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RESEARCH ARTICLE

Assessment of genetic diversity and population structure in melon (*Cucumis melo* L.) germplasm using microsatellite markers: Implications towards its varietal improvement

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Abstract

A total of 96 melon germplasm from four horticultural groups were undertaken for genetic characterization using 107 microsatellite markers. The average diversity indices of microsatellite markers, *viz.,* allele number, major allelic frequency, gene diversity, expected heterozygosity and polymorphic information content, were 2.69, 0.84, 0.25, 0.06 and 0.22, respectively. The neighbor-joining dendrogram grouped the melon germplasm into four major clusters with distinct separation of Indian *reticulatus* germplasm from that of the exotic germplasm adapted in India and wild *agrestis* germplasm. Population structure analysis deciphered two main subpopulations broadly corresponding sweet melon preferred by consumers from sub-species *melo* and non-sweet wild *agrestis* melon separately along with admixtures. This finding was validated by principal coordinate analysis. AMOVA analysis further partitioned the whole genetic variation among individuals (74%), within individuals (22%) and among populations (4%) with low genetic differentiation and high levels of gene flow among subpopulations. A total of 12 microsatellite markers produced 19 unique alleles among 24 germplasm, which would act as a distinct DNA fingerprint for germplasm identification and legal protection. The present study provided a deeper understanding of the genetic structure of melon germplasm and will assist in formulating future breeding programmes.

Keywords: Melon (*Cucumis melo* L.), horticultural groups, genetic diversity, population structure, microsatellite markers, AMOVA

Introduction

Melon (*Cucumis melo* L.; 2n = 24) is an important horticultural crop cultivated in tropical and sub-tropical regions worldwide, known for its delicious taste, sweetness, and rich vitamin and mineral contents (Munshi and Choudhary 2014). Many of recent studies specified that melon might have originated in Asia, particularly India (Sebastian et al. 2010; Endl et al. 2018), with further support from Gonzalo et al. (2019) reaffirming India as the epicenter of melon diversity. Melon intraspecific groups were classified into six horticultural groups based on their intended uses: *cantalupensis, inodorus, flexuosus, conomon, dudaim* and *momordica*, which became widely popular (Robinson and Deckers-Walters 1997). In the latest classification, Pitrat (2017) reported 19 intraspecific melon groups, with a recommendation of merging the groups, *cantalupensis* and *reticulatus*. All these infraspecific groups of melon are cross-compatible with one another, resulting in intermediate forms that are widely domesticated (Reddy et al. 2016).

Several genetic diversity studies focused on Indian melon germplasm (Bhimappa et al. 2019), highlighting the presence of beneficial genes conferring resistance to various stresses, making Indian melon genetic resources highly sought after in breeding programs worldwide (Pitrat 2008; Dhillon et al. 2012, Padmanabha et al. 2023). Molecular

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markers are crucial for precise genetic characterization and assessing the relatedness of germplasm. Previous research has utilized microsatellite markers to examine the genetic diversity and population structures of melon (Tzitzikas et al. 2009; Raghami et al. 2014; Hu et al. 2019; Chikh-Rouhou et al. 2021). However, despite India's probable status as the center of origin and domestication, there have been limited investigations conducted on the genetic relationships between native and exotic melons and their wild relatives (Reddy et al. 2016; Saha et al. 2022) with a larger set of germplasm and molecular markers. Therefore, the present study aimed at classifying the genetic diversity and population structure of 96 melon germplasms, comprising native and exotic genotypes from six varietal (*cantalupensis*, *reticulatus*, *inodorus*, *momordica*, *conomon* and *callosus*) classes from four horticultural groups, using microsatellite markers.

Materials and methods

Plant materials

The current investigation included 96 melon germplasm maintained at the Division of Vegetable Science, ICAR-Indian Agricultural Research Institute (IARI) (Supplementary Table S1). Among the entire germplasm panel, 67.71% (65) belonged to the sub-species *melo*, including derived intercrossed populations, while 23.96% (23) of the germplasm were categorized under sub-species *agrestis* (Pitrat 2008). The germplasm assortment comprised eight commercially cultivated North Indian *reticulatus* varieties, two exotic varieties (*inodorus*) bred and adapted in India, a reference of exotic origin from the *cantalupensis* group and several significant breeding lines originating from the wild *agrestis* group.

Genomic DNA extraction, SSR analysis and PCR amplification

The genomic DNA was extracted from tender leaf samples from all the selected germplasm following the standard CTAB procedure (Doyle and Doyle 1990). The extracted DNA samples were subsequently stored in at deep fridge (-20°C) for future genotyping study of melon. A total of 123 microsatellite markers from the Cucurbits Genomics Database (https://www.icugi.org/), evenly distributed (9–12 markers each) across the melon chromosomes (n = 12) were employed for diversity studies. The detailed information regarding 123 SSR primers is presented in Supplementary Table S2**.** The PCR reactions were carried out in a 10 µL reaction volume containing 5 µL master mix (Promega, Madison, WI, USA), 1.5 µL of template DNA, 2.5 µL of TE buffer and 0.5 µL of each primer. The PCR amplification was carried out in Eppendorf Master Cycler (model *pro*-S, Hamburg, Germany) and the program was set with an initial denaturation for 5 minutes at 94°C, followed by 35 cycles of denaturation at 1 min, annealing at 50 to 54°C for 45 seconds, and extension at 72°C for 45 seconds, and a final extension period at 72°C for 10 minutes. The amplified PCR products were electrophoresed on a 3.5% polyacrylamide gel electrophoresis, stained with ethidium bromide and visualized under a Dark Reader trans-illuminator (Alpha Innotech, San Leandro, CA, USA), gel documentation system.

Data analysis

Amplicon sizes of each co-dominant marker were scored and gene diversity parameters such as allele frequency, number of alleles, gene diversity, heterozygosity and polymorphic information content were computed using Power Marker 3.5 (Liu and Muse, 2005). The data obtained were used for generating a Neighbor-Joining (NJ) dendrogram using Power Marker 3.5. The population structure was analyzed using the Bayesian model software STRUCTURE v 2.3.4 (Pritchard et al. 2000). The membership of each accession was tested from K = 1-10, each having ten iterations and coupled with a burn-in period of 1,00,000 steps followed by 1,00,000 Markov Chain Monte Carlo (MCMC) replications. The estimated log probability of data delta K obtained for every K was plotted using STRUCTURE HARVESTER to decipher the assumed estimate of K (Evanno et al. 2005). A membership likelihood score of ≥ 0.70 (Kimaro et al. 2020) was taken into consideration when assigning germplasm to a population and germplasm with membership likelihood below this value was considered as admixture group.

Principal coordinate analysis (PCoA) and analysis of molecular variance (AMOVA) was performed using the GeneAIEx 6.51 program. Additionally, seven allelic genetic parameters, including number of different alleles (*Na*), number of effective alleles (*Ne*), Shannon's information index (*I*), observed heterozygosity (*Ho*), expected heterozygosity (*He*), unbiased expected heterozygosity (*uHe*) and percentage of polymorphic loci (PPL), were assessed based on sub-populations and horticultural groups using GeneAIEx 6.51 program (Peakall and Smouse 2012).

Results

SSR markers-based phylogenetic analysis

The characterization of 96 melon germplasm with 107 SSR markers revealed a total of 288 alleles spanning from 2 to 5 alleles, with an average of 2.69 alleles per locus (Supplementary Table S3). The observed heterozygosity varied between 0.00 to 0.1, with an average of 0.06. Similarly, the gene diversity fluctuated between 0.01 and 0.60, averaging 0.25 per locus. The major allele frequency ranged from 0.48 to 0.99, with a mean value of 0.84, while the PIC values ranged from 0.01 to 0.53, with an average of 0.22. The results also revealed a group of 12 markers showcasing 19 unique alleles in 24 melon germplasm (Supplementary Table S3). Of the recognized germplasm, 12 originated from

the subspecies *melo* group, ten from the wild *agrestis* group and two from the resulting intercrossed populations. The relationships among the 96 germplasm were depicted in the NJ dendrogram (Fig. 1). The clustering process grouped the entire collection into four major clusters (I, II, III and IV) (Supplementary Table S1). Notably, cluster II emerged as the largest cluster, accounting for 48 genotypes, representing 50% of the total germplasm. Clusters I, IV and III contained 30 (31.25%), 11 (11.45%) and 7 (7.3%) genotypes, respectively.

Structure analysis

The Bayesian model analysis indicated the highest log likelihood value at $K = 2$ (Fig. 2), suggesting the presence of two distinct genetic subpopulations (Fig. 3) (Supplementary Table S1). The germplasm allocation to specific subpopulation was based on a minimum ancestry threshold ≥0.70, with 54 germplasm (56.25%) discovered in subpopulation I, 14 germplasm (14.58%) in subpopulation II and 28 (29.17%) considered as admixtures, because of likelihood less than ≤0.70. Subpopulation I encompassed all the popular North Indian melon varieties, commercially bred *inodorus* varieties in India and five derived intercrossed populations, whereas sub-population II contained 14 germplasm solely from the wild *agrestis* group. A total of 14 germplasm from each of the two subpopulations were recorded as admixtures.

The PCoA was performed to gain a different perspective on the structural relationship among the melon germplasm (Fig. 4). All the germplasm was marked with different symbols and colors, forming two distinct clusters that corresponded to the two subpopulations derived from STRUCTURE analysis. The sub-species *melo* were mostly positioned

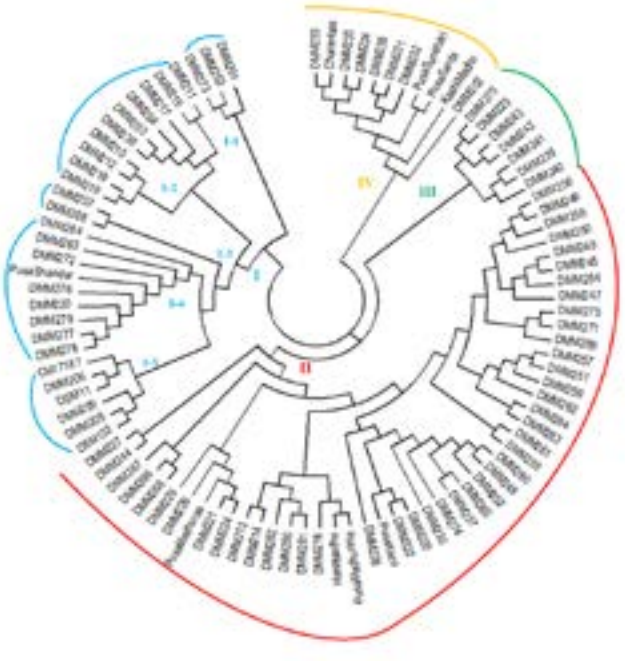

Fig. 1. Neighbor-*joining (NJ)* tree representing the genetic relationship among 96 melon germplasm

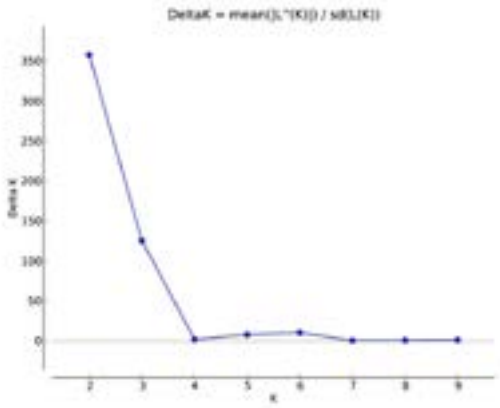

Fig. 2. Evaluation of population model (Evanno et al. 2005), the steep peak of delta $K = 2$ implying two subpopulations

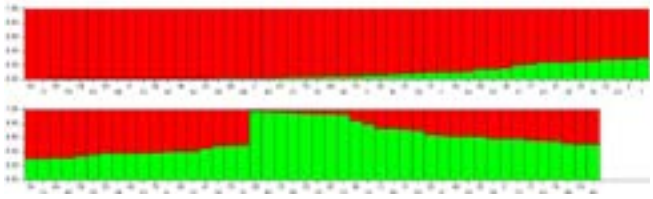

Fig. 3. Model-based subpopulations identified from STRUCTURE 2.3.4. Two subpopulations (K=2) were deciphered, coded with red and green colors mainly representing the commercial class and wild *agrestis* groups, respectively. A solitary color code within a discrete bar denotes purity, whereas, multiple colors within a discrete bar indicated that the particular accession had co-mixtures with genome from other accessions.

in the red region, whereas the wild *agrestis* groups were placed to the green area. The presence of admixtures in both subpopulations resulted in a lack of clear segregation of most germplasm (central portion). Some wild *agrestis* germplasm (e.g., No. 90, 89, 88, 15 and 29) were scattered across a broader area. Similarly, numerous wild *agrestis* germplasm also showed infiltration into the subspecies *melo* group (e.g., No. 17, 24, 20, 28 and 76). This observation highlighted the unique genetic background of wild *agrestis* and native *reticulatus* germplasm found in India.

Population differentiation

The AMOVA results revealed that majority of the genetic variation appeared among individuals (74%), while 22 and 4% of the variation were associated with individuals and among populations, respectively (Table 1 and Fig. S1). Wright's (1965) F-statistics was obtained, revealing F_{IS} (inbreeding coefficient) of 0.773 and F_{IT} (overall fixation index) of 0.781. Moreover, the study yielded a low F_{ST} (fixation index) of 0.037 and a high Nm (gene flow) of 6.564.

Allelic patterns across subpopulations

Seven genetic parameters were computed for the two subpopulations to correlate their diversity at the allelic

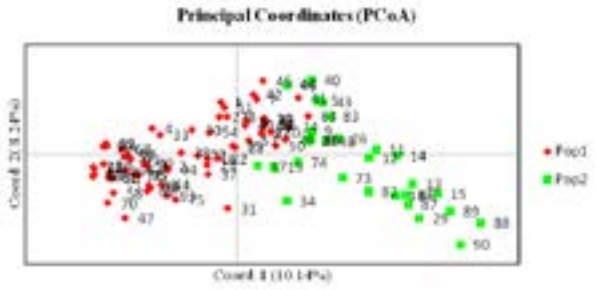

Fig. 4. Principal coordinate analysis (PCoA) displaying two subpopulations corresponding to that of STRUCTURE analysis within the investigated melon accessions

level (Table 2). At the allelic level, the mean values for the subpopulations *for Na, Ne, I, Ho, He, uHe* and PPL were 2.507, 1.467, 0.465, 0.071, 0.266, 0.272 and 93.46% respectively.

Discussion

Conservation and characterization of natural crop diversity are crucial for efficient utilization in crop improvement programs. The microsatellite markers in our study revealed an average of 2.69 alleles per locus, consistent with findings by Tzitzikas et al. (2009), Henane et al. (2015), and Zhang et al. (2017). However, other studies by Raghami et al. (2014), Reddy et al. (2016), Hu et al. (2019), and Chikh-Rouhou et al. (2021) reported higher mean alleles per locus. The differences in allele counts may stem from both genetic variation and methodologies used for identifying polymorphic markers. Generally, loci with more alleles are valuable for assessing genetic diversity. Additionally, a heterozygosity deficit was noted similar to the earlier record in Tunisian melon (Chikh-Rouhou et al. 2021), which could be possibly due to selection pressure. Our study uncovered 19 unique alleles across 24 germplasm lines, emphasizing the crucial role of identifying these unique alleles in preserving genetic diversity. This observation holds enormous importance for breeding implications (Thudi and Fakrudin 2011). Likewise, Singh et al. (2020) also reported seven unique alleles within 23 melon germplasm, with a remarkable representation of unique alleles from the *reticulatus* and *cantalupensis* group. These unique alleles can be further examined for germplasm identification or used DNA in fingerprinting of cultivars and F_1 hybrids.

The NJ dendrogram classified 96 germplasms into four clusters and cluster I comprised all 23 wild *agrestis* germplasm. Out of total 49 *reticulatus* germplasm of Indian origin, 48 of them could be clubbed together in cluster II except, Kashi Madhu variety developed by ICAR-IIVR, Varanasi, which was placed in cluster IV. Most of the exotic germplasm from *cantalupensis* and *inodorus* groups were grouped in clusters III and IV, respectively. However, one advanced breeding line DMM 203 (*C. melo* var. *inodorus*) developed from a crossing of exotic germplasm from *inodorous* group and *cantalupensis* group of Indian germplasm was placed in Cluster I along with majority of germplasm from *agrestis* group of Indian origin. The SSR markers employed in our study proved highly effective in differentiating the typical Indian *reticulatus* melon from that of the wild *agrestis* melon and exotic varieties with minimal assimilation of different varietal or horticultural affiliations. Similarly, Singh et al. (2020) observed the intermixing of germplasm between Indian and exotic melon germplasm using SSR markers, independent of geographical origins and taxonomical groups. This study successfully differentiated non-sweet wild *agrestis* melons from sweet native *reticulatus* melons and exotic varieties, demonstrating the value of SSR markers in genetic diversity studies for accurate melon germplasm classification.

Understanding the genetic diversity and structure of germplasm collections is crucial for crop improvement strategies and association mapping research to prevent incorrect associations among the germplasm (Flint-Garcia et al. 2005). The structuring of genetic variation may depend on evolutionary processes associated with domestication, gene flow resulting from natural or artificial selection and genetic drift (Raja et al. 2022). The Bayesian model analysis identified two sub-populations together with admixture group. Two subpopulations identified in STRUCTURE analysis were identical to the genetic clustering of the dendrogram, where the STRUCTURE deciphered the sub-populations with individuals from subspecies *melo* predominated in subpopulation I, while individuals from the subspecies *agrestis* predominated in subpopulation II. This finding fits with Pitrat's (2008) classifications, showing that subspecies are more closely tied to genetic differentiation than are varietals or horticultural groups, whereas NJ dendrogram identified four clusters with affiliations towards varietal groupings. Similarly, Hu et al. (2019) identified four clusters

Table 1. Analysis of molecular variance (AMOVA) of 96 melon germplasm

Source	d.f.	SS	MSS	Est. Var.	% Variation	F-Stat	F-value	F-Statistics
Among Pops	1	65.213	65.213	0.518	4%	F_{ST}	0.037	0.001
Among Individuals	94	2266.491	24.112	10.509	74%	F_{IS}	0.773	0.001
Within Individuals	96	297.000	3.094	3.094	22%	F_{IT}	0.781	0.001
Total	191	2628.703		14.121	100%	Nm	6.564	

Est. Var.= Estimated variance; F_{ST} = Fixation index; F_{IS} = Inbreeding coefficient; F_{IT} = Overall fixation index and Nm = Gene flow

Table 2. Mean values of different genetic parameters in each of the two subpopulations along with admixtures group

Pop	N	Na	Ne	I	Ho	He	uHe	PPL %
Pop. I (56.25%)	54	2.57	1.346	0.385	0.037	0.211	0.213	94.39%
Pop. II (14.58%)	14	2.449	1.584	0.531	0.097	0.311	0.322	91.59%
Admixtures (29.17%)	28	2.504	1.467	0.467	0.078	0.276	0.281	94.39%
Mean	96 (Total)	2.507	1.467	0.465	0.071	0.266	0.272	93.46%

N = Number of genotypes; Na = No. of different alleles; Ne = No. of effective alleles = 1/ (Sum pi ^2); *I* = Shannon's Information Index = −1 ∗ Sum [pi ∗ Ln (pi)]; *Ho*= Observed heterozygosity = no. of Hets/N; *He* = Expected heterozygosity = 1 − (Sum pi ^2); *uHe* = Unbiased expected heterozygosity = [2N/(2N-1)] ∗ He; PPL (%) = Percentage of polymorphic loci

using cluster analysis, while their STRUCTURE analysis indicated three subpopulations, roughly corresponding to the varietal melon germplasm used in their study. Previous studies employing SSR markers in Indian melon accessions revealed two structural groups ($K = 2$) (Reddy et al. 2016; Saha et al. 2022), corroborated by PCoA clustering into two distinct groups. The study discovered 28 genotypes with admixed lines containing genetic material from another population (Falush et al. 2003). Population density, bottlenecks and gene flow collectively influence population genetic structure. High gene flow (6.564) recorded in our investigation indicated robust exchange and minimal differentiation between subpopulations. This extensive gene flow likely accounts for the prevalence of numerous admixed lines within the germplasm collection. The notable factors contributing to this high gene flow could be ongoing anthropogenic seed dispersal over time and space, cross-pollination behavior, genetic drift, as well as natural and artificial hybridization between improved cultivars and local landraces, which may have facilitated the domestication of diverse and intermediate forms of melon (Reddy et al. 2016). F_{ST} serves as a genetic measure of population variation, with values exceeding 0.15 signifying significant differentiation (Frankham et al. 2002). In our study, a low F_{ST} value of 0.037 suggested limited genetic variance. This was supported by the AMOVA results.

Utilizing wild *agrestis* germplasm to broaden the genetic diversity of melon and integrate it into resistance breeding is crucial (Dhillon et al. 2012; Choudhary et al. 2020). Our study revealed a limited genetic exchange between subspecies *melo* and subspecies *agrestis* germplasm, suggesting the underutilization of wild *agrestis* germplasm in sweet melon improvement efforts. Notably, only partial genetic exchange was observed in key breeding lines ('CM17187', 'DSM 11' and 'DSM 132') intended for disease resistance breeding. Breeders have influenced the crop's population structure by selectively incorporating specific traits from a limited number of donor species within certain varietal groups through one-way selection pressure. For example, 'CM 17187' and 'DSM 132' lines showed the varying amount of genetic exchange with subpopulation I. 'CM 17187' is widely used for developing Fusarium wilt-resistant cultivars (Oumouloud et al. 2013), it has recorded the higher genetic exchange. However, 'DSM 132' exhibited limited genetic exchange due to its recent identification for resistance to ToLCNDV in melon (Padmanabha et al. 2022, 2023). Furthermore, the aggregation of *callosus* and *conomon* germplasm in subpopulation II with less than 10% genetic exchange with subpopulation I, indicates the need for further research to explore potential beneficial traits and specific genes within these wild *agrestis* groups for melon enhancement.

Allelic diversity investigations yielded crucial insights into allelic richness for the two subpopulations and horticultural groups examined. Subpopulation II demonstrated greater expected heterozygosity (He) compared to subpopulation I, indicating greater diversity within subpopulation II. Similar patterns emerged when evaluating allelic diversity parameters within the germplasm group based on horticultural groups, highlighting substantial heterogeneity and rich genomic diversity in the wild *agrestis* group. This finding is consistent with Hu et al. (2019), who reported higher allelic diversity in the wild melon group compared to the thin-skinned and thick-skinned melon groups.

In summary, the population structure analysis provided significant insights into the genetic basis of melon germplasm utilization in varietal improvement programmes in India. The distinction between subspecies *melo* and subspecies *agrestis*, highlighted their unique genetic characteristics, emphasizing the importance of preserving these genetic resources. High gene flow led to admixtures within the subpopulations, which can be effectively identified and excluded through population structure analysis, reducing false positives. To enhance future research, we recommend equal representation of germplasm from different varietal groups and the use of high-density markers for a more precise understanding of the population's genetic structure. Despite limitations, our study highlights the effectiveness of microsatellite markers in characterizing melon germplasm with precision.

Author's contribution

Conceptualization of research (HC, RKY, JK); Designing of the experiments (HC, RKY, JK); Contribution of experimental materials (HC); Execution of field/lab experiments and data collection (KKT); Analysis of data and interpretation (DCM,

JK, CK, KKT); Preparation of the manuscript (KKT, HC, RKY).

Supplementary materials

Supplementary Tables S1 to S4 and Figure S1 are provided and can be accessed, www.isgpb.org

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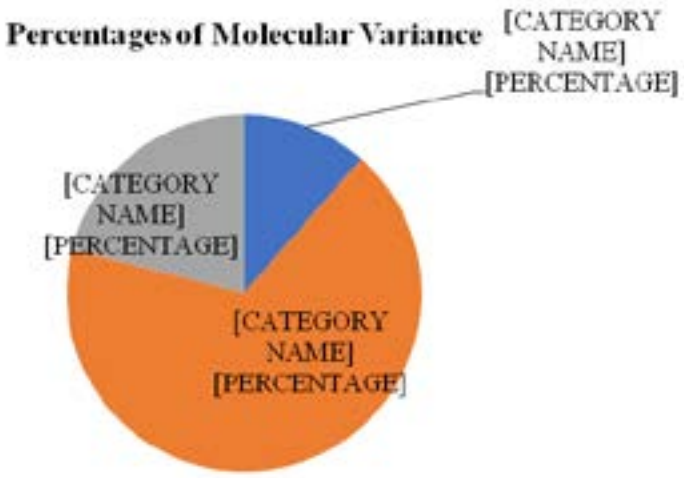

Supplementary Fig. S1. Analysis of Molecular Variance (AMOVA) of 96 melon germplasm based on populations deciphered through STRUCTURE analysis

Supplementary Table S1. Descriptions of 96 melon germplasm used in the current study

No.	Accession	Varietal group	Type	Cluster derived from SSR markers	Population derived from STRUCTURE analysis
1	Kashi Madhu	*reticulatus*	Commercially Released Variety	IV	I
2	Hara Madhu	*reticulatus*	Commercially Released Variety	II	I
3	Pusa Madhurima	*reticulatus*	Commercially Released Variety	II	I
4	Pusa Madhuras	*reticulatus*	Commercially Released Variety	II	I
5	Charentais	*cantalupensis*	Exotic Reference germplasm	IV	II
6	DMM 201	*reticulatus* x *momordica*	Derived Intercrossed population	I	I
7	Pusa Sarda	*inodorus*	Commercially Released Variety	IV	I
8	DMM 202	*inodorus*	Advanced Breeding Line	IV	I
9	DMM 203	*inodorus*	Advanced Breeding Line	I	II
10	DMM 204	*reticulatus* x *momordica*	Derived Intercross population	I	II
11	CM17187	*momordica*	Breeding stock from Wild *agrestis*	I	II
12	DSM 11	*momordica*	Breeding stock from Wild *agrestis*	I	II
13	DMM 205	*conomon*	Wild *agrestis*	I	II
14	DMM 206	*momordica*	Wild *agrestis*	I	II
15	DSM 132	*callosus*	Breeding stock from Wild *agrestis*	I	II
16	DMM 207	*momordica*	Wild *agrestis*	I	I
17	DMM 208	*momordica*	Wild *agrestis*	I	II
18	DMM 209	*callosus*	Wild *agrestis*	I	II
19	DMM 210	*reticulatus* x *momordica*	Derived Intercrossedpopulation	I	II
20	DMM 211	*momordica*	Wild *agrestis*	I	I
21	DMM 212	*momordica*	Wild *agrestis*	I	I
22	DMM 213	*reticulatus*	Advanced Breeding Line	II	I
23	DMM 214	*reticulatus*	Advanced Breeding Line	II	I
24	DMM 215	*momordica*	Wild *agrestis*	I	I
25	DMM 216	*reticulatus*	Advanced Breeding Line	II	I
26	DMM 217	*momordica*	Wild *agrestis*	I	II
27	DMM 218	*momordica*	Wild *agrestis*	I	I
28	DMM 219	*momordica*	Wild *agrestis*	I	II
29	DMM 220	*momordica*	Wild *agrestis*	I	II
30	DMM 221	*reticulatus*	Advanced Breeding Line	II	I
31	DMM 222	*reticulatus*	Advanced Breeding Line	II	I
32	DMM 223	*cantalupensis*	Advanced Breeding Line	III	I
33	DMM 224	*reticulatus*	Advanced Breeding Line	II	I
34	DMM 225	*reticulatus*	Advanced Breeding Line	II	II
35	DMM 226	*reticulatus*	Advanced Breeding Line	II	I
36	DMM 227	*reticulatus*	Advanced Breeding Line	II	I

37	DMM 228	*reticulatus*	Advanced Breeding Line	II	I
38	DMM 229	*reticulatus*	Advanced Breeding Line	II	I
39	DMM 230	*reticulatus*	Advanced Breeding Line	II	I
40	DMM 231	*inodorus*	Advanced Breeding Line	IV	II
41	DMM 232	*inodorus*	Advanced Breeding Line	IV	I
42	Pusa Sunehari	*inodorus*	Commercially Released Variety	IV	I
43	DMM 233	*cantalupensis*	Advanced Breeding Line	IV	II
44	DMM 234	*inodorus*	Advanced Breeding Line	IV	I
45	DMM 235	*inodorus*	Advanced Breeding Line	IV	I
46	DMM 236	*cantalupensis*	Advanced Breeding Line	IV	II
47	DMM 237	*reticulatus*	Advanced Breeding Line	II	I
48	DMM 238	*reticulatus* x *momordica*	Derived Intercrossed population	I	II
49	DMM 239	*inodorus*	Advanced Breeding Line	III	I
50	DMM 240	*inodorus* x *cantalupensis*	Derived Intercrossed population	III	I
51	DMM 241	*inodorus* x *cantalupensis*	Derived Intercrossed population	III	I
52	DMM 242	*cantalupensis*	Advanced Breeding Line	III	I
53	DMM 243	*cantalupensis*	Advanced Breeding Line	III	I
54	DMM 244	*reticulatus*	Advanced Breeding Line	II	I
55	DMM 245	*reticulatus*	Advanced Breeding Line	II	I
56	DMM 246	*reticulatus*	Advanced Breeding Line	II	I
57	DMM 247	*reticulatus*	Advanced Breeding Line	II	I
58	DMM 248	*reticulatus*	Advanced Breeding Line	II	I
59	DMM 249	*reticulatus*	Advanced Breeding Line	II	I
60	DMM 250	*reticulatus*	Advanced Breeding Line	II	I
61	DMM 251	*reticulatus*	Advanced Breeding Line	II	I
62	DMM 252	*reticulatus*	Advanced Breeding Line	II	I
63	DMM 253	*reticulatus* x *momordica*	Derived Intercrossed population	I	I
64	DMM 254	*reticulatus*	Advanced Breeding Line	II	I
65	DMM 255	*reticulatus*	Advanced Breeding Line	II	I
66	DMM 256	*reticulatus*	Advanced Breeding Line	II	I
67	DMM 257	*reticulatus*	Advanced Breeding Line	II	I
68	DMM 258	*reticulatus*	Advanced Breeding Line	II	I
69	DMM 259	*reticulatus*	Advanced Breeding Line	II	I
70	DMM 260	*reticulatus*	Advanced Breeding Line	II	I
71	DMM 261	*reticulatus*	Advanced Breeding Line	II	I
72	DMM 262	*reticulatus*	Advanced Breeding Line	II	I
73	DMM 263	*momordica*	Wild *agrestis*	I	II
74	DMM 264	*momordica*	Wild *agrestis*	I	II
75	DMM 265	*reticulatus*	Advanced Breeding Line	II	I

76	DMM 266	*reticulatus*	Advanced Breeding Line	II	I
77	DMM 267	*reticulatus*	Advanced Breeding Line	II	I
78	DMM 268	*reticulatus*	Advanced Breeding Line	II	I
79	DMM 269	*reticulatus*	Advanced Breeding Line	II	I
80	DMM 270	*cantalupensis*	Advanced Breeding Line	III	I
81	DMM 271	*reticulatus*	Advanced Breeding Line	II	I
82	DMM 272	*momordica*	Wild *agrestis*	I	II
83	DMM 273	*reticulatus* x *momordica*	Derived Intercrossed population	I	II
84	DMM 274	*reticulatus*	Advanced Breeding Line	II	I

Supplementary Table S2. A list of SSR markers used in the genotyping of 96 melon germplasm

S. No.	SSR primers	Chro. No.	Forward primer	Reverse primer	Position (cM)	Size
1	DM0300	1	CATTATTGAAGTTAGGTCCC	GGGGGTTGAGTTAGAAAAG	7	300
2	TJ22	1	GGGCTTGAAGAAAATCCCTC	GCCATTGAAGGTAGAGTCGG	17	100
3	DE1582	1	TATTCATATGCAAGCCAGC	GCACAATTATTTAAAAGTTTAGGG	22	135
4	CMCTN86	1	GTGACAGTTATCAAGGATGC	AAGGGAATGCATGTGGAC	35	180
5	DM0699	1	CTTGACTGTGATTCCAAGG	TCACCTAGCGTACCAAATC	36	190
6	DM0073	1	CTCATCGCAAAACCATATC	AGTTTGTGGATCGTTTAGG	46	130
7	DE1774	1	CAGAAATGTGGTTCTTCCC	GTGATCAGAAGAAGCTGCC	56	250
8	DM0198	1	GTGTAGGCCATGAAAATG	TTCCTTCTCTTCCTTCATC	66	150
9	DE1337	1	CTTCATCTTCTCGCAGAGC	ATAGACCTAGTCGCCCTCC	75	200
10	DM0339	1	TAATAAATACGTCCCTGCG	ATACAATGGTCAATGCGAG	94	300
11	CMAT141	1	AAGCACACCACCACCCGTAA	GTGAATGGTATGTTATCCTTG	127	170
12	DM0298	2	GTTCGACGTTTACTCATCC	AGTGAAAGATGGGTGCTTC	4	270
13	CMAGN39	2	GGGCCATTTTCTTTTTACAT	TCTCTTAACTTTCTCTCTCC	8	155
14	DE1135	2	TTCAGCAAAAGAACCGAAC	TTGCTCTTTAGGTTTCATCG	23	160
15	CMAGN16	2	CGATAAATGTTGATGAAAGTC	TTCCTCAGGTCATATTCTTC	36	150
16	DE1463	2	CTAAGACCAAAGGACACCG	CCAAGTCTGAGGCTCGTAG	42	110
17	DM0528	2	ATTAAACACAACAGGTGCG	CAATGACCCATGAAGAAAC	53	320
18	CMBR066	2	TCAAGCAAAAACCATAATCAGAA	TCCCTTTTCATCATTTCTCTTCA	64	120
19	DE1240	2	CATCCCAATTTCTCTTTGC	GACTTTACGATCATTCCGC	74	190
20	CMGCTN187	2	GTCTACTCTCTGCCTTTCAAC	TAATGCCTCTATCTTCTCG	85	140
21	CMCT44	2	TCAACTGTCCATTTCTCGCTG	CCGTAAAGACGAAAACCCTTC	91	105
22	DE2020	2	AGTCACAATTCCACAACCC	TCGCCACACTAATCAACTG	96	220
23	GCM548	2	AACAGGTAGAGGAAAGCATG	TGACCCACTAGTACATCTCTC	-	140
24	DE1187	3	CACTCCTTTTCCGTTTCAC	GAAAAGCAGGGATCTAGGG	0	150
25	DE1206	3	GCTCATTTTTGGGTGTAGTG	AAGTCCAAAAACACAAGCG	20	200
26	DE1602	3	CCTCCTCAAGAACTCATCG	GTCGCAGAACAGAAATCAAC	30	230
27	DM0071	3	AAGAAAGTCCCTCAGTTCAC	CAATACGTTGTGGCCTAAG	42	140
28	CMCTN5	3	CACCTTAAAGTTTAGCCCC	AAAAATGCAATGAACTGAGCGC	53	210
29	DE1533	3	CTGTTTCGAGAAAGGATGC	GGCAACTCATTTATCAGGC	60	170
30	DM0587	3	GAACTTCATCCTACAACGC	TTTATGCTCCTTTGAGTGC	64	340

31	TJ10	3	ACGAGGAAAACGCAAAATCA	TGAACGTGGACGACATTTTT	66	120
32	DM0192	3	ACACCATCACCAAACTCTC	TGGGATTTTCCATACCTC	80	110
33	DM0369	4	AGAGCTAAAGGAGAGGCAG	AAATAGGGTGAAGAATACGC	0	250
34	DE1234	4	CGGGACATAATTTGCTGAC	AGGGGTTAATAATTGTGTTGTG	11	170
35	CMTTTGN209	4	CCATTCATTAGCTTTCCTC	GCCATTGAAACTCTGAAAC	25	165
36	DE1885	4	CGCAAAGGAAATGTGATTC	TTGGTGGGTATTGAATTTTG	45	180
37	DE1130	4	AAACCTGTGATAAACAAGCG	TCATATGTTGCCTGACATTG	54	200
38	DM0744	4	CTCAATGAGAAGGAAGTCG	ATCCCTCAAATCTTTAACC	56	300
39	DM0448	4	AGATTTGCTGAAGGATTCG	AGACAACCCTATGAACCAAC	77	220
40	DM0152	4	GCAAAATCATAAACTTCCC	TTTGTGGTGTAAATGGTTC	93	90
41	DM0168	4	CATTTCATTTCATCACTTCC	GCGGCTGTTAATGATAAAG	114	260
42	DE1824	4	TTTCAACCTTCACCACTACC	AAGCAGTCGGTATCTGTGG	123	250
43	DE1059	4	TTCAGCTTCTTGACTTCCG	AGAGGACGAGGAGGAAGAG	129	230
44	DE1810	4	AAAAGAAGACAAGGAAAGCAG	TAATTAGGATGCCTTTGCC	137	190
45	DE1035	5	TCTTCATTTTCTTTGCCTTTC	CTTCCAAGGGTCTTCAATG	15	150
46	DM0768	5	AATTTCCGACCCATTTTAC	TGGAGAGGTAGATCATTGC	23	350
47	CMATN101	5	GCTTGTCTTTGTGTTTGC	GAGAACAAGACTCCTTAATCC	34	170
48	DE1809	5	AAGAACAAAGAGTTTTGGGG	TCATCTTTTCATCCGTTGTC	45	210
49	DM0552	5	TTTTAATGCCCATGGTATC	AAAAGGAACAGAACAAGGG	68	310
50	DM0638	5	ATGAATGATCTGGTTGGTG	CTAAGATCACACCACTGCC	77	100
51	CMTCN227	5	CCTCCGAACTCTCTCATC	ACCATCGTCATAGCCTTG	85	180
52	DE1644	5	AGCCATTTTCAAGTTGTGC	GTTGTATAACCAAAAATGCAAG	95	200
53	DE1500	5	GGACATATGGTTACTGAACTTTG	CACAGAACTTTTTCTTCTCTCAG	102	300
54	CMTCN50	6	TCTACTTCCATGAATCCATC	TAGAATGGTTAGGAAACCCT	1	220
55	CMTAN263	6	CAAAACTCTAAACAACGAC	ATGTAAATAGCAAAGGAAC	15	90
56	DE1250	6	AGGGGAGGCTCTGTAGAAG	ACACACCCTTCCCTAAACC	30	260
57	DE1591	6	AACTTTTCCCATTTCCGAC	TTTGTTACCTTAAATGATTGGTG	47	250
58	DE1981	6	TGTGGTTTATGGTTGGACC	TTGCGATGCATCTTGATAG	48	230
59	DE1491	6	CTAACCTCGCAATCTCTGG	TTGGGTCGTTACATGTGG	60	190
60	DE1926	6	AGAAGGTTCTTGCAACAGG	TCAAGCACTCACTTAAGCATC	70	150
61	DE1762	6	CTAAGGGAAAAAGGCAAGG	CCGTCGGTCTAGAAGAATG	80	150
62	DM0890	6	TTGAGAGGATGGTTTTCTTTC	TTTGTGGTGCAAACTTCTG	93	200
63	DE1487	6	TCTAAAATCCCAAAACCCC	AAAACCCAATAAGGATCGG	106	220
64	CMCTN38	6	TAAAACACTCTCGTGACTCC	GATCTGAGGTTGAAGCAAAG	120	150
65	DM0228	7	GACGAGAATTTGTTGGAAG	AGTGCCAGAGATGATGAAC	0	300
66	DE1295	7	AAGGTCCAAACTTTGAGGG	TATGCCCAATGGTACTTCC	12	120
67	DM0309	7	GGCAGTAAATGACCATGAC	GGTGACGAACAAACTGAAG	23	250
68	DM0104	7	TCTTGGACACATGGAAGTC	CGAGATGCACATAAACTTTC	35	200
69	DE1406	7	GGTCAGGATAGAGGGCAG	CCCAAATTTCGAGGTAAG	50	230
70	CMAGN141	7	TTTGTGAGGGTGCAGCTAG	CAACACAACACATGGCAATTC	64	175
71	DE1378	7	TGTTGTTCTTCATTGCGAC	ACTCTGTACATTGCCCAAC	72	150

72	DE1083	7	TATGACCAATTGGAGAATG	GATACCGAGAAAAAGCTTCC	87	200
73	DE1350	7	AGGGTGATTTTTGTGCAAC	AGTTTCACGTCCGAATCTG	105	200
74	DE1457	7	AGGATGCAAAGGTAGTTGC	CGACCAAACCTAAACCAAG	114	230
75	DM0043	8	GGTATTTGGTAATCGTATCC	GACAGTGAAGACCGTTACAG	1	140
76	CMCTT144	8	CAAAAGGTTTCGATTGGTGGG	AAATGGTGGGGGTTGAATAGG	13	190
77	DM0637	8	ATCTGCAACATCAAAAACC	TTGATCAAGAAAAGCATCC	28	160
78	DE1170	8	CACAGACAAAGTATCGAAAAGAG	TAGCGAGTCGAAACCTCTC	38	140
79	DM0091	8	ACTTGTAGTTAACCGCTGG	TTCTTTCACTGTGTTGATAGG	69	200
80	DM0640	8	CTGGAGAAGACAACAATGG	TTCATTCCCTATTTTTCCC	79	330
81	DE1366	8	TTCTCCGATGTGTCCTCTC	GTCGCTTGGAATATATCGG	85	150
82	DM0020	8	GCGATCTTGAAGTTTGTAAG	CAAAACCTAACAATCCACC	95	100
83	DM0353	8	GTTTTTGACATGAACAGCC	AAGCATTTTGAACCTCCTC	107	300
84	DE1614	8	AAGTGGAATTGGATGGATG	GATAAGTGGGAAGGGGAG	121	160
85	CMAG59	8	TTGGGTGGCAATGAGGAA	ATATGATCTTCCATTTCCA	-	140
86	DE1752	9	CCAAAGCATACTCGAGACC	CGCCTTCTTGAATCAGTTC	1	220
87	DE1400	9	AACTTTTGCTTTCCCTTCC	TGGGGAATTAGGGTTAGATG	5	200
88	CMTC47	9	GCATAAAAGAATTTGCAGAC	AGAATTGAGAAGAGATAGAG	12	160
89	DE1725	9	AAAAGCTTAAGGCCATTCC	GGGGGCCTTAAAATATGAC	25	150
90	DE1215	9	TTTCTCTTTTTGGAACTCCC	TTGGGAGATCGTAAGGTTG	33	230
91	DM0030	9	CCAAAGTAAAAGTGAAGTCC	CTTGAAATGAATTTGAGGTG	42	150
92	CMATN22	9	CGGCAATCATCTTATCTTTC	AAGATTGAAGTGGGAAAATG	67	170
93	DM0456	9	CATCAGAGGACAAGCATTC	TTACATGAGAAAAGACATGTAAG	78	250
94	SSR13420	9	GGGTTTGGGTTGGTTTAGGT	CTTTCATCACACCCTCCTCC	-	200
95	DM0580	10	CCACGAAATCAAAAATCAC	TTTTTCAACTTGCTTCGAC	3	220
96	CMCTN71	10	TCAATTTTTGCCAAACAAGC	CAAGGACACAGATTTAATAC	6	160
97	DE1887	10	CGTGCTTCCCTCTTAAATC	GAAGGGAGTATTGAGTTGGG	17	200
98	CMGAAN233	10	TGCAGGCTTTTTCATAAC	TGTTTATCAATGGCAGCG	25	150
99	DE1868	10	GCAAATTGATTTTGACTAATAGC	TTGATGTATGAAAAGTAGAGTTGC	32	250
100	DM0253	10	CATTTTGATTGCCAACTTC	TTCACTCGGTTCTCGATAG	36	170
101	DE1495	10	GTGAACGAAGAGACGAAGC	AAAACCCCAAACCCTAGTC	45	210
102	DE1275	10	AATTGCATTCACCAAACAAC	AGCTGTTTTCCACTGATCG	54	100
103	DM0173	10	ATCGTCAGTCACCTTTTTC	AAGGAGGAGTTTGTTGAAG	60	250
104	CMGA165	10	CTTGTTTCGAGACTATGGTG	TTCAACTACAGCAAGGTCAGC	68	100
105	DM0262	11	TTTGGAGATTAAGCAATCG	ATTCCCCATTAAACGACAC	4	200
106	DE1941	11	AAAGCACTATTTCCTTTCCC	TTGAAGGTATCTCTTCGCTG	8	250
107	DE1282	11	TATGCCACCTAAAGGGATG	CATAGTTTGTGCCTATTGCC	35	210
108	DE1348	11	CACACGTTTTTCTTCATTCC	GCAACTTTGTATGTTGCCTAC	44	230
109	DM0203	11	AAGTCGTAAGAACTCGCAC	TAACGGCCTCATAATTTTC	55	160
110	DM0331	11	AAACAGTGGCCAAATACTG	CTCAAACAAACTCCTCCAC	72	270
111	DE1034	11	AAACTGATCGACGCATCC	AATTGAATTGGCATTTTGG	85	210
112	DM0229	11	GACTTGACGAAAATTCCAC	TCTTCTTGTCCACCATCTC	94	170

113	DE1167	11	CTGAATGGCAAGAAAGAGG	TCAAGTTTGGGAATTTTGC	102	160
114	TJ147	11	GAAAGGTAGGAAGAAAGTGAAGA	ACTCTTGAAGCTGACCGATG	122.7	120
115	CMTCN34	12	TCCTCTCTTTTCTTTCATCC	GTTGCTGATTTTTGCATTCC	12	160
116	DE1299	12	GTGAGCCTTTCTCATAGTTGAC	GTCGTCCCAACAAATGAAG	24	160
117	CMN2155	12	TCATTGATCTTTTGCTTTTGC	TGGTAGCAAACATCTGCCTG	37	370
118	5A6U	12	TCCATTGGTTAAAAAGAAAGACG	TTCATTTTTGTATTCACTGCATTT	45	160
119	CMACGN289	12	TCATGTCAACCGAAGCTAG	CAGATACTGTCCGAACGTG	60	140
120	CMBR150	12	TTTTTACTGTGTGTTTTGATTTGTT	TTGGTGGACTGGAATCCATA	72	250
121	DE1185	12	GTCGCAACACACAACATTC	ATCCGTTCCAAACACAAAC	82	125
122	DE1610	12	AACCATGGAGACGAGATTG	ACGACTCCTCCCCAGCTC	102	150
123	DE1560	12	AAAACAGCATTGAAAACCG	ATCTGTTTCGATCCCACAC	106	200

Supplementary Table S3. Genetic diversity parameters revealed by 107 polymorphic SSR markers

Primers	MAF	K	GD	Ho	PIC	Primers	MAF	K	GD	Ho	PIC
DM0300	0.81	3	0.33	0.16	0.30	DM0890	0.73	2	0.40	0.02	0.32
TJ22	0.84	4	0.28	0.06	0.26	DE1487	0.89	3	0.21	0.06	0.20
DE1582	0.91	3	0.17	0.02	0.16	CMCTN38	0.86	3	0.25	0.07	0.24
CMTCN86	0.58	3	0.53	0.11	0.43	DM0228	0.88	2	0.21	0.05	0.19
DM0699	0.51	2	0.50	0.04	0.38	DE1295	0.98	3	0.04	0.04	0.04
DM0073	0.62	2	0.47	0.08	0.36	DM0309	0.97	3	0.06	0.04	0.06
DE1774	0.72	2	0.40	0.08	0.32	DE0104	0.96	2	0.08	0.00	0.08
DM0198	0.54	3	0.60	0.06	0.53	DE1406	0.76	4	0.41	0.04	0.39
DE1337	0.65	3	0.52	0.15	0.46	CMAGN141	0.95	3	0.10	0.02	0.10
DM0339	0.77	3	0.38	0.02	0.35	DE1378	0.56	3	0.50	0.13	0.38
CMAT141	0.96	4	0.08	0.05	0.08	DE1083	0.95	3	0.09	0.01	0.09
DM0298	0.87	3	0.24	0.12	0.22	DE1350	0.83	2	0.29	0.05	0.24
CMAGN39	0.71	4	0.46	0.12	0.42	DE1457	0.98	2	0.03	0.01	0.03
DE1135	0.90	2	0.19	0.13	0.17	DM0043	0.81	4	0.33	0.09	0.32
CMAGN16	0.61	3	0.51	0.00	0.42	CMCTT144	0.83	3	0.28	0.01	0.25
DE1463	0.82	3	0.30	0.05	0.26	DE1170	0.83	2	0.28	0.04	0.24
DM0528	0.68	4	0.45	0.14	0.37	DM0640	0.97	3	0.06	0.00	0.06
CMBR066	0.66	3	0.51	0.15	0.46	DM0020	0.99	2	0.02	0.02	0.02
DE1240	0.85	2	0.25	0.06	0.22	DM0353	0.92	3	0.15	0.08	0.14
CMCT44	0.96	2	0.08	0.04	0.08	CMAGN59	0.98	3	0.03	0.01	0.03
DE2020	0.85	3	0.26	0.13	0.24	DE1400	0.72	3	0.42	0.05	0.36
GCM548	0.88	4	0.23	0.06	0.22	CMTC47	0.93	3	0.14	0.02	0.13
DE1187	0.79	3	0.35	0.04	0.32	DE1725	0.91	2	0.17	0.00	0.16
DE1206	0.87	4	0.24	0.06	0.23	DM0030	0.96	2	0.08	0.02	0.08
DE1602	0.83	3	0.29	0.13	0.27	CMATN22	0.91	2	0.17	0.00	0.16
DM0071	0.67	2	0.44	0.17	0.35	DM0456	0.88	2	0.21	0.03	0.19
CMCTN5	0.57	5	0.58	0.12	0.51	SSR13420	0.92	3	0.15	0.10	0.14

DE1533	0.86	5	0.25	0.10	0.24	DM0580	0.85	2	0.25	0.00	0.22
DM0587	0.93	2	0.14	0.08	0.13	CMCTN71	0.87	4	0.25	0.06	0.24
TJ10	0.86	3	0.25	0.08	0.24	DE1887	0.81	2	0.31	0.07	0.26
DM0192	0.71	3	0.45	0.01	0.41	DE1868	0.95	2	0.09	0.07	0.09
DE1234	0.80	2	0.32	0.09	0.27	DM0253	0.85	3	0.26	0.09	0.24
CMTTGN209	1.00	2	0.01	0.01	0.01	DE1495	0.83	3	0.28	0.10	0.25
DE1885	0.96	3	0.10	0.02	0.08	DE1275	0.48	3	0.54	0.10	0.44
DM0448	0.80	2	0.32	0.08	0.27	DM0173	0.90	3	0.19	0.05	0.18
DM0152	0.92	2	0.15	0.00	0.14	CMGA165	0.91	3	0.17	0.00	0.17
DM0168	0.81	3	0.32	0.01	0.27	DM0262	0.98	2	0.03	0.01	0.03
DE1059	0.92	2	0.15	0.00	0.14	DE1941	0.92	2	0.15	0.08	0.14
DE1810	0.88	2	0.22	0.02	0.20	DE1282	0.95	2	0.09	0.03	0.09
DE1035	0.85	2	0.25	0.02	0.22	DE1348	0.98	2	0.03	0.01	0.03
CMATN101	0.96	2	0.08	0.08	0.08	DM0203	0.91	2	0.14	0.06	0.13
DE1809	0.95	2	0.10	0.00	0.09	DM0331	0.98	2	0.04	0.04	0.04
DM0552	0.60	4	0.54	0.04	0.46	DE1034	0.97	2	0.06	0.02	0.06
DM0638	0.96	2	0.08	0.04	0.08	DE1167	0.77	3	0.37	0.15	0.33
DE1664	0.56	4	0.59	0.06	0.53	TJ147	0.82	2	0.29	0.08	0.25
DE1500	0.82	2	0.29	0.08	0.25	CMCTN34	0.69	2	0.43	0.04	0.34
CMTCN50	0.69	3	0.47	0.07	0.42	DE1299	0.93	2	0.13	0.03	0.12
CMTAN263	0.58	4	0.57	0.13	0.51	CMN2155	1.00	2	0.01	0.01	0.01
DE1250	0.79	4	0.36	0.13	0.34	5A6U	0.97	2	0.06	0.00	0.06
DE1591	0.84	3	0.28	0.10	0.26	CMACGN289	0.97	2	0.06	0.63	0.59
DE1981	0.89	2	0.20	0.00	0.18	DE1185	0.51	2	0.50	0.03	0.38
DE1491	0.97	2	0.06	0.00	0.06	DE1610	0.94	3	0.12	0.10	0.12
DE1926	0.92	2	0.14	0.05	0.13	DE1560	0.58	3	0.52	0.10	0.43
DE1762	0.87	3	0.23	0.10	0.22						
Mean	0.84	2.69	0.25	0.06	0.22						

LG = Linkage group, MAF = Major allele frequency, K = Number of alleles, GD = Gene diversity, Ho = Observed heterozygosity, and PIC = Polymorphic information content

Supplementary Table S4. Unique alleles detected by SSR markers and identified melon germplasm

S. No	Ch. No.	SSR Markers	Total no. of alleles detected	No. of gen. identified	No. of unique alleles	Amplified size	Genotype (s) identified
1	1	DE1582	3	1	1	135	DMM 276 (*momordica*)
2	1	DM0339	3	2	1	500	DMM 244 (*reticulatus*) DMM 223 (*cantalupensis*)
3	2	CMAGN39	4	4	2	165	DSM 132 (*callosus*), DMM 209 (*callosus*)
						180	Charentais (*cantalupensis*), DMM 244 (*reticulatus*)
4	2	DE1463	3	2	1	50	DMM 244 (*reticulatus*), DMM 243 (*cantalupensis*)
5	2	GCM548	4	2	2	160	DMM 243 (*cantalupensis*)
						180	DMM 210 (*reticulatus*)

6	3	CMCTN5	5	4	2	170	DMM 263 (*momordica*), DMM 277 (*momordica*)
						180	DMM 228 (*reticulatus*)
7	3	DE1533	5	3	2	270	DMM 223 (*cantalupensis*)
						330	DMM 208 (*momordica*), DMM 244 (*reticulatus*)
8	5	DE1644	4	2	1	200	DMM 238 (*R*×*M*), DMM 279 (*conomon*)
9	6	CMTAN263	4	1	1	150	DMM 279 (*conomon*)
10	6	DE1250	4	7	2	190	DMM 203 (*inodorous*), DMM 238 (*R*×*M*), DMM 217 (*momordica*), DMM 210 (*reticulatus*), DMM 209 (*callosus*), DMM 243 (*cantalupensis*)
						220	DMM 211(*reticulatus*)
11	9	CMTC47	3	6	2	250	DMM 204 (*R* x *M*), DMM 211(*reticulatus*), Pusa Shandar (*momordica*), DMM 212 (*reticulatus*)
						180	DSM 132 (*callosus*), DMM 277 (*momordica*)
12	10	CMCTN71	4	4	2	180	DMM 220 (*momordica*)
						200	DMM 236 (*cantalupensis*), DMM 239 (*inodorous*) DMM 274 (*reticulatus*)