# Genetic Diversity in
# *Beta vulgaris* ssp. *maritima* under
# Subtropical Climate of North India

## H. M. Srivastava, H. N. Shahi,
## R. Kumar and S. Bhatnagar

*Sugarcrops Germplasm & Breeding Laboratory,*
*Indian Institute of Sugarcane Research (ICAR),*
*Lucknow-226 002, India*

## ABSTRACT

*Beta vulgaris* ssp. *maritima* is generally a self-incompatible, cross pollinated perennial species which grows from Mediterranean coasts to European Atlantic coasts. Thirty-four accessions of this species obtained from the BGRC collection located at Braunschweig (Germany) were evaluated for nine quantitative traits under the subtropical climate of North India. The characters studied were root weight, root length, crown size, number of rings, shape and color of leaf, leaf length and width, the ratio of leaf length to leaf width, petiole length, flowering (annual/biennial), and tolerance to temperatures of 40°C and above. Multivariate analysis revealed variation within and among groups of accessions and identified important traits to consider in a selection program. Four principal components (PCs) accounted for 82% of the variability. The first PC accounted for 44% of the variability and was associated with root weight, root length, and crown diameter. The second PC was associated with top weight and accounted for 20% of the variability. Cluster analysis by a non-hierarchical method resulted in six clusters, the largest cluster having nine genotypes, the smallest two.

**Additional Key Words**: Cluster analysis, Genetic diversity, Genetic resources, Multivariate analysis, Principal components.

*Beta vulgaris* ssp. *maritima* is generally a self-incompatible, cross pollinated perennial species that grows from Mediterranean coasts to European Atlantic coasts. This subspecies grows along sea coasts and is,

therefore, salt tolerant (Letschert et.al., 1994 Van dijk and Boundry, 1992).
*Beta vulgaris* ssp. *maritima* has attracted the attention of taxonomists, cu-
rators, and plant breeders, because of its reported  tolerance to salt, and
drought, and also as a source of cytoplasmic male sterility (CMS) (Coe and
Steward, 1977). The origin and geographic distribution of *B. vulgaris* ssp.
*maritima*  sources of CMS collected from Turkey, Greece, Morocco, Tuni-
sia, England, and France has been documented (Bosemark, 1998 ).

Wild *Beta* species contain genes for economically important quan-
titative traits and attributes.  The evaluation of this quantitative variation
under a wide range of environment and climatic conditions provides useful
information regarding the variability and genetic diversity within the sub-
species.  The present study was conducted with 34 accessions of *B. vul-
garis* ssp. *maritima* obtained from the BGRC collection maintained at
Braunschweig, (Germany) with the following objectives: (i) to determine
genetic variability for important quantitative traits, (ii) to evaluate these
genotypes under the subtropical conditions of North India, and (iii) to iden-
tify genotypes which may provide characteristics to enhance drought and
high temperature tolerance, for use in breeding programs (Srivastava, 1995
and 1998 ) Drought and high temperature tolerance would also be benefi-
cial in Pakistan, Iraq, Iran, Egypt, Morocco, Spain, and other countries
with similar climates (Srivastava et.al., 1992).

## MATERIALS AND METHODS

Seed of 34 genotypes of *B. vulgaris* ssp. *maritima* was obtained
from the BGRC, *Beta* collection, located at Braunschweig, Germany
(Table 1). These genotypes were evaluated for nine quantitative characters
(Table 2).  The experiment was sown in November 1996 and data were
recorded from May through June 1997 on ten randomly selected plants
from each plot. At the time of harvest the maximum air temperature ranged
from 40 to 45°C and minimum temperatures from 26 to 30°C, with frequent
hot dry winds.  In addition to the nine quantitative characters, data on root
shape and color were recorded.  Total soluble solids in the juice was mea-
sured in those genotypes from which sufficient juice could be extracted.

Nine characters were analysed by Principal Component Analysis
(PCA) (Spark 1973). Principal components with Eigen values above 0.8
were examined.  Correlations between quantitative characters and princi-
pal components were obtained by multiplying the square root of the eigen
value for each component by the eigen vector for individual characters.
Cluster analysis utilized the non-hierarchical method of Spark (1973) and
was performed using programs developed by the Indian Agricultural Sta-
tistics Research Institute, New Delhi.

**Table 1**: Accession number, IDBB* number, country of origin, and annuality in *Beta. vulgaris* ssp. *maritima* genotypes examined at Luchnow, 1997.

| Genotype No. | BGRC Acc. No. | IDBB-NR | COUNTRY | ANNUAL/ BIENNIAL |
|---|---|---|---|---|
| 1 | 28885 | 2722 | ITA | 1,2 |
| 2 | 51428 | 3735 | ITA | 1 |
| 3 | 58214 | 7119 | CYP | 1 |
| 4 | 28924 | 2205 | ITA | 1 |
| 5 | 51430 | 3737 | GRC | 1 |
| 6 | 58259 | 8534 | ITA | 1,2 |
| 8 | 53301 | 3798 | ISR | 1 |
| 9 | 54781 | 6090 | ESP | 1 |
| 11 | 45502 | 3387 | ITA | 1 |
| 12 | 62109 | 8623 | IRN | - |
| 13 | 62101 | 8615 | MLT | - |
| 14 | 62110 | 8624 | IRN | - |
| 15 | 54760 | 6069 | PRT | 1,2 |
| 16 | 53035 | 3802 | ISR | 1,2 |
| 17 | 51427 | 3734 | GRC | 1 |
| 18 | 28893 | 2222 | ITA | 1 |
| 19 | 48819 | 3555 | TUN | 1 |
| 20 | 32646 | 3108 | GRC | 1 |
| 21 | 28922 | 2711 | ITA | 1,2 |
| 23 | 56770 | 6951 | GRC | 1,2 |
| 24 | 28891 | 2728 | ITA | 1,2 |
| 25 | 28884 | 2721 | ITA | 1 |
| 26 | 45486 | 3371 | GRC | 1,2 |
| 27 | 28899 | 2228 | ITA | 1,2 |
| 28 | 45504 | 3389 | ITA | 1,2 |
| 29 | 28876 | 2713 | ITA | 1 |
| 30 | 28928 | 2209 | ITA | 1,2 |
| 31 | 28892 | 2221 | ITA | 1 |
| 32 | 28937 | 2218 | ITA | 2,1 |
| 33 | 18273 | 2301 | SWE | 2 |
| 34 | 62108 | 8622 | IRN | - |
| 35 | 28878 | 2715 | ITA | 1,2 |
| 36 | 28931 | 2212 | ITA | 1 |
| 37 | Beta-17 | 6208 | FRA | - |

**1**=Annual , **2**=Biennial

*International Data Base for *Beta* numbers.( World Beta Network ).

**Table 2:** Characters studied in 34 genotypes of *Beta vulgaris* ssp. *maritima* in subtropical North India, 1997.

| Name of the character | Code for character | Parameters studied |
|---|---|---|
| Root weight | Rt wt. | Weight of single root. |
| Top weight | Top wt. | Weight of foliage and petioles. |
| Root length | Rt. Length | Length of root at harvest. |
| Crown size | Cr.size | Crown diameter at harvest. |
| No. rings/root | Ring.No. | No. of concentric rings at crown at the time of harvest. |
| Length of leaf | Leaf.length | Length of largest leaf at harvest. |
| Leaf width | Leaf width | Width of largest leaf at harvest . |
| L/W Ratio | L/W ratio | Ratio of length and width of the above measured leaf. |
| Petiole Length | Petiole length | Length of the petiole of the largest leaf. |
| Root shape and color | Rt. Shp. Col. | Shape and color of root |
| Soluble solids | Tss | Total soluble solids in juice |

## RESULTS AND DISCUSSION

The mean and range for all attributes are presented in Table 3. The analysis of variance revealed highly significant differences among the 34 genotypes for all attributes studied.

**Table 3:** Mean and range for nine attributes of *Beta vulgaris* ssp. *maritima* under sub-tropical conditions of North India, 1997.

| Character | Mean | Range | |
|---|---|---|---|
| | | Max. | Min. |
| Root weight/plant, g | 38.89 | 115.0 - | 10.0 |
| Top weight/plant, g | 67.05 | 410.0 - | 10.0 |
| Root length, cm | 18.09 | 33.4 - | 12.6 |
| Crown size, cm | 2.23 | 6.5 - | 0.8 |
| No. concentric rings/plant | 4.85 | 9.0 - | 3.9 |
| Leaf length, cm | 7.85 | 24.1 - | 2.1 |
| Leaf length, cm | 4.43 | 17.6 - | 1.0 |
| L/W, ratio | 1.88 | 3.6 - | 0.7 |
| Petiole length, cm | 49.66 | 101.0 - | 10.9 |

Based on the cluster analysis, genotypes were grouped into six clusters (Table 4). Cluster I was the largest, containing nine genotypes, followed by cluster V with eight genotypes. Clusters II, IV, and VI contained six genotypes each. Cluster III was smallest, containing only two genotypes. No association between geographic origin of genotypes and cluster group was observed. Maximum genetic variability was present in clusters I and V. This was indicated by the magnitude of the variation for different attributes in these two clusters. Minimum variability was observed in cluster II. The means of different characteristics associated with each cluster are shown in Table 5. Cluster II, III, and IV had root weights between 48 g and 74 g. In the other three clusters, the roots were small, ranging from 20 to 26 g. The top weight was also greater for genotypes in clusters II, III, and IV, compared to the other clusters (Table 5). Leaves were largest in genotypes of cluster III. However, the greatest leaf length/width (L/W) ratio was observed in cluster V.

**Table 4:** Clustering of 34 *Beta vulgaris* ssp. *maritima* genotypes growth at Lucknow, India, 1997.

| Cluster number | Number of genotypes | Accession numbers in each cluster |
|---|---|---|
| Cluster I | 9 | 12, 24, 25, 27, 28, 29, 34, 36, 37 |
| Cluster II | 5 | 2, 18, 23, 26, 31 |
| Cluster III | 2 | 4, 9 |
| Cluster IV | 6 | 1, 5, 6, 11, 32,33 |
| Cluster V | 8 | 3, 8, 13, 17, 19, 20, 30, 35 |
| Cluster VI | 4 | 14, 15, 16, 21 |

**Table 5:** Means of nine attributes in each of six clusters, Lucknow, 1997.

| Characters | Cluster | | | | | |
|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | 6 |
| Root wt., g | 20.50 | 73.75 | 67.50 | 48.33 | 26.12 | 26.67 |
| Top wt., g | 28.33 | 89.17 | 285.0 | 112.50 | 34.50 | 28.33 |
| Root length, cm | 15.85 | 15.90 | 17.62 | 14.57 | 18.74 | 26.48 |
| Crown size, cm | 1.80 | 3.40 | 5.78 | 2.07 | 1.46 | 1.70 |
| No of rings | 4.84 | 5.12 | 4.05 | 5.18 | 5.16 | 4.13 |
| Leaf length, cm | 7.18 | 12.78 | 23.30 | 5.79 | 4.80 | 3.68 |
| Leaf width, cm | 3.91 | 7.56 | 15.73 | 3.73 | 1.69 | 2.67 |
| L/W, ratio | 1.78 | 1.72 | 1.51 | 1.57 | 2.74 | 1.52 |
| Petiole length, cm | 72.99 | 32.66 | 19.75 | 36.19 | 45.92 | 60.12 |

Four principal components (PCs) with Eigen values greater than 0.8 accounted for 83% of the variability (Table 6). The first principal component accounted for 44% and was associated with root weight and size. The second principal component explained 20% of the variability and was influenced by top weight, leaf size and shape, number of leaves/plant, and petiole length. The third component explained 10% of the variation and was dominated by root length and shape. The fourth component accounted for only 9% of the variability. The correlation coefficients of the nine attributes with their principal components are given in Table 7.

Clustering of genotypes, their mean performance, and principal component analysis suggested that crosses involving selected parents from these genetically diverse clusters would manifest maximum heterosis and

**Table 6:** Eigen value and percent of variability explained by each of four principal components.

| Principal components | Eigen value | % variability | Accumulated variability |
|---|---|---|---|
| 1 | 3.95 | 43.96 | 43.96 |
| 2 | 1.76 | 19.56 | 63.52 |
| 3 | 0.90 | 9.99 | 73.51 |
| 4 | 0.80 | 8.78 | 82.29 |

**Table 7:** Correlation coefficient of nine attributes and four principal components, Luchnow, 1997.

| Characters | PC-1 | PC-2 | PC-3 | PC-4 |
|---|---|---|---|---|
| Root wt. | 0.33 | 0.38 | -0.12 | 0.46 |
| Top wt. | 0.17 | -0.06 | -0.50 | -0.04 |
| Root length | -0.20 | -0.17 | -0.39 | 0.15 |
| Crown size | -0.62 | 0.15 | 0.32 | -0.05 |
| No. of rings | 0.44 | -0.14 | 0.60 | 0.29 |
| Leaf length | -0.01 | 0.67 | 0.28 | -0.03 |
| Leaf width | 0.31 | 0.40 | -0.11 | 0.06 |
| L/W Ratio | -0.37 | -0.04 | -0.06 | 0.81 |
| Length of petiole | -0.07 | -0.09 | -0.03 | -0.04 |

increase variability in the architecture of the progeny. Crosses among these selected but diverse lines are also likely to produce recombinants with desirable traits (Murthy and Arunachalam, 1966; Srivastava et al., 1999).

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