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Genetic diversity of cucumber (*Cucumis sativus*) accessions differing in quantitative traits and microsatellite markers

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ABSTRACT

The genetic diversity among 78 cucumber (*Cucumis sativus* L.) accessions was analyzed using 8 morphological traits and 60 SSR markers under two environmental (open field and protected cultivation) conditions. D^2 analysis had grouped the 78 accessions in five major clusters. Cluster I comprised 51 accessions followed by 14, 5, 7 and 1 in cluster II, III, IV, and V respectively. The variation was observed for morphological characters like days to first female flower anthesis (37.53-58.64), days to first fruit harvest (47.28-67.43), fruit length (9.47-26.84 cm), average fruit weight (67.46-417.56 g) and vine length (96.23-170.13 cm). The first four principal components explained 87.72% of the total variation. A total of 171 alleles were amplified with a mean of 2.85 alleles per locus. The polymorphism information content (PIC) varied from 0.05 (UW084478) to 0.59 (UW084186) with a mean value of 0.36. The major allele frequency, gene diversity, and heterozygosity of these SSR markers were 0.36-0.97, 0.05-0.67 and 0.00-0.68, respectively. The dendrogram based on SSR marker analysis classified the 78 genotypes into two major groups those were subdivided into ten subgroups. Collectively, the information obtained will provide a valuable resource for germplasm conservation, genetic analyses and gene discovery in cucumber breeding.

Key words: *Cucumis sativus,* Genetic diversity, Morphological, Simple sequence repeat (SSR) Morphological markers,

Assessment of genetic diversity based only on morphological characters is greatly influenced by environmental conditions. Combining both morphological and molecular information is the most comprehensive way for assessment of diversity (Collard *et al.* 2005). Cucumber (*Cucumis sativus* L.) has a narrow genetic base with 3-12% polymorphism (Behera *et al.* 2011) but molecular markers are widely utilized to assess its genetic diversity. Due to neutrality, high level of transferability and co-dominance nature of SSRs, they are used more frequently in comparison to other PCR based markers (Yang *et al.* 2015). SSR markers have been utilised for genetic diversity, population structure, genome wide association (Wang 2018), mapping of genes/ QTLs (Jat *et al.* 2018), association mapping and marker-assisted selection (Miao *et al.* 2011).

The aim of this study was to assess genetic diversity among 78 cucumber core collections of different regions of India and few exotic collections for 8 horticultural traits under two environments (open field and net house condition). The diversity was also analyzed using 60 SSR markers representing all 7 chromosomes (Yang *et al.* 2013) to determine the association among the markers and morphological traits. The information obtained from the present study will provide ample scope for selection of the cucumber accessions representing high genetic diversity for the development of high yielding cultivars and conservation of cucumber accessions.

MATERIALS AND METHODS

Plant materials

78 cucumber accessions including indigenous and exotic accessions were utilized for the current study (Supplementary Table 1).

Phenotypic characterization

Phenotypic characterization for 8 horticultural traits was carried out at experimental field of Division of Vegetable Science, ICAR-IARI, New Delhi, India during summer 2016-17 and 2017-18 in a randomized block design (RBD)

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Table 1 Number of alleles**,** major allele frequency (MAF), gene diversity (GD), heterozygosity (H) and polymorphism information content (PIC) of the SSR markers

Marker	Reverse	Forward	No. of alleles	MAF	GD	H	PIC
SSR00688	CCGAAGATTTTAATGGGAGGA	CAGCCGAGACAATCAAACAA	1	0.96	0.07	0	0.07
UW084478	TTGTGATTCTTAATGTTATTTTGTC-CA	GGGTGATCACTAACCCCAAA	2	0.97	0.05	0	0.05
SSR16346	TTTTGTTTGAATTGGGGTTTTT	TCCTGACGACACCCTTCTTC	2	0.95	0.1	0	0.09
UW083909	CCCCCAAGTTATCACCATTG	TGCCTTGCCGGATAAGTTAC	2	0.94	0.11	0.01	0.1
SSR16683	CTGCTTCTTCCCATCCAATG	TCAATCCAAACAGACATTTTCG	3	0.9	0.18	0.01	0.17
UW084817	TTTCATTGTTGTGATCCGTGA	CCGCTAAAATGAAGGGCATA	3	0.9	0.19	0	0.17
UW085408	AAAGATGATGTCTATCACTCA-CAAAA	CCATTTTAAAGTTTGTGGAGACC	3	0.87	0.24	0.01	0.23
UW028811	TGACCGGAAGTATCATTGGAG	TCCTTTCCTTGTGAATGGAAT	3	0.87	0.24	0.24	0.21
UW084265	GAAAACATGAAGGCCGTTGT	CCATTTGTCAGTGCCTTTCA	2	0.86	0.24	0.18	0.21
UW085171	CACTTTCCTTTTTCCTGTTCTTG	CTGAGTCCTACCAAGTCAATCG	3	0.85	0.26	0.14	0.24
UW084624	GGACGAGGAATACATTCTCTGA	ATGAGGCAGAGATTCCACGA	2	0.85	0.26	0	0.23
SSR03235	TGAATGAGAATTAATACAAAAC-CACAA	TGCACAGGAAATGAAATGGA	3	0.85	0.27	0	0.25
UW083908	GGTGAGCAAGGGTTTTCTTG	AAGGCGTTCCGATGATTTTT	2	0.84	0.27	0.22	0.23
UW085185	TTGAGAGTACTTAACAA-CAAAAAGGTG	GACATGTCGTTTTGTGGGTG	3	0.83	0.29	0	0.27
UW083941	GGCCTCCCGAAGATTGTATT	TCCAATGATTTCATTCACACCT	3	0.83	0.29	0.17	0.26
UW084347	AGGGATTGGAAGTGAACAGC	ATACCGTCCATTTGGTCGAA	3	0.81	0.32	0.09	0.29
UW084279	GCTGTAGTTAATGCTCTTTCTGTCT	GGGGACGAGGGAAATAGAGA	3	0.79	0.34	0	0.31
UW084028	TGGAGATCAACTCAACATTTGC	TTTTCTTTTTCAAAATCTCACCA	3	0.76	0.39	0.06	0.36
UW023709	TGGATCTTTGATTTCTGGGC	AACACAGTCTGCATTTGCCA	3	0.76	0.34	0	0.36
UW084541	CAACCTTACCTTCATACATCCAAA	AAACTTGCATGTCTTATCTTCGTG	3	0.74	0.41	0.03	0.38
UW085421	GGCGTTGGGTTAAGCATTTA	CGTGGGTTTTTACCGTCATT	3	0.74	0.41	0	0.37
UW029623	AAGGATGCTGATTGACAGCC	TTTTCATTCCCTTCTCGACG	3	0.73	0.43	0.1	0.39
UW043623	AAAATTTCAAAAATAGAACCTTTCC	TGATGGTCACGTGCTCAAAC	3	0.73	0.42	0.03	0.38
SSR03552	CCAACTTGGAAAATTGCTACA	TTCAGTTCGCTCGTGAAAGA	3	0.72	0.42	0.09	0.37
UW084033	CAAAAATAAACAAATGAAAA-CATCG	CACTCTTTCTCCCCCATCAA	3	0.72	0.42	0.35	0.36
SSR18640	AATGCCTCCTGCCTACTGTC	TGTGAATTGTTTATTTTCATTTTCA	2	0.72	0.41	0	0.32
SSR22777	AGAGTCACCCCTCCAAACAA	CGTACGAAAAACCTCTATTCCC	3	0.71	0.42	0.19	0.34
UW085303	AAATCAAAAGGCCAACATCC	GGGAATTAAAGTGAGGAAAAGC	3	0.7	0.47	0.04	0.42
UW083916	AGGGTCCAACTCAAACTCAAA	GCCCACCCTTAACATCTTACC	3	0.69	0.47	0	0.41
UW062953	AACGAAAGTAACGCCGTTTG	ACGGAGGAAATCAGAACCCT	3	0.69	0.45	0.03	0.38
UW084787	CATGTGTGACGCTTCTTTATTTTT	TGGTGCTCCCTTTCTACACA	3	0.68	0.48	0	0.43
SSR22469	ATCGGGAAGCTTCACTCAAA	TCCCCATTATGGTTCTTTTCC	3	0.68	0.49	0.15	0.44
UW083711	ATCCTCTCTCCCTCCACCAT	TTGAAAGAGTGTCGGTGATGTC	3	0.68	0.48	0.1	0.43
UW041955	GATATTTTTCCAACCTTCCC	TGTGTGATTTTCATTGCTGT	3	0.68	0.47	0.33	0.4
UW085138	ACCAAATCGCTTCTGAGGTT	GGCATGAAAGAAACACCGTT	3	0.67	0.46	0	0.38
SSR15108	GTACATAATGCTCCAAAGGC	AAAGCAGTGGAAGATTGAAA	3	0.66	0.46	0.24	0.38
SSR14340	TCACACCTGCATTTTTCATCA	GAGGCGTTCTCAACATACCC	3	0.65	0.51	0.15	0.46
UW084490	CAATCGGTAAAAGCATGCAA	TTCGTATCATATTCTCCACGTTTC	3	0.65	0.52	0.24	0.46

Contd.

Table 1 (*Concluded*)

Marker	Reverse	Forward	No. of alleles	MAF	GD	H	PIC
UW085093	AAATGGGTCATACCCAAAAGG	GCCAATGCAATTACTTCAGG	3	0.64	0.5	0	0.42
UW083862	CCTTGGGGAGTTTCATTTTTG	TCCTTTAGTTGATGATATCCTAATTTC	3	0.64	0.49	0.18	0.4
UW083899	TTGGTGGATTACACGAACACA	TGTTGACTGAGACATTTTT	3	0.63	0.49	0.32	0.4
UW044712	AGCCTTGGTGAAAAGGAAAT	GCCTACAATGACACACCAACC	3	0.63	0.52	0	0.45
SSR06011	GAAACACAAAGTTAAAA-CAAAAATCC	GACATCACGACGTGGAACC	3	0.63	0.54	0.08	0.48
UW083821	ATGACAGCGGAAAGGGTTTA	CCAGCTTCACCAGCTGTTCT	3	0.62	0.5	0.19	0.42
UW084483	CTCTTCCTCTGCTCATCCAA	GAGCCCCAGTAAGTGAAACAA	3	0.61	0.5	0.01	0.4
UW082747	CAATGGAAGATTCTCAAATTGTTG	TTGAGAGGCACTTGATGTTCA	3	0.6	0.5	0.05	0.4
UW085227	GGGTGAGGAATTGGAGGATT	CCTAAACATGGCTTCCTCCTC	3	0.6	0.51	0	0.42
SSR16869	CCAACTACAGCCTACCTGAG	ATTCCTTTTTAGAGATGGGG	3	0.59	0.52	0.31	0.43
SSR22203	TCTTGATTTTGTGTTTGTGAGAGG	ATAAGAGAAAATGATTGCCGTGA	3	0.58	0.58	0	0.51
SSR13262	TGGTGATTAGTAGAGGGTCAAAT-TC	TGTCCTTTCCTTCTACTTCTTGC	3	0.56	0.58	0.18	0.52
SSR11632	TGAGGTGAAGCGTGAGAAGA	TTCAACTCATTATGGATTGGATT	3	0.56	0.59	0.17	0.53
UW084942	GAAAATCATCGTTACAACAGAAA-CA	CTTTGACTGCCTCCATTGAT	3	0.53	0.59	0	0.51
UW084916	TATTCTCATCGGAAAACGCC	TTTGCCCTACTACCCCTCCT	3	0.52	0.53	0.22	0.43
UW084188	TGAACACACACGATTATTGTCA	TTTCATAAAGTTGGAGGTAGTATTCC	3	0.52	0.61	0.12	0.54
SSR00182	CTTCTCTCGGCCCAGTACAC	TTAATGTCCCACACTTGGCA	3	0.51	0.53	0	0.43
SSR12414	CATCTCCCTCAATGCATCCT	CACTTTTCACGTACAAAACACG	3	0.51	0.53	0.22	0.43
UW084967	GGTCTTCCTTTTCAAATCATTG	AAAAATTCCTAAGACGACGATCA	3	0.5	0.61	0	0.53
UW084351	TTTGCATAATGGGAAGAAGG	CCCCACAAGAATGGAGAATG	3	0.48	0.54	0.68	0.43
SSR00607	AAGCCACCTTCCCTCTCAAT	GCAAACTGTGGGACGTTTCT	3	0.44	0.63	0.06	0.55
UW084186	TTCAAGAACATCGCCATGAG	CAGAAAGAAATGGCAGGGAA	3	0.36	0.67	0	0.59
Mean			2.85	0.7	0.42	0.1	0.36

with three replications. Five plants were randomly chosen and tagged to record data on 8 quantitative traits.

Genomic DNA isolation

The total genomic DNA was extracted following a modified CTAB method (Miao *et al.* 2011) and DNA quality was checked through 0.8% agarose gel electrophoresis and quantity by using a spectrophotometer at wavelength of 260 nm, and finally stored at -20°C for further use.

PCR amplification

The PCR reactions were prepared in a volume of 20µl reaction mixture each containing 2µl of 10X reaction buffer, 0.30µl of 10 mM dNTPs, 1µl each of forward and reverse primers, 2.0µl of template genomic DNA (50 ng), 0.2µl of Taq DNA polymerase (0.75 U) and 13.5µl MQ water. The PCR products were separated by electrophoresis in 3.0% agarose gels containing 0.1µg/ml ethidium bromide in 1X TBE buffer at 120 Volts for 3 hours. DNA fragments were visualized and documented using the ALPHA IMAGER gel documentation system (Alpha Innotech, USA).

Statistical data analysis

The data were analyzed using the ANOVA procedure of SAS 9.2 (SAS Institute, Cary, NC, USA). The D^2 analysis was done (Indostat services, Hyderabad, India). Polymorphic information content (PIC), major allele frequency (MAF), heterozygosity and genetic distance based clustering was measured using Power Maker v3.25 (Liu and Muse 2004). The dendrogram was constructed by Unweighted Pair-Group Method of Arithmetic Average (UPGMA). GenAlEx V6.5 (Peakall *et al.* 2012) software was used for Principle Coordinate Analysis (PCoA) and Analysis of Molecular Variance (AMOVA).

RESULTS AND DISCUSSION

Phenotypic performance of accessions

The highest variation was observed for average fruit weight with the CV of 46.53% followed by fruit length/ diameter ratio (29.26), fruit length (25.99), node number of first female flower (15.38), vine length (8.60), fruit diameter (8.27). Days to first fruit harvest and days to first

Table 2 Summary statistics of horticultural traits evaluated in 78 cucumber genotypes

Variable	Mean	Standard Deviation	C V
Node number of first female flower	6.76	1.04	15.38
Days to first female flower	48.85	3.19	6.53
Days to first fruit harvest	59.97	3.70	6.17
Fruit length (cm)	13.89	3.61	25.99
Fruit diameter (cm)	5.20	0.43	8.27
Fruit length/diameter ratio	2.70	0.79	29.26
Average fruit weight (g)	157.50	73.29	46.53
Vine length (cm)	147.40	12.68	8.60

female flower had shown the least variation with the CV of 6.17% and 6.53% respectively (Table 2).

The node number of first female flower and days to first female flower anthesis are the indicator of earliness in cucumber. The accession RS1 (4.75) followed by DG4 (5.09) and EC636505 (5.17) produced female flower on the lowest node. Days to first female flower anthesis and days to first fruit harvest were lowest for Gy421 (37.53, 47.28) followed by Gy14 (38.22, 47.52), determined early harvesting of the accessions. The accessions CL746 (26.84cm), CL758 (25.64cm) and EC636517 (24.44cm) were recorded for maximum fruit length. The accession CL758 (417.56 g) produced maximum fruit weight followed by DARL106 (365.62 g).

Relationship among accessions based on horticultural traits

D^2 analysis of 78 cucumber accessions had categorized them into five distinct clusters (Fig 1). Cluster I comprised of the maximum number of accessions (51) those were represented from different states of India and few exotic collections. Cluster II had 14 accessions, while cluster III had 5 accessions consisting of two gynoecious line Gy14 and Gy421 along with 3 Indian accessions like Pahari77, DC21, and Barsha Magal. Cluster IV had 7 accessions, while cluster V had only one accession CL758. The intra-cluster distance was the highest in cluster IV (57.30) showing the existence of maximum variability among the accessions of this cluster. The maximum inter-cluster distance was found between cluster III and V (340.56) followed by cluster I and V (294.61) suggesting the more diverse nature of the accessions belonging to these clusters.

The cluster V had maximum mean value for node number of first female flower (7.35), fruit length (25.63 cm), fruit length: diameter ratio (5.43), average fruit weight (417.55g) followed by vine length (163.39 cm). However, cluster IV had maximum mean value for days to first female

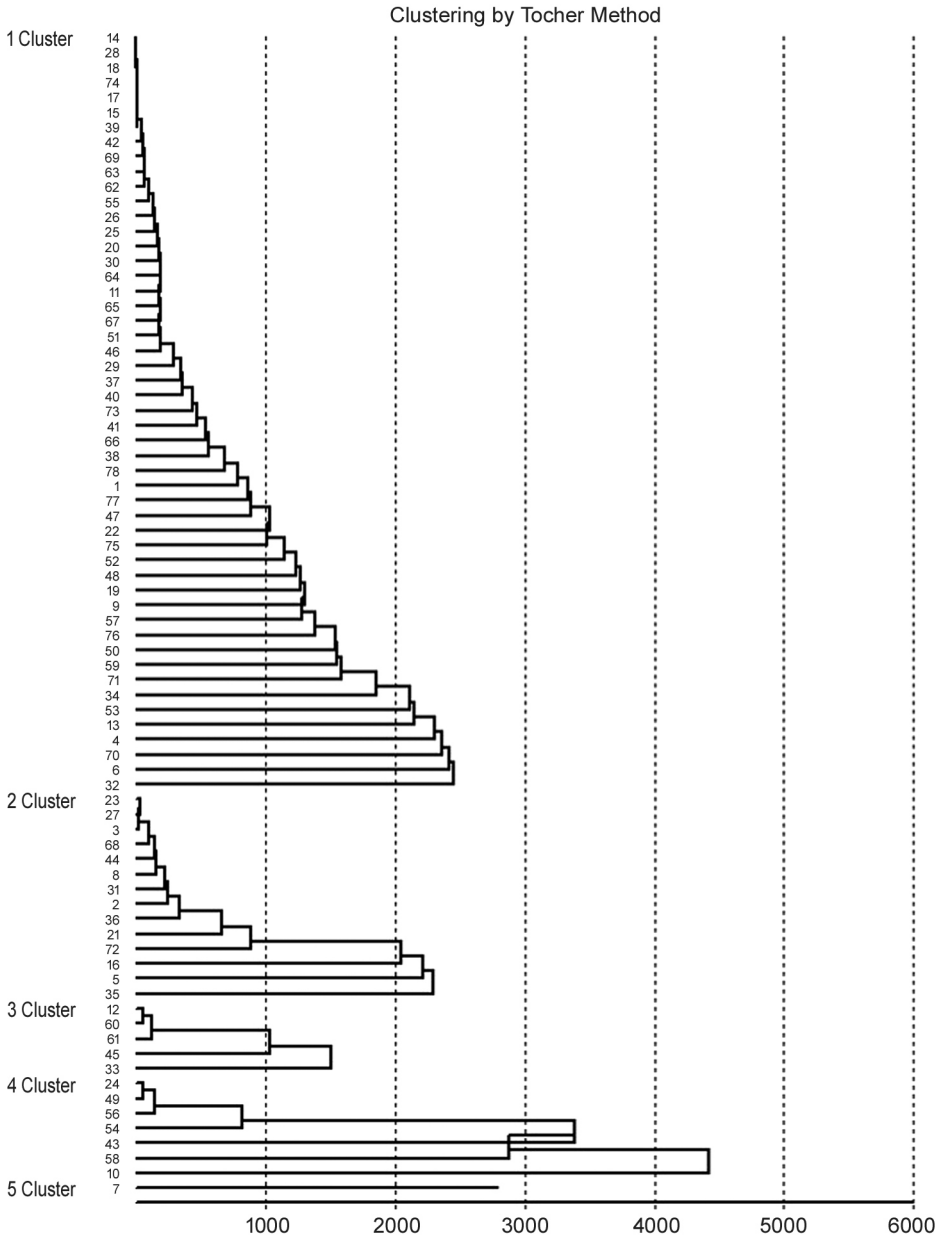

Fig 1 Genetic relationship among 78 cucumber genotypes based on eight horticultural traits using UPGMA cluster analysis of the distance matrix.

Table 3 Cluster mean of 8 horticultural traits for 78 accessions of cucumber

Trait	Node number of first female flower	Days to first female flower anthesis	Days to first fruit harvest	Fruit length (cm)	Fruit diameter (cm)	Fruit length/ diameter ratio	Average fruit weight (g)	Vine length (cm)
I	6.76	49.00	60.00	12.81	5.24	2.46	124.63	148.36
II	6.55	49.42	60.08	15.35	4.99	3.15	203.56	145.50
III	6.43	43.88	55.74	10.36	5.10	2.08	80.36	124.50
IV	7.25	50.05	62.77	19.67	5.42	3.64	323.05	157.97
V	7.35	49.67	58.72	25.63	4.61	5.43	417.55	163.39

flower anthesis (50.05), days to first fruit harvest (62.77) and fruit diameter (5.42 cm) (Table 3).

Principal component analysis (PCA) for the 8 morphological traits the first two components had an Eigen value of more than 1.0. The first and second components had explained 43.11 and 23.95% of the variation (Table 4). The other two principal components (third and fourth) with the Eigen value more than 0.5 cumulatively with first and second PC explained a total variation of 87.72% existing among the genotypes. A scatter plot was drawn between PC1 and PC2 depicted a clear pattern of grouping among accessions in the factor plane. All the accessions were widely scattered across the quarters.

The different morphological traits contributed for total variation was calculated as component 1, 2, 3 and 4. Component 1 showed the contribution of node number for first female flower (0.25), days to first female flower (0.36), days to first fruit harvest (0.37), fruit length (0.44), fruit length: diameter ratio (0.40), average fruit weight (0.40) and vine length (0.39) for 43.11% of the total variability. Component 2 showed the contribution of fruit diameter (0.42) and fruit length: diameter ratio (-0.46) for 23.95% of the total variability. Similarly, fruit diameter (0.81) and node number of first female flower (0.90) contributed to the total variation of 11.98% and 8.68% from component 3 and component 4, respectively (Table 4).

Molecular characterization through SSR loci

A total of 60 SSRs were amplified across all 78 accessions of cucumber (Table 1) which produced 171 alleles ranging from 1 to 3 with a mean of 2.85 alleles per locus. The major allele frequency (MAF) at the SSR loci varied between 0.36 (UW084186) to 0.97 (UW084478) with a mean value of 0.70 (Table 2). The PIC values (represent allelic diversity and frequency) had an average value of 0.36 per marker for SSR across all the accessions which varied from 0.05 to 0.59. In terms of PIC values, UW084186 (0.59), SSR00607 (0.55), UW084967 (0.53), UW084188 (0.54), SSR11632 (0.53), SSR13262 (0.52), SSR22203 (0.51) and UW084942 (0.51) were recorded to be most informative markers, while marker UW084478 recorded least PIC value (0.05). Out of 60 SSRs, 22 did not show any heterozygosity.

Table 4 Eigen value and percent of total variation and component matrix for the principal component axes

	PC1	PC2	PC3	PC4
Eigen value	3.45	1.92	0.96	0.69
% of variance	43.11	23.95	11.98	8.68
Cumulative %	43.11	67.06	79.04	87.72
Node number of first female flower	0.25	0.33	-0.10	0.90
Days to first female flower	0.36	0.33	-0.38	-0.21
Days to first fruit harvest	0.37	0.37	-0.09	-0.32
Fruit length (cm)	0.44	-0.35	0.21	-0.01
Fruit diameter (cm)	-0.03	0.42	0.81	-0.04
Fruit length/diameter ratio	0.40	-0.46	-0.04	0.05
Average fruit weight (g)	0.40	-0.25	0.37	0.05
Vine length (cm)	0.39	0.29	0.06	-0.19

Genetic relationship among accessions based on SSR markers

The analysis based on the UPGMA tree revealed that 78 cucumber accessions were grouped into two major clusters A and B consisting of 6 and 72 accessions, respectively (Fig 2). The UPGMA tree showed a close similarity among HS5, HS9, GS3, Swarna Sheetal, Swarna Ageti and WBC27-1. Cluster B could be subdivided into 10 sub clusters V (3 accessions), I, VI and VII (4 accessions in each), IV and IX (5 accessions each), II (7 accessions), X (8 accessions) and III (10 accessions) while VIII was the largest sub cluster containing a total of 19 accessions. The accessions, Dharwad Green, WBC21, and WBC5 were distinct from other accessions and were singly represented from the node in the cluster B. Sub-cluster I grouped two gynoecious accessions Gy14, Gy421 along with DC22 and GLK1 indicating their close association. Major sub-cluster VIII consisted of 19 diverse accessions, 6 from USA, 5 from West Bengal, India, 4 from Uttarakhand, India, 2 each from Haryana and Western Uttar Pradesh, India. The random grouping of accessions was observed in the dendrogram, while out of 5 accessions of China, 4 accessions (CL758, CL773, 702-6-B76, and CL746) appeared in the same cluster.

The principal coordinate analysis (PCoA) results were in close agreement with UPGMA based tree. A variation of 23.75% was recorded by the first three coordinate axes. The first axis explained 10.09% of genetic variation followed by 7.64% explained by the second axis. Most of the accessions were from the USA, Western Uttar Pradesh (India) and Haryana (India) were plotted in the first half and the second half of the coordinates while other accessions were plotted in second lower half of the coordinates. Based on SSR marker analysis the percentage of genetic variation within

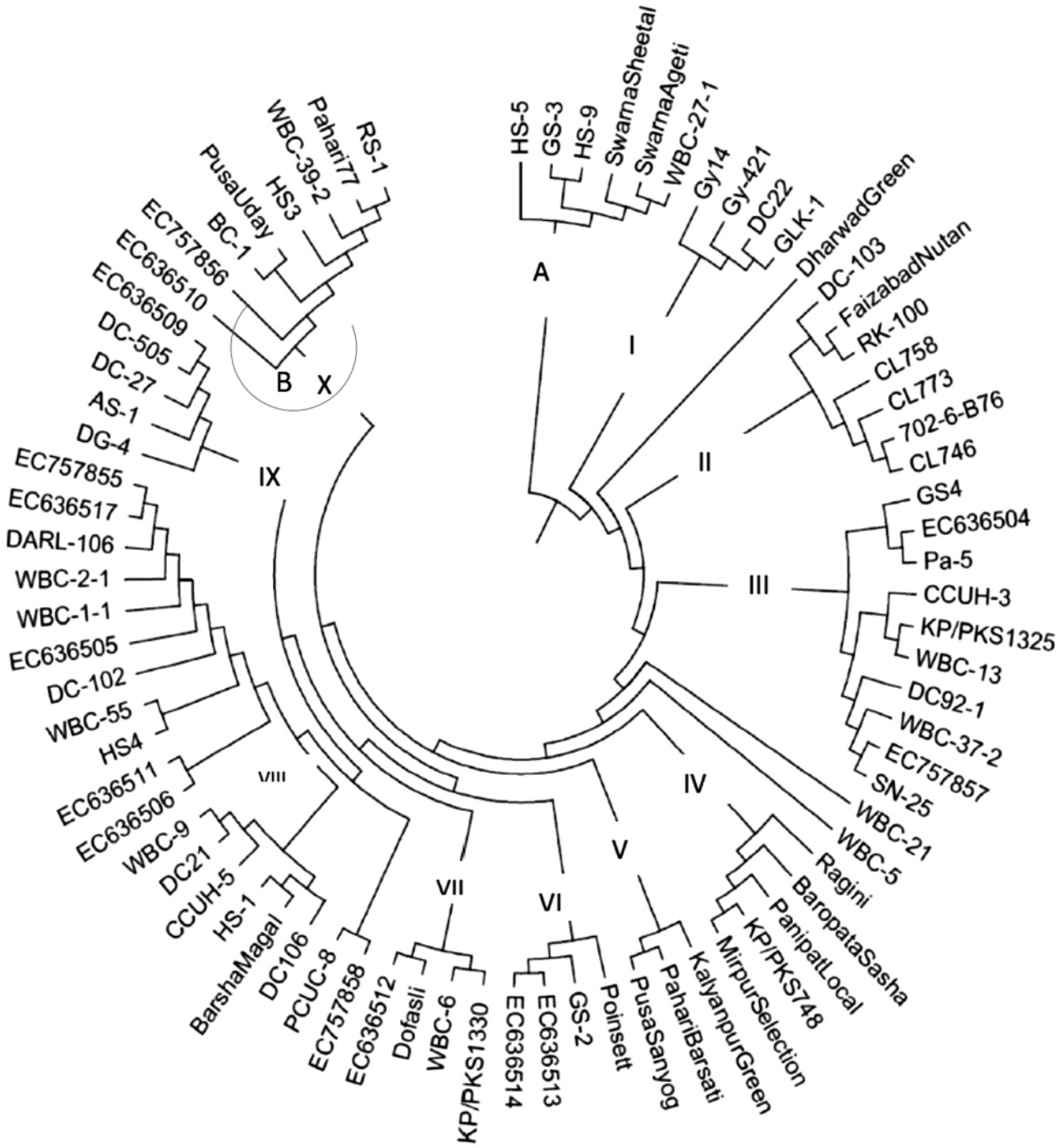

Fig 2 UPGMA tree based on dissimilarity index of 60 SSR markers for 78 cucumber genotypes.

the population was 97%, whereas the remaining genetic variation (3%) was observed among populations (Table 5).

D^2 statistics are often used to classify the genotype into groups based on multiple characters (Mahalanobis 1928). The clustering pattern of introduced accessions indicated that the germplasm collected from Indian states during Indo-US joint expedition have been re-introduced to India from the USA, is phenotypically similar to Indian collections (Pandey *et al.* 2013). The highest inter-cluster distance was observed for cluster V comprised of one genotype CL758 derived from China. This genotype represented the unique semi-wild landraces found in Xishuangbanna in South West China. The inter-cluster distances may be used for the selection of diverse genotypes which would be further utilized for breeding heterotic combinations.

In present experiment an average PIC was 0.36 and similar PIC were also observed in Indian cucumber accessions (0.31 by Pandey *et al.* 2013), (0.33 by Dar *et al.* 2017) and Chinese cucumber (0.39 by Hua *et al.* 2010). However, it was interesting to note that the polymorphism reported by Watcharawongpaiboon and Chunwongse (2008) in the accessions from Thailand (0.47) was higher than the

Table 5 AMOVA summary for SSR markers used in the study

Source	df	SS	MS	Est. Var.	%
Among pops	10	158.01	15.80	0.387	3%
Within pops	67	891.46	13.30	13.31	97%
Total	77	1049.47		13.69	100%

reports of PIC from Indian accessions. The UPGMA tree based on microsatellite marker has distributed the accessions from USA randomly in almost every sub-cluster of cluster B. The cucumber accessions were mostly collected from Uttar Pradesh (India) thus, a frequent grouping of the USA and Uttar Pradesh (India) accessions were observed (Staub *et al.*1997). All the Chinese accessions were grouped together with the accessions from eastern Uttar Pradesh, indicating a high level of similarity among Uttar Pradesh (India) and Chinese accessions. Two gynoecious lines namely Gy14 and Gy421 clustered in the same cluster based on D^2 analysis as well as SSR markers. The finding suggested that source of the origin of gynoecious trait was limited and subsequently utilized by all the cucumber breeders in a short span of time. Formation of two clusters based on microsatellite data showed grouping of all the Indian accessions in a single big cluster is an indication of narrow genetic base and genetic erosion of Indian cucumber (Pandey *et al.* 2013; Dar *et al.* 2017; Pandey *et al.* 2018).

The results of principal coordinate analysis (PCoA) were in contrast to the earlier reports (Pandey *et al.* 2013). Both the UPGMA and PCoA had grouped the genotypes in two distinct clusters. Based on SSR markers, AMOVA analysis fractioned the variation of 97% was due to genetic variation within a population and the remaining genetic variation of 3% was observed among populations. However, in Chinese, the USA and Dutch accessions, 68.1% variation within a population and 31.9% among the population of cucumber were reported (Lv *et al.* 2012).

Our results confirmed that phenotypic data and SSR markers derived genetic diversity analysis could be powerful tools for the detection of genetic diversity among cucumber accessions. Efforts are required to minimize genetic erosion and broaden the genetic diversity by conserving the highly variable accessions.

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