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GENETIC DIVERSITY OF *BRASSICA RAPA* L. INDIGENOUS LANDRACES BASED ON CLUSTER AND PRINCIPAL COMPONENT ANALYSES

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Abstract

Genetic variability was explored in locally collected 85 *Brassica rapa* accessions by using morphological markers. The experimental material was collected from diverse locations of Pakistan. These experiments were conducted under the agro-climatic conditions of Haripur, Khyber Pakhtunkhwa, Pakistan for two consecutive years 2012 and 2013. Data were recorded on various morphological and biochemical traits vacillating from flowering till its maturity and was analyzed by using two statistical procedures i.e., cluster and principal component analysis. Reasonable level of variation was recorded for various morphological and oil quality traits. High level of variation was recorded for seed yield followed by maturity, glucosinolate contents, plant height and flowering time. During 2012, cluster analysis categorized the 85 accessions into seven main groups, while in 2013 the same accessions were divided into six main groups. During 2012, first five principal components (PCs) accounted for 52.02% of variations among the studied accessions using morphological traits. Out of 52.02%, PC1 had 17.29%, PC2 contributed 10.13%, PC3 (9.51%), PC4 (7.98%) and the share of variability produced by PC5 was 7.11%. During 2013, the contributions of these accessions were 27.46% (PC1), 11.33% (PC2), 8.70% (PC3), 7.27% (PC4) and 6.38% (PC5) with an overall contribution of 61.14% variability. Based on present study, the four accessions i.e., 821, 844, 850 and 860 have been identified as potential genotypes which could be used in future breeding program.

Key words: Genetic diversity, Morphological and biochemical traits, Cluster and multivariate analyses, *Brassica rapa* L.

Introduction

Collections of local landraces/germplasm from diverse locations have great value from breeding point of view as containing many hidden desirable genes. For a successful plant breeding program, it is necessary that germplasm have diversity, reproducible and easily available to be used in the development of new cultivars (Naushad *et al.*, 2015; Zada *et al.*, 2013). While studying the genetic diversity in any crop, first to collect the germplasm and then evaluate by using different modern techniques. Often, indigenous cultivars of oilseed crops are of exceptional quality/flavors and have a good level of resistance against various biotic and abiotic stresses and may be superior to foreign materials (Williams *et al*., 1991).

To estimate variability in various cultivars, morphological characters, molecular evaluations and cytogenetic studies are commonly used (Singh *et al.*, 2010). In Pakistan two types of oilseed crops i.e., traditional (rapeseed-mustard, groundnut and sesame) and non-traditional (sunflower, safflower and soybean) are grown (Yousaf *et al.*, 2011). Rapeseed and Mustard belong to the tribe *Cruciferae (Brassiceae).* The family comprised of 51 genera and 37 species. According to literature, *B. campestris* recently known as *B. rapa* is native to Himalayan region and then introduced in the European-Mediterranean area and Asia. Mustard seed contains 40 and 24% oil and protein, respectively (Khaleque, 1985).

Main purpose of growing oil seed crops is mainly edible oil, containing vitamin A, D, E and K. After the extraction of oil from seeds, the cake comprises proteins of great biological worth and considerable amount of calcium and phosphorus which is a good source of animal feed and also to use in the fertilizers for different crops. Genetic divergence plays a vital part in the development of new varieties because hybrid is the result of hybridization between genotypes of diverse origin (Singh, 1984). Evaluations of genetic assortment and associations among genotypes assemblages are very valuable for assisting effective germplasm collection and management (Ghulam *et. al.*, 2010).

For identification of collected germplasm, nowadays different modern sophisticated techniques are available for the exploration of variability and the associations among genotypes including SDS-PAGE, isozymes and several molecular markers (Ana *et al.*, 2009; Krstkowiak *et al.*, 2009; Hartings *et al.*, 2009; Cheng *et al.*, 2009. Among these tools, morphological identification is the basic phase in the depiction and cataloguing of germplasm (Smith & Smith, 1989; Smykal *et al.*, 2008). To classify and measure the patterns of phenotypic diversity in the relationships of species and germplasm collections of variety of crops, various numerical taxonomic techniques have been successfully used (Naushad *et al.*, 2015; Li *et al.*, 1995).

Cluster and principal component analysis is a useful technique to be used for the classification of different biological populations at genotypic level and to evaluate comparative influence of various components to the total divergence both at intra- and inter-cluster levels (Zahan *et al.*, 2008). In plant breeding programs, several characters are simultaneously considered making it feasible to approximate the genetic divergence using multivariate techniques. Multivariate analyses have equivalent

usefulness to create the most proper cross combinations. Previously this technique had been used for the assessment of variability among various genotypes for various morphological traits of different crops (Mujaju & Chakuya, 2008; Chozin, 2007; Tesso *et al.,* 2005; Hasanuzzaman *et al.,* 2002; Ahlawat *et al.,* 2008; Golabadi *et al.,* 2006). In the present study, the genotypes with wide-ranging heritable background were collected and used to select best genotypes for future breeding programs.

Materials and Methods

Breeding material, procedure and traits measurement: A total of 85 *Brassica rapa* accessions (with two check cultivars; BSA and Toria-A) were collected from different sites of Pakistan. The collected materials were planted at newly developed Agriculture Farm of University of Haripur, Pakistan for two consecutive years (2012 and 2013). Recommended and same cultural practices were applied during both the growing seasons. Days were recorded on days to flower initiation, days to 50% flowering, days to flower completion, days to maturity, leaf petiole length (cm), leaf length (cm), leaf width (cm), leaf length/width ratio, leaves per plant, plant height (cm), length of main racemes (cm), silique per main raceme, silique length (cm), silique width, seeds per silique, 1000 seeds weight (g) and seed yield per plant (g). The oil quality traits i.e., oil content (%), protein content (%), oleic acid contents (%), linolenic acid contents (%), erucic acid contents (%) and glucosinolates contents (μMg^{-1}) were determined by Near Infrared-Reflectance spectroscopy (NIRS) at Nuclear Institute for Food and agriculture (NIFA), Tarnab, Peshawar, Pakistan.

Statistical analysis: Gomez & Gomez (1984) software were used for the calculation of basic statistical analysis for various morphological and biochemical traits. Multivariate analysis technique were used for all the recorded data for both years separately using "Statistica" Version 6.0 and "NTYSys 2.1", respectively as described by Sneath & Sokal (1973).

Results

Significant level of variations was observed for morphological traits among the studied accessions by using descriptive statistics analysis (Tables 1, 2). During 2012, 85 accessions were distributed into seven clusters (Fig. 5). Cluster-I had 18 accessions which were earlier in flowering (46.50 days) and maturity (125.80 days) while higher in protein (27.10%). Cluster-II comprised of 15 accessions with the distinguish features of low glucosinolate (91.90 μMg^{-1}) and linolenic acid (9.90%) and high oleic acid (43.80%). Cluster-III had 22 accessions with high seed yield per plant (35.40 g) and oil content (44.7%) (Table 5). Cluster-IV was the largest one and having 23 accessions having main raceme length (48.40 cm) and high protein content. Cluster-V had two accessions having earlier maturity (131.20 cm), more seed main $raceme^{-1}$ (58.30) and moderate to high oil and protein content (45.30% and 26.30%). The cluster-VI had one accession having leaf length (25.30 cm) and moderate to high oil and protein content (46.00% and 26.60%), respectively (Table 5). Accessions in cluster-VII was having 10 accessions and had more leaf length (39.00 cm) and seed/silique (24.70).

Table 1. Basic statistic data of all the accessions used in the study during 2012 year.

Traits	Mean ± SD	Range	CV (%)
Days to flower initiation	62.44 ± 11.36	37.00-104.0	18.19
Days to 50% flowering	79.89 ± 11.29	52-120	14.13
Days to flower completion	93.03 ± 10.65	66-131	11.45
Days to maturity	134.12 ± 9.29	113-162	6.93
Leaf petiole length (cm)	8.89 ± 4.96	0.7-21.3	55.78
Leaf length (cm)	25.07 ± 8.02	8.5-44.0	31.99
Leaf width (cm)	9.66 ± 6.85	1.9-34.1	70.92
Leaf length/width ratio	3.39 ± 1.85	0.81-13.16	54.71
Leaves $plant^{-1}$	17.78 ± 12.11	7.0-61.0	68.10
Plant height (cm)	160.84 ± 14.32	129-224	8.90
Primary branches $plant^{-1}$	7.17 ± 2.34	5-19	32.60
Main inflorescence length (cm)	52.36 ± 11.96	30.86	22.84
Silique per main inflorescence	49.26 ± 15.29	26-95	31.03
Siliqua length	4.12 ± 0.89	3.2-6.2	21.69
Siliqua width	0.45 ± 0.11	0.2-0.7	25.27
Siliqua length/width ratio	9.61 ± 2.99	4.86-18.33	31.12
Seeds $silique^{-1}$	17.32 ± 3.38	14-28	19.53
Seed yield $plant^{-1}$	32.98 ± 6.10	18.3-45.4	18.50
1000-seed weight (g)	2.50 ± 0.34	1.7-4	13.58
Oil contents %	43.99 ± 3.78	26.2-50.2	8.58
Protein contents %	26.93 ± 1.97	21.9-31.0	7.33
Glucosinolates (μMg-1)	110.54 ± 28.65	43.9-182	25.92
Oleic acid %	38.52 ± 6.04	27.9-56.9	15.68
Linolenic acid %	11.14 ± 2.31	1.9-19.0	20.74
Erucic acid %	55.35 ± 5.46	21.4-60.8	9.87

Table 2. Basic statistic data of all the accessions used in the study during 2013.

Traits	Mean ± SD	Range	CV
Days to flower initiation	61.58 ± 11.15	34-102	18.11
Days to 50% flowering	72.49 ± 11.84	40-118	16.33
Days to flower completion	80.60 ± 12.72	45-126	15.78
Days to maturity	136.43 ± 10.79	115-169	7.91
Leaf petiole length (cm)	12.19 ±	4.1-29	42.42
Leaf length (cm)	35.66 ± 5.17	18.1-53.2	21.69
Leaf width (cm)	12.05 ± 7.74	5.4-32.8	40.89
Leaf length/width ratio	3.26 ± 1.03	1.06-6.19	31.68
Leaves plant^{-1}	18.76 ± 3.39	11-28	18.07
Plant height (cm)	184.51 ± 117.64	142-240	9.56
Primary branches plant^{-1}	12.56 ± 2.94	7-18	23.44
Main inflorescence length (cm)	60.84 ± 12.79	39-96	21.01
Silique per main inflorescence	53.06 ± 11.20	32-82	21.11
Siliqua length	4.76 ± 1.51	3-14	31.64
Siliqua width	0.40 ± 0.09	0.22-0.62	21.55
Siliqua length/width ratio	12.21 ± 3.12	7.14-25	25.54
Seeds silique^{-1}	20.43 ± 5.61	8-34	27.44
Seed yield plant^{-1}	38.47 ± 11.93	18.3-69.2	31.01
1000-seed weight (g)	2.89 ± 0.76	1.4-5	26.14
Oil contents %	47.59 ± 2.85	41.1-55.5	5.98
Protein contents %	25.06 ± 1.88	20.9-29.4	7.49
Glucosinolates (μMg-1)	107.12 ± 19.34	70.2-160.4	18.05
Oleic acid %	39.77 ± 5.34	31-61.1	13.44
Linolenic acid %	9.77 ± 1.75	6.6-14.6	17.91
Erucic acid %	55.05 ± 6.05	23.9-60.9	11.00

During 2013, the same accessions were sub-divided into six main clusters. Cluster-I encompassed of 12 accessions, cluster-II had 20 accessions, cluster-III had six accessions and cluster-IV had 16 accessions. Cluster-V was larger one and covered of 21 accessions while 10 accessions were part of cluster VI (Fig. 6). Main features of the accessions included in cluster-I had high oil content (45.00%) and protein content (26.90%). Accessions decorated cluster-II were low in linolenic acid (9.50%), more seed silique^{-1} (21.50) and sufficient oil (48.50%). Cluster-III had early matured (131.50 days), leaves with long length (37.90 cm), high oleic acid (39.3%) and longer silique (4.60 cm) while accessions take part in cluster-IV were high yielding (51.80 g), more seed silique^{-1} (30.80), more oil (48.30%) and low linolenic acid (9.80%) (Table 6). Cluster-V had those accessions having more seed main raceme^{-1} (66.00), longer main raceme length (80.00 cm) and low linolenic acid (9.2%). Cluster-VI had those accessions having longer main raceme length (66.00 cm), low glucosinolates content (91.40 μMg^{-1}) and relatively low erucic acid (49.70%) (Table 6).

During 2012, principal component analysis (PCA) was carried out for 19 morphological and six oil quality traits which showed an eigenvalue of 52.01% in the *B. rapa* (Table 3). The coefficients defining five principal components which are given in Table 3. PC1 demonstrated glucosinoletes (0.28) and protein contents (0.17), PC2 had linolenic acid (0.20), protein contents (0.19), primary branches plant^{-1} (0.16), PC3 had leaf length/width ratio (0.33), 1000-seed weight (0.23), PC4 had erucic acid (0.39), silique length/width ratio (0.31), silique length (0.23) and glucosinolates (0.19). However, PC5 had 50% flower imitation (0.37), linolenic acid (0.36), days to flower completion (0.33), flower initiation (0.28) and protein (0.21) (Table 3). Informative outcome from present study for most of the quantitative traits in *B. rapa* accessions by using principal component analysis are provided in Figs. 1 and 2. Likewise principal component analysis of the *B. rapa* discovered assorted grouping pattern, which in general supported cluster analysis (Figs. 4, 5). Main reason behind the variability among the studied accessions was the diverse background of the collected materials.

During 2013, principal component analysis was performed for nineteen morphological and six biochemical traits which revealed an eigenvalue of 61.13% in the *B. rapa* (Table 4). The coefficients defining five principal components are given Table 4. PC1 accounted leaf width (0.33), leaves plant^{-1} (0.33), silique main inflorescence^{-1} (0.27), 50% flowering (0.27), flower completion (0.27), flower initiation (0.25), maturity (0.28). PC2 accounted for linolenic acid % (0.37), erucic acid (0.35), glucosinolates (μMg-1) (0.33), silique main inflorescence^{-1} (0.244). PC3 explained the linolenic acid (0.376), glucosinolates (μMg-1) (0.34), 50% flower in initiation (0.29), flower in initiation (0.29), flower completion (0.28) (Table 4). PC4 had leaf petiole length (0.39), Silique length/width ratio (0.34), leaf length (0.31), leaf length/width ratio (0.29) and plant height (0.28). PC5 accounted for oil content (0.43), primary branches plant^{-1} (0.36), plant height (0.33) and silique length/width ratio (0.18) (Table 4).

Table 3. Principal components analysis for morpho-physiological and seed quality traits in 85 accessions of *Brassica rapa* during 2012.

Eigenvalue and variances	PC1	PC2	PC3	PC4	PC5
Eigenvalue	4.32	2.53	2.38	1.99	1.78
Cumulative Eigenvalue	4.32	6.86	9.23	11.23	13.00
% Total variance	17.29	10.13	9.51	7.98	7.11
Cumulative %	17.29	27.42	36.93	44.90	52.01
Traits	**Eigenvectors**				
Days to flower initiation	-0.338	-0.078	0.070	0.080	0.282
Days to 50% flower imitation	-0.367	-0.088	-0.005	0.054	0.367
Days to flower completion	-0.389	-0.075	-0.035	0.045	0.326
Days to maturity	0.023	-0.031	-0.251	-0.278	0.093
Leaf petiole length (cm)	0.090	-0.315	0.087	-0.236	-0.002
Leaf length (cm)	-0.079	-0.269	0.063	-0.227	-0.089
Leaf width (cm)	-0.321	0.028	-0.197	0.120	-0.058
Leaf length/width ratio	0.223	-0.178	0.327	-0.307	0.025
Leaves plant^{-1}	-0.315	0.134	0.061	0.006	-0.233
Plant height (cm)	-0.207	0.105	0.041	-0.046	-0.141
Primary branches plant^{-1}	-0.258	0.160	-0.122	0.014	-0.219
Main inflorescence length (cm)	-0.026	0.111	-0.180	-0.342	-0.300
Silique per main inflorescence	-0.215	0.109	-0.138	-0.003	-0.414
Siliqua length	0.044	-0.467	-0.211	0.229	-0.088
Siliqua width	0.034	-0.259	-0.398	-0.001	-0.126
Siliqua length/width ratio	0.015	-0.313	0.079	0.309	-0.010
Seeds silique^{-1}	0.050	-0.368	-0.323	0.146	-0.101
Seed yield plant^{-1}	-0.030	0.012	-0.264	-0.290	0.006
1000-seed weight (g)	0.001	-0.006	0.234	0.068	0.032
Oil contents %	-0.125	-0.185	-0.071	-0.010	-0.045
Protein contents %	0.170	0.188	-0.307	-0.050	0.214
Glucosinolates (µMg-1)	0.283	0.146	-0.215	0.193	0.149
Oleic acid %	-0.186	-0.180	0.074	-0.348	0.064
Linolenic acid %	0.065	0.201	-0.329	-0.085	0.362
Erucic acid %	0.078	0.123	0.071	0.387	-0.186

Discussion

Cluster analysis divided genotypes into various groups based on morphological data and not on ecological background of the genotypes. In the present study, genotypes collected from diverse places were fall in the same cluster, while many others fell into different clusters. Present study revealed that groups in the cluster were mainly based on its morphological differences irrespective of its geographic affiliation (Nazim *et al*., 2015). Thus, from the findings of present study it cannot be assumed that the genotypes collected from same locality would always have low variability among them. In past findings, *B. juncea* accessions were grouped by various morphological traits, where geographic locations had no effect on grouping of different accessions (Naushad *et. al.,* 2015). Similarly, Zada *et al.* (2013) reported that genotypes and geographical origin had heterogeneous relationship in cluster formation.

Accessions from diverse locality were pooled in one cluster. On the other hand Padilla *et al*. (2005) collected *B. rapa* sub-spp *rapa* L. from northwestern Spain and they reported that cluster were formed on the basis of geographical origins and concluded that there were some relationships between their geographical origins. Past studies agree to the present outcome that this method can better clarify the complex relationships between populations of diverse origins in a more simplified way. By hierarchical cluster analysis, the present study revealed that some of the accessions collected from various geographical regions were grouped into the same cluster, while some other accessions fell into different clusters. Our findings were further strengthened by Youaf *et al*. (2011), who evaluated 114 accessions of *Brassica rapa* for two years for different morphological characters. They reported that genotypes collected from diverse locations with similar traits were placed in same cluster irrespective of its collection location.

Similarly greater variations were estimated in various groups of brassica accessions and concluded that morphological differences has major role in the formation of clusters not with its area of collection (Mahalakshmi *et al*., 2006; Wu *et al*., 2007; Gulam *et al*., 2010). Present findings also got support from the previous work of Verma and Sachan (2000), who reported that 12 clusters were formed in rapeseed and mustard purely on the basis of variation for various traits not on its geographic affinity.

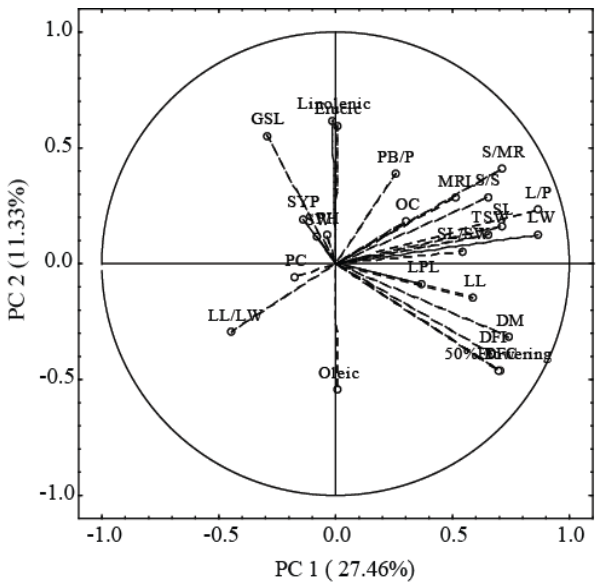

Fig. 1. Contribution of quantitative and qualitative traits in 1st and 2nd PC in *Brassica rapa* accessions.

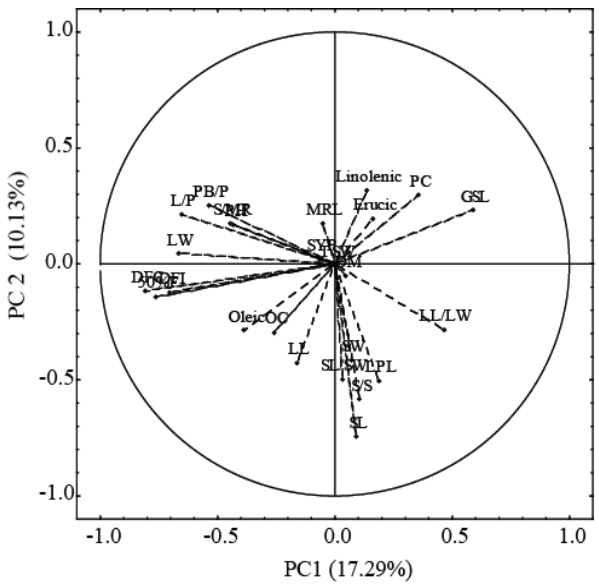

Fig. 2. Contribution of quantitative and qualitative traits in 1st and 2nd PCs in *Brassica rapa* accessions.

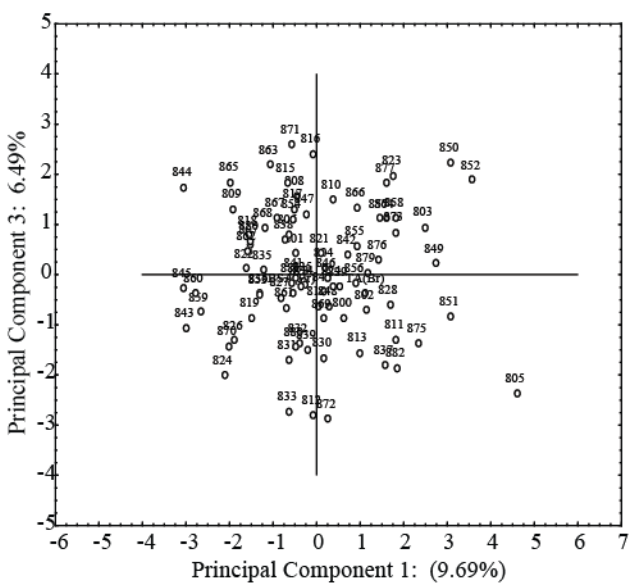

Fig. 3. Scatter diagram for 1st and 2nd PC for nineteen morpho-physiological and six seed quality traits in 85 accessions of *Brassica rapa* L. during 2012.

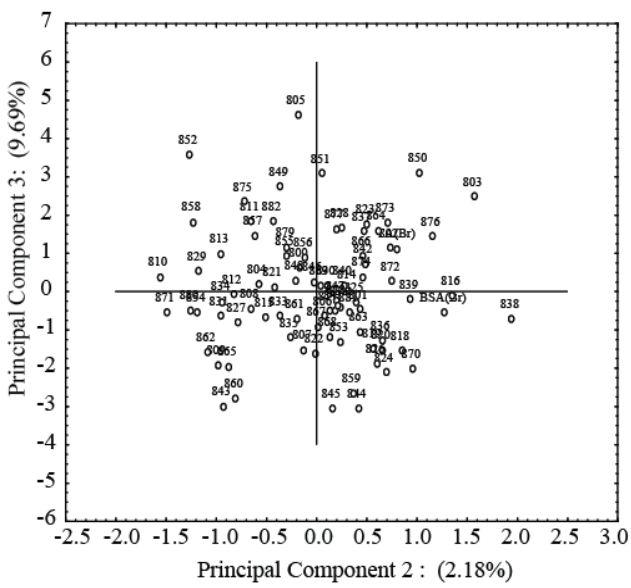

Fig. 4. Scatter diagram for 1st and 2nd PC for nineteen morpho-physiological and six seed quality traits in 85 accessions of *Brassica rapa* L. during 2013.

Principal component analysis helping the breeders in selecting certain genotypes for specific traits to achieve the breeding objectives easily. Different researchers used cluster and principal component analysis for various morph-physiological traits and seed related attributes (Balkaya *et al*., 2005; Warwick *et al*., 2006; Khan *et al.,* 2013; Jatoi *et al.,* 2011). However, present studies got support from past findings about cluster and principal component analyses which disclosed the complex relationship among the accessions in a more understandable way. The results obtained based on variability among the accessions from different locations related primarily to their morphological differences and secondly to horticultural use. Current study discovered a significant range of genetic diversity in *B. rapa* genotypes. Important morphological traits i.e., early maturity, branches/plant, seeds/silique, silique/plant, seed yield, and oil content could serve as major criteria for selection of promising *B. rapa* genotypes.

Accessions used in the present study showed high level of variability for majority of the characters of economic significance which can be used as a base line for future crop improvement programs. These findings also got support from past findings of Amiriyan *et al*. (2010), Zaman *et al*. (2010) and Alamayeha & Becker (2002), who reported that accessions with high genetic variation for various morpho-physiological and seed traits were grouped together. It was also reported that different morphological and yield characters contribute towards genetic divergence in various genotypes of Brassica. Present results were also in line with past findings as they proposed that principal component analysis revealed

multifaceted associations between the accessions and qualities and yield components and growing period contributed maximum towards genetic variation in 36 Ethiopian mustard accessions (Elizabeth *et al*., 2001; Choudhry & Joshi, 2001; Alamayeha & Becker, 2002).

Cluster constructed for various genotypes used in the present study showed that genotypes collected from the same area were also placed into different clusters. The genotypes belonging to different locations were grouped in the same cluster. This shows that geographic diversity was not related to genetic diversity of the genotypes, as also confirmed earlier by Jahan *et al.* (2013). If breeders want to conduct more specific breeding programs, multivariate analysis assist them about the importance of certain characters of genotypes in a specific group. For development of *B. rapa*, it would be necessary to use the local genotypes with broad genetic background in future breeding programs.

Table 4. Principal components analysis for morpho-physiological and seed quality traits in 85 accessions of *Brassica rapa* during 2013.

Eigenvalue and variances	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
Eigenvalue	6.86	2.83	2.17	1.82	1.60
Cumulative Eigenvalue	6.86	9.70	11.87	13.69	15.28
% Total variance	27.46	11.33	8.69	7.27	6.38
Cumulative %	27.46	38.79	47.48	54.75	61.13
Traits			**Eigenvectors**		
Days to flower initiation	0.254	-0.231	0.288	-0.038	0.145
Days to 50% flower imitation	0.268	-0.272	0.296	0.015	0.077
Days to flower completion	0.267	-0.274	0.284	-0.009	0.020
Days to maturity	0.282	-0.188	0.235	0.067	0.033
Leaf petiole length (cm)	0.141	-0.052	-0.079	0.398	-0.317
Leaf length (cm)	0.223	-0.087	-0.041	0.305	-0.220
Leaf width (cm)	0.331	0.076	-0.063	-0.081	-0.112
Leaf length/width ratio	-0.170	-0.175	0.051	0.293	-0.023
Leaves plant^{-1}	0.329	0.139	-0.046	-0.027	-0.180
Plant height (cm)	-0.015	0.074	0.092	0.275	0.327
Primary branches plant^{-1}	0.098	0.231	-0.160	0.200	0.363
main inflorescence length (cm)	0.195	0.170	-0.179	-0.123	0.016
Silique per main inflorescence	0.272	0.244	-0.206	-0.060	-0.096
Siliqua length	0.271	0.097	0.101	-0.100	-0.086
Siliqua width	-0.031	0.070	0.274	-0.405	-0.284
Siliqua length/width ratio	0.207	0.033	-0.181	0.338	0.178
Seeds per silique	0.248	0.171	-0.148	-0.050	-0.216
Seed yield plant^{-1}	-0.053	0.115	-0.043	0.020	-0.227
1000-seed weight (g)	0.250	0.076	-0.114	-0.008	0.169
Oil contents %	0.115	0.111	-0.054	-0.145	0.433
Protein contents %	-0.066	-0.033	-0.111	0.248	-0.265
Glucosinolates (µMg-1)	-0.112	0.329	0.342	0.267	-0.134
Oleic acid %	0.004	-0.321	-0.348	-0.152	0.023
Linolenic acid %	-0.004	0.367	0.376	0.156	0.060
Erucic acid %	0.003	0.354	0.137	-0.151	0.052

Table 5. Mean ± SD of nine clusters based on morphological and seed quality traits of 85 *Brassica rapa* accessions during 2012.

Trait	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5	Cluster-6
	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD
DFI	46.5 ± 7.5	59.9 ± 10.0	64.2 ± 5.3	65.0 ± 7.0	64.0 ± 3.9	69.0 ± 14.5
50%DFI	63.8 ± 7.0	76.8 ± 8.6	78.7 ± 7.0	82.9 ± 5.2	79.8 ± 5.3	92.7 ± 8.1
DFC	77.6 ± 7.9	91.5 ± 5.6	90.8 ± 5.9	96.0 ± 5.3	91.5 ± 5.1	106.0 ± 7.5
DM	125.8 ± 9.3	131.7 ± 8.1	131.8 ± 5.7	135.4 ± 4.2	131.2 ± 2.4	147.0 ± 7.2
LPL	9.3 ± 6.0	7.1 ± 5.2	7.4 ± 4.0	8.9 ± 4.3	5.9 ± 5.0	13.9 ± 3.9
LL	22.7 ± 6.8	23.7 ± 6.8	22.2 ± 3.7	24.6 ± 4.0	15.1 ± 4.7	39.0 ± 4.8
LW	6.7 ± 2.5	7.7 ± 3.4	7.3 ± 2.4	7.8 ± 2.7	6.1 ± 3.1	19.5 ± 6.7
LL/LW	3.6 ± 1.1	3.9 ± 2.9	3.3 ± 0.9	3.6 ± 1.5	3.2 ± 2.3	2.1 ± 0.4
L/P	14.2 ± 3.0	12.5 ± 2.0	13.4 ± 2.5	12.5 ± 1.9	15.0 ± 2.5	48.7 ± 8.5
PH	163.6 ± 10.5	160.1 ± 12.7	157.8 ± 14.8	162.6 ± 10.3	160.0 ± 10.8	165.0 ± 5.6
PB/P	7.9 ± 2.8	6.2 ± 0.9	6.4 ± 1.0	6.5 ± 1.2	7.0 ± 0.6	7.0 ± 0.0
MRL	54.6 ± 15.0	48.5 ± 8.6	43.1 ± 6.5	48.4 ± 9.3	54.7 ± 3.9	69.7 ± 13.7
S/MR	50.2 ± 12.1	41.4 ± 11.4	40.7 ± 7.9	40.1 ± 6.2	58.3 ± 5.5	78.0 ± 14.8
SL	4.0 ± 0.8	3.7 ± 0.6	3.9 ± 0.7	4.0 ± 0.7	3.9 ± 0.7	5.4 ± 0.5
SW	0.5 ± 0.1	0.5 ± 0.1	0.5 ± 0.1	0.4 ± 0.1	0.5 ± 0.1	0.5 ± 0.1
SL/SW	9.5 ± 3.8	8.1 ± 1.6	8.7 ± 1.4	9.9 ± 3.7	8.6 ± 1.9	11.0 ± 2.0
S/S	16.8 ± 3.4	16.4 ± 2.2	17.0 ± 2.0	15.9 ± 2.0	16.2 ± 2.6	24.7 ± 4.2
SYP	35.3 ± 5.7	34.0 ± 6.4	35.4 ± 4.1	31.9 ± 6.6	34.0 ± 3.2	32.5 ± 6.3
TSW	2.3 ± 0.4	2.4 ± 0.1	2.4 ± 0.3	2.5 ± 0.2	2.5 ± 0.1	3.0 ± 0.2
OC	42.1 ± 5.3	43.0 ± 3.5	44.7 ± 2.7	43.4 ± 3.3	45.3 ± 2.9	43.5 ± 2.0
PC	27.1 ± 2.7	27.1 ± 1.4	26.8 ± 1.7	27.3 ± 1.9	26.9 ± 2.3	28.4 ± 2.5
GSL	137.3 ± 21.4	91.9 ± 16.6	138.1 ± 14.5	116.2 ± 7.9	120.1 ± 7.7	144.9 ± 5.6
OA	35.6 ± 4.4	43.8 ± 6.1	32.3 ± 3.3	37.7 ± 4.2	36.2 ± 3.7	33.0 ± 2.5
LA	12.4 ± 3.0	9.9 ± 1.5	13.1 ± 2.0	10.8 ± 1.0	10.6 ± 2.2	12.8 ± 2.5
EA	57.8 ± 2.5	54.9 ± 4.9	56.5 ± 3.4	55.7 ± 4.2	52.6 ± 4.3	54.8 ± 4.8

Table 6. Mean ± SD of six clusters based on morphological and seed quality traits of 85 *Brassica rapa* accessions during 2013.

Trait	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD
DFI	54.9 ± 9.2	68.4 ± 3.3	60.1 ± 5.0	59.5 ± 7.2	62.0 ± 8.5	63.1 ± 11.5
50%DFI	67.6 ± 6.0	78.3 ± 7.3	68.8 ± 4.7	67.0 ± 6.1	69.5 ± 4.9	75.3 ± 7.8
DFC	76.3 ± 6.1	82.4 ± 6.2	76.2 ± 5.0	74.5 ± 4.4	76.0 ± 7.1	85.1 ± 8.7
DM	139.9 ± 10.7	135.3 ± 7.9	131.5 ± 5.7	132.8 ± 5.6	137.0 ± 4.2	139.1 ± 13.8
LPL	11.6 ± 6.2	12.8 ± 2.9	12.3 ± 5.7	13.5 ± 6.1	7.1 ± 0.6	12.7 ± 4.9
LL	33.7 ± 8.8	33.0 ± 3.3	37.9 ± 5.7	39.0 ± 4.8	24.6 ± 1.0	38.4 ± 9.1
LW	11.3 ± 3.4	10.9 ± 3.2	10.4 ± 2.3	11.9 ± 3.2	7.3 ± 0.8	15.1 ± 7.1
LL/LW	3.1 ± 0.9	3.2 ± 0.8	3.8 ± 1.0	3.4 ± 0.9	3.4 ± 0.3	3.0 ± 1.3
L/P	18.8 ± 3.0	16.1 ± 2.2	18.3 ± 2.2	18.3 ± 2.8	19.0 ± 2.8	21.2 ± 4.5
PH	186.2 ± 14.2	173.4 ± 8.5	189.1 ± 8.3	179.0 ± 8.2	209.5 ± 10.6	194.3 ± 16.9
PB/P	12.7 ± 2.8	10.6 ± 2.5	11.9 ± 2.7	10.8 ± 2.1	15.5 ± 3.5	13.9 ± 3.6
MRL	55.5 ± 7.8	53.1 ± 7.8	54.9 ± 9.6	51.5 ± 3.7	80.0 ± 14.1	66.3 ± 11.1
S/MR	53.5 ± 8.8	43.8 ± 8.7	47.6 ± 7.0	51.0 ± 8.8	66.0 ± 9.9	59.5 ± 9.3
SL	4.5 ± 0.9	5.7 ± 2.8	4.6 ± 1.4	6.1 ± 0.6	4.2 ± 1.6	4.4 ± 1.2
SW	0.4 ± 0.1	0.4 ± 0.1	0.4 ± 0.1	0.6 ± 0.1	0.4 ± 0.1	0.4 ± 0.1
SL/SW	11.9 ± 2.3	13.8 ± 4.0	13.5 ± 4.0	10.6 ± 1.2	10.8 ± 0.1	11.4 ± 2.4
S/S	20.0 ± 5.9	21.5 ± 5.5	19.4 ± 3.7	30.8 ± 4.6	17.0 ± 5.7	19.1 ± 5.6
SYP	30.9 ± 6.9	34.6 ± 6.7	30.2 ± 6.8	51.8 ± 9.5	42.7 ± 2.1	38.0 ± 10.8
TSW	3.0 ± 0.8	3.4 ± 1.1	2.7 ± 0.5	2.5 ± 0.3	3.0 ± 0.1	2.9 ± 0.6
OC	45.3 ± 2.8	48.5 ± 4.3	47.8 ± 1.8	48.3 ± 2.6	46.7 ± 3.7	47.1 ± 2.4
PC	26.9 ± 1.3	24.5 ± 1.4	23.8 ± 1.1	25.1 ± 1.6	26.5 ± 2.1	24.8 ± 1.7
GSL	130.6 ±	103.4 ± 7.2	107.3 ± 8.9	119.2 ± 6.0	118.3 ± 1.3	91.4 ± 15.8
OA	36.2 ± 3.6	38.7 ± 2.5	39.3 ± 3.1	37.9 ± 1.6	35.2 ± 5.9	43.8 ± 6.0
LA	11.0 ± 1.8	9.5 ± 1.6	8.8 ± 0.9	9.8 ± 1.4	9.2 ± 0.1	9.2 ± 2.0
EA	57.1 ± 3.8	54.5 ± 7.6	57.6 ± 2.9	55.5 ± 2.4	55.7 ± 3.8	49.7 ± 8.9

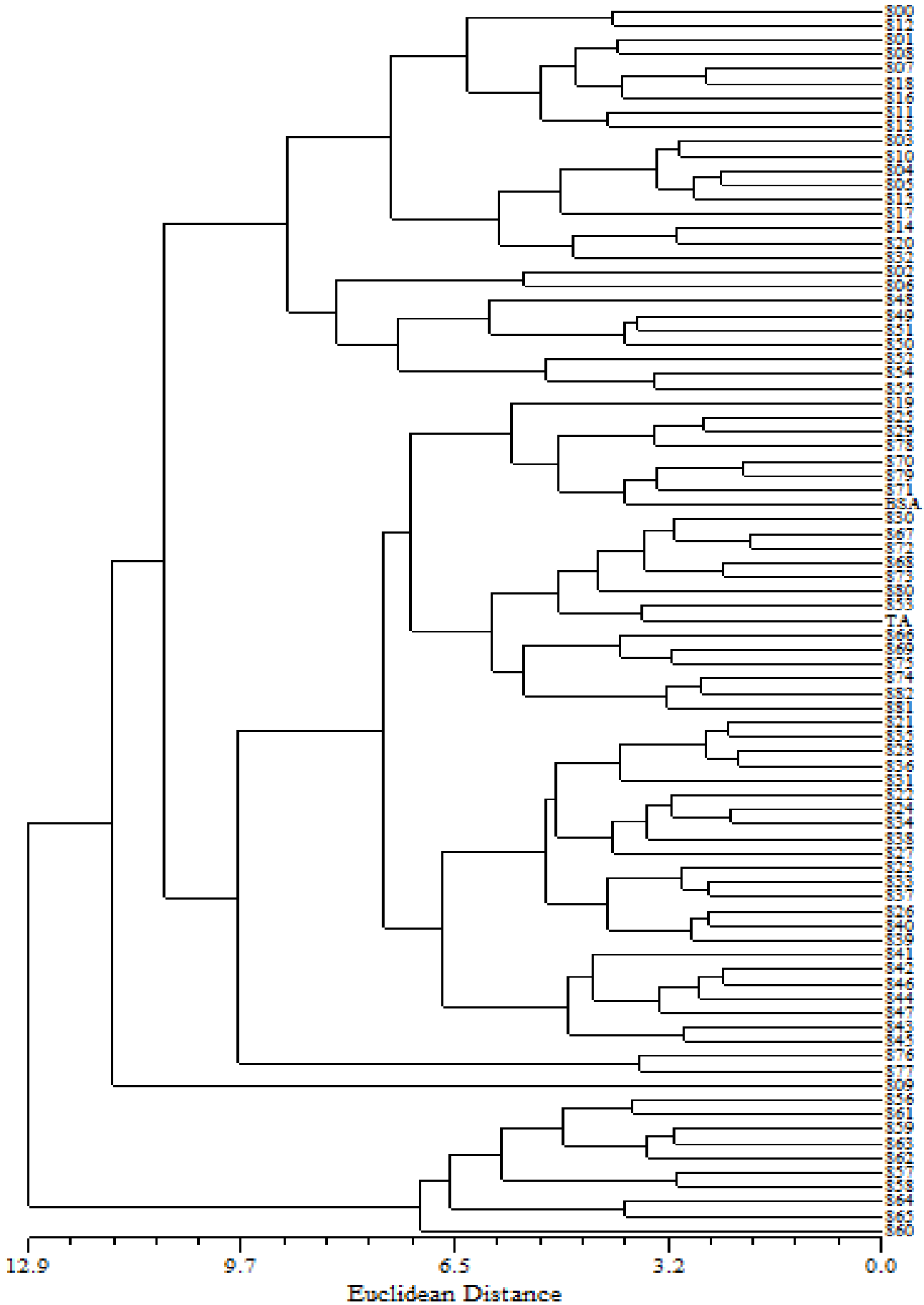

Fig. 5. Dendrogramical presentation for various *Brassica rapa* accessions used in the study during 2012.

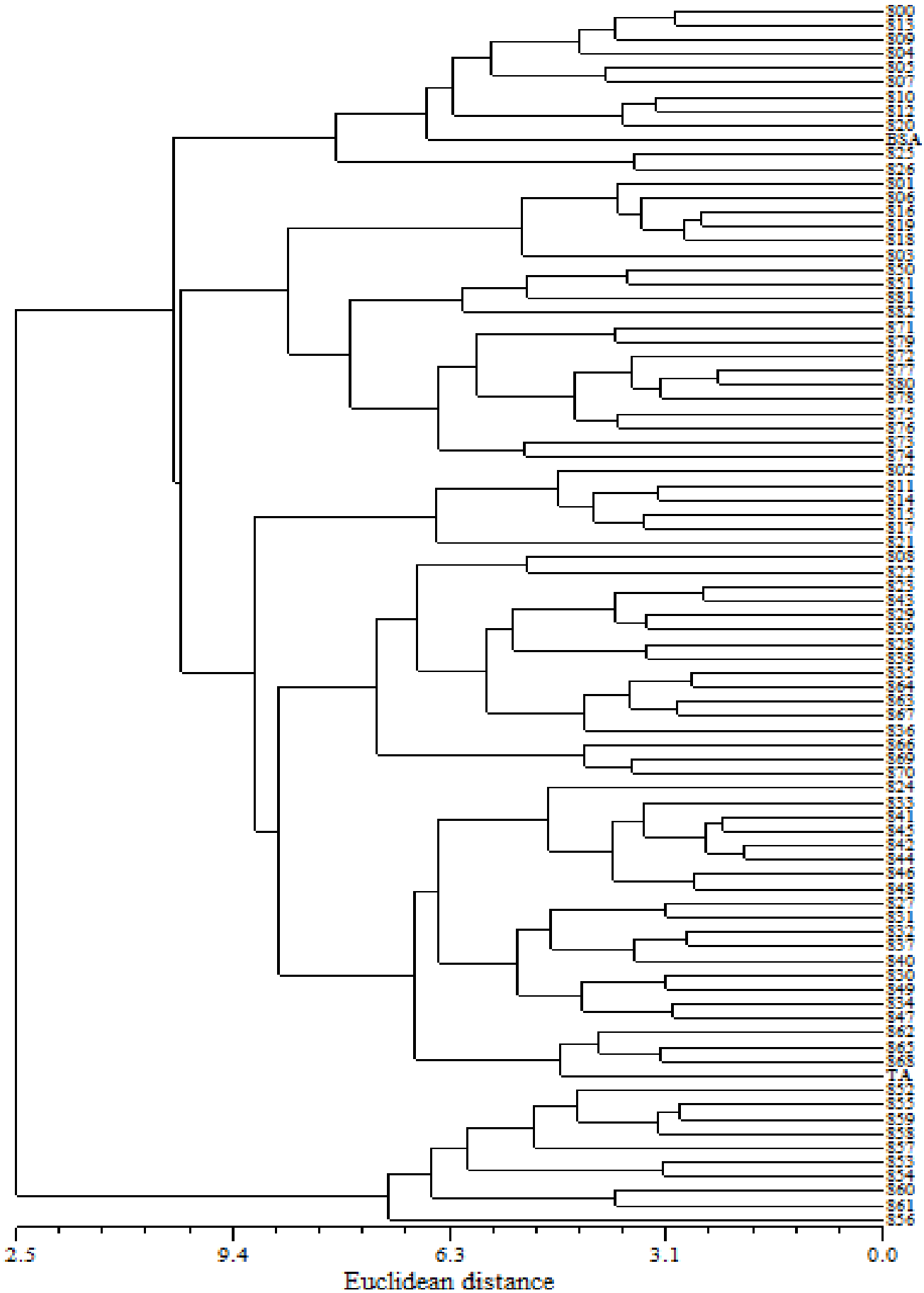

Fig. 6. Dendrogramical presentation for various *Brassica rapa* accessions used in the study during 2013.

Conclusion

Significant variations were recorded for various morphological and biochemical traits. High level of variation was recorded for seed yield followed by maturity, glucosinolate contents, plant height and flowering time. During 2012, cluster analysis categorized 85 accessions into seven main groups, while in 2013, the same accessions were subdivided into six main groups. During 2012, first five principal components (PCs) accounted for a total of 52.02% of variation among the studied accessions using morphological traits. During 2013, the overall contribution of variability was 61.14%. Based on present study, the four accessions i.e., 821, 844, 850 and 860 have been identified as potential genotypes which could be used in future breeding program.

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