RESEARCH ARTICLE

Studies on Traditional Melon '*Vellari*' (*Cucumis melo* var. *momordica* L.) in Tamil Nadu, India

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Abstract

The local snapmelon landrace known as "Vellari" is an important traditional crop in southern India, specifically in the districts of Tamil Nadu. However, it has received limited attention in global studies and gene bank collections, primarily due to the lack of germplasm collections and data on its morphological traits and significant quality characteristics. This study examined seventeen germplasm accessions of "Vellari" collected from five districts representing diverse climatic zones for their fruit morphology and phenotypic variability. Organoleptic assessments based on consumer preferences were also conducted. A total of 29 quantitative and 27 qualitative descriptors were used to estimate phenotypic diversity. Principal component analysis (PCA) was performed to assess variability between the collections. The analysis identified several defining characteristics that differentiate the snap melon accessions, including leaf pubescence, flower earliness, flowering time, peduncle length, fruit shape and size, and days to maturity. The first five components explained 84.29% of the cumulative percentage of variation. A wild taxon called "Sukkangai" (*Cucumis melo* ssp *agrestis* var *agrestis*) was also reported for local use in the surveyed area.

Keywords: Less-known, Landraces, Tamil Nadu, Snap melon, Vellari, Sukkangai.

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vitamin-C, 0.3 g protein, 95.7% moisture (Peter and Hazra 2012) and 74.0 kcal energy (Goyal and Sharma 2009).

Due to the fast replacement of the vegetable melon cultivars with improved varieties of muskmelon and cucumbers, the collection and conservation of these valuable germplasm deserves a top priority (Fregany *et al.*, 2011; Koli *et al.*, 2013; Manchali *et al.*, 2019). The south Indian melons denoted with a source of resistance to cucumber mosaic virus, zucchini yellow mosaic virus, powdery mildew (races 1, 2, 3, 5), *Fusarium* wilt (races 1, 2), *Aphis gossypii* and leaf miner (Fregany *et al.*, 2011). Despite producing climacteric fruits, the poor keeping qualities of snap melon cultivars prevents widespread commercial acceptance across the country. In the Indian national collections at ICAR-National Gene Bank, New Delhi, the snap melon from Tamil Nadu is barely represented.

Keeping the importance of snap melons from south India, the study was undertaken on the less-known melons "Vellari" with aim to: 1) Exploring unrepresented areas having distinct accessions in southern Indian districts of Tamil Nadu; 2) Characterization of collected germplasm for morphological traits, and to look for associations between morphological and geographical distances; 3) Organoleptic assessment to popularize and extend its use.

Materials and Methods

Germplasm Collection

Collection sites for germplasm of "Vellari" were identified after pre-surveying in the six districts of Tamil Nadu with help of the Department of Horticulture and Plantation Crops, Government of Tamil Nadu, Tamil Nadu. The exploration was undertaken in - Dindigul, Virudhunagar, Cuddalore, Kancheepuram, Ariyalur, and Namakkal districts during February-March 2020 and a total of 156 study sites were visited. Detailed passport data were recorded as per the standard methodology for collection (Dwivedi 2010). Farmer's fields and local markets of each district were thoroughly surveyed for variability in snap melon.

Germplasm Characterization and Data Analysis

A total of seventeen "Vellari" accessions were collected as mature fruits. The germplasm was evaluated in the field from February to May 2021. A total of 56 morphological characters were recorded, including 29 quantitative traits and 27 qualitative traits per the Cucumis melo descriptors published by IPGRI (2003) (Table 1).

Principal component analysis (PCA) was performed to determine which variable contributed more with its variance to the total variance observed in the collected accessions. Using the correlation matrix among 56 variables for 17 accessions, Eigenvalues and contribution percentages of each principal component axis were computed (Jeffers 1967). All computations were performed using SPSS 28.0.0 software, Euclidean distances were calculated across accessions, and a distance matrix was produced using DARwin 6.0.

Geo Reference Mapping and Organoleptic Assessment

Sampling sites were depicted using software (DIVA-GIS7.5) and the geo-referenced map was produced (Figure 1). The organoleptic assessment was done with the help of 36 informants. The data were recorded for edibility preferences and acceptability.

Identity Confirmation

After a study of the plants, the identity was confirmed as a snap melon. In accordance with regular herbarium procedures, herbarium specimens of chosen material with flowering and fruiting were made in the field and deposited at the National Herbarium of Cultivated Plants. (NHCP), ICAR-NBPGR, New Delhi.

Result and Discussion

Germplasm collection

During an exploration undertaken to six districts of Tamil Nadu viz., Dindigul, Virudhunagar, Cuddalore, Kancheepuram, Ariyalur and Namakkal in February-March 2020, a total of 17 accessions of distinct types of landraces of *"Vellari"* and two *Sukkangai* accessions were collected (Figure 2) from 156 study sites located in the farmers' field, local market and kitchen gardens. The study area lies in a wide range between 9.6° N and 12.9° N latitude, 77.6° E to 79.8° E longitude, and altitude ranging from 5 to 325 m above mean sea level. Two *Sukkangai* accessions were collected from the Dindigul district (PP 01, PP 02). Seventeen snap melon accessions were collected from the following five districts, Virudhunagar (PP 03-04), Kancheepuram (PP

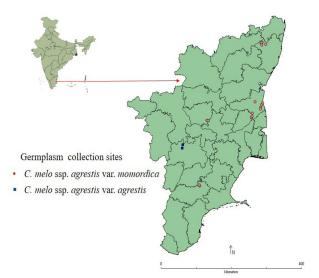


Figure 1: Area of study and collection sites

Table 1: List of descriptors used for morphological characterization

S. No	Descriptor code	Descriptor
1	PtSz	Plant size :3 (<1 m ³) 5 (1–3 m ³⁾ 7 (>3 m ³⁾
2	IL	Internode length: average internode length of 10–15 th node on main vine
3	NNFF	No. of nodes to first fruit
4	STT	Stem thickness in mm
5	NPB	No of plant branches: count only flowering branches
6	LS	Leaf shape:1 (entire) 2 (trilobite) 3 (pentalobate) 4 (3- palmately lobed) 5 (5-palmately lobed) 99 other
7	LL	Leaf lobes: 3 (shallow) 5 (intermediate) 7 (deep)
8	LP	Leaf pubescence type: 3 (soft) 5 (intermediate) 7 (hard)
9	GL	Glossiness: 3 (glossy) 5 (intermediate) 7 (dull)
10	LR	Leaf ratio: Leaf length divided by leaf width. Measures leaves in the middle of the branch
11	LPL	Leaf petiole length in cm
12	EM	Earliness of male: 3 (early) 5 (intermediate) 7 (late)
13	EF	Earliness of female: 3 (early) 5 (intermediate) 7 (late)
14	DFF	Days to first flowering
15	D50	Days to 50% flowering
16	PL	Peduncle length in cm
17	FBS	Flower bud shape: 1 (globular) 2 (intermediate) 3 (long) 99 (other)
18	LSP	Mean length of standard petal in cm
19	WSP	Mean Width of standard petal in cm
20	OP	Ovary pubescence: 1 (less) 3 (medium) 3 (dense)
21	OS	Ovary shape: 1 (flat) 2 (round) 3 (long) 4 (very long)
22	FS	Fruit shape: 1 (globular) 2 (flat) 3 (oblate) 4 (elliptical) 5 (pyriform) 6 (ovate) 7 (acorn) 8 (elongate) 9 (scallop) 99 (other)
23	FSZ	Fruit size/weight in g
24	FL	Fruit length width ratio: the length from stem end to blossom end of the fruit divided by the width at the broadest point
25	ТМ	Time of maturity: 1 (< 70 days) 2 (70–90 days) 3 (91–110) days 4 (>110 days)
26	DFFrt	Days to first fruit
27	SC	Predominant fruit skin color: 1 (white) 2 (light yellow) 3 (cream) 4 (pale green) 5 (green) 6 (dark green) 7 (blackish green) 8 (orange) 9 (brown) 10 (grey) 99 (other)
28	SFSC	Secondary fruit skin color: 1 (white) 2 (light yellow) 3 (cream) 4 (pale green) 5 (green) 6 (dark green) 7 (blackish green) 8 (orange) 9 (brown) 10 (grey) 99 (other)
29	IMFC	Primary color of immature fruit: 1 (light green) 2 (intermediate) 3 (dark green)
30	SSCP	Secondary skin color pattern: 0 (no secondary color) 1 (light green) 2 (intermediate) 3 (dark green)
31	FSRF	Fruit surface: 1 (smooth) 2 (grainy) 3 (finely wrinkled) 4 (deeply wrinkled) 5 (shallowly wavy) 6 (rarely warts) 7 (numerous warts) 8 (lightly corked/netted) 9 (heavily corked/netted) 10 (sutures) 99 (other)
32	FSL	Fruit stem length in cm
33	СН	Fruit splitting or cracking habit 3 (low) 5 (intermediate) 7 (high)
34	MCF	Main color of flesh: 1 (white) 2 (yellow) 3 (cream) 4 (pale green) 5 (green) 6 (pale orange) 7 (salmon)
35	FT	Flesh texture: 1 (smooth-firm) 2 (grainy-firm) 3 (soft-spongy) 4 (mealy) 5 (fibrous-gelatinous) 6 (fibrous dry)
36	FF	Flesh flavor: 3 (insipid) 5 (intermediate) 7 (sweet)
37	FTH	Flesh thickness in cm
38	SDLG	Seed length in cm
39	SDW	Seed width in cm
40	SDT	Seed thickness in cm

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05-07, PP18-19), Cuddalore (PP 08-12), Ariyalur (PP 13-15), and Namakkal (PP/KRR 01, PP/KRR 02). The collected germplasm was evaluated and multiplied in the Ariyalur district of Tamil Nadu from February to May 2021 and submitted to the National Gene Bank, New Delhi. Nine of 17 accessions received indigenous collection numbers (Table 2). The remaining accessions sent for multiplication. The study area includes four climatic zones of Tamil Nadu, i.e., the southern zone, Western zone, Northeastern zone, Western zone, and Cauvery delta zone (TN-ENVIS) (Figure 1).

Variability Study in "Vellari"

Genetic resources of exotic and native melons have widened our knowledge of understanding and utilization of the potential value of the melons (Sari and Solmaz 2005; Mohamed and Yousif, 2004; Laghetti et al., 2008; Joseph et al., 2013, 2017; Staub et al., 2004; Solmaz et al., 2016). Snap melons of southern India are less worked out with respect to their genetic resource potential. Accessions from south India are meagerly represented in the National Gene Bank holding compared to North Indian melons (Fregany 2011; Manchali et al., 2019). Collection and utilization of such variability are essential. For 56 selected qualitative and quantitative descriptors (IPGRI 2003) were assessed in the field. About 17 accessions of snap melon collected from Tamil Nadu state, Southern India, were evaluated to estimate the genetic diversity among the snap melon accessions. Across snap melon accessions, 16 descriptors were to be uniform, which are discarded from the analysis, and the remaining 40 descriptors were used for analysis (Table 1). The snap melon accessions used in the analysis showed substantial genetic diversity (Figure 3)

Principal component analysis was used to assess the variability in snap melon accessions. The percentage of variation explained by the first five components were 34.25, 25.81, 12.30, 6.33 and 5.58, respectively; the cumulative variance of first five components was 84.6% (Tables 2 & 3 and Figure 4) and the principal characters with higher Eigenvectors delineated the accessions into separate groups in the first five components are represented (Table 3). The analysis revealed that the variations in leaf pubescence type, earliness of male and female flower, days to first flowering, days to 50% of flowering, peduncle length, flower bud shape, ovary pubescence, ovary shape, fruit shape, fruit size, fruit length-width ratio, time of maturity, days to first fruit, predominant fruit skin color, the main color of flesh and flesh flavor were contributed more to distinguish snap melon accessions evaluated in the present study, accessions showing larger variation in days to first flowering (20-34), days to 50% of flowering (24-38), ovary shape (round, long and very long) fruit shape(elongate, ovate and oblate) fruit size (450–3000 g), predominant fruit skin color (light yellow, yellow, grey, and orange) and main color of flesh (white, cream, pale orange). A total of 22 characters out of



Figure 2: Collection of germplasm: (a) *C. melo* subsp. *agrestis* var. *momordica* growing in the farmer's field-; (b) *C. melo* subsp. *agrestis* var. *agrestis* in natural habitat; (c) melons sold in local market of Madurai, Tamil Nadu; (d) variability in melons



Figure 3: Variability in snap melon fruit morphology a & e - PP 04; b& f- PP/KRR 01; c& g- PP 18; d& h - PP 19

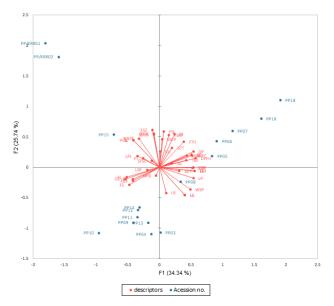


Figure 4: Principal component analysis biplot depicting the relationship of descriptors and accessions (axes F1 and F2: 60.08%)

S. No.	Accession	Collector-No.	Crop/Species	Cultivar name/bio-status
1	IC-0647724	PP-03	Snapmelon/Cucumis melo var. momordica	<i>Vellari</i> /landrace
2	IC-0647725	PP-04	Snapmelon/Cucumis melo var. momordica	<i>Vellari</i> /landrace
3	IC-0647726	PP-08	Snapmelon/Cucumis melo var. momordica	<i>Vellari</i> /landrace
4	IC-0647727	PP-09	Snapmelon/Cucumis melo var. momordica	<i>Vellari</i> /landrace
5	IC-0647728	PP-10	Snapmelon/Cucumis melo var. momordica	<i>Vellari</i> /landrace
6	IC-0647729	PP-15	Snapmelon/Cucumis melo var. momordica	<i>Vellari</i> /landrace
7	IC-0647730	PP-19	Snapmelon/Cucumis melo var. momordica	<i>Vellari</i> /landrace
8	IC-0647731	PP/KRR-01	Snapmelon/Cucumis melo var. momordica	<i>Vellari</i> /landrace
9	IC-0647732	PP/KRR-02	Snapmelon/Cucumis melo var. momordica	<i>Vellari</i> /landrace

Table 2: Indigenous collection number for collected germplasm

40 showed significant variance, and these characters were used to generate a dendrogram (Figure 5). The Euclidean distances were calculated across landraces and a distance matrix was produced using DARwin 6.0 software. The 17 accessions were separated into three clusters: the first cluster had eight accessions, the second cluster had seven accessions, and the third cluster had two accessions. These clusters were mainly separated by fruit shape and size. Accessions collected from each district have significant fruit size and shape variations, so most accessions from the same district were clustered together. According to the dissimilarity matrix, PP 10 and PP 15 are extremely distant accessions with a dissimilarity index of 33.9, while PP/KRR 01 and PP/KRR 02 are extremely similar with a dissimilarity index of 1.59.

The present collection included landraces producing fruits mostly appropriate for local trading and selfconsumption since seeds were exchanged between local farmers who grew snap melon for such purposes. So these snap melon cultivations are restricted to particular geographical areas based on local people's preferences because they are not suitable for distant markets due to their poor quality of keeping. We found that each district in our study area has distinct fruit types.

Germplasm collected from the Kancheepuram district was preferred in the same way as the muskmelon due to fruit taste, shape and skin type, showing intermediate characters between the muskmelon and snapmelon. Detailed morphological study coupled with the molecular study will better understand its identity and relation with other materials. A recent study (Pandey *et al.*, 2021) observed that a landrace called '*Arya*' in Rajasthan has some intermediate characteristics of snake melon and snap melon; a molecular study confirmed that '*Arya*' is a separate taxon. Crossability studies with other taxa of *melo* will enrich the gene pool and help to assign a distinct taxonomic status based on the outcome of the hybridization (Joseph *et al.*, 2013).

Organoleptic Assessment

The comparison was made based on an organoleptic assessment that included 36 people, mostly women folks

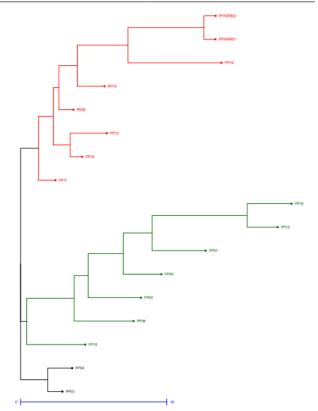


Figure 5: Euclidean distance clustering of 17 snap melon accessions based on 22 morphological descriptors

between the ages of 30 and 60. It was carried out to determine consumer preferences, and three fruit characteristics were evaluated: 1) Salad preference, 2) Dessert preference, 3) The aroma of ripened fruit. For a salad, the majority of participants preferred PP15 (40%), while none preferred the following accessions: PP05, PP06, PP07, PP18 and PP19. On the other hand, 72% of people highly preferred the above-mentioned accessories for dessert purposes because of their sweet flesh and aroma. These six accessions were collected from the Kancheepuram district, where they were primarily cultivated and used for desserts because of their sweet flesh and pleasant aroma. However, due to their rough skin, they were not suitable for salads. The remaining eleven

Table 3: Eigen value and percent of total variation and component matrix for the principal component axes

Principal component	F1	F2	F3	F4	F5
Eigenvalue	13.735	10.296	4.925	2.564	2.228
Variability (%)	34.337	25.739	12.311	6.409	5.569
Cumulative (%)	34.337	60.076	72.388	78.796	84.365
Descriptor code					
PtSz	-0.171	0.211	0.142	-0.078	0.058
IL	-0.171	0.211	0.142	-0.078	0.058
NNFF	-0.135	0.227	-0.001	-0.136	0.16
STT	0.084	0.153	0.293	0.022	0.1
NPB	-0.022	-0.066	-0.109	0.143	-0.196
LS	0.167	-0.219	0.137	0.081	-0.004
LL	0.167	-0.219	0.137	0.081	-0.004
LP	0.225	-0.085	-0.132	0.078	0.105
GL	0.083	0.031	-0.307	-0.142	0.215
LR	0.046	-0.201	0.165	-0.037	-0.114
LPL	-0.143	0.088	-0.243	-0.041	0.159
EM	0.232	-0.03	0.049	-0.02	0.31
EF	0.232	-0.03	0.049	-0.02	0.31
DFF	0.223	0	-0.01	0.062	0.321
D50	0.215	-0.005	0.019	0.042	0.367
PL	-0.174	-0.092	0.161	0.039	-0.03
FBS	-0.173	-0.106	0.068	-0.069	-0.042
LSP	-0.079	-0.019	0.374	0.007	0.116
WSP	0.204	-0.175	-0.086	0.01	0.089
OP	0.224	0.125	-0.006	0.01	-0.163
OS	-0.225	-0.092	0.019	0.068	0.181
FS	-0.197	-0.137	-0.127	0.003	0.117
FSZ	-0.044	0.292	0.086	0.099	0.013
FL	-0.213	-0.079	-0.149	-0.006	0.138
ТМ	0.178	0.054	0.156	-0.342	-0.124
DFFrt	0.236	0.07	0.086	-0.157	0.083
SC	0.211	0.099	-0.007	0.099	-0.231
SFSC	-0.049	0.052	0.414	-0.017	0.095
IMFC	0.212	0.091	-0.021	0.157	-0.285
SSCP	0.017	0.22	-0.242	-0.026	0.152
FSRF	0.062	0.251	-0.132	0.052	-0.112
FSL	0.028	0.281	-0.079	-0.013	0.021
СН	0.005	0.124	0.055	0.532	0.026
MCF	0.179	0.09	-0.082	0.169	0.047
FT	-0.105	0.07	0.149	0.49	0.116
FF	0.098	0.259	-0.095	-0.044	-0.148
FTH	0.159	0.201	0.108	0.102	-0.101
SDLG	-0.035	0.257	0.158	-0.03	0.149
SDW	-0.036	0.266	-0.002	-0.143	0.007
SDT	0.13	-0.028	0.184	-0.336	-0.074

accessions were cultivated for immature and mature fruits with delicate skin and excellent palatability, making them ideal for salads. In this study, two snapmelon accessions from Tamil Nadu were used for comparison in the National Gene Bank, i.e., IC597018 and IC597021.

Ethnobotany and Uses

Snap melon is used in a variety of ways in Tamil Nadu, including immature fruits as salad, mature fruits as dessert and summer drinks with jaggery or sugar that provide a soothing sensation during summer. The young fruits are often confused with cucumber (*Cucumis sativus* L.) fruit due to their similar utility and common name, '*Vellari*'. In some parts of the Cuddalore district, farmers get a good price for the seeds used to garnish sweets and savory dishes in the same way as other cucurbit seeds. In the same area, the immature fruits of "*Sukkangai*" (*Cucumis melo* ssp *agrestis* var *agrestis*) have a strong bitter taste. Local people were reported to process them for processed vegetables. The fruits are sliced into small pieces and soaked in buttermilk for a few days, then sun-dried and stored for future use. They are also used to cure stomach worm problems in children.

Focus needs to be placed on the following: fine grid survey, collection and conservation of germplasm from areas of availability (other districts and states in south India), diversity analysis, and comparative study with North Indian melons. South Indian snap melons, "Vellari," have been rapidly dwindling due to the improved cultivars of the common cucumber over the past two decades, and their significant traits can be used in crop improvement for better adaptability to drought conditions and other biotic stress tolerant traits.

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