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Full Length Research Paper

Estimation of phenotypic divergence and powdery mildew resistance in a collection of *Cucumis sativus* L.

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Genetic diversity in thirty cucumber (*Cucumis sativus* L. var. *sativus*) collections from Karnataka, Southern India, was assessed by examining variation among thirty phenotypic characters and powdery mildew resistance. The collection showed appreciable phenotypic diversity in vein length, leaf length, tendril length, fruit length, fruit breadth, fruit weight, seed index and seed weight. Principal component analysis (PCA) was performed on 19 quantitative and 11 qualitative characters to determine relationships among populations and to obtain information on the usefulness of those characters for the definition of groups. When the 30 populations were plotted on the first two principal components, accounting for 46% of the total variation, five clusters were identified, accounting for 28 morphological attributes used in the study. The greater part of diversity was accounted for leaf length, fruit length, cavity length, node number, flesh colour, fruit weight, colour of stripes, pericarp thickness, fruit shape, seed length and seed index. CSC-71 (yellow skin and 678 g/fruit) and CSC-83 (774 g/fruit) are considered to be the most important collections to be stressed for further breeding purpose. CSC- 04, CSC-76 and CSC-77 showed gene specific banding for both the sequence tagged site, specific to powdery mildew resistance (EAACMCAC391-395STS and EAAGMCAT280-282STS). Collection CSC-71 (yellow skin and 678 g/fruit) showed gene specific amplification in primer EAACMCAC391-395STS. This evaluation of fruit trait variability combined with powdery mildew resistance can assist geneticists and breeders to identify populations with desirable characteristics for inclusion in variety breeding programs.

Key words: *Cucumis sativus*, genetic diversity, phenotypic traits, principle component analysis.

INTRODUCTION

India is a home to a large reservoir of biological wealth. The diversity of this biological or genetic wealth is the foundation of sustainable food and nutritional security to the world. Access to a broad genetic base enables us to cope with the challenges to food production that can arise from several of biotic and abiotic stresses. Changes in soil and water conditions, new pest attacks, niche climate changes would all require new varieties. Breeding these varieties is only possible if a range of genes are available. Genetic diversity of concern to agriculture is available in the cultivated form, which is in the form of several crop varieties. Despite our crucial dependence on it, the threat to bio-wealth is increasing everyday. Genetic erosion has resulted in a depletion of both the number of crop species and the amount of genetic diversity within a species (Frankel, 1972; Harlan, 1975). Rapid development of elite cultivars has hastened the displacement of old varieties and landraces. Thus, in many species the broad genetic base needed for crop improvement continues to shrink.

Phenotypic characterization is the first step in the description and classification of genetic resources (Smith and Smith, 1989). With respect to diversity in characters among populations, cluster analysis has been used to identify morphological variability in different crop species (Decker and Willson, 1986; Escribano et al., 1991; Cartea et al., 2002; Balkaya and Karaagac, 2005; Balkaya et al., 2010). In analyzing genetic diversity among populations and determining the most important variables contributing to this variation, it has appeared that principal component analysis (PCA) is most useful.

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The genus *Cucumis* of the Cucurbitaceae contains two major commercially grown vegetables, cucumber (*Cucumis sativus* L. var. *sativus*; $2n = 2x = 14$) and melon (*Cucumis melo* L.; $2n = 2x = 24$; Jeffrey, 1980; Kirkbride, 1993). A genome sequence data of *C. sativus* var. *sativus* L. has also been reported by Huang et al. (2009). *C. sativus* is widely grown and consumed all over the world either raw or in pickled form. In recent years, market demand for slicing types has tremendously increased and the produce is available almost throughout the year. *C. sativus* indigenous to India and has been domesticated for at least 3,000 years (Whitaker and Davis, 1962). Genetic diversity of *C. sativus* in the primary centre of origin (India) and secondary center (China) has been described (Staub et al., 1997; 1999). Germplasm from these geographic areas are genetically different from each other and distinct from all other *C. sativus* germplasm in the U.S. National Plant Germplasm System (NPGS) (Staub et al., 1999). Within the species, wide variation with respect to fruit bearing habits, maturity, yield, shape, size, color, spines and vine habit of the crop has been observed in India (Robinson and Decker-Walters, 1997).

Molecular markers have extensively been used for studying genetic diversity and genetic relationship in cucumber, especially PCR-based markers, such as random amplified polymorphic DNA (RAPD) (Lang et al., 2007), amplification fragment length polymorphism (AFLP) (Li et al. 2004), inter-simple sequence repeat (ISSR) (Wang *et al*. 2007) express sequence tag (EST) (Hu et al., 2010) and simple sequence repeat (SSR) (Danin-Poleg *et al*. 2001). From all these studies, different estimates for the degree of genetic variation were obtained, reflecting the differences in the selected sets of genotypes or marker systems. Powdery mildew caused by *Podosphaera xanthii* (formerly known as *Sphaerotheca fuliginea* Schlech ex Fr. Poll.) or *Golovinomyces cicho-racearum* (formerly known as *Erysiphe cichoracearum* DC ex Me´ rat.) is one of the most serious diseases in cucumber. Several reports indicate the involvement of more than one gene for powdery mildew resistance in several cucumber accessions (Pierce and Wehner, 1990). Some linkages between the powdery mildew resistance locus and phenotypic markers have also been reported (Fanourakis and Simon, 1987; Walters et al., 2001).

In 1992, the U.S. and Indian governments sponsored an expedition to collect *Cucumis* spp. from North Indian states including Rajasthan, Madhya Pradesh, and Uttar Pradesh and the germplasm collected from this expedition have been maintained in USDA gene bank (Staub et al., 1997). There has been no comprehensive program for the collection, characterization, screening of phenoltypic diversity and powdery mildew resistance in *C. sativus* from Southern India. Therefore, we have collected *C. sativus* from various regions of Karnataka and assessed their phenotypic divergence and resistance towards powdery mildew.

MATERIALS AND METHODS

Plant materials and bio-agronomic traits

The study was performed on thirty landraces of *C. sativus* collected in the state of Karnataka, India (Table 1). The landraces were evaluated in field trials using a randomized complete-block design in triplicates during March to July 2009. Each plot consisted of 1 row, 7.5 m long, spaced 2 m apart, with 1.5 m spacing between plants within the row. For the analysis of phenotypic diversity, all characters (nineteen quantitative and eleven qualitative characters) were measured in the field and at the normal harvest time. The characters selected for the analysis were (Robinson and Munger, 1976; Kirkbride, 1993; Ramaswamy et al., 1977), mainly related to *C. sativus* breeding aims and were recorded for all genotypes in triplicates. The fruit characters studied at maturity included length, diameter, shape, brightness, color, skin and flesh thickness. Traits for fruit size and shape, such as flesh thickness, fruit length and width, placenta length, were measured using the drawing ruler. Cotton blue in lacto phenol stain was used for the analysis of pollen viability. Finally, with the aim to compare together qualitative and quantitative data, a numerical transformation was applied to traits such as flesh and rind color (Table 2). In particular, a numerical value, ranging from 1 to k (k equal to number of classes), was assigned to each phenotrait, to indicate different degrees of expression. For seed characters, 10 measurements were averaged for each plant.

Powdery mildew resistance

The DNA from young leaf (about 5 to 8 cm^2) of the randomly selected plants was isolated by a modified cetyltrimethyl ammonium bromide (CTAB) method (Murray and Thompson, 1980). DNA was purified by treating the sample with 10 µg/ml RNaseA at 37°C for 30 min. The concentration of DNA was estimated spectrophotometrically (Genequant Pro, Amersham Biosciences) at 260 nm and the purity was measured by the ratio of the absorbance at 260 and 280 nm. Two cucumber sequence tagged site (STS) primers EAACMCAC391-395STS and EAAGMCAT280-282STS (Sakata et al., 2006) were used for PCR amplification, which are closely linked to the powdery mildew resistance trait in cucumber.

Statistical analysis

All the original data were standardized to eliminate the difference in the variance of each character. Principal component analysis (PCA) was performed to generate a cluster diagram. Eigenvalues and contribution percentage of each principal component axis were calculated using the correlation matrix among thirty characters for thirty accessions (Jeffers, 1967). All computations were performed using the unscrambler 10 software (CAMO Software India Pvt. Ltd, Bangalore, India) and SPSS 17.0 for MS Windows (SPSS Inc).

RESULTS AND DISCUSSION

Thirty selected qualitative and quantitative characters (Table 2) were assessed in the uniform filed trials. All the cucumber accessions used in the analysis were monoecious and substantial genetic diversity was observed. Growth duration of the cucumber plants varied greatly, four collections were short (within 90 days), thirteen were medium (within 120 days) and thirteen were long (more than 120 days). The range for primary branches/plant

Table 1. List of *C. sativus* collection, details of collection sites and analysis grouping.

Analysis code number	Collection ID	Locality	District	Analysis grouping*	Powdery mildew resistance†
1	CSC-04	Makri,	Haveri	2	1, 2
2	CSC-08	Kalgonda,	Haveri	2	2
3	CSC-22	Chamehalli	Shimoga	6	2
4	CSC-24	Odeyarakoppa	Shimoga	2	-
5	CSC-26	Isoor	Raichur	5	-
6	CSC-29	Chamehalli	Shimoga	2	-
7	CSC-35	Shikaripura	Shimoga	4	-
8	CSC-39	Mallapura	Shimoga	4	-
9	CSC-40	Chikapura	Shimoga	4	-
10	CSC-41	Kundhoor	Shimoga	4	2
11	CSC-43	Kundhoor	Shimoga	1	2
12	CSC-45	Chikapura	Shimoga	2	-
13	CSC-48	Mallapura	Shimoga	1	2
14	CSC-65	Bhatkala	Uttara Kannada	2	-
15	CSC-71	Shivapura	Hassan	3	1
16	CSC-72	Hethgodhanahalli	Hassan	3	2
17	CSC-73	Hethgodhanahalli	Hassan	3	1
18	CSC-75	Hethgodhanahalli	Hassan	2	-
19	CSC-76	Hethgodhanahalli	Hassan	2	1, 2
20	CSC-77	Hethgodhanahalli	Hassan	3	1, 2
21	CSC-78	Sankanhatti	Belgaum	3	1
22	CSC-81	Nanjanagudu	Mysore	1	-
23	CSC-82	Nanjanagudu	Mysore	1	-
24	CSC-83	Nanjanagudu	Mysore	1	-
25	CSC-84	Nanjanagudu	Mysore	3	-
26	CSC-89	Kanakapura	Bangalore rural	1	-
27	CSC-90	Hirehalli	Hassan	7	-
28	CSC-91	Kallimudhanahalli	Hassan	1	1
29	CSC-92	Honnaragi	Belgaum	1	-
30	CSC-109	Ilkal	Bagalokot	5	-

* Grouping according to the first two Principle components of the phenotypic characters.
† Accessions showing powdery mildew resistance with cucumber STS primer 1 (EAAGMCAT280-282STS) and primer 2 (EAACMCAC391-395STS).

was from three to eight. The highest number of primary branches was observed in CSC-90, which also possessed a longest vine length of 369 cm. Leaf blade in all the accessions was intermediate-lobed. There was large association between the weight of the fruit and the number of nodes on the 60th day. More the number of nodes (CSC-83 with 37 nodes) more are the number of leaves and larger is the size of the fruit (774 g/fruit), which could be linked to the maximum photosynthesis of the plant. Morphological variation was most apparent in fruit size which varied from 16.3 to 25.2 cm/fruit. Fruit color was also quite variable, the skin color of the collected genotypes was mainly dark green and light green, but two collections CSC-45 and CSC-71 had white skinned fruits. The flesh color of the cucumber was either white or cream in the collections. The flesh textures of the fruits in the collections were generally crisp at maturity. The average fruit weight of the collections varied greatly, with CSC-83 having a maximum weight of 774 g/fruit and CSC-84 having the lowest fruit weight of 230 g/fruit. The fruit length and the cavity length were directly proportional to each other. The thickness of the flesh varied from 1.4 to 2.3 cm across the collections. Variations were also observed in the seed length, seed width, seed index, 100 seed weight and all the seed characters were linked to each other.

Maximum, minimum, mean values and standard error in the quantitative characters are shown in Table 3. The results showed large variation among populations. The vein length and node number varied from 143 to 369 cm and 16 to 39, respectively. Fruit length varied widely, from 16.30 to 25.20 cm, respectively. Mature fruit color is

Table 2. List of the morphological attributes used as descriptors for *C. sativus.*

S/N	Character code	Character and descriptive value
1	Vl	Vein length at 60th day in cm
2	Gd	Growth duration: days from sowing to harvest (Days)
3	N60	Node numbers of plant at 60th days after sowing
4	Nb	Number of branches at 60th day
5	Sh	Stem hair: 1 (soft), 2 (intermediate), 3 (hard)
6	Ll	Leaf length in cm
7	Lw	Leaf width in cm
8	Lb	Leaf blade: 1(entire), 2 (light-lobed), 3 (intermediate-lobed)
9	Tl	Tendril length in cm
10	Sc	Spine color; 1 (white), 2 (black)
11	Pv	Pollen viability (%)
12	Fl	Fruit length in cm
13	Fd	Fruit diameter in cm
14	Fw	Fruit weight in g
15	Fs	Fruit shape: 1 (Elliptical elongate), 2 (oblong ellipsoid), 3 (globular), 4 (stem end tapering), 5 (Blossom end tapering)
16	Fsu	Fruit surface: 1 (smooth), 2 (bumps)
17	Rc	Rind coloration: 1 (monocolored), 2 (bicolored with longitudinal strips from base to apex)
18	Fc	Fruit color: cream: 1 (yellow), 2(light green), 3 (green), 4 (dark green), 5 (orange), 6 (pink), 7 (brown)
19	Cs	Color of stripes: 1 (absent), 2 (white), 3 (green), 4 (yellow)
20	Ft	Flesh thickness in cm
21	Flc	Flesh color: 1 (white), 2 (cream), 3 (yellow), 4 (orange), 5 (green)
22	Qf	Quality of flesh: 1 (crispy), 3 (intermediate), 5 (soft)
23	Cl	Cavity length in cm
24	Pt	Pericarp thickness
25	Bs	Blossom scar size in mm
26	Pl	Placenta length in mm
27	Sl	Seed length in cm
28	Sw	Seed width in cm
29	Si	Seed index: seed length/seed width
30	Ss	100 seed weight in g

an important phenotypic character in cucumber and we have observed off-white, yellow, light green and dark green colored fruits in our collection (Figure 1). The fruit weight varied from 330 to 774 g per fruit. Spine color is also an important characteristic of cucumber; in our collections we have observed fruits with black and white spine. Eleven of the thirty collections had black spines and the rest possessed white spines. These spines generally wither off at maturity; however, fruits in some populations had persistent spines even after harvesting (Figure 1, CSC-77 and CSC-78). The flesh of the fruits was generally white to off-white in color and crispy in nature. In terms of flesh and pericarp thickness, there were low differences among the populations (Table 3). The average fruit weight across populations was 511.46 g and average fruit weight of individual populations varied from 230 to 774 g (Table 3).

The original set of thirty variables (Table 2) was reduced by PCA to twenty eight, which accounted for about 74% of the total genetic diversity by 6 PC's. The degrees of association of characters with this axis were also obtained and are given as their factor scores or Eigen vectors (Table 4). This information was used to construct two dimensional ordinations of *C. sativus* genotypes (Figure 2). PCA results indicated that, the first two PCs explained 46% of the total variation. The first principal component (PC1) accounted for the greatest amount of variance in the original data, while PC2 accounted for the greatest amount of variation in the residual variation, which was unaccounted for by the first principal axis. PC3 accounted for the greatest amount of variation in the residual variation unaccounted by PC2. The same process unfolded for principal axes 4, 5 and 6 (Table 4). Characters with higher coefficients on the PC axes should be considered more important (Jeffers, 1967; Balkaya et al., 2010).

Table 3. Variability in some quantitative characters of *C. sativus* collections.

Trait	Mean ± SD*		
	Maximum value	Minimum value	Average value of populations
Vl	369	143	243.06 ± 62.05
Gd	3	1	2.30 ± 0.70
N60	16	39	28.00 ± 6.70
Nb	8	3	4.80 ± 1.03
Ll	18.50	10.60	14.01 ± 2.30
Lw	26.20	9.60	17.18 ± 3.76
Tl	30.80	19.60	24.55 ± 3.15
Pv	100	67	92.10 ± 9.08
Fl	25.20	16.30	19.77 ± 2.32
Fd	26.10	14.70	19.85 ± 2.74
Fw	774	230	511.46 ± 137.43
Ft	2.30	1.40	1.65 ± 0.25
Cl	20.50	13.10	15.56 ± 2.31
Pt	4.60	2.80	3.13 ± 0.50
Bs	9.00	2.00	5.83 ± 1.62
Pl	6.00	4.00	5.30 ± 0.70
Sl	1.40	0.97	1.15 ± 0.13
Sw	1.33	0.53	0.39 ± 0.17
Ss	1.12	0.53	0.79 ± 0.14
Si	4.67	0.98	3.13 ± 0.74

* Table shows minimum, maximum and mean values and standard deviation (SD) for thirty populations.

Leaf length had higher co-efficient on the first PC axis than on the other axes. The second axis had the highest coefficient for fruit weight, flesh thickness, flesh color and pericarp thickness scores, the third axis had the highest coefficients for tendril length, fruit weight and fruit surface, the fourth PC axis had the highest coefficient for spine color, pollen viability and flesh color. The PC5 had the highest coefficient for vein length, seed length and seed index and finally, PC6 was mainly related to placenta length. To understand the overall diversity of the *C. sativus* populations, the data were analyzed by cluster analysis which revealed the distribution of genetic diversity displayed in Table 4. Cluster analysis was performed to group populations according to their variability and five clusters were obtained.

The means and standard deviations for the traits for each cluster are presented in Table 5. The first cluster includes eight collections. This cluster was formed mainly on the vegetative characters of plants (Ll, Sw, N60, Tl, Vl, Lw, Nb) and two fruit characters (Fc, Fl, Cl). The fruits of this cluster generally possessed a maximum fruit weight ranging from 496 to 774 g per fruit, with CSC 83 gaining the maximum fruit weight of 774 g per fruit. The second cluster also included eight populations characterized on the fruits variables (Flc, Fw, Cs, Fc, Pl, Rc, Fd) and pollen viability. The fruits of this cluster were generally the smallest of all the collections and had a fruit weight ranging from 306 to 461 g per fruit. The CSC 45 (fruit weight 461 g) belonging to Cluster 2 is a white skinned cucumber, the skin of these fruits are generally tender and need not peeled before consumption. The third cluster incorporated six populations characterized based on stem hairs and spine color. Large variations were observed in the fruit weight of the third cluster (303 to 678 g per fruit). The CSC 71 belonging to Cluster 3 is white skinned cucumber, with a fruit weight of 678 g per fruit. The fourth cluster was characterized based on seed length, 100 seed weight, blossom scar, pericarp and flesh thickness. The fruits of this cluster also possessed a large fruit weight ranging from 649 to 704 g per fruit. Cluster five had 2 populations with a medium fruit weight of 429 to 447 g per fruit. CSC-22 and CSC-90 were segregated as a separated individual from the rest of the cultures and had a fruit weight of 462 and 574 g per fruit, respectively. CSC 71 (678 g) had a heavy fruit weight when compared with CSC 45 (461 g) among the white skinned cucumber. CSC 83 (774 g) and CSC 71 (yellow skin and 678 g) are considered to be the most important

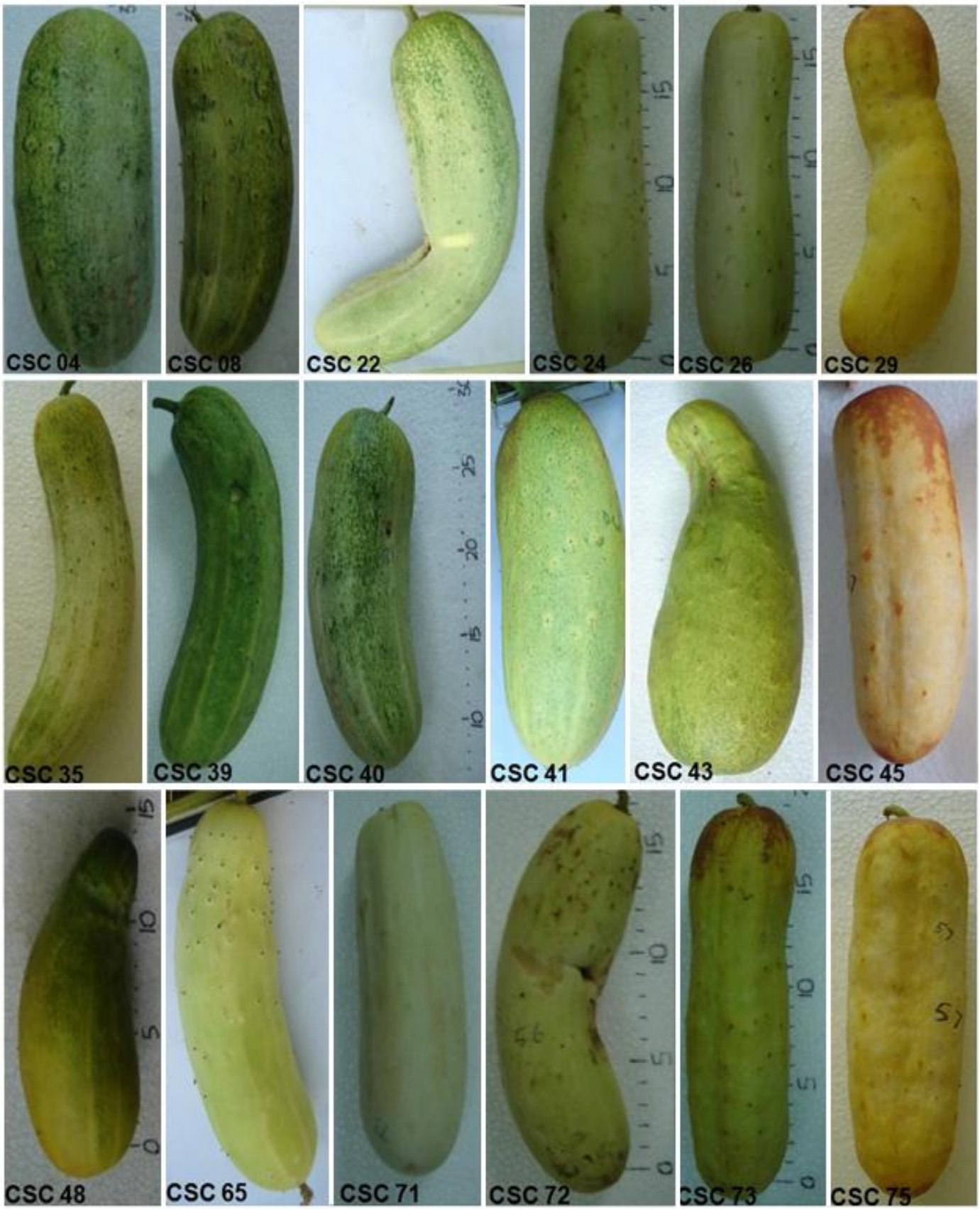

Figure 1. Diversity of fruit size, shape and color of *C. sativus* collections collected from Karnataka, India.

Figure 1. Continued.

collections to be stressed for further breeding purpose. To determine whether the collections had disease resistance against powdery mildew, 30 collections were tested against two STS primers which were specific to powdery mildew QTL of cucumbers (Sakata et al., 2006). A total of 13 collections showed gene specific resistance against the powdery mildew. 7 collections showed amplification against the primer EAAGMCAT280-282STS with a band size of 229 base pair and 9 collections showed a band size of 140 base pair against EAACMCAC391-395STS primer (Table 1). CSC-04, CSC-76 and CSC-77 showed banding in both primers. These two primers were derived from two loci on LG II of PI197088-1, a cucumber variety of Indian origin and the QTL analysis had showed that, the locus on LG II is most effective (Sakata et al., 2006). The study by Sakata et al. (2006) provides evidence that, the combination of the multiple loci could play an important role in expressing the high level of resistance to powdery mildew under varying temperature. Accession PI197088-1 used for breeding of disease resistance variety is of Indian origin collected from the Northern India, a better disease resistant variety could be obtained by screening the collections throughout the country. The high degree of polymorphism observed bet-

Table 4. Principal component analysis (PCA) of characters associated with thirty *C. sativus* populations. Proportions of variations are associated with first six PC axes.

	PC1	PC2	PC3	PC4	PC5	PC6
Explained proportion of variation (%)	**25**	**21**	**10**	**8**	**5**	**5**
Cumulative proportion of variation (%)	**25**	**46**	**56**	**64**	**69**	**74**
Trait	**Eigen vector**					
Vl	-0.190	0.051	0.258	0.137	0.420	-0.084
Gd	0.228	0.004	-0.164	0.173	-0.083	-0.265
N60	-0.272	0.026	-0.067	-0.239	0.134	-0.090
Nb	-0.145	0.111	0.150	-0.101	0.284	-0.206
Sh	-0.237	-0.101	-0.104	-0.014	0.113	-0.216
Ll	-0.313	0.096	0.038	-0.191	0.021	0.067
Lw	-0.189	0.032	0.113	-0.286	0.059	0.280
Tl	-0.204	0.0581	-0.301	0.185	0.210	-0.070
Sc	-0.151	-0.083	-0.083	0.302	-0.040	-0.175
Pv	-0.071	0.208	-0.178	0.340	0.252	-0.170
Fl	-0.254	0.198	-0.157	-0.013	0.056	0.209
Fd	0.077	0.225	-0.275	-0.295	-0.215	-0.245
Fw	-0.059	0.307	-0.326	-0.070	-0.010	0.090
Fs	0.194	0.237	0.145	0.195	-0.010	0.175
Fsu	0.088	0.021	0.455	0.143	0.079	-0.052
Rc	0.045	0.232	0.168	-0.221	0.037	-0.267
Fc	-0.063	0.270	0.254	0.277	-0.199	-0.054
Cs	-0.047	0.294	0.083	-0.035	0.153	0.057
Ft	0.173	0.328	-0.061	-0.110	-0.101	-0.150
Flc	-0.077	0.315	0.046	0.338	-0.098	-0.065
Cl	-0.257	0.197	-0.124	0.040	0.038	0.252
Pt	0.173	0.328	-0.061	-0.110	-0.101	-0.150
Bs	0.224	0.081	0.119	-0.121	0.267	0.066
P	-0.020	0.219	0.093	0.088	-0.248	0.487
Sl	0.273	0.110	-0.107	0.024	0.358	0.117
Sw	-0.252	0.094	0.218	-0.036	-0.198	-0.214
Ss	0.133	0.156	0.205	-0.278	0.155	-0.082
Si	0.295	0.007	-0.194	0.042	0.334	0.176

ween the collections and powdery resistance provide the needed information to follow the transmission of resistance alleles from the donors in advancing breeding lines.

There is a constant need to conserve genetic resources because plant breeding efforts depend on a continuing and expanding supply of genetic resources. Indian *C. sativus* have undergone natural selection for adaptation to the different agro-ecological zones (Sharma et al., 1986 to 92). The north-eastern region has shown to hold special significance for wild and cultivated germplasm. Useful breeding traits and their sources among Indian wild and cultivated *Cucumis* has been mentioned by Sharma et al. (1986 to 92). Analysis of cucumber collections showed variations among the collections from North *sativus*, the whole range of variability has not even been collected and conserved. So, attempts have to be made for the collection and conservation of *C. sativus* from other parts of India. In view of the above, the collections from southern India showed large variability with respect to fruit characteristics and are an important germplasm (CSC 71 and CSC 83) to select out salad varieties and the collection, also had powdery mildew resistance varieties, of them, CSC-04, CSC-76 and CSC-77 are also to be stressed out for future breeding programme.

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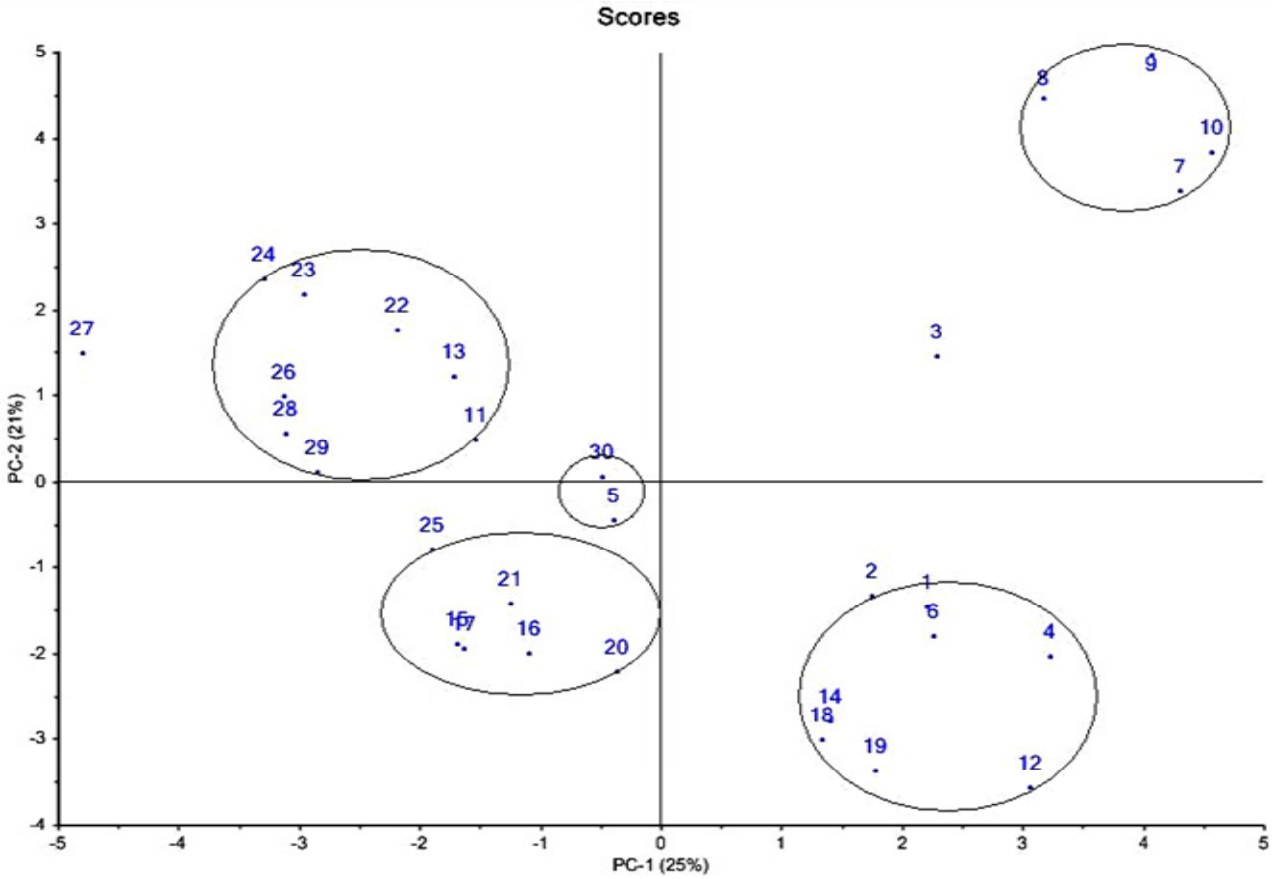

Figure 2. Cluster diagram constructed on the basis the first two principal component axes, which contain 46% of the total variation.

Table 5. Mean trait values used in *C. sativus* cluster identification.

Trait	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Vl	266.6 ± 56.1	206.6 ± 54.9	250.3 ± 66.0	215.4 ± 46.1	242.0 ±57.98	290.0	369.0
Gd	2.0 ± 0.53	2.6 ± 0.51	1.8 ± 0.75	2.7 ± 0.50	3.0 ± 0.0	3.0	1.0
N60	32.5 ± 5.39	22.5 ± 4.84	33.3 ± 3.61	22.7 ± 5.73	25.5 ± 0.70	23.0	35
Nb	5.00 ±0.92	4.25 ±0.88	4.66 ±0.81	4.75 ±0.95	5.00 ± 0.0	5.0	8.0
Ll	15.8 ± 1.27	11.47 ± 0.80	15.43 ± 0.72	12.62 ± 2.68	15.05 ± 0.63	11.7	16.7
Lw	17.76 ± 4.97	14.93 ± 2.13	19.43 ± 1.94	15.82 ± 5.07	17.70 ± 2.21	16.5	22.1
Tl	26.85 ± 2.21	22.16 ± 2.75	25.70 ± 3.69	22.75 ± 2.21	23.85 ± 0.35	24.2	27.4
Pv	96.12 ± 2.35	86.12 ± 12.22	90.83 ± 11.87	96.25 ± 4.50	91.00 ± 2.82	96.0	97.0
Fl	22.47 ± 1.65	17.92 ± 1.07	18.90 ± 1.27	19.25 ± 0.60	18.65 ±1.06	17.9	24.5
Fd	19.97 ± 2.28	18.07 ± 1.66	18.98 ± 2.32	23.72 ± 0.93	22.50 ± 5.09	19.0	18.5
Fw	626.75 ± 88.28	394.00 ± 48.76	431.66 ± 143.68	669.00 ± 24.83	438.00 ± 12.72	462.0	574.0
Ft	1.61 ± 0.12	1.50 ± 0.01	1.51 ± 0.07	2.20 ± 0.08	1.75 ± 0.21	1.9	1.5
Cl	18.35 ± 1.68	13.90 ± 0.56	15.50 ± 1.16	15.05 ± 0.34	13.85 ± 0.35	13.6	20.5
Pt	3.22 ± 0.24	3.00 ± 0.10	3.03 ± 0.15	4.40 ± 0.16	3.50 ± 0.42	3.8	3.0
Bs	4.75 ± 1.38	5.75 ± 0.46	6.33 ± 1.36	8.50 ± 0.57	4.50 ± 2.12	6.0	4.0
Pl	5.75 ± 0.46	5.00 ± 0.53	5.00 ± 0.89	5.75 ± 0.50	4.50 ± 0.70	6.0	5.0
Sl	1.05 ± 0.08	1.20 ± 0.10	1.06 ± 0.06	1.35 ± 0.02	1.17 ± 0.29	1.2	1.16
Sw	0.38 ± 0.01	0.33 ± 0.04	0.37 ± 0.01	0.60 ± 0.48	0.39 ± 0.0	0.34	0.39
Ss	0.69 ± 0.05	0.77 ± 0.15	0.79 ± 0.07	1.01 ±0.10	0.75 ± 0.10	0.818	0.9416
Si	2.79 ± 0.32	3.71 ± 0.72	2.83 ± 0.23	3.13 ± 1.14	3.00 ± 0.75	3.52	2.93

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