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M Priyadarshini

Department of Seed Science & Technology, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India

S Das

All India Coordinated Research Project on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India

KC Muduli

Department of Seed Science & Technology, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India

S Mohanty

All India Coordinated Research Project on Seed Technology Research (NSP) Crops, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India

S Sahoo

Department of Seed Science & Technology, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India

BR Pradhan

Regional Research Technology Transfer Station, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India

Corresponding Author:**S Das**

All India Coordinated Research Project on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India

Characterisation of cucumber genotypes through seed morphological characters

M Priyadarshini, S Das, KC Muduli, S Mohanty, S Sahoo and BR Pradhan

Abstract

The discrimination of crop varieties, especially by examination of the seed is increasingly important in order to protect the breeders and farmers rights. Several techniques could be used for varietal identification, but it is necessary to find simple, rapid and cost effective techniques for characterisation and identification. In present investigation an attempt has been made to identify some cucumber varieties through seed morphological characters. The experiment was laid out in a completely randomized design with 3 replications in the year 2019 by taking 12 cucumber varieties which are cultivated in Odisha. Observations were recorded on seed length, breadth, thickness, L/B, L/T and B/T ratios and 100 seed weight. Cucumber genotypes showed significant differences in respect of seed length, breadth, thickness and 100 seed weight. Based on seed length, three genotypes were grouped into short length (9.705 – 10.622 mm); six genotypes as medium length (10.623 – 11.540 mm) and three genotypes as long length (> 11.540 mm). Based on seed breadth the genotypes were grouped as narrow width (4.193- 4.518 mm), medium width (4.519 - 4.844 mm) and wider width (> 4.844 mm). Based on seed thickness the genotypes were grouped as low (2.206 – 2.412 mm), medium and high (> 2.619 mm). Based on seven seed morphological characters Gower's similarity coefficient was estimated and the dendrogram was constructed following UPGMA method. At 70% phenon level 12 cucumber genotypes were divided into three clusters.

Keywords: cucumber, characterisation, morphological characters, numerical taxonomy

Introduction

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetable crops grown extensively in tropical and sub-tropical parts of the country. It is grown for its tender fruits, which are consumed either raw as salad, cooked as vegetable or as pickled in its immature stage. The fruits of cucumber is said to have cooling effect, prevent constipation, checks jaundice and indigestion. Besides this, the seed of cucumber is also used in Ayurvedic preparations and raw fruits are being used for cosmetic purpose.

At present, the advent of large number of high yielding varieties and hybrids having better nutritional quality, tolerant to biotic and abiotic stresses are under cultivation throughout the country. In recent years public institutions and private companies introduces one after the other hybrids/varieties for commercial cultivation. Therefore, the discrimination of cucumber varieties, especially by examination of the seed is increasingly important in order to protect the breeders and farmers rights (Wang *et al.*, 2000)^[7] and to ensure genetic purity or genuineness of variety which is most important characteristics of a quality seed. The aspects of Distinctness, Uniformity and Stability (DUS) are fundamental for characterization of varieties. Varietal characterization could be done following taxonomic approach (use of morphological descriptors). These morphological descriptors have a traditional significance and are immediately accessible on the spot without need of equipment. However, the approach demands a field assessment, which depends on the degree of experience of the operator. The discrimination of crop varieties, especially by examination of the seed is increasingly important in order to protect the breeders and farmers rights. Several techniques could be used for varietal identification, but it is necessary to find simple, rapid and cost effective techniques for characterisation and identification. In present investigation an attempt has been made to identify some cucumber varieties through seed morphological characters.

Materials and Methods

Fifty seeds per each replication were taken randomly from each genotype to measure length (mm), breadth (mm) and thickness (mm) by using Dial thickness gauge. Then L/B, L/T & B/T ratio was calculated.

One hundred seeds were taken randomly per replication for each genotype to estimate test weight (g). The data were statistically analysed following SAS 9.0 version. The level of significance used in F test was $P = 0.01$.

$$\text{Gower's scale value} = \frac{\text{Real value} - \text{minimum value}}{R_i}$$

The raw data on seed length, width, thickness; length-breadth, length-thickness and breadth- thickness ratios; and 100 seed weight were converted to Gower's scale value as follows.

Where R_i is the range.

The purpose of this conversion was to classify the cucumber genotypes based on seven seed characters at a time following the principles of numerical taxonomy. Besides Gower's scale value was scored for easy comparison of the genotypes. The scale value between 0.000 – 0.330 was scored as "0"; 0.331 – 0.661 as "1" and > 0.661 as "2" indicating low, medium and high value in respect of a particular character. Based on Gower's similarity coefficient the dendrogram was constructed following UPGMA (unweighted pair group mathematical average) method for grouping of genotypes.

Results and Discussion

Seed morphological characters of cucumber genotypes

Seed morphological characters of cucumber genotypes are presented in Table 1. Significant differences were observed

among the genotypes for seed length, width, thickness and 100 seed weight. Measurement on seed length showed that V1 had the lowest seed length (9.075 mm) and V6 had the highest seed length (12.456 mm). Based on seed length, three genotypes (V1, V10, and V12) were grouped into short length (9.705 – 10.622 mm); six genotypes (V2, V3, V5, V7, V8 and V11) as medium length (10.623 – 11.540 mm) and three genotypes (V4, V6 and V9) as long length (> 11.540 mm). Seed breadth varied from 4.193 mm to 5.167 mm. Based on seed breadth the genotypes were grouped as narrow width (4.193- 4.518 mm), medium width (4.519 - 4.844 mm) and wider width (> 4.844 mm). V1, V2, V5, V6 and V11 had narrow width whereas V7 recorded the widest width (5.167 mm). Seed thickness of cucumber genotypes varied from 2.206 to 2.824 mm and the genotypes V2 and V5 had low thickness (2.206 – 2.412 mm) and V1, V9, V11 and V12 had the high thickness (> 2.619 mm). 100 seed weight ranged from 2.178 to 3.034 g. Based on seed weight, three genotypes (V1, V2 and V10) were grouped into light seed size (2.178 – 2.649 g); eight genotypes as medium seed size (2.650 – 3.121 g) and one genotype (V9) as bold seed size (> 3.121 g). Seed shape that depends on length to breadth ratio (L/B) is a very stable varietal property that can be used to measure the varietal purity of a sample. Length to breadth ratio in the present study varied from 2.199 to 2.793. Grouping of the genotypes based on seed length, width, thickness and seed weight is presented in Table 2.

Table 1: Seed morphological characters of cucumber genotypes

Genotype		Seed length (L) (mm)	Seed breadth (B) (mm)	Seed thickness (T) (mm)	L/B ratio	L/T ratio	B/T ratio	100 seed weight (g)
Var.	Name							
V1	Kumud	9.705	4.193	2.638	2.315	3.679	1.589	2.178
V2	R.K.-180	11.059	4.406	2.206	2.510	5.013	1.997	2.347
V3	Cucumber 12 PATA	11.193	4.699	2.547	2.382	4.395	1.845	3.034
V4	BarshaMangal	11.612	4.778	2.430	2.430	4.779	1.966	2.837
V5	Desi Green	11.288	4.381	2.408	2.591	4.688	1.819	2.718
V6	BCU-1	12.456	4.453	2.420	2.793	5.147	1.840	2.845
V7	Rajmata	11.360	5.167	2.597	2.199	4.374	1.990	3.030
V8	Supriya	10.962	4.790	2.525	2.289	4.341	1.897	2.840
V9	Mohini	11.578	4.752	2.662	2.436	4.349	1.785	3.590
V10	CU ₃	10.518	4.530	2.556	2.322	4.115	1.772	2.570
V11	CU ₁	10.955	4.452	2.692	2.461	4.069	1.654	2.690
V12	CU ₂	10.553	4.637	2.824	2.276	3.737	1.642	2.890
Grand Mean		11.103	4.603	2.521	2.416	4.363	1.834	2.800
Range		2.751	0.974	0.618	0.598	1.468	0.408	1.412
CD (0.01)		1.20	0.46	0.24	0.20	0.25	0.18	0.27
CV(%)		4.71	4.41	4.15	3.56	2.15	4.29	4.33

Table 2: Grouping of cucumber genotypes based on raw data of different seed characters

Character	Low value	Medium value	High value
Seed length (mm)	9.705 – 10.622	10.623 – 11.540	> 11.540
	V1, V10, V12 (short)	V2, V3, V5, V7, V8, V11 (medium)	V4, V6, V9 (long)
Seed breadth (mm)	4.193 – 4.518	4.519 – 4.844	> 4.844
	V1, V2, V5, V6, V11 (narrow)	V3, V4, V8, V9, V10, V12 (medium)	V7 (wide)
Seed thickness (mm)	2.206 – 2.412	2.413 – 2.619	> 2.619
	V2, V5 (thin)	V3, V4, V6, V7, V8, V10 (moderately thin)	V1, V9, V11, V12 (thick)
100 seed weight (g)	2.178 – 2.649	2.650 – 3.121	> 3.121
	V1, V2, V10 (light)	V3, V4, V5, V6, V7, V8, V11, V12 (medium bold)	V9 (bold)

Characterisation of cucumber genotypes through Gower's scale value

Gower's scale value is presented in Table 3 and the scored value is mentioned in the parenthesis of Table 3. From Table 3 it was observed that seeds of V1 had short length, narrow width, light weight, L/B, L/T, B/T ratios were low except high thickness and it was unique among all. Seeds of V2 had

medium length, narrow width, thin, light weight, L/B ratio was medium but L/T and B/T ratios were high. Seeds of V3 were medium in length and width; moderately thin, medium bold in size (100 seed weight), L/B ratio was low but L/T and B/T ratios were medium. Seeds of V4 were long in length, medium in width; moderately thin, medium bold in size (100 seed weight), L/B ratio was medium but L/T and B/T ratios

were high. Seeds of V5 were medium in length and width; moderately thin, medium bold in size (100 seed weight), L/B ratio was medium but L/T and B/T ratios were high. Seeds of V6 were long in length, narrow width; moderately thin, medium bold in size (100 seed weight), L/B and L/T ratios were high and B/T ratio was medium. Seeds of V7 were unique among all the genotypes due to its widest width; its length was medium, thickness was moderately thin, medium bold in size (100 seed weight), L/B ratio was low, L/T ratio was medium and B/T ratio was high. Seed characteristics of V8 were almost similar to V3 except B/T ratio which was

high in V8 and medium in V3. Seeds of V9 were long in length, medium in width; thick, bold in size; L/B, L/T and B/T ratios were medium. Seeds of V10 were short in length, medium in width, moderately thin, light in size, L/B and L/T ratios were low whereas B/T ratio was medium. Seeds of V11 were medium in length, narrow in width, thick, medium bold in size, L/B ratio was medium, L/T and B/T ratios were low. Seed morphological characteristics of V12 were almost similar to V1 except seed breadth and seed size which were medium in V12 and low in V1.

Table 3: Gower's scale value for different seed characters

Genotype	Seed length (L)	Seed Breadth (B)	Seed Thickness (T)	L/B	L/T	B/T	100 seed weight (g)
V1	0.000 (0)	0.000(0)	0.699(2)	0.194 (0)	0.000 (0)	0.000 (0)	0.000(0)
V2	0.492(1)	0.219(0)	0.000(0)	0.520(1)	0.909(2)	1.000(2)	0.120(0)
V3	0.541(1)	0.520(1)	0.552(1)	0.306(0)	0.488(1)	0.627(1)	0.606(1)
V4	0.693(2)	0.601(1)	0.362(1)	0.386(1)	0.749(2)	0.924(2)	0.467(1)
V5	0.575(1)	0.193(0)	0.327(0)	0.632(1)	0.687(2)	0.564(1)	0.382(1)
V6	1.000(2)	0.267(0)	0.346(1)	1.000(2)	1.000(2)	0.615(1)	0.472(1)
V7	0.602(1)	1.000(2)	0.633(1)	0.000(0)	0.473(1)	0.982(2)	0.603(1)
V8	0.457(1)	0.613(1)	0.516(1)	0.151(0)	0.451(1)	0.755(2)	0.469(1)
V9	0.681(2)	0.574(1)	0.738(2)	0.396(1)	0.456(1)	0.480(1)	1.000(2)
V10	0.296(0)	0.346(1)	0.566(1)	0.206(0)	0.320(0)	0.449(1)	0.278(0)
V11	0.454(1)	0.266(0)	0.786(2)	0.438(1)	0.266(0)	0.159(0)	0.363(1)
V12	0.308(0)	0.456(1)	1.000(2)	0.129(0)	0.040(0)	0.130(0)	0.504(1)

*Number inside parentheses indicates scored value

Based on seven seed morphological characters Gower's similarity coefficient was estimated and the dendrogram was constructed following UPGMA method. The matrix of Gower's similarity coefficient among 12 genotypes is mentioned in Table 4. Similarity coefficient value ranged from 0.375 to 0.906. The highest similarity coefficient value (0.906) was observed between V3 and V8 followed by 0.867 between V10 and V11. The lowest similarity coefficient value was observed between V1 and V6. The dendrogram based on Gower's similarity coefficient (Fig.1) was constructed following UPGMA (unweighted pair group mathematical average) method. It indicates how much similarity exists among the twelve genotypes based on seven seed characters. From the Fig. 1 it was observed that at 60% phenon level all the 12 genotypes appeared as a single unit and at 100% phenon level all the genotypes are different from each other. This indicates that all the genotypes taken for the study have 60% similarity. At 70% phenon level (considering 70% similarity) the genotypes were divided into three clusters or

groups. Cluster-I (CI-I) comprised of four genotypes (V10, V11, V12 & V1); CI-II consisted of five genotypes (V3, V8, V4, V7 & V9) and CI-III consisted of three genotypes (V5, V6 & V2). V10 & V11 of CI-I, V3 & V8 of CI-II and V5 & V6 of CI-III exhibited 80% similarity. V3 & V8 of CI-II exhibited more than 90% similarity. Based on the variation in seed morphological characteristics, the cucumber genotypes were grouped into different categories. The seed morphological characteristics helped in identifying and grouping of the genotypes. Similar observation and grouping of genotypes based on seed morphological characters were made by Naghavi *et al.* (2009) [3] in wheat; Vanangamudi *et al.* (1988b) [6] in rice; Paukens (1975) [4] and Nagapadma *et al.* (1996) [2] in maize; Arunkumar *et al.* (2004) [1] in pearl millet; Thangvel *et al.* (2005) [5] in sorghum.

From the present investigation it may be concluded that seed morphological characters were found to be useful in classification of cucumber genotypes.

Table 4: Matrix of similarity coefficient among 12 genotypes of cucumber based on 7 seed characters

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12
V1	1.00	0.500	0.574	0.452	0.562	0.375	0.444	0.586	0.512	0.694	0.742	0.759
V2		1.00	0.688	0.782	0.808	0.703	0.609	0.690	0.574	0.712	0.660	0.492
V3			1.00	0.839	0.813	0.687	0.819	0.906	0.861	0.805	0.778	0.743
V4				1.00	0.814	0.738	0.783	0.850	0.778	0.707	0.680	0.611
V5					1.00	0.810	0.642	0.764	0.727	0.824	0.783	0.621
V6						1.00	0.524	0.638	0.618	0.658	0.617	0.481
V7							1.00	0.837	0.731	0.632	0.616	0.631
V8								1.00	0.792	0.785	0.758	0.757
V9									1.00	0.746	0.749	0.688
V10										1.00	0.867	0.764
V11											1.00	0.832
V12												1.00

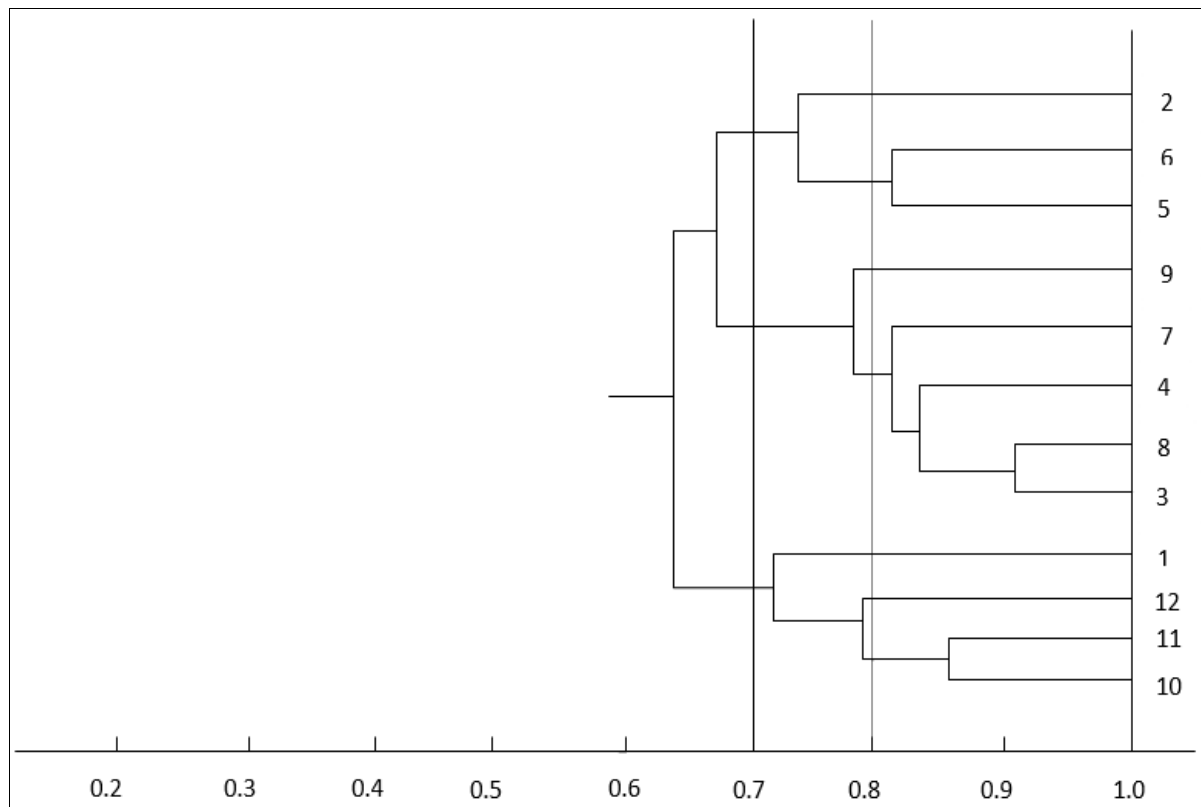


Fig 1: Dendrogram based on Gower's similarity coefficient for classification of cucumber genotypes through seed characters

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