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GENETIC DIVERSITY AND DOWNY MILDEW RESISTANCE IN MUSKMELON (*CUCUMIS MELO* L.)

Koushik S. M.[1], Padmanabha K.[2*], Sangeetha C. G.[3], Ramchandra R. K.[4], Shivanand Veerappa Hongal[5], Yoshita Shrikrishna Shastri [2], Sreenatha A.[6] and Raghavendra S.[7]
[1]Department of Vegetable Science, RHREC, UHSB Campus, GKVK Post-560065, Karnataka, India
[2]Department of vegetable Science, College of Horticulture, Bengaluru, UHSB campus,
GKVK Post-560065, Karnataka, India
[3]Department of Plant Pathology NH-75, Tamaka, Kolar-563103, Karnataka, India
[4]Department of BCI, COH, Bengaluru, UHSB Campus, GKVK post-560065, Karnataka, India
[5]KVK Kolar, NH-75, Tamaka, Kolar-563103, Karnataka, India
[6]College of Horticulture, NH-75, Tamaka, Kolar-563103, Karnataka, India
[7]Department of Biochemistry, Division of Plant Science, COA, Navuli, Shivamogga,
KSNUAHS, Karnataka, India
*Corresponding author E-mail: padduhort@gmail.com

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ABSTRACT

An experiment was conducted at College of Horticulture Bengaluru in the year 2025 in a randomized block design. The ANOVA inferred that all the observed parameters are significant. High genotypic coefficient of variance and phenotypic coefficient of variance was observed for fruit yield per vine, average fruit weight, number of fruits per vine, sex ratio, rind thickness, cavity diameter, fruit shape index, total soluble solids and vine length. Estimates of high heritability coupled with high genetic advance as per cent over mean recorded for days to first male flower appearance, days to first female flower appearance, node at first male flower appearance, node at first female flower appearance, sex ratio, number of fruits per vine, average fruit weight, fruit yield per vine and total soluble solids inferring that selection could improve these traits by highlighting the significance of additive gene action. The D^2 statistics is used to assess the genetic diversity, 12 clusters were constructed using ward method. Cluster IV contains the highest number of genotypes (18) and least in cluster VII-XII (1 each). The highest intra-cluster value was observed for Cluster VI (16.64), indicating a high level of genetic diversity within this cluster. The maximum inter-cluster value is present between Cluster III and Cluster XI indicating its use in hybrid breeding and selection of transgressive segregants. In the field experiment on downy mildew disease screening, the genotypes Meghalaya melon-6 and Meghalaya melon-5 were identified as resistant. They recorded percent disease index (PDI) values of 19.50 and 19.82, respectively, along with AUPDC values of 557.48 and 577.64. These results suggest that both genotypes can be effectively utilized in breeding programs for downy mildew resistance.

***Keywords* :** muskmelon, variability, downy mildew, diversity.

Introduction

In the tropical and subtropical regions of the world the production and consumption of the cucurbitaceous vegetables is renowned; these include 118 genera and 825 species, in the family (Jeffrey, 1990). The economic important desert vegetable of this family is muskmelon. Muskmelon thrives in hot and dry climates with its deep root system, making it well-suited for the subtropical conditions of India. Currently, India ranks fifth in global melon production, yielding approximately 1,346 million tons from 0.69 million hectares (Anonymous, 2022).

Muskmelon is primarily cultivated as a dessert fruit that helps to quench thirst and enhances the nutritional value of the human diet, while non-dessert types are consumed as vegetables. It is also commonly used in salads and served fresh at the table. Having known its enormous importance, still a mere work is carried out in crop improvement in muskmelon. To achieve higher yield and productivity the knowledge of genetic variability and diversity of various yield contributing traits is important.

Various devastating diseases like cucumber mosaic virus, cucumber green mottle mosaic virus, downy and powdery mildews and Fusarium wilt attack this crop. Among these, downy mildew (*Pseudoperonospora cubensis* (B & C) Rostow.) is the wide spread and most devastating disease worldwide (Call 2012; Lebeda and Cohen 2011). Due to the changing climate the identified resistance sources are turning susceptible so there is a need for new sources of resistance. Thus, this study was formulated to study the genetic diversity for yield and yield related traits in muskmelon and to screen the genotypes for downy mildew resistance.

Material and Methods

During 2024-2025 at department of vegetable science research plot College of Horticulture Bengaluru two experiments were conducted to study the magnitude of genetic variability for yield and yield attributing traits and screening of melon genotypes for downy mildew resistance under natural field condition. The experimental site is at 12°58' latitude north, 77°11' longitude East, with an elevation of 930 meters above mean sea level in the Eastern region of Karnataka. In both the experiment sixty-nine genotypes were led in randomized block design with two replications in *zaid* (diversity for yield and yield related traits) and *kharif* (screening for downy mildew) season with the spacing of 2.0m × 0.6m. The observations were recorded for morphological fruit traits related to fruit yield and quality traits on five randomly selected plants in each replication. Genetic diversity was analysed by Mahalanobis's (Mahalanobis 1936) generalized distance (D2) and clustering of genotypes was done according to Tocher's method (Rao 1952). Average intra and inter cluster distance was calculated as per the standard procedures.

Disease screening

To screen for downy mildew disease, the crop was raised in a field without any chemical sprays for disease control, and the plants were scored at weekly intervals based on disease symptoms on leaves of the selected individual plant using the 0- 9 scale as described by Jenkins and Wehner (1983).

Per cent disease index (Wheeler, 1969) was calculated using the formula,

$$\text{Percent disease index (PDI)} = \frac{\textit{sum of the individual disease rating}}{\textit{total number of observations} \times \textit{maximum scale}} \times 100$$

Based on the PDI, the genotypes were classified as resistant (R) (0-20%), Moderately resistant (MR) (21-40%), Susceptible (S) (41-60%), Highly susceptible (HS) (>60%) respectively.

Area under disease progress curve (AUDPC)

AUDPC is another criterion that represents the speed of progression of pathogen in plant tissue and used to differentiate between resistant and susceptible genotypes. This was calculated using a formula (Perchepied *et al*., 2005),

$$\text{AUDPC}=\sum_{i}^{n}\left[\frac{x_i+x_{i+1}}{2}\right](ti+1-ti)$$

Results and Discussion

Analysis of variance showed significance for all the characters under study. In this investigation, the results revealed that there is low difference between genotypic variance and phenotypic variance indicating higher contribution of genotype in expression of phenotype. Highest phenotypic and genotypic coefficient of variance was observed in fruit yield per vine (36.33 and 33.71 respectively) followed by average fruit weight, number of fruits per vine, sex ratio and vine length showing presence significant amount of variability for the selection of the traits with least influence of environment (Shivakumara, 2019) and Gaikwad *et al.* (2020). Days to first male and female flower appearance, and node at first male and female flower appearance showed moderate coefficient of variance both phenotypically and genotypically. The trait days to first harvest had low GCV (2.90) and PCV (3.26%) inferring there is low variability and limited scope for selection for this trait. Comparable findings were observed by Kavya (2017), Mehta *et al.* (2012) and Tara *et al.* (2023).

Table 1 : Estimates of variability and other genetic parameters for growth, fruit and yield traits in muskmelon genotypes

Sl. No.	Genotypes	Mean	Range		GV	PV	GCV (%)	PCV (%)	Heritability (%)	GA	GAM
			Min	Max							
1.	Vine length (m)	1.21	0.81	2.26	0.08	0.09	23.44	24.43	32.06	0.56	46.32
2.	Days to first male flower appearance	37.34	28.67	50.17	24.54	26.26	12.89	13.34	93.46	9.87	25.68
3.	Days to first female flower appearance	40.51	30	52	23.97	24.68	12.08	12.26	97.14	9.94	24.53
4.	Node at first male flower appearance	4.04	2.50	5.67	0.31	0.48	13.70	17.12	64.08	0.91	22.60
5.	Node at first female flower appearance	5.09	3.33	6.67	0.37	0.53	11.92	14.24	70.08	1.05	20.56
6.	Days to first harvest	74.57	68.00	79.00	04.69	05.9	02.90	03.26	79.49	3.98	5.33
7.	Sex ratio	10.38	15.44	2.99	4.39	5.47	20.11	22.44	80.32	3.87	37.13
8.	Number of fruits per vine	4.53	1.67	7	1.30	1.55	25.14	27.43	84	2.15	47.47
9.	Average fruit weight (g)	801.49	89	1516.67	68472.03	71173.66	32.65	33.29	96.20	0.53	65.97
10.	Fruit yield per vine (kg)	3.47	0.59	6.62	1.37	1.59	33.71	36.33	65.34	1.66	46.08

PCV =Phenotypic co-efficient of variability; GCV = Genotypic co-efficient of variability; GA = Genetic advance; GAM= Genetic advance as percent mean

Fruit yield per vine and other traits such as average fruit weight (Table 1), number of fruits per vine, sex ratio, days to first male and female flower appearance and node at first male and female flower appearance, exhibited high broad sense heritability (>60 %) along with high genetic advance as percentage over mean (GAM >20 %). These results were in line with the findings of Gaikwad *et al.* (2020) and Indraja *et al.*, 2021 explaining these characters are under the influence of additive gene action which can be improved through selection. Days to first harvest had higher heritability with low GAM expressing direct selection is not useful. Vine length is moderately heritable with high GAM indicating presence of additive gene action along with careful selection in the further generation is required.

Genetic diversity

Based on the D^2 clustering, these sixty-nine genotypes were grouped into 12 clusters (Table 2). The cluster IV contains maximum number (18) of genotypes which includes the *momordica* group, *agrestis* group and *cantaloupe* group. Followed by cluster II which comprises of 14 genotypes from both muskmelon and snap melon inferring that the genotypes within the clusters are closely related (Bhimappa *et al.*, 2019). Cluster VII to cluster XII are singleton clusters showing the uniqueness of the genotypes in these clusters belonging to *cantaloupensis, inodorus* and *reticulatus groups*. The results showed that the clustering pattern does not correspond to the horticultural groups, taxonomic categories, or geographic origins of the accessions (Singh *et al.*, 2020). Genetic diversity observed among the genotypes may be due to factors like history of selection, selection under diverse environments, heterogeneity and genetic drift.

Table 2 : Classification of muskmelon genotype into different clusters based on D^2 values

Cluster No.	Genotypes Included	No. of Genotypes
I	Ic-524117, IC-34781, IC-278413, IC-524129, IC-524110B, IC-524121, IC-524132, IC-315327, IC-524177B, Pusa Kazri	10
II	IC-514135, IC-315312C, IC-315312B, COHB 38, IC-256242, IC-256241, IC-524115B, IC-524116, IC-524143A, Punjab Sunheri, IC-524177A, HUB-28, IC315312A, HUB-10	14
III	Banaspathre -1, Banaspathre-2, Manipur melon, Banaspathre-10	4
IV	Meghalaya melon-1, Meghalaya melon-3, Meghalaya melon-5, Meghalaya melon-6, Meghalaya melon-4, SJDP-7, IC-524118, IC-265204B, Meghalaya melon-2, IC524106B, IC-524105C, HUB-20, Durgapur Madhu, SJDP-8, Snapmelon local, Hara Madhu, IC-524117, IC-524105A	18
V	SL-2, SL-3, SL-1, SL-5, SL-4, IC-524143B, IC-285515, IC-276305, IC-524115C	9
VI	4SJDP20, KJDP-1, SJDP-1, KJDP-11, SJDP-17, HUB-9, Valuk Maharashtra snap melon, Thar Mahima	8
VII	Muskmelon local	1
VIII	Pusa Sarda	1
IX	Kashi Madhu	1
X	Arka Siri	1
XI	Arka Jeet	1
XII	IC-524105B	1

Based on inter clusters (table 3), the statistical distance was maximum (34.17) between Cluster III and Cluster XI, closely followed by Cluster III and Cluster IX (32.23), Cluster I and Cluster III (31.71), Cluster III and Cluster VII (31.34), and Cluster III and Cluster VIII (30.45). These results clearly suggest that the genotypes found in any of these pairs of clusters were highly divergent. While the statistical distance was least between Cluster VIII and Cluster IX (9.34), followed by Cluster X and Cluster XI (10.84) and Cluster IX and Cluster X (11.36), indicating closer genetic relationships among genotypes within these cluster pairs. The highest intra-cluster distance (table 3) was present in cluster VI (16.64) followed by Cluster V (14.38) and Cluster IV (12.72). High magnitude of intra-cluster distance indicates that there is a good scope for selection for many traits of interest (Bhimappa *et al.*, 2019). The singleton clusters depicted uniqueness of the genotypes.

Table 3 : Average intra and inter cluster distance value for 15 characters formed by 69 genotypes muskmelon

	cluster 1	**cluster 2**	**cluster 3**	**cluster 4**	**cluster 5**	**cluster 6**	**cluster 7**	**cluster 8**	**cluster 9**	**cluster 10**	**cluster 11**	**cluster 12**
Cluster1	9.29	16.41	31.71	18.04	17.70	26.03	12.68	13.72	13.36	15.82	15.54	22.83
Cluster 2		10.73	25.73	14.47	16.23	21.35	17.47	16.65	18.08	22.22	22.43	19.83
Cluster 3			10.12	21.40	30.20	21.92	31.34	30.45	32.23	30.08	34.17	20.55
Cluster 4				12.72	19.91	19.22	17.09	16.12	17.50	18.74	20.79	17.66
Cluster 5					14.38	29.11	17.70	22.05	22.16	26.81	26.91	21.50
Cluster 6						16.64	28.12	21.16	24.74	23.58	24.81	24.23
Cluster 7							0.00	15.02	13.90	17.49	16.49	22.81
Cluster 8								0.00	9.34	12.17	10.76	25.34
Cluster 9									0.00	11.36	14.08	26.08
Cluster10										0.00	10.84	26.91
Cluster 11											0.00	29.43
Cluster 12												0.00

A detailed examination of the mean values highlights different clusters were superior for different characters, demonstrating the potential for selective breeding depending on trait-specific objectives (Table 4). Cluster III exhibited the highest mean values for days to first female (49.29) and male flowering (47.13) and node at first female flower (6.04) and male flower (4.05), suggesting selection of these genotypes for earliness and reproductive growth traits.

Table 4 : Mean values of 16 character for 12 cluster in melon genotype

Cluster	**DFF**	**DMF**	**DFH**	**NAFMF**	**NAFFF**	**NFPP**	**SR**	**TSS**	**AFW**	**FYPV**	**FSI**	**FT**	**RT**	**CD**	**VL**	**NBPV**
1	36.77	34.65	74.38	3.98	4.98	4.83	3.02	6.66	0.63	3.01	0.93	2.6	1.53	8.5	1.34	3.98
2	37.61	35.8	75.33	3.87	5.05	4.69	3.09	7.76	0.8	3.72	1.26	2.36	1.32	8.38	1.01	3.76
3	49.29	47.13	74.1	4.05	6.04	4.51	4.09	9.86	1.04	2.11	1.94	2.46	1.29	9.83	1.39	3.96
4	42.91	40.64	74.9	4.04	5.14	4.45	4.01	9.1	0.88	3.87	1.4	2.67	1.79	7.84	1.49	4.15
5	34.39	32.48	72.84	3.61	4.66	5.56	3.06	7.65	1.12	4.2	1.36	2.63	1.75	5.84	1.04	4.21
6	46.58	44.48	73	4.05	4.95	5.06	4.06	7.55	0.46	2.36	1.43	2.97	1.57	11.42	1.01	3.85
7	39	36.33	70.6	4.03	4.91	6	4.04	7.42	1.03	4.21	0.93	2.38	1.01	8.38	1.39	3.94
8	40.67	39.67	72.33	3.84	4	7	11.92	11.16	0.69	4.58	1.05	3.18	2.31	11.73	1.07	3.98
9	43.38	40.17	74.3	3.47	5.34	5.33	4.04	13.61	0.51	2.17	0.99	2.63	1.38	11.73	0.86	4.16
10	43.83	40.17	74.33	3.84	4.47	5.34	3.84	13.15	0.43	1.41	0.87	1.75	0.94	5.67	0.9	3.84
11	41.43	36.5	75.03	3.66	4.34	5.34	3.54	11.51	0.3	1.34	1.03	2.83	0.94	10.12	2.26	3.84
12	44.33	42.5	76.33	3.66	4.83	5.34	11.51	8.1	1.11	5.88	2.83	2.72	0.94	10.12	2.26	3.84

DFF-Days to first female flower appearance
DMF- Days to first male flower appearance
DFH-Days to first harvest
NAFMF-Node at first male flower appearance
NAFFF- Node at first female flower appearance
NFPP-Number fruits per plant
SR-Sex ratio
TSS-Total Soluble solid
AFW-Average fruit weight
FYPV-Fruit yield per vine
FSI-Fruit shape index
FT-Flesh thickness
RT-Rind thickness
CD-Cavity diameter
VL-Vine length
NBPV-Number of branches per vine

On the other hand, cluster XII was characterized by exceptionally high values for vine length (2.26 m) and fruit yield per plant (5.88), which makes the genotypes in these cluster a potential source for yield improvement and vigorous growth (Bhimappa *et al.*, 2019). Similarly, cluster VIII recorded the highest mean for TSS (11.92) and flesh thickness (3.18) indicating its importance for quality improvement.

In contrast, some clusters were notable for their lower mean performance. Cluster V had the lowest values for days to female flowering (32.48), rind thickness (0.75), and cavity diameter (5.84), while cluster VI exhibited the least number of branches per vine (3.85) and fruit thickness (1.57). These clusters, though inferior for certain traits, may be useful in reducing unwanted characters such as excessive rind thickness and late flowering when used in hybridization. Thus, crosses between genetically divergent clusters (e.g., cluster III × cluster XII, cluster VIII × cluster IX) are expected to yield transgressive segregants combining earliness, fruit quality, and yield potential (Tomar *et al*., 2008).

Screening for downy mildew

All the genotypes were screened for downy mildew in field condition during the *Kharif* season which is congenial for spread of the disease. The PDI when calculated on weekly basis inferred that the genotype Meghalaya melon-5 and Meghalaya melon-6 are resistant with the PDI score of 19.82 and 19.50 respectively (Table 5) at the eighth week conferring the slow disease progress in these genotypes. The AUDPC points were also estimated, 577.64 and 557.48 respectively. Thus, these genotypes can be used as a promising source for donor material in breeding efforts. Their inclusion in hybridization schemes may hasten the progress toward resistant cultivar development. A significant number of genotypes of fifty-five, such as Arka Jeet, Arka Siri, Pusa Sarda, Hara Madhu, Punjab Sunheri, Thar Mahima, several IC accessions, SJDP lines, SL lines and other local varieties, were classified as highly susceptible based on the PDI of disease progression and AUDPC score. Similar results were obtained in cucumber by Pitchaimuthu *et* al., 2022 and in watermelon by These genotypes can be utilized in breeding experiments acting as susceptible check. The wide range of responses to Downy mildew among muskmelon genotypes underscores the rich genetic diversity present within Indian melon germplasm. Genotypes identified as resistant or moderately resistant represent important resources for breeding durable downy mildew-resistant cultivars (Sudhakara, 2014). These findings align with earlier reports and reinforce the necessity of continuous evaluation and utilization of germplasm in resistance breeding programs.

Table 5 : Evaluation of muskmelon genotypes for per cent disease index of Downy mildew under natural screening

Genotype name	PDI (1st interval)	PDI (2nd interval)	PDI (3rd interval)	PDI (4th interval)	PDI (5th interval)	PDI (6th interval)	PDI (7th interval)	PDI (8th interval)	AUPDC POINTS	Disease reaction
Arka jeet	3.7	12.3	17.4	23.6	37.5	42.2	52.6	100	2012.15	HS
Arka Siri	5.3	22.6	35.7	47.4	82.3	86.8	95.3	100	3309.25	HS
Pusa sarda	2.5	26.3	34.3	42.2	56.3	82	93.2	100	3048.85	HS
Hara Madhu	8.1	22.5	29.3	48.2	63	78.3	92	100	3061.45	HS
Kashi Madhu	4.4	28.4	38.3	50.3	58.3	85	97.2	100	3217.9	HS
Punjab Sunheri	2.9	27.6	34.2	45	66.2	82	91	100	3132.15	HS
Durgapur Madhu	10.7	21.8	35	49.2	63.4	76	87.4	100	3067.05	HS
Thar Mahima	0.2	23.7	37.2	50.2	73.2	84.2	92	100	3224.2	HS
IC-524117	5.14	32.2	38	43	74	87	90.2	100	3268.79	HS
IC-524151	3.08	30.2	38	45.3	70.8	82.3	87.5	100	3189.48	HS
IC-524177B	0.7	36.9	46.3	50.5	62.8	77.4	88	100	3235.75	HS
IC-524143B	1.2	28.4	33	45.6	65.8	78	87.8	100	3074.4	HS
IC-524121	2.4	24.3	35	57.8	73.8	85	90.3	100	3271.8	HS
IC-347781	0.1	29.5	32	46.7	78.3	88	96.5	100	3297.35	HS
IC-276305	6.8	30.1	40	47	54.6	75	84	100	3038.7	HS
IC-524132	0.37	34.3	39	43.5	54	69.6	82.3	100	2960.195	HS
IC-524110B	0.34	20.4	31	39.6	64.6	75.3	86.5	100	2922.99	HS
IC-315327	1.6	26.3	34	48.2	56	73.2	85.9	100	2970.8	HS
IC-278413	0	32.2	45.6	52.8	67.3	78.2	87.3	100	3243.8	HS
IC-514135	1.4	38.2	45	54.3	69.2	76.5	94.8	100	3350.9	HS
IC-524129	0.6	38	42.3	47.7	58.4	79.3	86	100	3164	HS
Muskmelon local	1.2	25	39.2	59.4	66.7	84.8	92.3	100	3276	HS
Pusa Kazri	0.6	18.9	37.7	48.8	69.3	79.3	86.4	100	3084.9	HS
IC-524105A	5.8	22.3	40.3	59.5	66.4	78.8	84.2	100	3180.8	HS
IC-524105B	0.6	33.8	46.7	54	69.4	73.2	87.2	100	3252.2	HS
IC-524105C	0.5	38.3	44.5	57.9	70.2	75.3	84.4	100	3295.95	HS
IC-524106B	0.2	31.9	43.4	46	64	73.9	93.2	100	3167.5	HS
HUB-9	0.4	16.2	24.6	28.5	32.2	35.5	40	41.3	1529.5	S

HUB-20	0	16.2	24.6	28.5	37.03	36.04	32.03	41.3	1509.9	S
Snapmelon local	0.1	12.5	28.4	38.7	40.6	56.7	60.2	68.3	2138.15	HS
HUB-28	0.3	14.4	22.4	27.5	30.06	34.2	37.7	40.3	1446.97	S
HUB-10	0	16.2	23.3	30.3	32.4	38.2	40.7	43.8	1574.3	S
Banaspathre-10	0	18.2	19.1	32.4	37.3	36.03	42.3	44.7	1610.21	S
IC-524177A	2.4	33.2	46	57.6	69.3	83.5	82.5	100	3313.1	HS
IC-524116	0.1	38.4	44.2	57	72.3	82	87.3	100	3368.75	HS
IC-256242	0	34.5	48.3	58.9	67	75	80.3	100	3248	HS
IC-524143A	0	31.5	52.4	65.2	80.3	78	80.8	100	3417.4	HS
IC-256241	0.7	27.9	48	57.3	64.8	84.9	90	100	3312.75	HS
IC-524115B	5.16	30.3	46.6	53.5	68.3	77.4	94.6	100	3312.96	HS
SJDP17	0.4	25.7	38.9	67	78.6	82	87.4	100	3358.6	HS
SJDP20	0	27.9	42.3	62	73.5	78.7	87.3	100	3301.9	HS
KJDP-1	0.8	38.7	47.7	54.7	66	83.2	90.5	100	3368.4	HS
KJDP-11	0.6	40	47.5	56	67.3	77.4	92.3	100	3365.6	HS
SJDP-1	0.5	37.9	50.3	57.7	62.5	74.2	82.3	100	3256.05	HS
SJDP-8	0	37	52.4	63	66.2	80.3	90.3	100	3424.4	HS
B-1	3.6	12.3	18.7	22.4	27.3	35.5	38.2	48.3	1431.5	S
B-2	0	16	22.5	37.3	41.2	47.3	50.3	53.8	1878.8	S
Meghalaya melon-1	0	1.1	6.3	12.6	9.7	15.1	19.3	23.6	613.9	MR
Meghalaya melon-2	0	2	7.3	10.4	12.4	10.2	14.2	24.3	565.6	MR
Meghalaya melon-3	0	2.03	5.02	11.2	15.03	12.4	17.3	26.4	625.66	MR
Meghalaya melon-4	0	4.1	8.3	9.2	11.6	15	17.9	23.02	623.84	MR
Meghalaya melon-5	0	3.2	4.7	8.5	13.6	16.7	16	19.82	577.64	R
Meghalaya melon-6	0	0.44	7.3	9.4	12.5	15.5	15	19.50	557.48	R
IC-265204B	7.3	20.3	36.2	44.3	53	69.5	74.2	100	2808.05	HS
Valuk Maharashtra snap melon	10.2	35	40.6	52.2	62.3	72.3	93.4	100	3226.3	HS
SJDP-7	14.2	30.3	47	53.2	62.8	77.7	87	100	3255.7	HS
Manipur melon	5.2	17.5	38	50.2	68.7	72.3	82	100	3019.1	HS
SL-1	30.1	37.6	42.5	44.2	53.7	32.3	98	100	3246.95	HS
SL-2	27	34.4	46.8	52.7	60.2	90.04	90.2	100	3414.88	HS
SL-3	26	37.2	44.3	45.3	57.3	82.02	88.3	100	3271.94	HS
SL-4	22.9	32.2	40.3	48.3	56.6	90.3	94.3	100	3314.15	HS
SL-5	32	38.2	44.2	52.7	72.3	88.3	93.4	100	3535.7	HS
IC-315312A	10.2	19.3	28.3	40	68.9	82.7	92.3	100	3056.2	HS
IC-524118	9.5	17.9	22.4	57.3	67.6	86	96.3	100	3165.75	HS
IC524115C	12.3	20.4	40.7	58.2	73.6	76.7	87.6	100	3243.45	HS
IC-285515	7.3	25.4	32	65	78.7	83.2	90.6	100	3349.85	HS
IC-315312C	8	29.2	46	47.4	58.3	79	93.2	100	3199.7	HS
IC-315312B	13.3	26.2	37.2	53.9	62.3	73.5	86.7	100	3125.15	HS
COHB 38	1.03	13.2	15.7	18.3	18.8	20.4	22.6	25.2	943.005	MR
Mean	4.67	25.05	34.81	44.98	56.81	67.89	75.83	86.14	2756.91	
Range	0-32	0.44-40	4.7-52.4	8.5-67	9.7-82.3	10.2-90.3	14.2-98	19.5-100	544.6-3535.7	

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