

Genetic Variability and Factor Analysis in Rapeseed (*Brassica Rapa L.*) Germplasm Collection for Yield Related Traits

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Abstract: The Principal Component Analysis (PCA), one of multivariate analysis methods elucidates among a set of the traits which ones are decisive in genotypic differentiation and selection. The present study was undertaken in rabi 2013-14 at three locations. The collection comprising of 10 genotypes including two checks namely SS-1 and farmer's variety was studied using factor analysis. Ten quantitative traits related to seed yield namely days to flowering, days to maturity, plant height, primary branches plant⁻¹, length of main raceme (cm), number of siliquae on main raceme, number of siliqua/plant, number of seeds siliqua⁻¹, 1000-seed weight and seed yield/plant. Analysis of variance revealed that there were significant differences between checks and accessions between accessions and between checks for all the traits. It indicated presence of substantial amount of variation among the test entries. The factor analysis was based on Pearson correlation matrix and euclidean distances. Total variance explained by the first principal component was 67.03% and the variation explained by the second component with 10.6%. Latent roots (eigen values) are between 6.703 for the first and 1.06 for the second. Plant height and 1000-seed weight were the important traits in the first principal component. Primary branches per plant and number of siliqua on main raceme were the important traits in second principal component.

Key words: Genotype; principal component, trait, variation, eigen values, euclidean distances

INTRODUCTION

Brassica rapa L. commonly known as field mustard or turnip mustard belonging to the family Brassicaceae. The seeds of *Brassica rapa* L. contain 42% oil and 25% protein. It also serves as important source of raw material for industrial use such as in making soaps, paints, hair oils, lubricants, textile auxiliaries, pharmaceuticals and so, on. It is the third most important oil crop in the world accounting for over 16% of the world's edible oil supply. India holds a premier position in rapeseed-mustard economy of the world with 2nd and 3rd rank in area and production, respectively. It is the third largest rapeseed-mustard producer in the world after China and Canada with 12% of world's total production (Gupta and Pratap, 2007). It is grown on an area of 5.8 m ha with a production of 6.8 mt and an average productivity of 1.17 t ha⁻¹ (Anonymous, 2013). This crop accounts for nearly one third of the oil produced in India, making it the country's key edible oilseed crop after groundnut and soybean. This group of oilseed crops is gaining wide acceptance because of adaptability for both rainfed as well as irrigated areas and suitability for sole as well as mixed cropping. Being a major rabi (winter season) oilseed crop it has greater potential to increase the availability of edible oil from the domestic production. Despite its wide

adaptability for varied agro-climatic conditions, the area, production and yield of rapeseed-mustard in India have been fluctuating due to various biotic and abiotic stresses coupled with India's domestic price support programmes. Nevertheless, the crop has a potential to ensure the nutritional security and contribute to livelihood security as well.

In the state of Jammu and Kashmir, brown sarson is the major oilseed crop cultivated on a large scale. During the year 2012-13, the crop was grown on an area of 0.67 lakh ha with a production of 5.32 lakh quintals and an average productivity of 7.94 quintals ha⁻¹ (Anonymous, 2013). Not much work has been carried out on genetic improvement of brown sarson. In order to achieve higher production and consequently change the edible oilseed scenario of the state it is imperative to develop improved varieties with high yielding ability, high oil content and early maturity. Besides yield potential, the variety should also possess stability in its performance over a range of environments. Knowledge on the interaction and stability is foremost in breeding varieties for wider adaptation in adverse agro-climatic conditions. The aim of the breeding programme should be to develop genotypes that can withstand unpredictable transient environmental fluctuations.

In order to increase the existing genetic variability and to develop rapeseed cultivars that will have high seed and oil yield potential, exploitation of the gene pool is of foremost importance. Many researchers have been evaluating the diversity in different collections of rapeseed genotypes using multivariate techniques (Choudhary and Joshi, 2001). Existence of genetic diversity is very essential to meet the present and future crop breeding challenges. It is a prerequisite for the development of improved cultivars with wider adaptability and broad genetic base. It can be estimated through biometrical procedures such as mahalanobis's D²-statistic and is possible to choose genetically diverse parents. Diversity analysis greatly helps the breeder in identification and proper choice of parents for specific breeding objectives. The selection of potential varieties in a breeding program is based on the knowledge of genetic diversity amongst them. Therefore the present study was undertaken to collect information on genetic divergence in the genotypes and selection of suitable diverse parents for the utilization in future hybridization program.

The Principal Component Analysis (PCA), one of multivariate analysis methods elucidates among a set of the traits which ones are decisive in genotypic differentiation. PCA enables easier understanding of impacts and connections among different traits by identifying them and explaining their roles. This method is a powerful multiple method to apply evaluation yield component, identify biological relationships among traits (Acquaah *et al.*, 1992) decrease associated-traits to a few factors (Johnson and Wichern, 1996) and description of correlations among variables. Factor analysis has the potential of enhancing our knowledge of causal relationship of variables and can help to know the nature and sequences of traits to be selected for breeding program (Khameneh *et al.*, 2012).

MATERIAL AND METHODS

The present study was undertaken in rabi 2013-14. The basic material for the study comprised 10 genotypes of brown sarson (*Brassica rapa* L.). Each genotype was grown in a 3-row experimental plot of 3 m length with

inter and intra row spacing of 30 and 10 cm, respectively. The plants were space planted for optimal expression of traits and lack of prior knowledge about growth habit of the genotypes. Data was collected from five randomly selected competitive plants on various morphological, maturity, yield and yield contributing traits. The analysis of variance was done using WINDOSTAT advanced biometrics software. We considered ten quantitative traits related to seed yield namely days to flowering, days to maturity, plant height, primary branches plant⁻¹, length of main raceme (cm), number of siliquae on main raceme, number of siliqua/plant, number of seeds siliqua⁻¹, 1000-seed weight and seed yield/plant. The factor analysis was based on Pearson correlation matrix and Euclidean distances. Latent roots or eigen values for all principal components were shown. The variability of the collection in was interpreted based on the seven principal components. Non-rotated and rotated values of latent vectors (component weights, factor loadings) were shown. The Varimax method was used for the rotation of principal components. Both the unrotated and the varimax rotated PCA values were calculated by the statistical package StatistixXL.

RESULTS AND DISCUSSION

Principal Component Analysis (PCA): PCA is a statistical method which attempts to describe the total variation in multivariate sample using fewer variables than in the original data set. In the end, the analysis results in the identification of the major attributes that are responsible for the observed variation within a given collection. Principal component analysis was carried out with 10 genotypes of *Brassica rapa* L. (Table 1). The computed eigen values for the 9 variables subjected to principal component analysis, together with the corresponding proportion and cumulative explained variances are given in Table 2. The first principal component accounted for 64.57% of the total variation while principal components two and three accounted for 9.22 and 4.30%, respectively. The fourth principal component accounted for 2.43% and 1.020 variability.

Table 1: Mean performance for 10 rapeseed genotypes for 10 quantitative traits

Genotypes	DF	DM	PH	PBPP	LMR	NSMR	NSPP	NSPS	100SW	SYPP
KBS-69	170.1	222.8	122.2	6.1	0.01	57.65	220.7	18.66	3.13	6.34
KBS-33	168.4	222.6	122.8	6.64	0.006	55.73	220.1	19.18	3.12	6.15
KBS-49	167.6	221.7	126.2	6.89	0.016	57.67	229.6	20.02	3.19	6.68
KBS-38	170.2	222.8	124.2	6.61	0.01	56.76	225.9	16.11	3.17	6.53
KBS-5	168.8	224.8	119.8	6.32	0.012	49.79	214.8	18.85	3.11	5.64
KBS-40	171	223.9	114.3	6.11	0.019	49.06	210.4	16.27	2.89	5.41
FV	171.6	225.1	110.8	5.88	0.02	48.39	209.2	14.78	2.7	4.32
KBS-28	171.1	225.7	118	6.4	0.02	53.2	215.1	17.74	3.08	5.12
KS-101	170.1	223.4	113.5	5.51	0.017	54.36	209.6	17.06	3.01	3.67
SS-1	170.6	224.3	120.5	5.42	0.018	55.39	219.1	17.53	2.99	3.52
Mean	169.95	223.71	119.23	6.188	0.0148	53.8	217.45	17.62	3.039	5.338

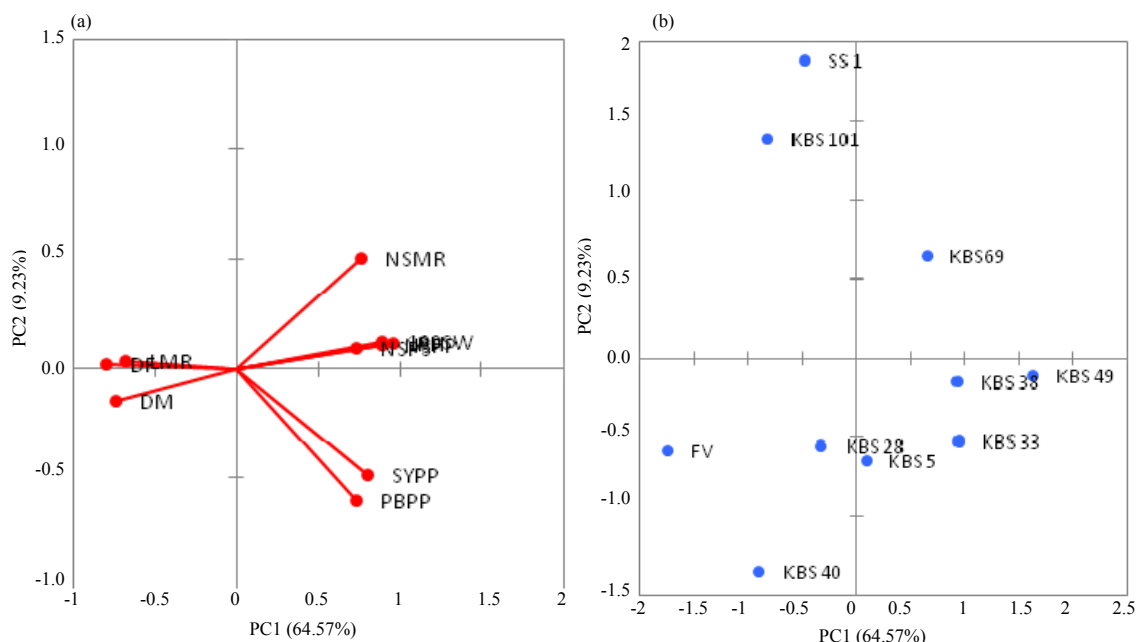


Fig. 1(a-b): Genotype v/s trait biplot for yield traits (a) Factor loadings (axes F1 and F2: 73.80 %) and (b) Observations (axes F1 and F2: 73.80 %)

Table 2: Eigen values (Latent roots) and rotated component loadings (values of principal component traits of rapeseed)

Principal component	Eigen value	Variability (%)	Cumulative variability (%)
PC 1	6.457	64.571	64.571
PC 2	0.923	9.228	73.800
PC 3	0.430	4.305	78.104
PC 4	0.243	2.432	80.536
PC 5	0.102	1.020	81.557

Table 3: Factors loadings for component character traits in principal component 1-5

Trait	PC 1	PC 2	PC 3	PC 4	PC 5
DF	-0.315	0.020	0.540	-0.206	0.345
DM	-0.290	-0.154	-0.142	-0.589	0.322
PH	0.376	0.115	0.105	-0.371	0.079
PBPP	0.290	-0.625	0.089	-0.229	-0.264
LMR	-0.268	0.035	0.054	-0.451	-0.472
NSMR	0.303	0.525	0.343	0.035	0.016
NSPP	0.349	0.109	0.352	-0.256	-0.362
NSPS	0.291	0.096	-0.569	-0.139	-0.079
100SW	0.349	0.126	-0.186	-0.289	0.513
SYPP	0.315	-0.508	0.259	0.219	0.278

Contribution of characters towards divergence of the genotypes: The factor loadings of characters from PCA retained five components identified the major characters responsible for maximum variability Table 3. The largest contribution to PC1 was by plant height (0.376) followed by 100-seed weight and number of siliqua per plant. Maximum contribution to PC2 was by number of siliqua on main raceme followed by 100-seed weight (0.126) and plant height (0.115). The largest contribution to PC3 was by days to flowering (0.540) followed by number of siliqua per plant (0.352) and number of siliqua on main raceme (0.343). For PC4, number of siliqua on main

raceme (0.035) contributed the most and days to maturity (-0.589) contributed the least. Days to flowering (0.345) contributed the most to PC5 and length of main raceme (-0.472) the least (Fig. 1).

CONCLUSION

The principal component analysis was effective for classification of the quantitative traits that explained most of the variability of the studied genotypes. In this data set, the characters were appointed to five PCs, out of which the first three PCs explained 63% of the total variance. It served as a useful tool for detection of traits for which the genotypes expressed the highest differences and facilitated the choice of variables based on which the clustering of the germplasm could be performed.

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