Classification and Selection of Representative Varieties of *Eruca sativa* Mill. (Taramira)

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A total of 235 accessions of *Eruca sativa* Mill. (Taramira) , including two checks were grown in augmented design for evaluation. Observations on 11 characters namely plant height; primary branches per plant, secondary branches per plant; main shoot length, number of siliqua on main shoot, siliqua length, number of seeds per siliqua, yield per plant, 1000-seed weight, oil content and protein content were recorded. Oil content and protein content together were also calculated for this study. Using principal component analysis, all the 235 accessions, were classified into nine clusters. Subjective classification of different characters between the clusters based on coefficient of variance was also done. It revealed that there are significant differences in the pattern of subjective classification of different characters between the clusters.

Key words: Taramira, *Eruca sativa* Mill., Cluster analysis, Principal component analysis, Subjective classification

Eruca sativa Mill. (taramira), a rapeseed and close relative of mustard is believed to be a native of southern Europe and North Africa. It is grown in the drier part of North-west India comprising the states of Punjab, Haryana, Uttar Pradesh and Rajasthan. Maintenance of a huge germplasm of rapeseed at the National Research Centre on Rapeseed-Mustard (NRCRM), Bharatpur, Rajasthan is not only a cumbersome task but also quite difficult for the breeders, to select the varieties for breeding programme. Hence, this study was carried out to classify huge taramira germplasm into different groups based on principal component analysis (Jaiswal and Sangwan, 1998). The representative varieties of different groups are also selected to make ease of the breeder to maintain and select the varieties for breeding purposes (Mishra *et al.,* 1991).

Materials and Methods

Two hundred and thirty five accessions including checks of *Eruca sativa* (taramira) were grown in augmented design for germplasm evaluation during *rabi* 1999-2000-01 at the National Research Centre on Rapeseed-Mustard, Bharatpur (Rajasthan). Two check varieties (RTM-314 and T-27) were grown repeatedly after each ten accession to evaluate the new one. Each accession was sown on two rows of four-meter at 45 cm distance and plant-to-plant spacing of 15 cm was maintained by thinning. Recommended doses of fertilizer (N: P: K@ 40:20:0 kg/ha) were applied. Suitable agronomic practices and plant protection measures were adopted.

Observations were recorded on five randomly selected plants. The traits studied were plant height (cm); primary branches per plant (nos.); secondary branches per plant (nos.); main shoot length (cm); siliqua on main shoot (nos.); siliqua length (cm); seed per siliqua (nos); yield per plant (gm); 1000-seed weight (gm); oil content (%) and protein content (%). Oil content plus protein content together were also considered for the classification.

Results and Discussion

A total of 235 accessions of taramira comprising BPTM 1 to 233 and two check varieties RTM-314 and T-27 have been classified in to 9 clusters (Mishra *et al.,* 1991 and 1998). Cluster, numbers of accession (N), within mean sum of square and cluster members were presented (Table 1). Considering within mean sum of square it revealed that most diverse cluster was cluster number 2 (10.18), followed by cluster number 5 (7.53), cluster number 7 (7.42), cluster number 4 (7.16), cluster number 1 (6.71), cluster number 6 (6.20), cluster number 8 (6.18), cluster number 3 (5.90) and cluster number 9 (4.32) (Table 1).

The mean, coefficient of variance (CV) and percentage contribution to divergence of different characters under study are presented (Table 2). The most divergent character was secondary branches per plant (CV = 32.42) followed by yield per plant (CV = 31.73); primary branches per plant (CV = 21.61); main shoot length (CV = 14.4); siliquae on main shoot (CV = 12.78); plant height (CV = 10.79) etc. (Table 2). If percentage contribution towards divergence for the individual characters kept in descending order like 1000-seed weight (10.60%); seed per siliqua (10.24%); main shoot length (9.34%); yield per plant (9.14%); plant height (8.55%); siliqua length (8.34%);

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Table 1. Classification of 235 *Eruca sativa* Mill. accessions into 9 clusters

Cluster (BPTM)	Accession Number in Cluster	Within MSS	Cluster members
1	30	6.71	104; 71; 27; 24; 77; 128; 10; 130; 56; 118; 115; 109; 107; 78; 26; 129; 131; 122; 125; 25; 121; 28; 113; 127; 116; 123; 167; 126; 124; 132
2	14	10.18	117; 74; 165; 135; 76; 136; 143; 204; 139; 140; 142; 144; 137; 141
3	37	5.90	194; 3; 227; 229; 186; RTM-314; 1; 228; 181; T-27; 119; 231; 225; 199; 99; 179; 213; 134; 138; 156; 201; 191; 189; 173; 112; 180; 200; 205; 114; 215; 206; 230; 198; 190; 188; 208; 32
4	15	7.16	57; 192; 233; 174; 232; 153; 154; 21; 8; 193; 168; 146; 160; 145; 159;
5	30	7.53	59; 106; 61; 23; 7; 4; 14; 67; 212; 12; 20; 11; 65; 19; 13; 5; 152; 16; 30; 66; 158; 68; 149; 18; 148; 17; 147; 150; 161; 151
6	21	6.20	98; 92; 84; 89; 81; 87; 80; 79; 95; 91; 90; 86; 94; 82; 111; 85; 83; 93; 100; 110; 162
7	35	7.42	203; 226; 101; 172; 202; 97; 184; 219; 170; 178; 196; 169; 103; 222; 2; 88; 163; 105; 120; 183; 166; 108; 64; 157; 171; 182; 164; 175; 102; 197; 177; 176; 195; 185; 223
8	18	6.18	155; 44; 210; 214; 39; 216; 211; 36; 224; 209; 35; 49; 220; 217; 221; 218; 207; 33
9	35	4.32	52; 62; 75; 53; 72; 63; 60; 38; 55; 70; 69; 54; 50; 42; 41; 15; 187; 9; 22; 48; 37; 58; 46; 133; 51; 40; 47; 45; 6; 73; 43; 29; 31; 34; 96

Table 2. Mean, CV and percentage contribution to divergence of different characters under study

Character	Mean	CV	Percentage contribution to divergence
Plant height (PH)	84.55	10.79	8.55
Primary branches (PB)	7.45	21.61	8.33
Secondary branches (SB)	14.96	32.42	7.85
Main shoot length (MSL)	38.48	14.40	9.34
Siliquae on main shoot (SMS)	17.06	12.78	7.59
Siliqua length (SL)	1.92	8.85	8.34
Seeds per siliqua (SS)	19.3	9.17	10.24
Yield per plant (YPP)	9.77	31.73	9.14
1000 seed weight (1000 SW)	4.11	6.81	10.60
Oil content (OC)%	35.12	1.74	8.33
Protein content (PC)%	22.51	2.22	6.86
OC and PC	57.63	1.35	4.42

primary branches (8.33%) and oil content (8.33%), these eight characters explained 72.87% variation (Table 2), whereas, the principal component analysis revealed that only five principal component explained 73.72% and eight principal component explained 93.20% towards genetic divergence (Hepziba *et al.*, 1995). Therefore, use of principal component is more appropriate than the use of individual character's contribution towards the study of genetic divergence.

Seed is usually marketed for both oil and protein content but oil content is negatively correlated to protein content in taramira (Table 3). In the evaluated accessions of taramira, oil content, protein content and oil plus protein content were not observed to be important characters for the study of the genetic divergence (CV's are 1.74; 22.2 and 1.35 % respectively) (Table 2) (Aluko and Mcintosh, 2001). After comparing the Table 2 and 3 simultaneously, highly correlated variable oil content with oil plus protein content ($r^2 = 0.726$) and PC with OC plus PC (r^2=0.533) could be ignored but important variables for breeding purposes such as SB, PB ($r^2 = 0.689$); SMS, MSL ($r^2 = 0.564$); SS, SL ($r^2 = 0.538$); MSL, PB ($r^2 = 0.486$); YPP, SB ($r^2 = 0.459$) and 1000-SW, YPP ($r^2 = 0.375$) could be selected.

Characteristics of classified clusters

All the 235 accession of taramira were classified into nine distinct clusters. The feature of the distinct cluster is explained as cluster number 3 had 37 accessions including two check varieties (RTM-314 & T-27). It revealed that accessions of cluster number 3 had the characteristics of two check varieties and the most variable characters in cluster number 3 is YPP followed by SB, PB and SMS (Table 4). Cluster number 9 had unique feature in CV not more than 2.846 in any character under

Table 3. Correlation coefficient of different characters

Character	Correlation matrix											
	PH	PB	SB	MSL	SMS	SL	SS	YPP	1000-SW	OC	PC	OC&PC
PH		0.106	0.302	0.203	0.294	0.026	-0.033	0.362	0.282	-0.304	-0.027	-0.281
PB			0.689	0.486	0.204	0.004	-0.089	0.172	0.041	0.054	-0.141	-0.053
SB				0.308	0.232	-0.034	-0.059	0.459	0.099	-0.004	-0.181	-0.129
MSL					0.564	0.169	0.021	-0.059	0.096	-0.006	-0.106	-0.079
SMS						0.038	0.003	0.177	0.103	-0.059	-0.161	-0.164
SL							0.538	0.035	0.097	-0.084	0.124	0.015
SS								0.147	-0.147	-0.028	0.001	-0.024
YPP									0.375	-0.190	-0.119	-0.248
1000-SW										-0.105	-0.020	-0.105
OC											-0.195	0.726
PC												0.533
OC&PC												

Table 4. Coefficient of variance of individual characters along with over all CV in different clusters

Character	Cluster (CV)									Overall
	1	2	3	4	5	6	7	8	9	CV
PH	9.508	7.443	9.891	12.906	11.686	9.083	8.915	10.881	2.846	10.79
PB	22.431	20.759	13.970	22.062	18.426	17.528	11.779	24.436	0.372	21.61
SB	29.458	35.233	35.694	34.071	17.034	17.512	19.534	66.640	0.864	32.42
MSL	14.911	11.959	9.681	9.497	12.685	10.391	10.271	16.269	1.006	14.4
SMS	13.596	17.685	10.926	11.545	10.204	16.182	13.594	11.941	0.617	12.78
SL	7.112	12.077	8.062	12.348	8.898	9.176	9.936	7.059	0.051	8.85
SS	10.188	6.685	9.025	8.524	7.458	6.473	8.848	10.724	0.550	9.17
YPP	33.171	37.542	40.853	22.860	40.093	37.405	29.249	41.803	1.390	31.73
1000-SW	12.905	8.041	10.013	11.398	12.434	9.807	10.173	12.762	0.158	6.81
OC	1.804	2.259	3.154	1.513	2.331	2.230	1.871	1.726	0.202	1.74
PC	2.545	5.926	3.735	1.844	2.446	2.360	2.839	2.717	0.143	2.22
OC & PC	1.448	2.411	2.936	0.644	1.456	1.292	1.496	1.419	0.204	**1.35**

study (Table 4). Cluster number 1 had the most variable characters YPP followed by SB, PB and MSL. The most variable characters in cluster number 2 was also YPP followed SB, PB and SMS. Cluster number 4 and number 8 had most variable characters SB followed by YPP and PB but separated by the forth-variable character i.e. PH in cluster number 4 but MSL in cluster number 8 (Mishra *et al.*, 1998).

Similarly, cluster number 5 and number 6 had most variable characters YPP followed by PB and SB but it can be distinguished with the forth-variable character MSL in cluster number 5 and SMS in cluster number 6. Cluster number 7 can identify with the characteristics of most variable character YPP followed by SB, SMS and PB. Presence of some peculiar characteristics in every cluster may help the breeders to select the clusters having characters of their choice for their breeding programme.

Ignoring the three characters namely oil content, protein content and oil plus protein content because of their low CV's (< 6%), the subjective classification of rest characters in the different clusters was made based on their CV's (Table 5). Chi-square test was applied to the subjective classification. The calculated, chi-square value at 3 d.f. was significant at 1 % level of significance (Calculated value = 14.28; tabulated value = 11.34). It can therefore, be concluded that there are significant differences in the pattern of presented subjective classification of different agro-morphological characters between the clusters and classification of all the accessions into nine clusters.

The study was also an attempt to select the few representative varieties from the different classified clusters to make ease for the scientists to maintain the germplasm. For this purpose individual recorded observation of different characters in different clusters and over all mean of the all the characters of 235 accessions was taken into account.

The observed record of characters in different clusters that were more than over all mean were selected and taken into consideration to select the representative

Table 5. Subjective classification of different characters between the clusters based on CV

Characters	1	2	3	4	5	6	7	8	9
PH	L	L	M	H	H	L	L	M	VL
PB	H	H	L	H	M	M	L	H	VL
SB	M	H	H	H	L	L	L	H	VL
MSL	H	H	L	L	H	M	M	H	VL
SMS	H	H	M	H	M	H	H	H	VL
SL	L	H	L	H	L	L	L	L	VL
SS	M	L	L	L	L	L	L	M	VL
YPP	M	H	H	L	H	H	L	H	VL
1000-SW	H	L	M	H	H	L	M	H	VL

VL = Very less ; L = Less ; M = Medium ; H = High

varieties of the individual cluster. Individual variety of different clusters was selected as representative varieties, which ranked first more times in respect to individual character of that particular variety (Mishra *et al.*, 1998). All the selected 59 representative varieties of different clusters were presented in Table 6. By this, we can suggest to maintain only 59 accessions (25%) in place of 235 accessions and taken into account for breeding programme, selecting the varieties from the individual cluster with specific character which suits the breeder for their breeding programme.

Table 6. Representative varieties of different clusters

Cluster/Total Number of Varieties	Representative varieties (BPTM)
1(8)	10; 118; 115; 131; 122; 125; 167; 132
2(5)	117; 165; 135; 139; 144;
3(9)	194; 3; 1; 119; 179; 134; 112; 188; 32
4(5)	232; 193; 146; 145; 159
5(9)	59; 61; 4; 212; 12; 68; 18; 150; 151
6(6)	98; 84; 111; 83; 100; 110
7(9)	226; 219; 196; 222; 2; 183; 182; 175; 223
8(4)	155; 216; 221; 207
9(4)	60; 42; 22; 58

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References

Aluko RE and T Mcintosh (2001) Polypeptide profile and functional properties of defatted meals protein isolates of canola seeds. *Journal of Science of Food and Agriculture* **81:** 391-393.

Hepziba SJ, M Theradimani, R Saraswathi and S Palanisamy (1995) Genetic divergence in pearmillet, *Crop Research* (Hisar) **9:** 96-104.

Jaiswal UC and ML Sangwan (1998) Variable selection for discrimination-A principal component analysis approach. Recent Advances in Information Theory, Statistics and Computer Application. p 86-88.

Kour Anupreet and SP Singh (2004) Evaluation of genetic diversity in different genotypes of *Brassica juncea*, In: Proc. 4th International Crop Science Congress, Brisbane.

Mishra AP, J Sarangi and SD Sharma (1991) Classification of the varieties of rice of India, In: Statistical Research Report, Deptt. of Statistics, Utkal University, Bhubaneswar. p 1-51.

Mishra AP, LS Kaushik and SD Sharma (1998) A study of the origin of rice varieties of India through Principal Component. In: Proceedings of First Annual Conference of Society of Statistics, Computer and Application (SSCA). p 41-57.