils attain the higher value in agricultural commodities. (Naheed *et al*., 2017). It belongs to the family *Brassicaceae* with 375 genera and 3200 species. Domestic needs of edible oil are brought about by 100 species of this genera. (Abideen *et al.*, 2013, Aftab *et al.*, 2020). The production of 0.466 million tons of oil was taken by growing rapeseed on an area of 0.193 million acres. (Anonymous, 2016-2017). The per unit area production of rapeseed is increased from 922 kg/ha to 1406 kg/ha, yet has wide range of potential which is 3500kg/ha (Agricultural statistics of Pakistan, 2018-19). There are many factors which are involved in the low yield per unit area which include non-availability of essential plant nutrients, dearth of well adapted genotypes, use of marginal lands for cultivation, insect and disease prevalence, competition with the

other major Rabi season crops like wheat, chickpea and lentil (Abbas *et al.*, 2020). Therefore, it is very important to adopt strategies for rapeseed crop improvement (Aftab *et al.*, 2020). In general, genetic improvement of crops can be accelerated when broad genetic diversity and the information of these genetic resources are available. At the same time, it is necessary to develop better methods of characterization and evaluation of germplasm collections, to improve strategies for conservation and collection of germplasm and to increase the utilization of plant genetic resources. A successful crop improvement program depends upon the genetic diversity of a crop for achieving the goals of producing high yielding and resistant varieties (Paulose, 1993). Genetic study based on the multivariate analysis is a powerful tool for determining the degree of divergence between populations, the relative contribution of different components to the total divergence and the nature of forces operating at different levels (Sing et al., 2007).

2.   Materials and methods

Present research was conducted at experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. Plant material was collected from Oilseed Research program section, Department of Plant Breeding and Genetics,

University of Agriculture, Faisalabad. Fifteen accessions of *Brassica napus* namely (DGL, Cyclone, Punjab Sarsoon, Zn-R-1, Shiralee, Zn-M-5, Zn-M-6, Zn-M-9, Chakwal Sarsoon, Napus-2, Zm-21, Ah-Rooh, Zn-R-8, Dunkled and Rainbow) were planted and evaluated on morphological basis under field conditions. Randomized complete block design along with three replications was used for uniform placement of experimental units under field conditions. Seeds of *Brassica napus* were sown in field after maintaining 75 cm and 25 cm row to row and plant to plant distance respectively. All the agronomic properties were followed for the trial. Data was recorded of the planted material against following parameters, plant height (cm), primary branches, secondary branches, silique per plant, seed per silique, seed yield (g), 1000 seed weight, oil proportion (%), protein proportion (%), fatty acid content (%)

Statistical Analysis:

The recorded data against various morphological and chemical characters was analyzed by using standard analysis of variance method given by Steel et al. (1997).

3. Results and discussion

The analysis of variance showed significant differences for plant height, primary branches, secondary branches, number of seeds in a silique, seed yield of a plant, 1000 seed weight, oil contents, protein contents, oleic acid contents, linolenic acid and erucic acid contents. All genotypes differed from each other for understudied traits. The cluster analysis was applied to differentiate and group the genotypes on the basis of variation among them for the traits under study (Khodadadi *et al.*, 2011). In this study 15 genotypes were selected and clustering was carried out on the basis of 12 traits i.e. plant height, primary branches, secondary branches, silique per plant, seeds per silique, seed yield, 1000 grain weight, oil contents, protein contents, oleic acid, linolenic acid and erucic acid. The cluster analysis grouped these genotypes into five clusters. A Dendrogram was obtained with this analysis (Figure 1). According to it, cluster 1 contained 2 genotypes i.e. 1 and 9. Six genotypes were grouped in cluster 2 i.e. 2, 8, 6 and 7. Genotypes; 3 and 4 were grouped in cluster 3. The cluster 4 contained three genotypes i.e. 5, 13 and 10. The cluster 5 contained eight genotypes; 8, 35, 23, 61, 9, 12, 66 and 70. The cluster six contained four genotypes; 11, 12, 14 and 15. (Figure 1).

Table 1. Analysis of variance for yield attributing traits

Source of variation	DF	PH	PB	SB	SP	SS	SY	1000 SW
Replication	2	9.18	0.82	6.67	28.3	89.84	0.291	0.01
Treatment	14	5851.38**	2.26*	68.33**	17617.4**	3.75*	152.70*	5.18*
Error	28	18.53	0.75	1.70	33.8	3.68	0.996	0.00
Total	44							

Table 2. Analysis of variance for chemical traits

Source of variation	DF	Oil %	Protein %	OA %	LA %	EA %
Replication	2	8.08	0.60	0.01	0.10	0.13
Treatment	14	19.25**	6.55*	435.17**	14.69**	433.88**
Error	28	2.30	0.30	0.07	0.09	0.46
Total	44					

PH = Plant height   Oil % = Oil proportion
PB = Primary branches   Pro % = Protein proportion
SB = Secondary branches OA % = Oleic acid proportion
SP = Silique in a plant   LA% = Linolenic acid proportion
SS = Seeds in a silique   EA % = Erucic acid proportion
SY = Seed yield   1000 SW = Seed weight

After constructing the Dendrogram, the distance between the clusters displayed difference between them. It was observed that members of cluster 1, cluster 4 and cluster 5 were most diverse clusters and their members had great genetic diversity for the traits

under study. There is also greater distance between cluster 3 and 5 so they are also diverse from each other. Cluster 2 and 3 showed least diversity for the selected traits. It indicated presence of low genetic diversity in both clusters. As we move from cluster

one to six, the similarity index between the clusters increased which indicated presence of some common parents in the genotypes. Genotypes of heterogeneous origin often grouped in the same cluster indicate the presence of partial ancestral relationship between genotypes (Rai *et al*., 2010).

In cluster 1 and 2 and 3, silique per plant indicated maximum value and 1000-seed weight showed minimum effect. The members of same cluster group show very low diversity for most of the evaluated traits. In cluster 4, silique per plant indicated maximum and positive effect. While seed yield showed minimum values in this cluster. In cluster 5, silique per plant indicated maximum and positive effect followed by plant height. Seed weight has minimum value like cluster 1, 2 and 3. Generally silique per plant indicated highest and positive effects in all clusters (Table 3). So, silique per plant showed high level of diversity and this trait could be used for selection criteria in these genotypes.

Table 3. Cluster Centroids for twelve variables

| Variable	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Centroid
PH	188.667	155.944	184.167	243.667	103.750	156.000
PB	5.333	5.000	6.333	4.333	5.250	5.244
SB	9.833	9.278	6.500	14.000	5.250	8.222
SP	212.167	293.556	342.333	350.333	150.917	254.956
SS	11.333	15.056	15.500	8.000	15.167	14.178
SW	3.400	3.865	3.877	5.243	6.536	4.609
Yield	16.467	13.595	20.233	3.740	14.182	14.362
Oil	38.073	39.899	38.433	41.247	35.937	38.493
Protein	26.945	25.270	26.255	25.540	25.009	25.573
Oleic	53.145	50.868	51.208	68.240	36.661	48.587
Linolenic	14.102	10.729	10.142	12.643	10.145	11.072
Erucic	30.633	29.227	26.708	16.543	17.343	25.064
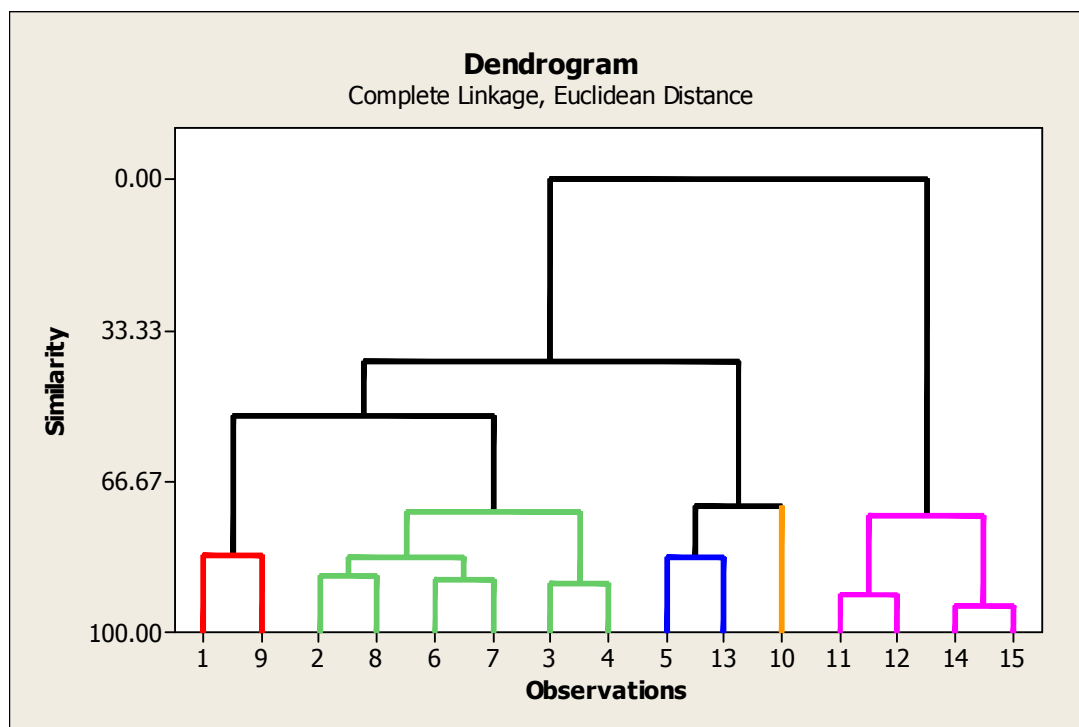
Fig. 1: Dendrogram showing 15 genotypes for 12 yield related traits.

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References
1. Arshad Abbas, Usman Saleem, Sadia Kaukab, Salman Saleem, Aqsa Tahirand Zubair Ahmed. Genetic Evaluation of Maize (*Zea mays* L.) genotypes at seedling stage under moisture stress condition. *Life Sci J* 2020;17(4):65-74.
2. Anonymous. 2016-17. Economic Survey of Pakistan, Ministry of Finance, Economic Advisor Wing, Islamabad.
3. Abideen, S.N.Ul., F. Nadeem and S.A. Abideen. 2013. Genetic Variability and Correlation Studies in *Brassica Napus* L. Genotypes. International Journal of Innovation and Applied Studies. 4(2):574-581.
4. Khodadadi, M., Fotokian, M. H., & Miransari, M. (2011). Genetic diversity of wheat (Triticum aestivum L.) genotypes based on cluster and principal component analyses for breeding strategies. *Australian Journal of Crop Science*, *5*(1), 17.
5. Muhammad Aftab, Rizwana Qamar, Sajida Habib, Momna Mehmood, Muhammad Aslam, Ali Hassan, Amir Bibi, Shamsa Kanwal, Hafiz Saad Bin Mustafa, Shazia Saeed, Ahmad Nawaz Gill. Assessment of Genetic Diversity Among Sunflower Inbred Lines for the Development of Recombinants having Better Achene Yield and Oil Quality. Life Sci J 2020;17(3):28-33.
6. Muhammad Aftab, Samia Fatima, Huma Qamar, Mariam Hassan, Muhammad Zubair, Adnan Arshad, Tariq Mahmood, Sikander Ali, Sundas Shahazad, Muhammad Rizwan Khurshid, Muhammad Kamil Malik, Ahsan Mohyo-Din, Naeem Arshad Maan, Muhammad Ilyas. Study of Morphological Characters Give an Insight into the Genetic Variation Present in Brassica napus L. Germplasm. Life Sci J 2020;17(3):56-61.
7. Naheed. H, R. Uddin, F.Ullah, Q. Sohail and N. Khan. 2017. Genetic Analysis for Yield and Yield Components in Rapeseed. Turkish J. Agri. and Nature. Sci. 4(4): 376–384.
8. Rai, S. K., Rai, G. K., & Singh, A. K. (2010). Hierarchical cluster analysis in exotic introductions of chilli (Capsicum annuum L.). *Environment and Ecology*, *28*(4A), 2423-2425.
9. Singh, P. and S.S Narayanam. 2007. Biometrical techniques in plant breeding. Kalyani publishers, Dehli, India.

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