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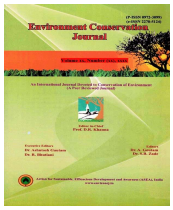

Genetic divergence analysis in Taramira (*Eruca sativa* Mill.) under different environment conditions with special reference to principal component analysis

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ABSTRACT

The field experiment was conducted to identify the principal component among ten morphological one (biochemical) oil content traits of thirty germplasm lines from the All India coordinate research project oilseeds (Taramira) in a randomize block design (RBD) with three replications in each of the test conditions, which were generated using 3 separate sowing dates with fifteen days interval from October 2nd week to November 3rd week (15th October, 30th October & 15th November 2018-19). First three principal components contributed 76.8% proportion of variation with an eigen value more than one (1.329). The largest percent contribution (30.11) to overall genetic divergence was shown by siliqua per plant followed by test weight, number of primary & secondary branches per plant & seed yield per plant. The genotypes were divided into nine groups, with Cluster II having the most genotypes (12), followed by Cluster I with five genotypes. Based on mean value of seed yield, oil content & cluster analysis, eight germplasms with cross combination viz., RTM-1806 X (RTM-314, RTM-1351, RTM-1805, RTM-1810, RTM-1800, RTM-1791, RTM-1815) & RTM-1804 X (RTM-314, RTM-1351) were identified as high yielding which can be widely utilized as a parents in hybridization programme for the development of 9 new diverse varieties/ hybrids for enhanced seed yield as well as oil content.

Introduction

Oilseed crops are the basis of an agricultural economy like India's, and they're mostly grown for oil production across the world with total output of 32.26 million tonnes and area of 25.50 million hectares and average yield of 1265 kg/hectare, India is one of the world's leading oilseed producers (Anonymous, 2019). The toria seed & mustard group of the family Brassicaceae includes Eruca sativa (L.) Miller (Rocket plant or Taramira). This plant's name is derived from the Latin word eruca, which means cabbage (Garg & Sharma, 2014). Taramira is an important oilseed crop suitable to be grown under in drought-prone areas of northwestern India, & it has gained attracted interest as a possible biodiesel crop. Taramira oil is used in medications, cosmetics, & in the manufacturing of grease, plastics, lubricants, soaps, & paints, among other things (Warwick *et al*.,

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2007; Yaniv *et al*., 1998). Salads, cooked veggies, & functional foods are all made with the plant.

Groundnut, soybean, rapeseed-mustard, sesamum, & taramira are the most important oilseed crops farmed in Rajasthan. Due to the native ecological circumstances of Rajasthan & its potential application in bio-diesel generation, taramira has grown in popularity among all oilseed crops. Taramira is produced on 7.63 lakh hectares in Rajasthan, yielding 4.62 lakh kg with an average productivity of 606 kg/hectare (Anonymous, 2019).

Presence of optimal genetic divergence between the parents is a significant pre-requisite for the success of crop improvement initiatives in various crops. Because superior transgressive segregates arise in segregating generations in crossings between genetically diverse parents, the Thus, crossing genetically different parents in any breeding effort can result in a wide range of gene combinations, which can then be used to either exploit heterosis for the development of hybrid varieties or to obtain superior recombinants for the development of pure line varieties. As a result, a preliminary assessment of the genetic diversity available in the breeding materials is a necessary precondition for any breeding program's success (Deep *et al*., 2019). Correlation studies provide trustworthy & relevant information about the type, scope, & direction of any selection process.

In light of the foregoing, the current research was conducted to evaluate the character association & relationship between distinct Taramira germplasm using a clustering & PCA approach in order to find different germplasms suited for the crop's hybridization programme.

Material and Methods

The experimental material included 30 germplasm lines from the All India Coordinated Research Projects, Oilseeds (Taramira), Department of Plant Breeding & Genetics, S.K.N. College of Agriculture, Jobner, as well as two checks, RTM-314 & RTM-1351. The experiment was set up in a (RBD) with three replications in each of the test conditions, which were established by three different sowing dates separated by fifteen days from October 2nd to November 3rd (15th October, 30th October & 15th November 2018-19). Within each replication, the germplasms were distributed at random, with inter & intra row spacing of 30 & 10 cm, respectively.

For 10 agro-morphology & 1 bio-chemical (Oil content), observations were recorded on ten randomly selected competing plants in each replication & in each environment, then the average of all replications of all environments for each character viz., days to 50% percent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, length of siliqua (cm), siliqua per plant, seed per siliqua, test weight (g), oil content (%) & seed yield per plant (g). The major descriptive statistics such as mean, range, standard deviation & coefficient of variation were calculated using standard methods as described by Panse & Sukhatme (1964) correlation coefficients were calculated using as per the method proposed by Al-jibouri *et al*. (1958). he data were subjected to analysis of genetic divergence through D^2 statistic (Mahalanobis 1936) to quantify genetic divergence as proposed by Rao (1952), while Tocher's method as used to form cluster.

Results and Discussion

The genetic variability available in the base population is the most important prerequisite for selection in any crop improvement effort. For all of the agromorphological & biochemical parameters under consideration, the experiment's pooled analysis of variance indicated significant differences across 30 germplasm (Table 1). Sujatha et al. (2002) investigated the extent of divergence in taramira and found that the majority of yield and its contributing features had considerable variability.

The checks i.e., popular cultivated varieties namely RTM-314 & RTM- 1351 showed superior performance for most of the characters under study. Variety RTM-314 exhibited superiority for days to 50 percent flowering, days to maturity, secondary branches per plant & oil content while RTM-1351 showed good performance for primary branches per plant, length of siliqua, siliqua per plant, seed per siliqua & seed yield per plant. Germplasm RTM-1797 exhibited superior performance for secondary branches per plant, length of siliqua & seed yield per plant (Table 2).

The correlation coefficient, which expresses the intensity of association among a group of characters, is an important biometrical technique

Tabel 1: Pooled ANOVA for seed yield & its component traits in taramira

Source of variation	d.f	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	Length of siliqua (cm)	Siliqua per plant	Seeds per siliqua	Test weight (g)	Oil content (%)	Seed yield per plant(g)
Environment	2	1590.28**	1091.24**	633.52**	59.05**	134.40**	3.72**	3117.15**	2.11	0.55**	75.78**	63.68**
Rep in Env.	6	16.31	83.30	40.84	0.18	0.44	0.02	22.10	2.24*	0.08	8.58	0.12
Genotype	29	27.13*	115.85**	77.14*	1.95*	3.26**	0.14*	539.70**	0.65	0.47**	18.18**	1.39**
Genotype x environment	58	15.69**	46.34	38.84**	1.06**	0.60	0.06**	50.50**	16.80*	0.09*	5.38	0.27**
Error	174	8.03	40.22	19.60	0.15	0.38	0.03	24.06	0.24	0.05	5.07	0.15

***Significant at 5% level of significance **Significant at 1% level of significance**

Table 2: mean of seed yield & its components of taramira evaluated under different environments

Gemplasm	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	Length of siliqua (cm)	Siliqua per plant	Seeds per siliqua	Test weight (g)	Oil content (%)	Seed yield per plant(g)
RTM-314	56.44	130.67	77.55	6.25	9.44	2.74	70.30	20.58	3.18	39.92	3.76
RTM-1791	54.89	130.00	75.13	5.89	8.23	2.57	62.33	19.38	3.25	38.37	3.37
RTM-1792	54.33	128.33	74.46	5.61	7.73	2.34	51.34	18.73	2.80	36.05	3.01
RTM-1793	49.78	122.22	74.52	5.86	7.54	2.45	50.37	18.73	2.98	36.50	2.98
RTM-1794	53.67	119.89	73.16	5.17	7.42	2.45	53.57	18.62	2.75	35.20	2.96
RTM-1795	50.45	119.45	72.51	6.37	8.00	2.59	60.80	17.75	2.97	38.04	3.37
RTM-1796	50.56	122.44	71.53	5.56	7.92	2.49	56.51	18.08	2.76	35.24	3.14
RTM-1797	51.89	128.44	67.53	6.54	6.77	2.25	56.33	18.18	2.98	36.35	2.73
RTM-1798	54.11	125.89	68.19	6.01	8.09	2.53	59.84	19.05	3.00	37.20	3.35
RTM-1799	51.22	124.78	71.37	5.77	8.03	2.54	62.17	18.40	2.97	37.07	3.32
RTM-1800	55.11	124.67	76.08	6.01	8.55	2.61	62.00	20.14	3.11	38.25	3.88
RTM-1801	54.22	120.56	68.68	5.65	7.51	2.44	45.23	19.16	2.54	36.58	2.73
RTM-1802	51.00	121.33	72.54	5.24	7.07	2.37	52.59	18.40	2.54	35.34	3.02
RTM-1803	51.00	122.00	71.99	5.42	7.94	2.32	54.53	19.17	2.93	34.47	2.87
RTM-1804	52.44	122.55	76.39	5.06	8.36	2.33	48.82	19.05	3.05	36.94	3.05
RTM-1805	52.22	121.00	79.18	5.92	8.54	2.57	66.03	20.14	3.21	38.14	3.78
RTM-1806	54.22	119.55	73.67	4.87	8.15	2.66	59.97	17.97	2.86	35.95	3.15
RTM-1807	51.11	120.33	76.07	5.55	8.11	2.34	53.64	17.86	2.72	36.73	3.14
RTM-1808	53.11	121.33	75.72	5.47	7.41	2.56	41.64	19.17	2.55	35.85	2.93
RTM-1809	52.22	127.11	72.33	5.58	6.95	2.56	55.46	17.86	2.67	35.79	2.87
RTM-1810	51.89	123.33	75.99	5.98	8.49	2.53	65.57	20.03	3.13	38.44	3.93
RTM-1811	54.89	118.34	71.14	4.88	7.89	2.49	49.98	19.38	2.63	36.23	2.94
RTM-1812	53.11	124.00	73.68	5.00	7.67	2.51	54.96	17.64	2.87	35.08	2.98
RTM-1813	52.33	119.22	70.73	5.10	8.19	2.40	53.05	19.38	2.66	35.04	2.85
RTM-1814	54.33	124.89	71.71	5.97	7.12	2.48	48.90	19.38	2.70	35.69	2.87
RTM-1815	55.33	125.33	78.26	6.06	8.03	2.58	59.71	20.14	3.05	39.27	3.91
RTM-1816	55.45	128.45	71.96	5.98	7.14	2.56	38.55	19.49	3.01	35.85	2.85
RTM-1817	51.78	126.11	70.73	6.13	7.35	2.42	56.42	18.40	2.69	36.85	2.93
RTM-1818	53.22	127.45	74.98	5.81	8.04	2.28	50.29	18.73	2.43	36.72	2.82
RTM-1351	52.11	129.33	76.65	6.52	9.00	2.75	72.60	20.80	3.25	39.52	3.99
Mean	52.95	123.97	73.48	5.71	7.89	2.49	55.78	18.99	2.87	36.76	3.18
Minimum	56.44	130.67	79.18	6.52	9.44	2.75	72.60	20.80	3.25	39.92	3.99
Maximum	49.78	118.34	68.68	4.87	6.77	2.25	38.55	17.75	2.43	34.47	2.73
C.V	3.33	3.04	3.29	4.30	4.54	4.49	4.71	4.23	4.63	3.53	7.25
S.E	1.02	2.18	1.40	0.14	0.21	0.06	1.52	0.46	0.08	0.75	0.13

for constructing the selection index. The phenotypic correlations were assessed among eleven traits in 30 Taramira genotypes, & these revealed an intrinsic relationship between any two variables, which might have occurred due to pleiotropic gene action, linkage, or most likely both. The phenotypic correlation coefficients between yield & its component characters are reported in this study (Table 3). The most economic trait i.e., seed yield per plant & oil content showed positive & significant association with plant height, number of primary & secondary branches per plant, length of siliqua, siliqua per plant, seed per siliqua & test weight. Seed yield per plant & oil content also showed positive correlation & were significantly associated with each other. Selection criteria based on these component traits, as well as seed yield, will be more useful as a result. Earlier researchers Yadav & Pandey, (2018), Rauf & Rahim, (2018) and Shinwari *et al*., (2013) noticed a similar type of correlation between yield & yield-related traits.

The mean data of eleven quantitative traits were submitted to principal component analysis in this study, which used a data reductionist technique employing a linear combination of optimally-weighted observed variables to discover the plant features that contribute the most to overall variance. Only three of the eleven PCs had an Eigen value greater than 1.0, indicating 76.8% diversity among 30 genotypes (Table 4). The first principal component (PC1) accounted for 51.3 percent of total variance, whereas PC2 & PC3 contributed 13.5 & 12.1 percent of total variation, respectively. This similar result agreement by Ara *et al*. (2018) and Parvin *et al*. (2019).

Table 5 shows the % contribution of individual characteristics to genetic divergence for all eleven characters. The character siliqua per plant contributed the most to total genetic divergence (30.11%), followed by test weight (22.53), number of primary branches per plant (18.62), number of secondary branches per plant (13.56), & seed yield per plant (13.56). The findings of Renuka Devi *et al*., (2017), Kumari & Kumari, (2017) were in similar direction to the present research findings. Table 6 shows the factor loadings of characters from PCA, which have five components that identify the main characters responsible for the most variability. All of the characteristics contributed to the overall variety in a good way. While the most significant contributions in PC1 were seed yield per plant, oil content, test weight, siliqua per plant, & secondary branches per plant, the most significant contributors in PC2 were seed yield per plant, oil content, test weight, siliqua per plant, & secondary branches per plant. Plant height (0.351), secondary branches per plant (0.329), & seed production per plant all contributed to the PC2 (0.154). siliqua per plant (0.357) made the most contribution to PC3, followed by secondary branches per plant (0.244), & test weight (0.244). (0.159). The goal of principal component analysis is to find the smallest number of components that may explain the most variability out of all the variables, as well as to rank items based on PC scores. Germplasms from clusters separated by a large statistical distance might be used in a hybridization programme to obtain a broad range of diversity among segregates. Cluster VII had the most intra-cluster distance, whereas clusters IV, V, VIII, & IX had none. Similar result was found by Sodani *et al*., (1990); Naznin *et al*., (2015), Doddabhimappa *et al*., (2010) and Chandra *et al*., (2018). Cluster analysis is a data classification approach that allows for the separation of genetic material into several homogeneous groups. It makes it easier to categories genotypes based on morpho-genetic characteristics. Cluster analysis also aids in the reduction of variance within a group while boosting variance between groups, as well as the detection of outliers.

For majority of the characters studied, there was a lot of variance in cluster mean performance. Using Tocher's approach, a hierarchical clustering methodology based on eleven quantitative trait data was able to arrange 30 germplasms into nine groups (Table 7 Fig. 1). Cluster II had the most germplasm (13), followed by cluster I (5), cluster III & cluster VII (3), cluster VI (2), & the other clusters each had one germplasm. Cluster VI & VII (15.66) had the greatest inter-cluster distance, followed by Cluster IV & Cluster VI (14.26), Cluster VI & Cluster IX (13.98), & Cluster V & Cluster IX (13.98). (13.68). Cluster II & III (6.07) & Cluster I & Cluster III (6.22) had the shortest inter-cluster distances. Except for days to 50% flowering (highest in cluster IV) & number of primary branches per plant (highest in cluster IX), Cluster VI had the highest mean value for all yield & component characters, while Cluster IX had the lowest mean value for

Table 3: Phenotypic correlation coefficients for different traits in 30 germplasms of taramira over the pooled environmental data.

Characters	Days to 50% flowering	Days to maturity	Plant height(cm)	No. of primary branches per plant	No. of secondary branches per plant	Length of siliqua(cm)	Siliqua per plant	Seeds per siliqua	Test weight(g)	Oil content (%)
Days to 50% flowering										
Days to maturity	0.184									
Plant height	0.021	-0.002								
primary branches per plant	0.031	0.386**	0.016							
secondary branches per plant	0.111	0.120	0.402**	0.165						
Length of siliqua	0.273**	0.064	0.263*	0.245*	0.312**					
Siliqua per plant	-0.019	0.218*	0.283**	0.391**	0.601**	0.427**				
Seeds per siliqua	0.410**	0.155	0.272**	0.250*	0.447**	0.297**	0.289**			
Test weight	0.107	0.280**	0.253*	0.396**	0.450**	0.456**	0.566**	0.354**		
Oil content	0.120	0.329**	0.431**	0.449**	0.527**	0.378**	0.528**	0.420**	0.489**	
Seed yield per plant	0.064	0.129	0.465**	0.377**	0.616**	0.522**	0.700**	0.436**	0.611**	0.608**

Table 4: Principal components showing the eigen values & proportion of variation.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Eigenvalues	5.644	1.481	1.329	0.688	0.493	0.461	0.372	0.226	0.177	0.071	0.06
Proportion	0.513	0.135	0.121	0.063	0.045	0.042	0.034	0.021	0.016	0.006	0.005
Cumulative Proportion	0.513	0.648	0.768	0.831	0.876	0.918	0.952	0.972	0.988	0.995	1

Table 5: Contribution of different characters towards genetics divergence among 30 taramira germplasm.

	Days to 50% flowering	Days to maturity	Plant height(cm)	No. of primary branches per plant	No. of secondary branches per plant	Length of siliqua(cm)	Siliqua per plant	Seeds per siliqua	Test weight(g)	Oil content (%)	Seed yield per plant(g)
Times Ranked	8	4	12	81	59	5	131	4	98	2	31
Contribution	1.84	0.92	2.76	18.62	13.56	1.15	30.11	0.92	22.53	0.46	7.13

Table 6: Principal component analysis for taramira germplasm accessions – non rotated loadings.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
1	0.129	-0.092	-0.774	0.203	-0.12	0.118	-0.111	0.415	0.179	0.3	-0.01
2	0.186	-0.622	-0.136	-0.151	-0.551	0.03	-0.087	-0.372	-0.037	-0.242	0.159
3	0.267	0.351	-0.07	-0.587	-0.315	-0.498	-0.001	-0.018	0.077	0.251	-0.197
4	0.236	-0.565	0.244	-0.094	0.395	-0.195	-0.115	0.095	-0.143	0.565	0.025
5	0.334	0.329	0.001	-0.057	-0.09	0.465	-0.282	-0.106	-0.618	0.199	0.2
6	0.298	0.113	-0.132	0.647	0.013	-0.528	0.095	-0.323	-0.254	-0.025	-0.064
7	0.331	0.058	0.357	0.29	-0.208	0.296	-0.263	-0.131	0.498	0.175	-0.424
8	0.306	0.009	-0.362	-0.261	0.547	0.234	0.213	-0.475	0.172	-0.132	-0.186
9	0.34	-0.073	0.159	0.033	-0.195	0.203	0.812	0.302	-0.123	0.015	-0.086
10	0.385	-0.088	0.041	-0.08	0.167	-0.112	-0.322	0.471	-0.158	-0.608	-0.274
11	0.392	0.154	0.122	0.027	0.099	-0.088	-0.016	0.089	0.419	-0.104	0.771

Table 7: Constituents of 9 clusters of 30 taramira germplasm

Cluster	No. of germplasm	Germplasm
Cluster I	5	RTM-1805, RTM-1810, RTM-1800, RTM-1791, RTM-1815
Cluster II	13	RTM-1794, RTM-1812, RTM-1796, RTM-1813, RTM-1807, RTM-1803, RTM-1809, RTM-1792, RTM-1818, RTM-1793, RTM-1817, RTM-1814
Cluster III	3	RTM-1798, RTM-1799, RTM-1795
Cluster IV	1	RTM-1811
Cluster V	1	RTM-1806
Cluster VI	2	RTM-314, RTM-1351
Cluster VII	3	RTM-1801, RTM-1808
Cluster VIII	1	RTM-1804
Cluster IX	1	RTM-1797

Table 8: Average intra (bold) & inter-cluster D^2 values for nine clusters in 30 taramira germplasm

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	**3.58**	9.06	6.22	11.06	9.42	5.45	12.23	7.81	11.11
Cluster II		**4.93**	6.07	6.13	7.76	12.37	7.18	6.29	8.57
Cluster III			**3.2**	8.27	7.42	8.84	9.8	7.37	7.99
Cluster IV				**0**	5.7	14.26	7.57	6.5	12.32
Cluster V					**0**	11.66	11.46	7.35	13.68
Cluster VI						**3.99**	15.66	11.37	13.98
Cluster VII							**5.76**	8.4	10
Cluster VIII								**0**	11.21
Cluk8ster IX									**0**

Table 9: Cluster means of 9 clusters of 30 taramira germplasm from three different environments

	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches per plant	No. of secondary branches per plant	Length of siliqua	Siliqua per plant	Seeds per siliqua	Test weight	Oil content	Seed yield per plant
Cluster I	53.89	124.87	76.93	5.97	8.37	2.57	63.13	19.97	3.15	38.49	3.77
Cluster II	52.19	123.49	72.96	5.54	7.62	2.42	53.2	18.54	2.73	35.75	2.96
Cluster III	51.93	123.37	70.69	6.05	8.04	2.55	60.94	18.4	2.98	37.44	3.35
Cluster IV	54.89	118.34	71.14	4.88	7.89	2.49	49.98	19.38	2.63	36.23	2.94
Cluster V	54.22	119.55	73.67	4.87	8.15	2.66	59.97	17.97	2.86	35.95	3.15
Cluster VI	54.28	130	77.1	6.38	9.22	2.74	71.45	20.69	3.21	39.72	3.88
Cluster VII	54.26	123.45	72.12	5.7	7.35	2.52	41.81	19.27	2.7	36.1	2.83
Cluster VIII	52.44	122.55	76.39	5.06	8.36	2.33	48.82	19.05	3.05	36.94	3.05
Cluster IX	51.89	128.44	67.53	6.54	6.77	2.25	56.33	18.18	2.98	36.35	2.73
Maximum	54.89(IV)	130(VI)	77.1 (VI)	6.54 (IX)	9.22 (VI)	2.74 (VI)	71.45 (VI)	20.69 (VI)	3.21 (VI)	39.72 (VI)	3.88 (VI)
Minimum	51.89 (IX)	118.34(IV)	67.53 (IX)	4.87 (V)	6.77 (IX)	2.25 (IX)	41.81(VII)	17.97 (V)	2.63 (IV)	35.75 (II)	2.73 (IX)

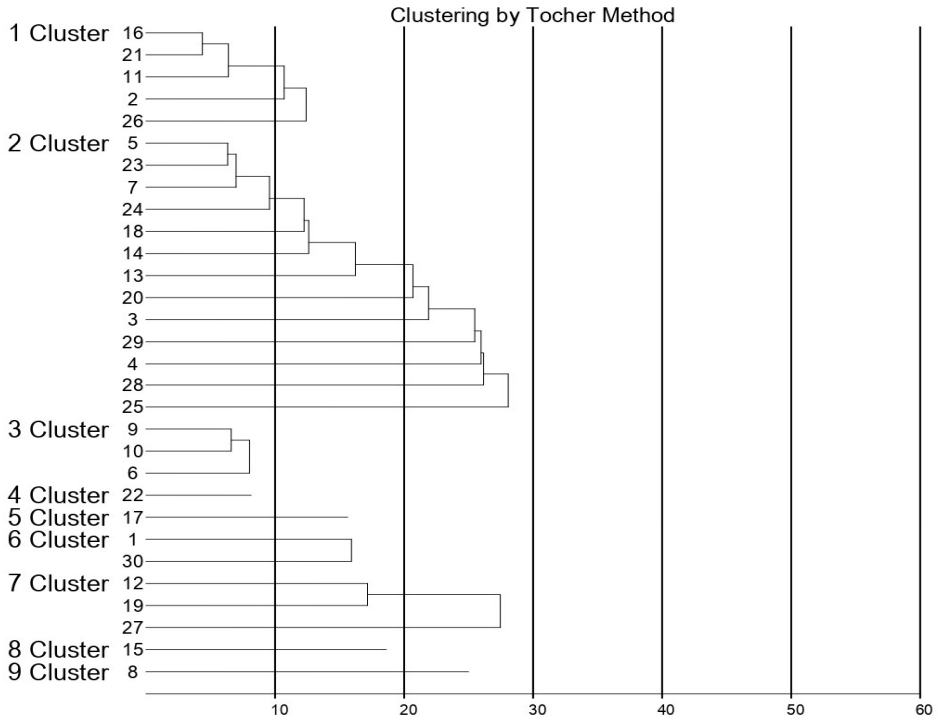

Figure 1: Dendogram of 30 taramira

days to 50% flowering, plant height, secondary branches per plant, length of siliqua, & seed yield per plant (Table 9). This result indicated that the germplasm under investigation was genetically diverse & that the base material included a significant degree of variability indicating that selection to produce new enhanced inbred lines is possible. Seed yield is such a complex & reliable character, crop improvement through indirect selection using these traits would be effective.

Conclusion

Mean sum of square of all characters under investigation showed significant variations i.e., existence of sufficient variability in selected germplasms. Selection of more than one character at a time can done because seed yield have significant positive correlation with its components. Characters i.e., length of siliqua, seed per siliqua, number of primary & secondary branches per plant are responsible to contributes to the total diversity because these characters have high contribution percentage. PC I to PC III contribute 75 % of total genetics divergence so more emphasized should be done in three principle components. High intra cluster distance accounts to higher genetic divergence between clusters & vice-versa. Gemplasm belongs to cluster I, cluster V, cluster VI & cluster VIII are suitable to serve as parents in development of hybrid varieties as these clusters have high inter cluster distance & high cluster mean for seed yield & oil content. Characters *i.e.,* length of siliqua, seed per siliqua, number of primary & secondary branches per plant are responsible to contributes to the total diversity because these characters have high contribution percentage will be exploited for crop improvement in taramira.

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Conflict of interest

The authors declare that they have no conflict of interest.

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