Metroglyph Analysis for the Yield and Quality Related Characters of *Brassica juncea* L.

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ABSTRACT

Eight accessions of *Brassica juncea* were sown in a Randomized Complete Block Design in four replications. Data on various economic characters of the plant were recorded for the comparative evaluation with the help of metroglyph techniques. Analysis of variance showed highly significant differences among *Brassica juncea* accessions for all the quantitative characters. Six clusters were obtained by the Anderson's Metroglyph analysis. The cluster number I and II were largest with two genotypes whereas the cluster III, IV, V and VI were formed by the single genotypes.

Key Words: Metroglyph analysis; Yield; Quality; *Brassica juncea* L.

INTRODUCTION

Pakistan is facing an acute shortage of edible oils during 2003-04, domestic production of edible oils could meet only 29% of the total requirement (Anonymous, 2004) while the remaining 71% was met through imports. This gap between the domestic production and consumption is further widening due to increasing population and changing food habit of the community. The import of edible oils exerts a great burden on the foreign exchange. Brassica have been an important source of edible oil in Pakistan and accounted for 23% of the total domestic production (Anonymous, 2002). There is dire need to develop high yielding varieties of Brassica so that it can contribute more to the domestic production of edible oils in the country. The present studies were undertaken to evaluate various yield components by using Metroglyph technique for brassica accessions. The purpose was to evaluate the genetic potential of these accessions for yield and yield components and to develop a selection criterion. Information thus obtained could be used for the development of comprehensive breeding programme to evolve high yielding brassica cultivars.

MATERIALS AND METHODS

Investigations on eight accessions of brassica viz., UCD-8/4, UCD-83, UCD-627, UCD-323/2, UCD-11/1, UCD/675, UCD-7/8 and RL-18 were carried out in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experiment was laid out in Randomized Complete Block Design (RCBD) with four replications. Row to row distance of 45 cm and plant to plant distance of 25 cm was maintained for the genotypes and 11 lines of each accession were sown. Ten well guarded plants were randomly selected from five middle rows from each plot in each replication. Data on plant height, number of primary branches, number of secondary branches, number of pods per plant, pod length, number of seed per pod, 1000-seed weight and seed yield per plot were collected using standard procedures. Data so collected were analysed by standard analysis of variance technique as given by Steel and Torrie (1980). The Metroglyph analysis was performed according to the method of Anderson (1957) who proposed this method to study the pattern of morphological variation in crop species. Sexena *et al.* (1978), Singh and Chaudhry (1977), Chandra (1976), Gumber and Sohoo (1988), Dewan *et al.* (1992) and Mahapatra *et al.* (1995) and many others also used this method. The method involves mean values of characters. Two characters which exhibited highest variance were selected as X and Y-axis coordinates. This resulted in scattered diagram where each glyph represented a genotype except for the characters on X and Y-axis. Other characters were represented as rays on each glyph. The length of ray depended upon the index score of genotype for that character (1-for lower value, 2-for medium and 3-for highest value). Then grouping of genotypes was carried out on the basis of sum of next index score of all the varieties in that group.

RESULTS AND DISCUSSION

Genetic variability analysis. The analysis of variance for plant height, number of primary branches per plant, number of secondary branches per plant, number of pods, number of seeds per pod, pod length, 1000-seed weight, seed yield per plot, oil content and protein content % is presented in Table I. Data indicated that the differences among all the accessions were highly significant for all the characters under investigation. The genotypic and phenotypic coefficients of variability are presented in Table II. Seed yield per plant showed highest genetic variability while pod

Table I. Mean squares from the analysis of variance of different plant characters among the eight accessions of *Brassica juncea*

Character	Blocks	Genotypes	Error
Plant height (cm)	38.228	314.226[**]	25.274
Number of primary branches per plant	0.102	1.938[**]	0.149
Number of secondary branches per plant	0.926	6.423[**]	0.889
Number of pods per plant	11.921	4384.604[**]	215.310
Number of seeds per pod	0.108	0.897[**]	0.103
Pod length (cm)	0.005	0.053[**]	0.018
1000-seed weight (g)	0.007	0.054[**]	0.009
Oil content (%)	0.061	6.981[**]	0.154
Protein content (%)	0.069	15.390[**]	0.058
Seed yield per plant(g)	7.147	21.178[**]	3.546
Seed yield per plot(g)	4511.318	5705.383[**]	1649.645

Table II. Genotypic and phenotypic coefficients of variability among eight accession of *Brassica juncea*

Character	Coefficient of variability (%)	
	Genotypic	Phenotypic
Plant height (cm)	3.95	4.12
Number of primary branches per plant	9.788	10.189
Number of secondary branches per plant	10.329	11.128
Number of pods per plant	8.196	8.405
Number of seeds per pod	3.367	3.579
Pod length (cm)	2.563	3.149
1000-seed weight (g)	2.789	3.071
Oil content (%)	2.839	2.872
Protein content (%)	10.756	10.777
Seed yield per plant (g)	11.076	12.138
Seed yield per plot (g)	7.485	8.878

length showed lowest genetic variability. The phenotypic coefficients were greater than the respective genotypic coefficients of variability due to high influence of environment.

Anderson's metroglyph is a relatively simple technique and is used for preliminary grouping of genotypes (Bahadra & Akhtar, 1991; Kotalah *et al.,* 1986; Gumber & Sohoo, 1988). According to this technique the eight genotypes of *Brassica juncea* formed six clusters (Fig. 1). The number to each cluster was allocated on the basis of index score of the cluster in ascending order (Table V). The index score allotted to each characters of the genotypes indicated the worth of that genotype regarding that character.

The mean index score for all the genotypes was 22.75 with a standard deviation of 0.29 on the basis of these two statistics (mean + standard deviation) the genotypes were divided into three groups.

1	Below 22.46
2	From 22.75 to 23.04
3	Above 23.04

The group number 1 included genotype numbers 1,3,5 and 6. These genotypes were scattered into various clusters on graph (Fig. 1) as follows.

Cluster Number	Genotype Number
I	6
II	3, 5
III	1

Group number 2 on the basis of standard deviation of index scores of genotypes ranged between 22.75 and 23.04. This group included the genotypes numbers 2, 4 and 7. These genotypes were dispersed among various clusters on graph (Fig. 1) as follows:

Cluster Number	Genotype Number
III	7
IV	2
V	4

Table III. Range of means and index scores for indicated palnt traits of *Brassica juncea*

Character		Score 1			Score 2		Score 3	
	Range of means	Value less than	Sign.		Value from	to Sign	Value more than	Sign
Plant height	200.7-225.2	205.63	•		205.6-224.8	•	224.8	•
Primary branches	4.98-8.13	6.09	•		6.09-7.57	•	7.57	•
Secondary branches	10.13-13.88	9.92	•		9.92-12.85	•	12.85	•
Pods per plant	359.4-441.4	350.2	•		360.2-427.6	•	427.6	•
Grains per pod	12.52-13.93	12.70	•		12.70-13.76	•	13.76	•
Pod length	3.45-3.80	3.49	•		3.49-3.80	•	3.80	•
1000-seed weight	3.65-3.98	3.64	•		3.64-3.92	•	3.92	•
Seed yield/plant	16.77-23.35	16.15	•		16.15-21.76	•	21.76	•
Seed yield/plot	377.5-500.0	372.0	•		372.0-473.3	•	478.8	•

Table IV. Score of the mean indicated traits of genotypes of *Brassica juncea*

Genotypes	Plant height	Primary branches per plant	Secondary branches per plant	Pods per plant	Grains per pod	Pod length	1000-seed weight	oil content	Protein content	Seed yield per palnt	Seed yield per plot	Total
RL-18	2	2	2	2	2	2	2	2	2	2	2	22
UCD-8/14	2	2	2	2	2	2	2	2	3	2	2	23
UCD-83	2	2	2	2	2	2	2	1	2	2	2	20
UCD-627	2	2	2	3	2	1	2	2	3	2	2	23
UCD-323/2	2	2	2	2	1	2	2	2	2	2	2	21
UCD-11/1	1	2	2	1	3	2	3	2	1	2	2	21
UCD-675	2	2	2	2	2	2	2	3	2	2	2	23
UCD-7/8	3	3	3	3	2	2	3	3	1	3	3	29

Following the same criterion, the third group of *Brassica juncea* genotypes which had an index score higher than 23.04 included genotype number 8. The relative dispersion of this genotype was as under.

Cluster Number	Genotype Number
1	8

Among all the genotypes, genotype number 8 had the highest index score as total and as well as for individual character except for protein content for which it scored 1, and grains per pod and pod length for which it scored 2. The minimum index score of 20 was scored by the genotype number 3. The cluster with lowest of 22 index score was cluster number VI which included a single genotype 1.

Table V. Cluster number, index score and genotypes included in each cluster following metroglyph technique

Cluster No.	Genotypes	Cluster index score
I	UCD-11/1, UCD-7/8	50
II	UCD-83, UCD-323/2	41
III	UCD-675	23
IV	UCD-8/4	23
V	UCD/627	23
VI	RL-18	22

Fig. 1. Metroglyph scattor diagram showing various groups formed from eight genotypes of Brassica
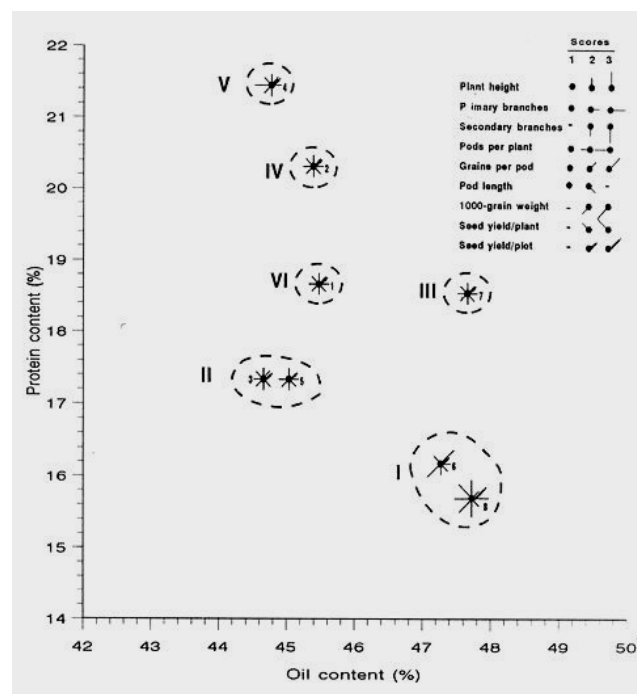
CONCLUSIONS

The studies revealed that these genotypes with high index score and fell into different clusters can be crossed to have maximum variability of good combinations of characters. The information could be helpful in identifying and engineering the crosses that could be attempted to obtain desired results. From the result it is clear that parents UCP-11/1 and UCP-7/8 are close enough and UCP-83 and UCP-323/2 show that same thing there is no need to cross these parents infect for better variability UCP-8/14 and UCP-627 can be crossed with above mentioned parent for better adaptable cross combination. This kind of studies will help for arrangement of cross combination for the best possible results (Kotalah *et al.,* 1986; Gumber & Sohoo, 1988; Bahadra & Akhtar, 1991).

REFERENCES

Anonymous, 2000. *Economic Survey*. Government of Pakistan. Finance Div., Economic Advisor's Wing, Islamabad

Anderson, E., 1957. A semigraphical method for the analysis of complex problems. *Proc. Nat. Acad. Sci. Washington*

Bahadra, S.K. and M.I. Akhtar, 1991. Genetic divergence of yield and its morphological components of mungbean (*Vigna radiata* L.). *SABRAO J.*, 23: 127–36

Chandra, S., 1976. Comparison of mahalanobis's methods and metroglyph technique in the study of genetic divergence in *Linum usitatissimum* L. germplasm collection. *Enphytica*, 26: 141–8

Dewan, D.B., M.A. Islam and M.A. Khaleque, 1992. Metroglyph analysis of morphological variation in Indian mustard (*Brassica juncea* L.). *Agric. Sci.*, 62: 766–77

Gumpber, R.K. and M.S. Sohoo, 1988. Metroglyph analysis in persian clover (*Trifolium resupinatum*). *Indian J. Agric. Sci.*, 58: 958–9

Kotalah, K.C., C. Panduranga and N. Sreerama, 1986. Mahalanobis's D^2 and Metroglyph analysis in mid–duration genotypes of rice. *Indian J. Agric. Sci.*, 56: 151–6

Mahapatra, K.L., H.P. Mishra and B. Acharya, 1995. Clustering of rice mutants by different methods of analysis. *Indian J. Genet.*, 55: 138–47

Sexena, M.B.L., G.V. Subba, G.K. Gupta and R.G. Verma, 1978. Bajra germplasm of arid areas of Kajasthan, *Indian Genet. Pl. Br.*, 38: 390–5

Singh, R.K. and B.D. Chaudhry, 1977. *Biometrical Methods in Quantitative Genetic Analysis*. pp. 224–32. Kalyani Publishers, New Dehli, India.

Steel, R.G.D. and J.H. Torrie, 1980. *Principles and Procedures of Statistics. A Biometrical Approach*. McGraw Hill Book Co., New York, USA