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Fruit Flesh Thickness Analysis in Local Cucumber (*Cucumis sativus* L.) Genotypes Through Morphological and Marker-Based Assay

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ABSTRACT

Cucumber (*Cucumis sativus* L.) is one of the commercially important and widely cultivated cucurbitaceous vegetable grown throughout the world. The immature fruits are consumed as salad or pickled. The present study involved 22 local cucumber genotypes collected from different places of Karnataka, India. Fruit flesh thickness is an important trait for cucumber fruit quality and a central determinant of yield. Among the evaluated genotypes, the fruit flesh thickness (1.92 cm), fruit diameter (6.87 cm) and yield per plant (3.05 kg) were higher in genotype (CSSL) collected from Shiralakoppa (Shivamogga) region. The higher fruit length (31.48 cm) and lower fruit flesh thickness (0.84 cm) was recorded in genotype (VLD) collected from Dharwad. The analysis of variance revealed significant differences for all the traits. Higher GCV, PCV and high heritability coupled with high GAM were recorded for fruit weight, fruit diameter, fruit flesh thickness, seed cavity width and yield per plant. The fruit flesh thickness in 22 local cucumber genotypes was analysed using candidate gene (*Csa2M058670.1*) markers. Among 13 SSR primers, SSR23420 and SSR10849 have shown higher PIC (0.37) and higher gene diversity (0.50). The cucumber genotypes such as CSSL,CSWL, CSHLC-1 and CSHL were found to be promising for fruit quality traits such as fruit length, diameter, flesh thickness and yield.

Keywords : Cucumber, Local genotypes, Fruit flesh thickness, Morphological, Markers

THE cucumber (*Cucumis sativus* L.) (2n = 14) is a member of Cucurbitaceae that comprises of 90 genera and 750 species. In Latin, *Cucumis* means 'Cucumber' and *sativus* means 'that is sown'. The cucumber is one of the oldest cultivated vegetable crops. It has been known in history for over 5,000 years and was originated in India (Sebastian *et al*., 2010). It is a thermophilic and frost-susceptible plant species. The African group contains the larger number of the species that are spread over large parts of Africa and the Middle East. The Asiatic group to which *Cucumis sativus* L. belongs, is found in south and east Himalayas.

The minerals and vitamins present in cucumber are known to hydrate the body as twice the amount of water. Eating peeled or a whole cucumber with seeds intact will help to obtain lots of fiber and β-carotene, an antioxidant that will boost immunity. Cucumber also helps to improve the absorption of calcium, enhancing the repair of bone muscles. It can reduce the spread of cancerous cells throughout the body and decrease the risk of cancer development in the body. It also plays a major role in regulating uric acid levels in the body and thus prevents the crystallization in kidneys. Consuming cucumber also ensures healthy and glowing skin. They also help to keep diabetes in check (Raaz *et al*., 2014).

Breeding cucumber for improving its yield, quality and disease resistance is a big target for the world-wide breeders. Fruit traits are considered most important in cucumber breeding. Some of the fruit traits such as fruit length, diameter, weight and number of fruits per plant have direct correlation with the yield. Fruit related characteristics are most important for cucumber varietal improvement hence considerable attention has been placed on fruit quality (Li *et al*., 2013 and Harshitha & Shyamalamma, 2021). Fruit flesh thickness is an important fruit quality trait in cucumber and a major determinant of yield. The thicker fruit flesh contributes to greater edible portion of cucumber. Fruit flesh enlargement is an important phase of fruit development in cucumber (Boonkorkaew *et al*., 2008). The assessment of genetic variability for fruit flesh thickness is essential before planning an appropriate breeding strategy for genetic improvement in cucumber.

A Quantitative Trait Locus (QTL) of 0.19 Mb located on chromosome 2 that controls fruit flesh thickness in cucumber (QTL fft2.1) was reported by Xu *et al*., (2015). Twenty genes were identified in 0.19 Mb QTL region and qRT-PCR revealed higher expression levels of *Csa2M058670.1* (a SET domain protein-lysine methyl transferase) in thick fruit flesh cucumber lines compared to thin fruit flesh cucumber lines. The sequence alignment showed 4 bp deletion from the thin flesh cucumber lines which is responsible for fruit flesh thickness. Further, Wang *et al*. (2020) confirmed that SET domain controls cell division and differentiation, which contains the possible candidate gene *Csa*2M058670.1 that controls fruit flesh thickness in cucumber and designed SSR primers for these regions. These primers were used in the present study for screening local cucumber genotypes with varied fruit flesh thickness.

Information related to genetic variations in cucumber fruit flesh thickness in local cucumber genotypes is lacking in the literature. Thus, a study on evaluation of diversity for fruit flesh thickness among local cucumber genotypes collected from different regions of Karnataka, India was carried out at phenotypic and molecular level with an objective of screening of local cucumber genotypes for fruit flesh thickness through morphological and molecular marker-based screening with candidate gene markers.

MATERIAL AND METHODS

Plant Materials and Crop Cultivation

Twenty-two local cucumber genotypes were collected from different regions of Karnataka known for its diversity in terms of fruit colour, flesh thickness, fruit size, shape, taste and likeness by the public. The details of the local types used as research materials has been provided in Table 1. The seeds of local cucumber types were sown in the field in basin method, with three seeds in three corners of a triangle prepared within the basin (Plate 1). The required quantity of manures and fertilizers were incorporated into the basins as per the package of practices followed for horticultural crops (Jyothishree and Prakash, 2024). The plants were irrigated by drip method and the plant protection measures were taken up as per the pest and disease problems identified.

Phenotypic Data Collection

Twenty-two local cucumber genotypes were sown in completely randomized design with three replications, in the field adjacent to department of plant biotechnology, UAS, Bangalore during January - 2022. The observations on fruit length (cm), fruit diameter (cm), fruit weight (g), fruit stalk length (cm), fruit flesh thickness (cm), seed cavity breadth (cm), seed cavity length (cm), TSS (°Brix), shelf-life (days), fruit weight at physiological maturity (g), number of fruits per plant and yield per plant (kg) were recorded. The observations were recorded as per the DUS guidelines provided by PPV and FRA, New Delhi.

TABLE 1
List of local cucumber (*Cucumis sativus* L.) genotypes used in the experiment

Genotypes	Place of collection in Karnataka
G1 - DGLM	Dharwad
G2 - CSLG	Bangalore
G3 - DGM	Dharwad
G4 - CSLW	Bangalore
G5 - VLD	Dharwad
G6 - MUCHANDA	Mysore
G7 - CSHLA	Arakalagudu
G8 - KPL	Koppal
G9 - CSHLH	Holenarasipur
G10 - CSG - 2	Golithadaka
G11 - CSG - 1	Golithadaka
G12 - CSG - 3	Golithadaka
G13 - CSHL	Hassan
G14 - NATTI	Bangalore
G15 - CSHLC - 2	Hassan
G16 - HVR	Haveri
G17 - CGLB (Check variety)	Bangalore
G18 - CSWL	Bangalore
G19 - CSHLC - 1	Channarayapatna
G20 - CSJ - 1	Jamakandi
G21 - CSGLD	Dharwad
G22 - CSSL	Shiralakoppa

Genomic DNA Isolation and Purification

For plant genomic DNA extraction, tender leaves were collected from 30 days old plants, washed well with tap and sterile water and stored at -20°C in a freezer. On the day of extraction, the samples were crushed using liquid Nitrogen and the DNA was isolated through CTAB method (Doyle and Doyle, 1987). Later, the DNA quality was checked on 0.8 per cent agarose gel through gel electrophoresis and the concentration was checked in Eppendorf Bio-spectrometer. The samples contaminated with RNA were treated with RNase enzyme (10 mg/ml)

Plate 1 : General view of cucumber field

and the purified DNA was diluted to 50 ng/µl for SSR marker analysis.

SSR Marker Analysis

Thirteen SSR markers (Table 2) specific to fruit flesh thickness gene were used for screening cucumber genotypes (Xu *et al*., 2015). The PCR reaction was performed using 10X PCR buffer with $MgCl_2$ (1.5 µl), 2 mMdNTP’s (1.0 µl), 10 µM forward primer (0.5 µl), 10 µM reverse primer (0.5 µl), 3 U *Taq* DNA Polymerase (0.4 µl), sterile water 7.5 µl and 50 ng/µl template DNA (1.2 µl) with a total volume of 12.6 µl. Amplification was carried out in a thermocycler (Eppendorf Master Cycler nexus gradient) withan initial denaturation temperature of 94°C for 4 min followed by 35 cycles of denaturation at 94°C for 1 min, primer annealing at 50- 65°C for 1 min, primer extension at 72°C for 1 min and final extension at 72°C for 10 min. Amplified products were separated on 1.8 per cent agarose gel. The gel was viewed in Gel Doc (Syngene’s G:BOX F3) and the DNA amplification

TABLE 2

List of candidate gene SSR primers for fruit flesh thickness in cucumber (Xu *et al*., 2015)

Primers		Sequence 5' ’! 3'	Anneal. temp. (ºC)
SSR00204	Forward	AACCCTATTTGCACGCATTC	51.4
	Reverse	GAGAAACAGCTGGAATTGGG	
SSR00289	Forward	AGGACGAGGCTAATGGGAGT	47.5
	Reverse	TTACAAGTCCCCCTCAAACG	
SSR18937	Forward	TTACTCCAAAGATGCTGGGC	54.9
	Reverse	CATTTGACCGAATCTTGACTTT	
SSR13532	Forward	AAACCCAAGAATTGTAAACCCA	56.5
	Reverse	TGATCCATTTCTATTCCTAACATTGA	
SSR03593	Forward	GATGATCAAATTTACAATCTTGCC	55.8
	Reverse	GGCAGCCTAATTAGAATAACTCAGA	
SSR23832	Forward	TGAAACAATCACCATCATCTCA	52.4
	Reverse	AAGTGGGAAGCTTTGGAGGT	
SSR22558	Forward	TCAACTTATCCCTCTTTCTATTTTCC	62
	Reverse	GGCAATCATTACCAAAAACCA	
SSR23420	Forward	GAAGGGATGGTAGATGAAGGG	59.8
	Reverse	CTTCTCCCCTTTCTTGGCTT	
SSR01374	Forward	GGGAGATTCTCAAAATGGATGA	56.5
	Reverse	TTGCGTGTAAGGAACGTCAC	
SSR10849	Forward	TCGATCTGGTTTACTGTAGATATGC	59.8
	Reverse	GAAGAATTTGAAAAGATAAAAACACA	
SSR20248	Forward	TCCTCAAACGTCTCTCTCCC	58.5
	Reverse	GATAGCATGCGGTGTCCTCT	
SSR00378	Forward	TCCCTAAAATTTCGACAACCC	55.9
	Reverse	TTAGTATGGCTTGAACACCCA	
SSR00030	Forward	TGAAATTGCTTACCCTTTGACC	58.2
	Reverse	CCATGTTTTGTAGGGATCGAG	

Plate 2 : Fruit length variations observed among the genotypes

TABLE 3
Estimates of genetic variability for fruit and yield related traits in twenty-two local cucumber genotypes

Traits	Mean	Range		PCV (%)	GCV (%)	h^2 (%)	GAM (%)
		Min	Max				
FL (cm)	20.92	14.01	31.48	15.82	15.59	97.13	31.65
FD (cm)	4.84	3.25	6.87	24.28	23.95	97.34	48.68
FW (g)	218.79	109.00	334.00	36.12	35.09	94.41	70.24
FSL (cm)	2.44	1.08	4.48	31.64	30.82	94.86	61.83
FFT (cm)	1.18	0.84	1.92	23.59	21.72	84.74	41.18
SCB (cm)	2.66	1.63	3.93	25.93	25.00	92.97	49.67
SCL (cm)	16.56	13.42	23.62	15.23	14.45	89.93	28.22
TSS (ŗBrix)	1.16	0.93	2.05	27.27	25.01	84.12	47.26
SL (days)	4.36	3.25	5.5	14.86	11.57	60.26	18.56
FWPM (g)	501.81	358.36	880.00	31.23	29.80	91.04	58.57
NFPP	8.66	5.25	11.25	22.76	21.44	88.74	41.60
YPP (kg)	1.97	1.12	3.05	31.63	30.60	93.56	60.96

(Index: FL-Fruit Length, FD- Fruit Diameter, FW-Fruit Weight, FSL-Fruit Stalk Length, FFT-Fruit Flesh Thickness, SCB-Seed Cavity Breadth, SCL-Seed Cavity Length, TSS, SL-Shelf-Life, FWPM-Fruit Weight at Physiological Maturity, NFPP-Number of Fruits Per Plant and YPP-Yield Per Plant) was recorded directly using Gel documentation unit. Presence of amplicon was scored as 1 and absence was scored as 0.

Data Analysis

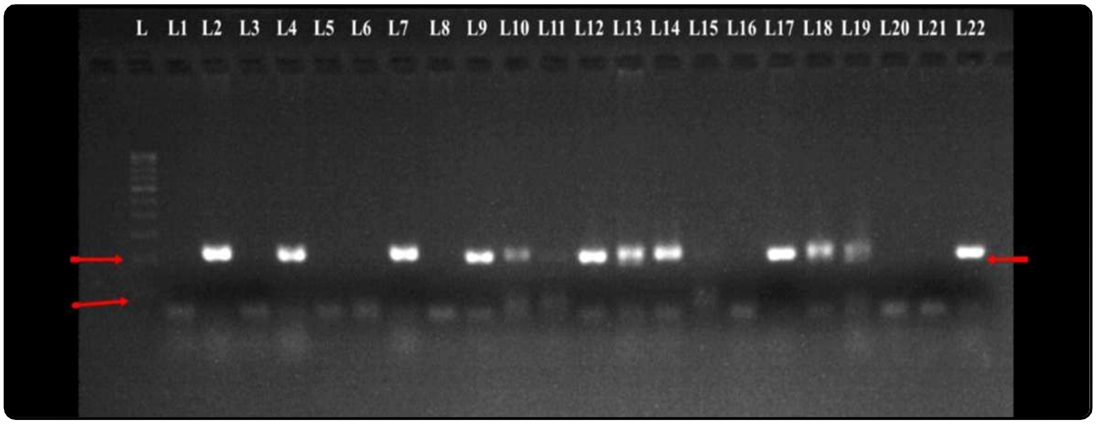
Analysis of variance (ANOVA) was computed for all the measurable traits to detect the variability among the twenty-two cucumber genotypes. The OPSTAT version 14.139.232.166 software was used for data analysis. The significance among the treatment differences were determined by comparing the calculated value of F with the tabulated value at five percent level of significance. The binary data generated from all the markers was entered in the NT edit program of NTSYSpc version 2.02 software. The similarity matrix was used to generate dendrogram using the SHAN module for cluster analysis. The summary statistics including the major allele frequency, gene diversity and polymorphic information content (PIC) values were determined using the software power maker version 3.23.

RESULTS AND DISCUSSION

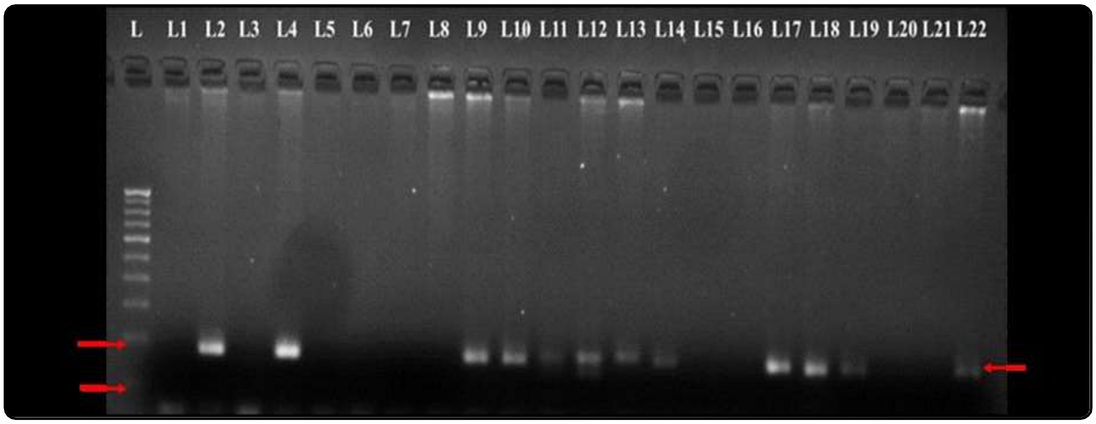
The analysis of variance indicated highly significant differences among the genotypes for all the characters studied, which has revealed the existence of sufficient variability in the Cucumber germplasm (Table 3). Fruit length ranged from 14.01 cm to 31.48 cm with a mean of 20.92 cm (Plate 2). Similar results for fruit length variations are reported by Valcarcel *et al*., (2018) with a range of 12.5 cm to 35.6 cm. The fruit diameter recorded at the middle portion of the fruit showed variations ranging from 3.25 cm to 6.87 cm. Jat *et al.* (2014) reported similar results for fruit diameter (4.16 to 6.82 cm). Significant variations were observed for individual fruit weight among genotypes and it ranged from109.00 g - 334 g with an average of 218.79g. Kumar *et al.* (2020) have reported similar results in cucumber accessions (124.63 g - 417.55 g). The stalk length of the fruit ranged from 1.08 cm to 4.48 cm. Zhang *et al.* (2012) reported similar results in the cucumber accessions for fruit stalk length (1.3 - 6.1 cm). The fruit flesh thickness was the most important fruit quality traits in cucumber and the results showed significant variations among genotypes studied, it ranged from 0.84 - 1.92 cm, with a mean of 1.18cm (Table 3). Shet *et al.* (2018) found similar results for fruit flesh thickness (0.50 - 3.00 cm) in the germplasm evaluated by them.

Seed cavity breadth was in the range of 1.63 cm - 3.93 cm with a mean of 2.66 cm (Plate 3). Higher the seed cavity breadth, lower was the fruit flesh thickness. The seed cavity length showed significant differences among the genotypes and it ranged from 13.42 cm to 23.62 cm, with a mean of 16.56 cm. Ranjan *et al.* (2015) reported

Plate 3 : Variations observed in fruit flesh thickness and seed cavity breadth among the genotypes



a) SSR23420



b) SSR10849

Legend: (L-Ladder L1-DGLM L2-CSLG L3-DGM L4-CSLW; L5-VLD L6-MUCHANDA; L7-CSHLAL8-KPLL9-CSHLH L10 G-2 L11-CSG-1 L12-CSG-3 L13-CSHL; L14-NATTI L15-CSHLC-2L16-HVR L17-CGLB L18-CSWL L19-CSHLC-1L20-CSJ - 1; L21-CSGLDL22-CSSL)

Plate 4 : Amplified gel pictures of local cucumber genotypes with higher gene diversity for fruit flesh thickness candidate gene markers a) SSR23420 and b) SSR 10849

seed cavity breadth (2.35 cm to 4.42 cm) and seed cavity length (3.15 - 7.0 cm) in cucumber genotypes. Total Soluble Solids (TSS) showed significant differences among the genotypes (0.93 to 2.05 °Brix). Similar variations in TSS (3.98-5.38 °Brix) has been reported by Jat *et al.* (2014). The shelf-life of the fruit increased with decrease in physiological loss in weight (PLW) and it was 3.25 - 5.5 days in the present study. Ranjan *et al.* (2015) observed similar variations in shelf-life (2.1-7.0 days).

The individual fruit weight was recorded at physiological maturity and the physiological maturity was judged based on a fruit turning green to yellow or brown depending on the local genotype. The fruit weight at physiological maturity ranged from 358.36 g to 880 g, with an average of 501.81g. Similar results for fruit weight variation at physiological maturity (326 g - 567 g) has been observed by Ranjan *et al.* (2019). Number of fruits per plant showed significant variations with a range of 5.25 - 11.25. Similar results for number of fruits per plant (1.33 - 5.80) are reported by Pandey *et al*., (2018). The total yield per plant (1.12 kg - 3.05 kg) varied significantly among 22 cucumber genotypes. Rajawat *et al*. (2017) reported similar variations in TFYPP in cucumber genotypes with a range of 1.13 - 2.31 kg per plant.

The genetic variability is the key factor for selection of superior genotypes in breeding programmes. The higher variations contribute to efficient selection. The PCV for all the traits was higher than GCV (Table 3). Fruit diameter, fruit weight, fruit stalk length, fruit flesh thickness, seed cavity breadth, TSS, fruit weight at physiological maturity, number of fruits per plant and yield per plant have high (20%) GCV and PCV. The traits such as fruit length, seed cavity length and shelf-life have exhibited medium (10-20%) GCV and PCV. Heritability of all the traits (fruit length, fruit diameter, fruit weight, fruit stalk length, fruit flesh thickness, seed cavity breadth, seed cavity length, TSS, shelf-life, fruit weight at physiological maturity, number of fruits per plant and yield per plant) were high (60%). was high (20%) for fruit length, fruit diameter, fruit weight, fruit stalk length, fruit flesh thickness, seed cavity breadth, seed cavity length, TSS, fruit weight at physiological maturity, number of fruits per plant and yield per plant. Only shelf-life had moderate Genetic advance as per cent mean (18.56%).

The correlation coefficient for twelve traits was analyzed among twenty-two local cucumber genotypes to understand the association between the traits (Table 5). The traits such as fruit weight (0.948), fruit flesh thickness (0.873), seed cavity breadth (0.924) and yield per plant (0.749) were positively correlated with fruit weight and fruit diameter.

Further, the fruit flesh thickness was positively correlated with seed cavity breadth (0.693) and yield per plant (0.612) and the fruit shelf life was also positively corelated with fruit weight at physiological maturity (0.639). The yield per plant was majorly correlated with fruit weight (0.844), fruit diameter (0.749), fruit flesh thickness (0.612) and seed cavity breadth (0.769). Hence, selection of the genotypes for these traits would lead to the higher production. Sharma *et al*. (2018) also reported similar results with significant positive correlation between yield per plot and number of fruits per plant (0.773, 0.850). Lakshmi and Reddy (2020) observed that, the fruit yield per plant was having significantly positive correlation with number of fruits per plant, fruit length, fruit diameter, fruit weight and TSS.

The Marker Assay

The SSR markers linked to fruit flesh thickness gene-*Csa2M058670.1* with a four base pair mutation in thin flesh genotypes were screened for the polymorphism. Thirteen SSR primers (Table 4) exhibited 0.25 to 0.37 PIC values with mean of 0.35. The markers SSR23420 and SSR10849 showed moderate PIC value (0.37), which was on par with Valcarcel *et al*. (2018) reports on SSR markers,with PIC values ranging from 0.04 to 0.49 with mean of 0.29. Normohamadi *et al*. (2017) also reported the PIC of 0.44 to 0.8.

The major allele frequency ranged from 0.55 to 0.82 with a mean of 0.64. The higher major allele

Table 4

List of candidate gene (fruit flesh thickness) markers showing major allele frequency, gene diversity and PIC

Marker	Major allele frequency	Gene diversity	PIC
SSR00204	0.64	0.46	0.36
SSR00289	0.64	0.46	0.36
SSR18937	0.64	0.46	0.36
SSR13532	0.64	0.46	0.36
SSR03593	0.64	0.46	0.36
SSR23832	0.64	0.46	0.36
SSR22558	0.64	0.46	0.36
SSR23420	0.55	0.50	0.37
SSR01374	0.64	0.46	0.36
SSR10849	0.55	0.50	0.37
SSR20248	0.82	0.30	0.25
SSR00378	0.64	0.46	0.36
SSR00030	0.64	0.46	0.36
Mean	0.64	0.46	0.35

TABLE 5
Correlation coefficient between fruit and yield traits among local cucumber genotypes

Traits	FL (cm)	FD (cm)	FW (g)	FSL (cm)	FFT (cm)	SCB (cm)	SCL (cm)	TSS (ºBrix)	SL (days)	FWPM (g)	NFPP	YPP (kg)
FL (cm)	1											
FD (cm)	-0.392	1										
FW (g)	-0.243	0.948 *	1									
FSL (cm)	0.322	-0.611 *	-0.598 **	1								
FFT (cm)	-0.335	0.873 *	0.817 **	-0.618 *	1							
SCB (cm)	-0.292	0.924 *	0.898 **	-0.440 **	0.693 *	1						
SCL (cm)	0.724 *	-0.177	-0.071	0.125	-0.026	-0.123	1					
TSS (ºBrix)	-0.064	0.429 **	0.380	-0.147	0.466 **	0.450 **	0.086	1				
SL (days	-0.063	-0.144	-0.123	0.363	-0.208	-0.196	-0.393	-0.071	1			
FWPM (g)	0.498 **	-0.093	0.032	-0.071	-0.127	-0.105	0.169	-0.224	0.409	1		
NFPP	0.660 *	-0.600 *	-0.505 **	0.639 *	-0.589 *	-0.476 **	0.256	0.038	0.403	0.400	1	
YPP (kg)	0.077	0.749 *	0.844 *	-0.345	0.612 *	0.769 *	-0.022	0.493 **	0.123	0.263	-0.030	1

frequency was observed in SSR20248 (0.82) and the minimum was found in SSR10849 (0.55). Kumar *et al*. (2020) reported the major allele frequency between 0.36 (UW084186) to 0.97 (UW084478) with a mean value of 0.70. The higher gene diversity was observed in SSR23420 and SSR10849 (0.50) Plate 4) and lower gene diversity was recorded in SSR20248 (0.30) with a mean of 0.46. Pandey *et al.* (2017) found similar results with gene diversity (0.074 - 0.428) and Lv *et al*. (2012) also reported gene diversity of 0.30 - 0.74.

Dendrogram analysis based on molecular data obtained from SSR markers grouped twenty-two local cucumber genotypes into two clusters *viz*., cluster-I and cluster II in the dendrogram (Fig. 1). Cluster I composed of 8 genotypes and cluster-II with 14 genotypes. Further cluster-I was divided into two sub-clusters, cluster-IA and cluster-IB. Cluster-IA included four genotypes (DGLM, DGM, VLD and KPL) and all exhibited fruit flesh thickness of 0.84 - 0.94 cm and cluster-IB included another fourgenotypes (MUCHANDA, CSGLD, HVR, CSJ-1) with fruit flesh thickness measured 0.85-0.99 cm. Similarly, cluster-II was divided into two sub-clusters, cluster-IIA and cluster-IIB. The cluster IIA grouped all the genotypes collected from three locations *viz.,* Hassan, Channarayapattana and Golithadaka (CSLG, CSLW, CSSL, CSHLH, CSHLC-1, CSWL, NATTI, CSG-3, CSHL-1, CSG-2, CGLB and CSG-1), all the fruits exhibited white peel and bigger core, with brown peel upon maturity. Whereas, the cluster-IIB contained only two genotypes *viz*., CSHLA and CSHLC-2 from same ecological regions *viz.,* Arakalagudu and Holenarasipur. All the genotypes in cluster II exhibited very close phenotypic traits, indicating common geographic origin and spread to local nearby regions, as these local types are cultivated even till date for commercial purpose, with some special features such as longer fruit length, uniform shape and size, white peel with crispy and tasty thick fruit flesh.

From the present investigation, it can be inferred that the genotypes with higher fruit length (CSGLD and CSHLC- 2), higher fruit diameter (CSSL, CSHLC - 2 and CSG - 1), higher fruit weight (CSSL, CSHLC - 2), higher fruit flesh thickness (CSSL, CSWL and CSHLC - 1) and higher yield per plant (CSSL and CSHLC - 2) are useful for further

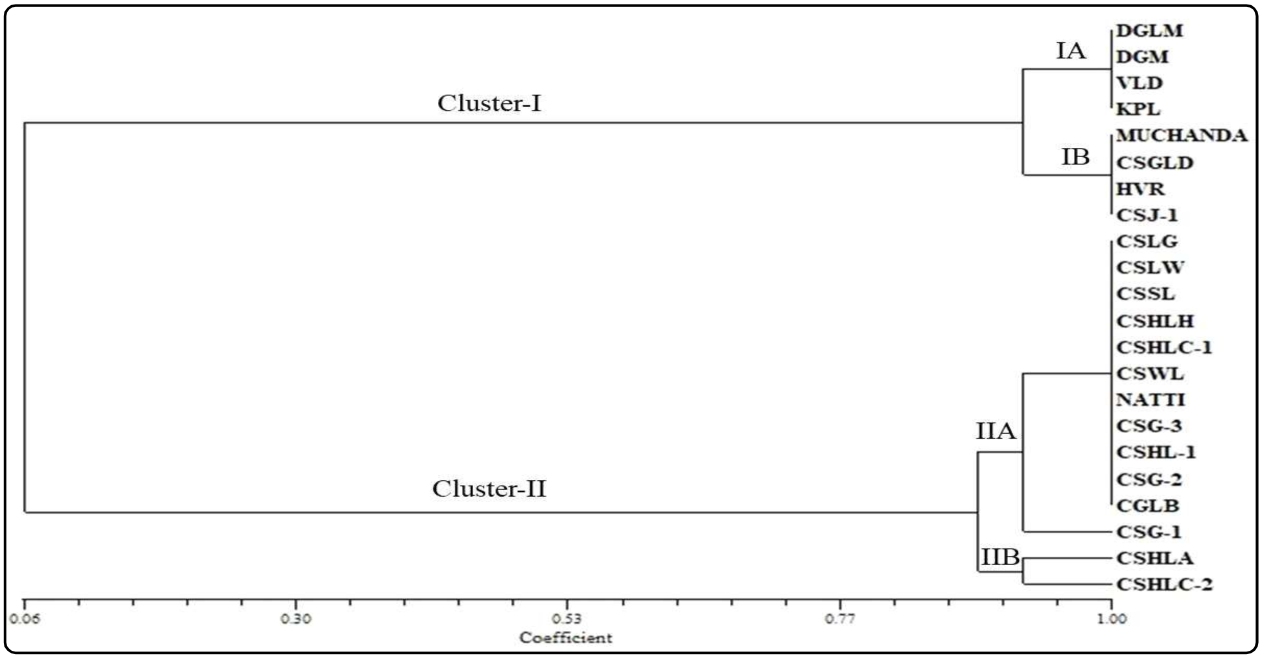


Fig. 1 : Dendrogram obtained from SSR markers data for twenty-two local Cucumber genotypes based on Jaccard's Similarity coefficient

evaluation in breeding programmes.

The genotype CSSL collected from Shivamogga is found to be promising with higher fruit diameter, fruit weight, fruit flesh thickness and yield per plant. The genotypes with higher fruit flesh thickness amplified in majority of the fruit flesh thickness candidate gene SSR markers used for molecular screening. Hence, these genotypes can be selected for further breeding approaches.

The results obtained in the present study indicates that thicker fruit flesh contributes to greater edible portion of the cucumber. The assessment of genetic variability for fruit flesh thickness is essential before planning an appropriate breeding strategy for genetic improvement in cucumber crop.

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