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The Extent of Intra-Specific Genetic Divergence in *Brassica Napus* L. Population Estimated through Various Agro-Morphological Traits

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Abstract:

To estimate the genetic diversity and association among agro-

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*morphological traits data was recorded on 12 qualitative and 21 quantitative traits among 211 genotypes of Brassica napus L. The recorded data were analyzed through two complementary methods i.e. cluster analysis and principal component analysis. Among the genotypes studied valuable variability was observed for different agronomic and morphological parameters in which the trait of shattering percentage was found to have leading variations (395.4) followed by plant height (200.7), days to 50% flowering (115.2) and day to 100% flowering (93). The greatest and highly significant correlation (0.95**) among all the traits was observed between days to 100% maturity and days to 50% flowering among the genotypes followed by correlation (0.83**) between silique length and silique length and width ratio and correlation of 0.79** between main raceme length and siliquae main raceme^{-1}. Through cluster analysis all the genotypes were divided into five main clusters. It was found that first 3 principal components (PCs) with an eigenvalue of above than 1.0 accounted for 45.94% of the overall differences found among 211 genotypes of Brassica napus L. studied during the present study. The contribution of first three PCs in over all PCs was 26.96%, 10.00% and 8.9%, respectively. Among all studied genotypes three accessions 1697, 26068 and 24854 showed great potential for the traits of seeds per silique, seed yield per plant and 1000-seed weight, respectively. So these accessions are recommended for use in future breeding programs for getting promising results.*

Key words: Cluster analysis; Principal component analysis; Variability; Correlation; Genotypes.

Introduction

Brassica oilseeds are important crops mainly grown for edible oil content, one of the main constituent of daily diet. In Pakistan five major species of rapeseed and mustard i.e., *Brassica napus* L., *Brassica campestris* L., *Brassica carinata* L., *Brassica juncea* L. and *Eruca sativa* are cultivated (Munir and Khan, 1984). Among these, *Brassica napus* L. is considered of

chief importance as its seed consist of 40 to 45% oil, 3.5 percent fats and 0.35 percent phosphorus (Downey and Robbelen, 1989). In addition, *Brassica napus* L. seed contain 18 to 22 percent proteins with important amino acids i.e. cystine, methionine and lysine. It is therefore considered as alternative to cereals which are deficient of these protein units (Rashid *et al*., 2005).

Due to its wide adaptability, around the world breeders have targeted the species for development of new improved cultivars with increased oil content and minimum level of erucic acid and glucosinulates (Anand and Downey, 1981; Chen *et al*., 1988; Brown *et al*., 2000). However, Pakistan still spent 187.1 Rs billion as import bill for edible oil to meet 70% of its local demand (PARC, 2013). Beside a number of other shortcomings, unavailability of improved cultivars with qualitative and quantitative value addition is the primary reason of this inadequacy (Khatri *et al*, 2005).

The existence of genetic diversity in any crop germplasm has vital role to play in the development of improved varieties for better yield and other desirable attributes like shorter life cycle, enhanced nutrition, resistance against biotic and abiotic stresses, high adaptability and many more. It is the base of crop improvement, in the absence of which goals of nutritional and food security is distant to achieve. Nonetheless, it should also be systematically examined evaluated and recorded as a pre-requisite for cultivar's development as well as for the future utilization by breeders (Todorrovska *et al.,* 2003). But during continuous selection process for better quality and productivity the gene pool of the selected final varieties has narrowed down due to elimination of genes for undesirable traits. For example in the process of selection for reduced amount of erucic acid and glucosinolates in oilseed of *Brassica napus* L other associated important alleles may be lost due to genetic drift and subsequent degradation of genetic diversity (Cowling, 2007; Ananga *et al*., 2008).

Among other factors habitat and ecosystem is considered the most important source of variation in species' genetic structure. Geographic distribution variation is considered to be strongly associated with ecologically motivated variability and consequently mentioned as "ecogeographic factors" (Rao and Hodgkin, 2002). Khan and Khan (2003) have suggested the collection of *Brassica* germplasm with diverse ecogeoraphical origin from within or outside the country to widen the base of available gene pool for selection. In that respect, worldwide efforts are being made to explore, evaluate and conserve the plant genetic resources and broaden the base of existing genetic stocks as a strategy to overcome risks posed by various diseases, rapidly changing climatic and environmental conditions and most importantly to meet the growing consumption demand (Rao and Hodgkin, 2002).

The present study was carried out to 1) Estimate extent of the genetic variation in terms of agro-morphological divergence among *Brassica napus* L. genotypes from Asian and European origin. 2) Evaluate performance of exotic *B. napus* accessions under Pakistani agro-climatic conditions and screening of superior genotypes. 3) Intra and inter-population variation and interrelatedness of genotypes from eco-geographically diverse background.

Materials and Methods

A total of 211 accessions (**Table 1**), from Pakistan (92), China (56), Sweden (3), Netherland (2), Germany (2) USA (1) and unknown (55) origin, preserved in the gene-bank of PGRI (Plant Genetic Resource Institute), National Agricultural Research Center (NARC), Islamabad-Pakistan (33° 33' N and 73° 06'E) were evaluated in the field of institute during the year 2012-2013. Pre-planting irrigation was carried out to prepare beds with adequate soil moisture while irrigation was withheld

during cropping period. In augmented field design each accession's seed was planted at a depth of 3-4 cm using hand drill, in a single line of 2 meter length with 75 cm line-to-line spacing. Recommended agronomic practices were carried out to maintain proper vigor and health of the plants. However no weedicides and pesticides were used to ensure the natural organic performance of the germplasm. The crop was harvested when more than 75% of plants turned yellowish in color and moisture content of the pod was reduced. For all the accessions, 5 randomly plants were tagged and evaluated for 33 morphological characters including 21 quantitative traits i.e. days to 50% flowering, days to 100% flowering, days to 50% maturity, days to 100% maturity, plant height (cm), primary branches plant$^{-1,}$ Leaves plant$^{-1,}$ main raceme length (cm), siliquae main raceme^{-1}, silique length (mm), silique width (mm), silique length and width ratio, seeds silique^{-1},seed yield plant^{-1}, 1000-seed weight, leaf length (cm), leaf width (cm), leaf length and width ratio, beak length (mm), stem thickness (mm) and shattering percentage and 12 qualitative traits i.e. emergence, leaf shape, leaf margins, leaf colour, flower colour, silique colour, seed colour, beak shape, stem shape, corolla shape, branching system, pedicel angle and length. The International Board for Plant Genetic Resources descriptors for *Brassica* and *Raphnus* (IBPGR, 1990) were used for selection and measurement of the traits.

Table1: Genotypes used during present study

S.No.	Country / region of origin	Number of accessions
1.	Pakistan	92
2.	China	56
3.	Unknown	55
4.	Sweden	3

5.	Netherlands	2
6.	Germany	2
7.	USA	1
Total		211

Data Analysis

All the recorded data were averaged and means of all the accessions were analyzed for simple statistics (mean, standard deviation and variance among the accessions), coefficient of variation and frequency distribution of all the genotypes for different parameters. Similarly the correlation coefficient in all pairs of parameters was deliberated to Steel and Torrie (1980) procedure by means of plot mean values. Histograms viewing the frequency distribution and range for different characters were organized to reveal genetic differences among all the accessions. All the recorded agronomic parameters were also examined by arithmetical taxonomic techniques through the 2 complementary procedures which are (1) cluster and (2) principle component analysis (Sneath and Sokal, 1973). Avoiding scaling differences effects the means of all the parameters were standardized through Z-scores before the cluster and PCA (principal component analysis). For the total pairs of genotypes estimates of Euclidean distances coefficient were made. The resultant Euclidean difference coefficient matrices were utilized to assess the associations between the *Brassica napus* L. accessions with cluster analysis (Statistica, Version 6.0). Principal component analysis (PCA) was also carried out with the similar data matrix. Scatter plots of initial three PCAs were formed to give a graphical image of pattern of differences among all the genotypes (Statistica, Version 6.0).

Results and Discussions

For all agro-morphological parameters common statistical data inferences i.e. coefficient of variation, range, variance and mean were noted during the present study (**Table 2**). Highest variance was found for shattering percentage and plant height followed by days to 50% flowering, days to 100% flowering, siliquae main raceme^{-1}, silique length, main raceme length, days to 100% maturity, days to 50% maturity, leaf length, beak length which were 395.4, 200.7, 115.2, 93, 69, 66, 49.3, 48.6, 42.6, 41.7, and 36.6, respectively. Comparatively low variations were found for the rest of traits. The results obtained from this study are in close agreement with that of Zada *et al*., (2013), who evaluated *Brassica carinata* L. germplasm and found high variability for the traits of plant height, main raceme length and siliquae on main raceme. Also Shinwari *et al*., (2013) and Abideen *et al.,* (2013) in their studies recorded highly significant variations among genotypes for the traits of silique length, main raceme length, siliquae on main raceme length, plant height, leaf length, days to flower completions (days to 100% flowering) and days to 50% flowering in *Eruca sativa* L.and *Brassica napus* L, respectively. Besides, Ali *et al*., (2003) and Nasim *et al.,* (2013) have observed highest degree of variability in the above mentioned traits in *Brassica napus* L populations which supported our findings with similar outcome.

Correlation analysis revealed highly significant positive association between DF 50% and traits like Days to flowering, Days to maturity, Plant height and leaves per plant (**Table 3**). Previous study by Nasim *et al*., (2013) also observed highly significant positive association between days to half flowering (days to 50% flowering) and days to full flowering (days to 100% flowering). Moreover, similar trend was reported by Alemayehu and Becker (2002) in the study of Ethiopian mustard germplasm as they found strong association between traits i.e. flower initiation, flower completion and days to maturity. Zare

(2011) in his study of morphological characterization in *Brassica napus* population reported highly significant strong correlation between flowering duration, plant height and days to physiological maturity which were in complete congruence with our findings. We found strong and positive association between raceme length and number of siliqua on main raceme which was also confirmed by previous studies in *Brassica napus* (Nasim *et al.,* (2013) and Indian mustard genotypes (Rabbani *et al*., 1999). Likewise, Seeds per silique, silique length and seed yield per plant were also found strongly correlated with each other in our analysis which corroborated with findings of , Rameeh (2011), Nasim *et al.,* (2013) and Khan *et al*., (2006) in *Brassica napus*.

In a UPGMA based dendrogram for agronomic traits, all the 211 accessions were distributed into 5 main clusters (**Figure 1**). Cluster I comprised of 14 early in maturing genotypes with medium height and highest number of primary branches per plant. Accession, 24864 was a lone member of Cluster II primarily due to its peculiar attributes i.e. higher number of leaves with smallest size, short height, maximum number of primary branches per plant, maximum number of siliquae on main raceme, highest number of seeds per silique, maximum 1000-seed weight, and highly resistant to shattering at harvest. Majority of the accessions (191) were distributed in Cluster III which were found as late maturing plants with larger leaves, greater number of leaves per plant, lower number of primary branches per plant, lower number of siliquae on main raceme, greater number of seeds per silique, medium in 1000-seed weight and lower seed yield. Cluster-IV included 4 late maturing tallest and shattering resistant genotypes, with broad leaves, and small sized grains but higher seed yield. Average performing genotype, 24860 was distinctly distributed in the cluster and considered as cluster V (**Table 4**). The standard deviation and mean for these clusters was calculated

and given in **Table 5**.

The division of studied *Brassica napus* L. genotypes into different groups was not because of its origination from different regions of the country and the world. But it was just because of their differences at agro-morphological levels. The result obtained during the present study of *Brassica napus* L. genotypes were given support by the findings of Zada *et al.,* (2013) in genotypes of *Brassica carinata* L., Shinwari *et al*., (2013) in genotypes of *Eruca sativa* L. and Amurrio *et al.,* (1995) through qualitative and quantitative traits of Iberian pea genotypes.

Principal Component Analysis

Principal component analysis, based on 21 quantitative agro-morphological parameters determined 3 PCs with Eigen value greater than unity (**Table 6**). Collectively these three PC accounted for 45.94% of the overall differences found among 211 genotypes of *Brassica napus* L. the first principal component (PC1) was found to have 26.96% variation in the population which were mainly due to traits i.e. leaf length and width ratio (0.232), primary branches per plant (0.710) and upto lesser extent, silique width and 1000-seed weight. On the other hand days to 50% flowering (-0.809), days to 100% flowering (-0.566), days to 50% maturity (-0.856), days to 100% maturity (-0.856), plant height (-0. 416), and shattering percentage (-0. 631) were found to have negative weights on first principal component. The PC2 accounted for 10.00% variation among germplasm as variables e.g. days to 50% flowering (0. 114), days to 50% maturity (0. 209), days to 100% maturity (0. 162), leaf length (0. 196), leaf length and width ratio (0. 157), leaves per plant (0. 270), plant height (0. 181), primary branches per plant (0. 104), silique width (0. 241), stem thickness (0. 133), seed yield per plant (0. 133) and shattering

percentage (0. 138) contributed positively. On the contrary, main raceme length (-0. 428), siliquae on main raceme (-0. 387), silique length (-0. 731), silique length and width ratio (-0. 755), beak length (-0. 396) and seeds per silique (-0. 356) were found to have negative load on PC2. The contribution of PC3 viz-a-viz overall variability was 8.9% which was primarily due to positive contribution of different traits i.e. leaf length (0. 169), leaf length and width ratio (0. 197), leaves per plant (0. 184), plant height (0. 165), main raceme length (0. 740), siliquae on main raceme (0. 777), silique width (0. 427), stem thickness (0. 159) and shattering percentage (0. 124). On the other hand days to flowering 50% (-0. 199), days to 100% flowering (-0. 293), days to 50% maturity (-0. 104), silique length (-0. 163), silique length and width ratio (-0. 385) and 1000-seed weight (-0. 255) contributed negatively in PC3. Like cluster analysis principal component analysis also made different groups of *Brassica napus* L. studied genotypes on the basis of agro-morphological similarities. The contribution and scatter diagram are given in **Figures**, **2, 3, 4, 5, 6,** and **7**, respectively. During this study it was found that the scattering and accumulation to the one point through PCA was beyond its origination from the different and same geographical regions. The present study is in close agreement with that of Zada *et al*., (2013), Yousuf *et al*., (2011) and Alamayeha & Becker (2002).

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Traits	**Mean**	**Minimum**	**Maximum**	**SD***	**CV (%) ****	**Variance**
DF 50%	105.4	73.0	143.0	10.7	10.2	115.2
DF 100%	120.3	78.0	155.0	9.6	8.0	93.0
DM 50%	159.2	151.0	188.0	6.5	4.1	42.6
DM100%	169.4	155.0	196.0	7.0	4.1	48.6
L L (cm)	22.0	11.9	58.5	6.5	29.3	41.7
L W (cm)	9.4	3.4	47.5	5.0	53.0	25.0
LL / LW (cm)	2.6	0.6	8.4	0.9	33.9	0.8
L/ P	16.2	9.4	25.4	3.1	19.1	9.5
PH (cm)	166.5	105.0	200.4	14.2	8.5	200.7
PB/P	11.2	5.8	18.6	2.8	24.6	7.6
MRL (cm)	64.5	46.3	81.0	7.0	10.9	49.3
S/MR	65.8	40.2	85.4	8.3	12.7	69.3
SL (mm)	53.5	29.6	85.4	8.1	15.2	66.3
SW (mm)	3.9	3.0	6.7	0.5	11.7	0.2
SL/ SW (mm)	13.8	7.0	23.9	2.6	18.5	6.5
BL (mm)	13.5	7.0	92.6	6.1	45.0	36.7
ST (mm)	18.5	12.1	68.4	4.8	25.8	22.8
S/S	19.1	10.2	28.6	3.7	19.6	14.1
TSW (grams)	3.1	1.0	5.9	0.8	26.6	0.7
SY/P	7.5	2.2	21.2	3.4	45.1	11.5
ST %	68.4	15.0	95.0	19.9	29.1	395.4

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Table 2: Basic statistics of different traits of the studied genotypes.

Table 3: Correlation among the traits for the studied genotypes of *Brassica napus* L.

Traits	DF50%	DF100%	DM50%	DM100%	LL	LW	LL/LW	L/P	PH	PB/P	MRL	S/MR	SL	SW	SL/SW	BL	ST	S/S	TSW	SY/P	ST%
DF50%	1.00																				
DF100%	0.72**	1.00																			
DM50%	0.75**	0.49**	1.00																		
DM100%	0.72**	0.43**	0.95**	1.00																	
LL	0.36**	0.24**	0.48**	0.48**	1.00																
LW	0.35**	0.20*	0.33**	0.36**	0.46**	1.00															
LL/LW	-0.19*	-0.15	-0.11	-0.10	0.26**	-0.51**	1.00														
L/P	0.52**	0.30**	0.58**	0.56**	0.48**	0.37**	-0.18*	1.00													
PH	0.24**	0.22**	0.23**	0.22**	0.31**	0.25**	-0.16*	0.43**	1.00												
PB/P	-0.53**	-0.27**	-0.54**	-0.56**	-0.44**	-0.43**	0.17*	-0.32**	-0.24**	1.00											
MRL	0.07	-0.02	0.02	0.06	0.07	0.08	-0.04	0.09	0.09	-0.18*	1.00										
S/MR	0.03	-0.02	0.06	0.13	0.12	0.08	-0.02	0.22**	0.11	-0.12	0.79**	1.00									
SL	0.23**	0.23**	0.21**	0.25**	0.16*	0.15	-0.09	0.04	0.03	-0.34**	0.16*	0.17*	1.00								
SW	-0.11	-0.06	-0.07	-0.01	0.05	-0.06	0.18*	-0.06	0.00	0.09	0.04	0.09	0.04	1.00							
SL/SW	0.27**	0.22**	0.23**	0.23**	0.12	0.16*	-0.16*	0.05	0.03	-0.35**	0.11	0.08	0.83**	-0.50**	1.00						
BL	0.00	0.00	-0.01	0.01	-0.01	0.00	-0.01	0.01	-0.09	0.00	0.10	0.13	0.18*	0.00	0.15	1.00					
ST	0.33**	0.17*	0.35**	0.33**	0.36**	0.24**	-0.10	0.52**	0.33**	-0.30**	0.12	0.11	0.12	-0.01	0.10	-0.01	1.00				
S/S	0.17*	0.16*	0.17*	0.21**	0.16*	0.11	-0.06	0.14	0.11	-0.16*	0.07	0.09	0.41**	0.13	0.29**	0.17*	0.11	1.00			
TSW	-0.04	0.03	-0.05	-0.02	0.02	0.00	0.03	-0.05	-0.02	0.06	-0.13	-0.10	0.04	-0.06	0.05	0.04	0.05	0.00	1.00		
SY/P	0.29**	0.21**	0.34**	0.34**	0.14	0.05	0.00	0.18*	0.07	-0.12	0.06	0.04	0.06	0.10	0.00	0.00	0.06	0.20**	0.04	1.00	
ST%	0.39**	0.14	0.56**	0.58**	0.39**	0.30**	-0.05	0.41**	0.17*	-0.53**	0.11	0.12	0.15	0.01	0.13	-0.10	0.24**	0.21**	-0.13	0.20**	1.00

Table 4: Different grouping of genotypes on the basis of divergence in their genetics and environment.

Clusters	No. of genotypes	Genotypes
I	**14**	1323, 1672, 1684, 1687, 1694, 1707, 1708, 1721, 16105, KP Raya, 24237, 24892, 24861, 24867.
II	**1**	24864
III	**191**	1691, 1693, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1705, 1706, 1720, 16104, 22851, 22853, 22855, 22856, 22858, 23632, 23633, 23698, 24169, 24170, 24210, 24211, 24212, 24213, 24214, 24215, 24216, 24217, 24218, 24219, 24220, 24221, 24222, 24223, 24224, 24229, 24230, 24231, 24232, 24233, 24234, 24235, 24236, 24238, 24239, 24240, 24241, 24242, 24243, 24244, 24245, 24246, 24247, 24248, 24249, 24250, 24251, 24252, 24253, 24254, 24255, 24256, 24257, 24258, 24259, 24842, 24843, 24844, 24845, 24846, 24847, 24848, 24849, 24850, 24851, 24852, 24853, 24854, 24855, 24856, 24857, 24858, 24859, 24862, 24863, 24865, 24866, 24868, 24869, 24870, 24871, 24872, 24873, 24874, 24875, 24876, 24877, 24878, 24879, 24880, 24881, 24882, 24883, 24884, 24885, 24886, 24887, 24888, 24889, 24890, 24891, 24893, 24894, 24895, 24896, 24897, 24898, 24899, 24900, 24901, 24902, 24903, 24904, 24905, 24906, 24907, 24908, 24909, 26317, 26318, 26319, 27380, 27381, 27382, 27383, 27384, 27385, 27386, 27387, 27388, 27389, 27390, 27391, 27392, 27393, 27394, 27395, 27396, 27397, 27398, 27399, 27400, 27401, 27402, 27403, 27404, 27405, 27406, 27407, 27408, 27410, 27411, 27412, 27413, 27414, 27415, 27416, 27418, 27419, 27420, 27421, 27422, 27423, 27424, 27425, 27426, 27428, 27429, 27430, 27431, 27432, 27898, 27899, 27900, 27901, 27902, 27903.
IV	**4**	26067, 26068, 26217, 26218
V	**1**	24860

Table 5: Standard deviation and mean of genotypes included in different clusters.

Traits	Cluster-I (13Accessions + 1 Check)	Cluster – II (1 Accession)	Cluster -III (191 Accessions)	Cluster -IV (4 Accessions)	Cluster -V (1 Accession)
DF 50%	94.65 ± 11.46	107	105.42 ± 9.07	143 ± 0	97
DF 100%	110.62 ± 12.62	120	120.36 ± 7.66	155 ± 0	111
DM 50%	153.51 ± 3.24	157	159.07±5.09	188 ± 0	152
DM100%	160.28 ± 5.66	167	169.54 ± 5.49	196 ± 0	162
L L (cm)	24.03 ± 14.93	15.80	22.69 ± 6.38	32.43 ± 0.98	21.10
L W (cm)	6.87 ± 1.89	6.00	9.56 ± 5.10	13.95 ± 1.77	8.40
LL / LW (cm)	3.58 ± 1.99	2.60	2.49 ± 0.89	2.35 ± 0.32	2.50
L/ P	15.28 ± 1.99	16.00	16.09 ± 3.00	22.95 ± 1.33	14.40
PH (cm)	164.47 ± 20.61	139.40	166.62 ± 13.56	175.60 ± 1.39	168.60
PB/P	13.64 ± 1.86	13.20	11.05 ± 2.65	8.40 ± 4.67	12.60
MRL (cm)	59.03 ± 7.58	65.90	64.83 ± 6.87	68.27 ± 0.48	69.10
S/MR	56.33 ± 8.09	67.80	66.33 ± 7.96	71.05 ± 2.76	67.40
SL (mm)	39.30 ± 7.53	52.40	54.54 ± 7.23	53.12 ± 6.07	50.70
SW (mm)	3.88 ± 0.95	3.60	3.93± 0.46	3.75 ± 0.12	4.00
SL/ SW (mm)	10.28 ± 1.42	14.60	14.04 ± 2.50	14.16 ± 1.55	12.80
BL (mm)	10.41 ± 3.06	92.60	13.33 ± 2.45	10.80 ± 1.82	11.50
ST (mm)	17.03 ± 3.25	16.80	18.53 ± 4.85	23.27 ± 1.55	18.00
S/S	15.07 ± 4.12	22.20	19.38 ± 3.56	18.30 ± 3.60	17.60
TSW (grams)	2.98 ± 1.07	3.90	3.13 ± 0.83	2.65 ± 0.69	4.30
SY/P	6.65 ± 2.82	9.60	7.37 ± 3.19	16.17 ± 4.11	9.80
ST %	55.63 ± 13.40	30	69 ± 19.87	90 ± 0	70

Table 6: Showing the share of the first three PCAs in the total divergence.

Traits	**PC1**	**PC2**	**PC3**
Eigenvalue	5.66	2.10	1.89
Comulative Eigenvalue	5.66	7.76	9.65
Percent Variance	26.96	10.00	8.98
Comulative Variance	26.96	36.96	45.94
DF 50%	-0.809	0.114	-0.199
DF 100%	-0.566	0.050	-0.293
DM 50%	-0.856	0.209	-0.104
DM100%	-0.857	0.162	-0.045
L L (cm)	-0.622	0.196	0.169
L W (cm)	-0.555	0.016	-0.025
LL / LW (cm)	0.232	0.157	0.197
L/ P	-0.697	0.270	0.184
PH (cm)	-0.416	0.181	0.165
PB/P	0.710	0.104	0.018
MRL (cm)	-0.190	-0.428	0.740
S/MR	-0.216	-0.387	0.777
SL (mm)	-0.410	-0.731	-0.163
SW (mm)	0.089	0.241	0.427
SL/ SW (mm)	-0.406	-0.755	-0.385
BL (mm)	-0.030	-0.396	0.056
ST (mm)	-0.511	0.133	0.159
S/S	-0.332	-0.356	-0.003
TSW (grams)	0.041	-0.024	-0.255
SY/P	-0.333	0.133	0.023
ST %	-0.631	0.138	0.124

Table 7: The promising genotypes identified during the present study.

Trait	Range	Accessions identified during the present study
DM 100%	< 160	001323, 001672, 001691, 1693, 1694, 1708, 1721, 16105.
PH (cm)	≥ 190	001687, 1694, 24217, 24848, 27387, 27388, 27390, 27391, 27393, 27394.
PB/P (No.)	>16	001687, 1694, 24215, 24231, 24232, 24240, 24859.
MRL(cm)	>75	1700, 1701, 22851, 24850, 24851, 24852, 24853, 24903, 27412, 27416, 27419.
S/MR (No)	>80	1701, 22851, 24851, 24878, 27391, 27395.
SL (mm)	>70	22853, 24217, 24220, 24221, 24862, 27381, 27384, 27402, 27421, 27423.
SW (mm)	≥5	24237, 24243, 24251, 24891, 24892, 24895, 27380, 27395.
S/S (No)	≥25	1665, 1697, 22853, 24235, 24251, 24257, 24856, 24874, 24875.
TSW (grams)	>5	22851, 24170, 24222, 24232, 24854.
SY/P (grams)	>15	24223, 24255, 24881, 26067, 26068,26217,27408,27903.
ST (%)	< 30	001691, 1702, 24219, 24222, 24854.

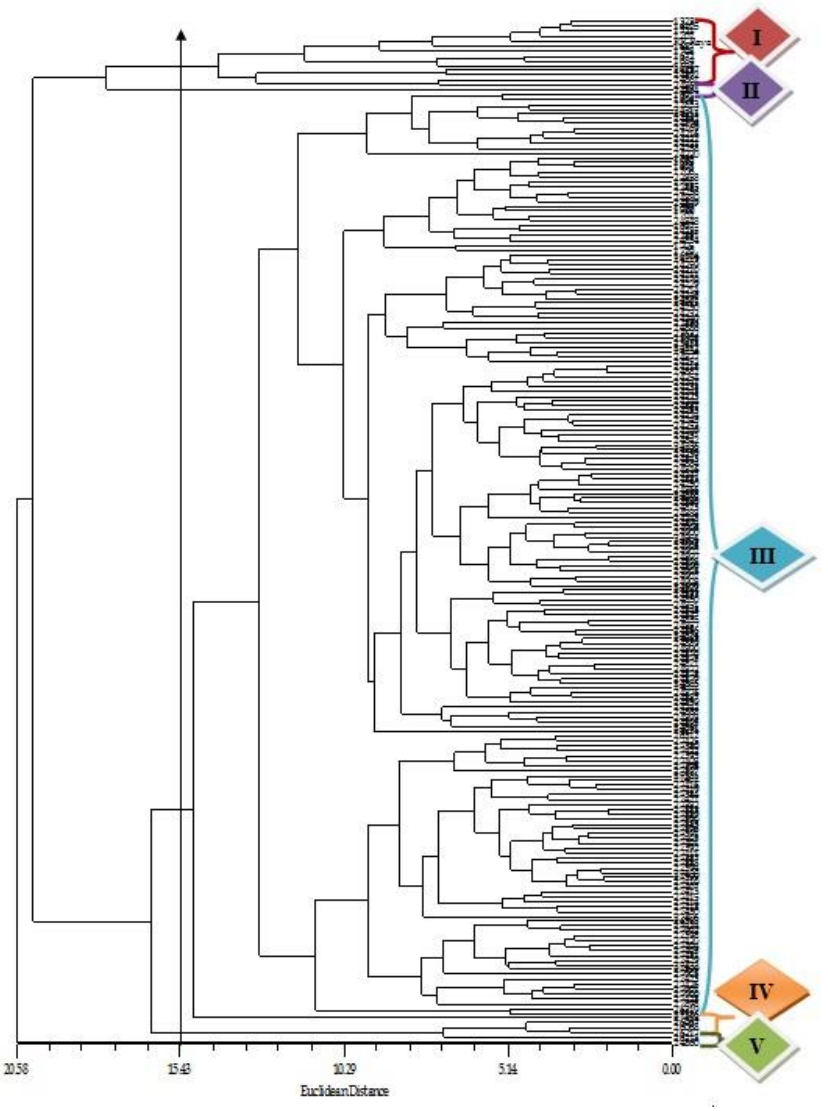

Figure 1: Dendrogram of the studied Brassica napus L. genotypes.

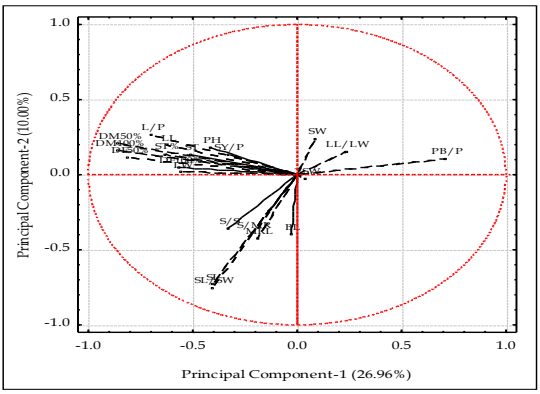

Figure 2: The contribution of the traits in the PC1 and PC2.

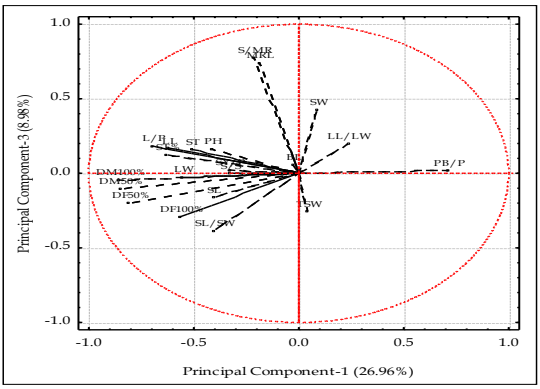

Figure 3: The contribution of the traits in the PC1 and PC3

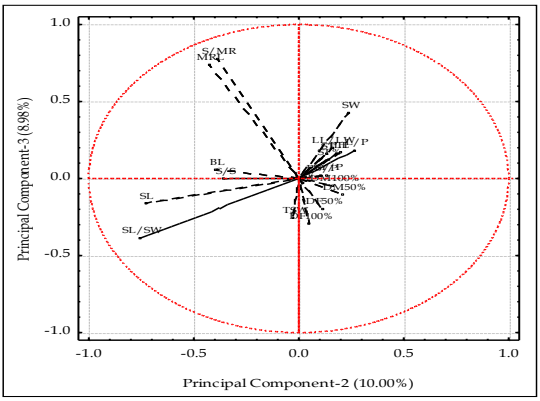

Figure 4: The contribution of the traits in the PC2 and PC3.

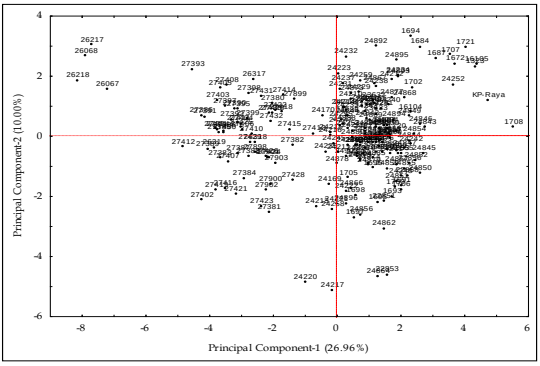

Figure 5: The scatter diagram showing the share of genotypes in the PC1 and PC2

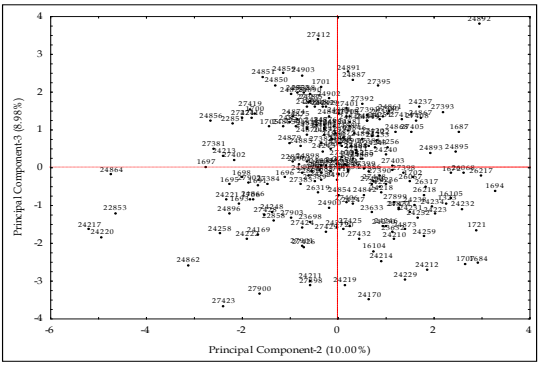

Figure 6: The scatter diagram showing the share of genotypes in the PC2 and PC3.

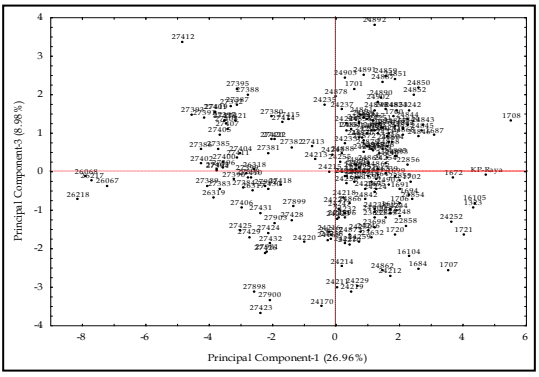

Figure 7: The scatter diagram showing the share of genotypes in the PC1 and PC3.