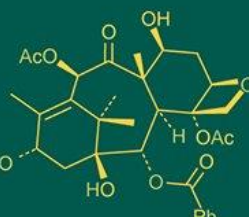


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Molecular and morphological assessment of cucumber germplasm leading to the discovery of ToLCNDV resistance

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Abstract

Cucumber (*Cucumis sativus* L.) is an economically important vegetable crop originating from India and widely cultivated across tropical and subtropical regions. Tomato leaf curl New Delhi virus (ToLCNDV) has emerged as a major constraint to cucumber production, resulting in severe yield losses due to its rapid spread by *Bemisia tabaci*. The present study aimed to characterize indigenous cucumber germplasm with respect to agro-morphological diversity, molecular variation, and response to ToLCNDV under natural disease pressure. A total of 100 germplasm lines maintained at ICAR-IARI were evaluated in a randomized block design for nine horticultural traits. Significant differences were observed across genotypes, indicating substantial genetic variability. High heritability and genetic advance for fruit yield, vine length, and fruit weight suggest strong additive gene effects. Correlation analysis identified fruit weight, fruit length, and vine length as key contributors to yield. Clustering analysis grouped genotypes into four divergent clusters, offering opportunities for breeding through strategic hybridization. Molecular characterization using 59 polymorphic SSR markers amplified 295 alleles with a mean PIC of 0.55, confirming considerable underlying genetic diversity. Field screening revealed wide variation in ToLCNDV response, with Vulnerability Index (VI) values ranging from 18.75% to 97.92%. Three genotypes, DC-61, DC-70 and DC-91 were identified as highly resistant, while seven were moderately resistant under field conditions. The study reports the first set of ToLCNDV-resistant cucumber genotypes derived from Indian germplasm. It demonstrates the value of integrating morphological, molecular, and disease-screening approaches for the utilization of germplasm. These resistant lines and diversity patterns provide a strong foundation for developing ToLCNDV-resistant cucumber cultivars through targeted breeding.

Keywords: *Cucumis sativus*, ToLCNDV, germplasm, SSR markers, resistance, GCV, heritability, yield

Introduction

Cucumber is believed to have originated in India (De Candolle, 1886) [3], which remains an important centre of diversity and primary gene pool for the species. It belongs to the genus *Cucumis*, which contains two major domesticated species: *C. sativus* (2n = 14) and *C. melo* (2n = 24). The cultivated cucumber and its wild progenitor, *C. sativus* var. *hardwickii*, form part of the Asiatic group distributed along the Himalayan foothills. Despite intensive global cultivation, modern cucumber cultivars often possess a narrow genetic base, increasing their vulnerability to rapidly evolving pathogens and emerging climatic stresses. Therefore, characterization and utilization of indigenous Indian germplasm are critical for broadening the genetic base and enhancing resilience.

In recent decades, tomato leaf curl New Delhi virus (ToLCNDV), a bipartite begomovirus belonging to the family Geminiviridae and transmitted by the whitefly *Bemisia tabaci*, has emerged as one of the most destructive viral pathogens affecting cucurbits. Since its initial detection in India in 1995 (Padidam *et al.*, 1995) [18], ToLCNDV has rapidly expanded its geographical distribution, causing epidemics across Asia, the Mediterranean basin, Africa, and parts of Europe. The virus poses a serious threat not only to cucumber but also to several other key crops such as tomato, pumpkin, zucchini, and bitter melon. Under conducive

Conditions, yield losses due to ToLCNDV can reach up to 100%, making it one of the most economically significant pathogens of cucurbits (Czosnek *et al.*, 1997; Zaidi *et al.*, 2016)^[2].

Despite the severity of ToLCNDV outbreaks, no verified sources of resistance have been identified in cultivated cucumber. This absence of confirmed resistance poses a significant bottleneck for breeding programs aiming to develop durable ToLCNDV-resistant varieties. However, given its Indian origin and the rich genetic diversity within local landraces, wild relatives, and indigenous germplasm, cucumber offers significant potential to uncover novel alleles conferring resistance to ToLCNDV and other viral pathogens. Recent studies have emphasized that resistance to leaf curl and related begomoviruses is often found within Indian cucurbit germplasm (Saez *et al.*, 2021), further underscoring the importance of systematic screening efforts. Therefore, identification and characterization of ToLCNDV resistance sources in Indian cucumber germplasm is an urgent research priority. Such efforts are essential not only for breeding disease-resistant cultivars but also for enhancing the overall genetic resilience of cucumber production systems. Integrating agro-morphological evaluation, molecular marker analysis, and field disease screening provides a comprehensive framework for identifying promising germplasm that can serve as valuable parental lines in future breeding programs.

Materials and Methods

Experimental site and plant material

The field experiment was conducted at the research farm of the Division of Vegetable Science, ICAR-Indian Agricultural Research Institute (IARI), New Delhi (28°35' N, 77°12' E; 228.6 m above mean sea level). The site has a semi-arid, sub-tropical climate with hot summers and mild winters. The experimental soil was loam in texture with an organic matter content of 0.75%. A total of 100 cucumber (*Cucumis sativus* L.) germplasm lines, maintained at the Division of Vegetable Science, IARI, were evaluated during the summer season of 2020. The trial was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was grown in a single row per replication, and recommended agronomic practices were followed to ensure uniform and healthy crop establishment. No insecticides were applied during the crop cycle to facilitate natural infestation by whitefly (*Bemisia tabaci*), the vector of Tomato leaf curl New Delhi virus (ToLCNDV). During the cropping period, the field exhibited pronounced leaf curl symptoms, and ToLCNDV was confirmed as the predominant causal agent in a parallel diagnostic study conducted at ICAR-IARI. This ensured a uniform and reliable natural disease pressure, enabling robust evaluation of genotype responses to ToLCNDV under field conditions.

Assessment of horticultural traits and disease scoring for ToLCNDV

Observations on horticultural traits were recorded for all cucumber genotypes evaluated under a randomized block design. Data from ten randomly selected plants per genotype per replication were used to compute replication-wise means, which were subsequently utilized for statistical analyses. The study comprised three replications. Quantitative traits recorded included node to first male flower, node to first female flower, days to first female

flower anthesis, number of fruits per plant, fruit length (cm), fruit diameter (cm), average fruit weight (g), vine length (cm), and yield per plant (g).

For disease assessment, tomato leaf curl New Delhi virus (ToLCNDV) scoring was performed on selected plants across all three replications. Disease severity was assessed visually based on characteristic viral symptoms. Observations were recorded at 10-day intervals on three dates during the cropping period: 35, 45, and 55 days after sowing. The mean score across these three assessment points was used to classify each genotype's response to ToLCNDV.

ToLCNDV symptom severity was evaluated using the 0-4 scoring scale described by Saez *et al.* (2020) for *Cucurbita moschata*, *Cucumis melo*, and *C. sativus*. Based on this scale, plants with a disease score of 0 or 1 were categorized as resistant, whereas plants scoring between 2 and 4 were classified as susceptible (Fig A). The overall disease reaction of each genotype was further categorized using the vulnerability index (VI), calculated following Havey (1996)^[7]:

$$\text{Vulnerability Index (VI)} = \frac{(0n_0 + 1n_1 + 2n_2 + 3n_3 + 4n_4)}{nt(nc-1)} \times 100$$

Where, n: represents the number of plants in each disease category, nt: total number of plants screened and nc: denotes the number of categories.

DNA extraction and SSR based genotyping

Genomic DNA was extracted from fresh leaf samples collected from healthy, field-grown plants at the Delhi site using the standard CTAB method (Doyle and Doyle, 1990)^[5]. DNA quantity and integrity were initially assessed on a 0.8% agarose gel. Further evaluation of DNA purity and precise concentration was performed using a Nano Drop spectrophotometer (Eppendorf). The DNA samples were subsequently diluted in TE buffer to obtain a working concentration of 25-30 ng µl⁻¹.

A total of 427 genomic SSR primers specific to *Cucumis sativus* were screened for PCR amplification. The sequence information for SSR markers that yielded polymorphic amplicons is provided in Table S1. PCR amplification was carried out in a 10 µl reaction volume containing 50 ng genomic DNA, 1.0 U Taq DNA polymerase (HiMedia Laboratories, Mumbai, India), 1× PCR buffer with 1.5 mM MgCl₂, 10 pmol each of forward and reverse primers, and 100 µM dNTP mix (Thermo Scientific).

Amplification was performed using a touchdown PCR protocol in an Eppendorf Mastercycler with the following conditions: an initial denaturation at 94 °C for 5 min; 30 cycles of denaturation at 94 °C for 1 min, primer annealing at 55-65 °C for 1 min (depending on primer-specific annealing temperature), and extension at 72 °C for 2 min; followed by a final extension at 72 °C for 10 min. Amplicons were held at 4 °C until retrieval and subsequently stored at -20 °C.

Electrophoresis and fragment detection

Amplified PCR products were mixed with 1 µl of 1× loading dye (bromophenol blue) and separated on 3% agarose gels prepared in 1× TAE buffer. Gels were stained with ethidium bromide, and DNA bands were visualized under UV light using a gel documentation system (Alpha Imager, Cell Biosciences, Santa Clara, CA). Amplicon sizes

were scored manually using a 50 bp DNA ladder as the reference. A binary data matrix was generated based on amplicon size. Power Marker v3.25 (Liu and Muse, 2005)^[14] was used to calculate polymorphism information content (PIC), major allele frequency, and to conduct cluster analysis. Genetic similarity indices were computed using Nei's coefficient (Nei and Li, 1979)^[17].

Statistical and molecular data analysis

Agro-morphological data were subjected to analysis of variance (ANOVA) using the online statistical package OPSTAT (<http://14.139.232.166/opstat/>). Mean and standard deviation values for each trait were computed using Microsoft Excel 2019. Diversity analysis and dendrogram construction for cucumber genotypes were performed using DAR win version 6.

Results

Analysis of variance and trait variability

Analysis of variance revealed highly significant differences among the cucumber genotypes for all nine horticultural traits, indicating substantial genetic variability. Traits including node to first male and female flower, days to first female flower anthesis, number of fruits per plant, fruit length, fruit diameter, average fruit weight, vine length, and fruit yield per plant showed wide and significant variation. Mean performance across the 100 genotypes also exhibited broad phenotypic variation. The node-to-first-male-flower averaged 4.78, with gynoeious lines such as DGC-102 and DGPC-58 producing no male flowers. The first female flower appeared between nodes 2.28 (769, AZMC-1) and 13.82 (DC-48), with a population mean of 7.02. Days to first female flower anthesis ranged from 26.58 (DGC-104) to 44.92 (Chaitali), with a mean of 37.94 days. Fruit number per plant ranged from 2.33 (DC-921) to 8.67 (DC-91), averaging 4.74. Fruit length varied from 5.65 cm (DC-70-26-1) to 15.27 cm (WBC-231) and fruit diameter from 1.76 cm (DC-70-26-1) to 4.92 cm (DC-209), with means of 10.76 cm and 3.43 cm, respectively. Average fruit weight ranged between 25.33 g and 158.82 g (mean 94.08 g). Vine length ranged from 60 cm (JLG) to 351.99 cm (DGC-103), with a mean of 139.22 cm. Fruit yield per plant showed extensive variation, ranging from 138.16 g to 991.19 g (DC-91), with a mean of 425.37 g. This range highlights considerable scope for selection in cucumber improvement.

Genetic parameters and trait associations

Genetic variability was further supported by high genotypic and phenotypic variances, particularly for fruit yield per plant (35046.02 and 38453.06), vine length (3631.94 and 3657.21), and average fruit weight (1265.04 and 1370.11). The highest GCV and PCV values were observed for node to first male flower (50.12% and 50.76%), fruit yield (44.00% and 46.09%), and vine length (43.28% and 43.43%). All traits exhibited high heritability, notably vine length (0.99), node to first male flower (0.97), and fruit yield per plant (0.91), indicating strong genetic control and the potential for effective selection (Table 1).

Phenotypic correlation analysis showed that fruit yield per plant had strong positive associations with average fruit weight (0.689), fruit diameter (0.761), fruit length (0.748), and vine length (0.459). Average fruit weight correlated strongly with fruit diameter (0.761) and fruit length (0.748). Conversely, number of fruits per plant showed negative

correlations with fruit weight (-0.388), fruit length (-0.327), and fruit diameter (-0.315). These results identify fruit weight, fruit length, and vine length as key yield-contributing traits.

Genetic divergence and cluster analysis

Genetic divergence assessed through the Hierarchical cluster analysis and Mahalanobis D² statistic grouped the 100 cucumber genotypes into four distinct clusters (Fig. C), with Cluster II being the largest, followed by Cluster I. The wide inter-cluster distances, particularly between Clusters II and I, suggest their potential for use in hybridization programmes. These genetically diverse clusters can be exploited to generate high-yielding, transgressive segregants owing to their broad genetic bases.

Molecular diversity

Molecular diversity among 96 cucumber genotypes was assessed using 59 polymorphic SSR markers out of 427 screened. A total of 295 alleles were amplified, with allele numbers per locus ranging from 3 to 8 and a mean of 5.0. The highest number of alleles (8) was observed with primers UW039642, SSR02771, UW084969, and SSR13511. PIC values ranged from 0.22 (UW085401) to 0.75 (UW084908), with an average of 0.55, indicating good marker informativeness. Gene diversity ranged from 0.24 to 0.78, and heterozygosity varied from 0 to 0.68 (mean 0.06), the highest being recorded for UW08450.

Evaluation of cucumber germplasm for resistance to ToLCNDV

A total of 100 cucumber genotypes were systematically screened under natural field conditions during the rainy season, a period conducive to high whitefly populations and severe Tomato Leaf Curl New Delhi Virus (ToLCNDV) pressure. The vulnerability index (VI), used as a quantitative measure of disease severity, showed considerable variation among the genotypes, ranging from as low as 18.75% to as high as 97.92%. This wide phenotypic spectrum clearly indicates substantial genetic diversity in the panel with respect to ToLCNDV response.

Among the evaluated materials, three genotypes DC-61 (18.75%), DC-70 (24.95%), and DC-91 (25.35%) consistently exhibited minimal symptom development, placing them in the highly resistant category. These genotypes maintained normal growth, flowered on time, and produced relatively healthy fruits despite intense disease pressure, highlighting their strong tolerance and potential underlying resistance mechanisms. In contrast, seven genotypes displayed moderate resistance, limiting disease progression to intermediate levels, whereas the majority 54 genotypes were categorized as moderately susceptible. These genotypes showed noticeable symptoms but still retained partial tolerance. The remaining thirty-six genotypes recorded VI values approaching the upper range and were classified as susceptible, exhibiting severe leaf curling, stunting, and significant yield reduction (Table 2).

The presence of highly resistant accessions such as DC-61, DC-70, and DC-91 is particularly promising for resistance breeding programmes. Their stable performance under natural epiphytotic conditions makes them potential donor lines for introgressing ToLCNDV resistance into elite, high-yielding cucumber backgrounds. Incorporating these resistant sources into hybridization and molecular breeding

strategies could accelerate the development of durable ToLCNDV-resistant cucumber cultivars suited for cultivation across disease-prone regions.

Discussion

The evaluation of 100 cucumber genotypes under natural field conditions with high Tomato leaf curl New Delhi virus (ToLCNDV) pressure revealed substantial genetic variability for yield, yield components, and disease resistance. The high mean sums of squares for vine length, average fruit weight, and fruit yield per plant demonstrate the presence of considerable genetic divergence that can be effectively utilized in breeding programmes. As phenotypic variances consistently exceeded genotypic variances, a moderate influence of the environment on trait expression is evident. Comparable trends have been documented in earlier studies on cucumber by Kumar (2006) [11], Munshi *et al.* (2007) [16], and Singh *et al.* (2013) [25], validating the robustness of the present findings. Traits such as node to first male flower, fruit yield per plant, and vine length exhibited high genotypic and phenotypic coefficients of variation, indicating a broad scope for improvement through phenotypic selection. The relatively narrow gap observed between GCV and PCV for most traits suggests a predominance of additive genetic variance and a minimal role of environmental fluctuation, thereby increasing the reliability of selection. These results are consistent with the observations of Kandasamy (2017) [9] and Deepa *et al.* (2018) [4], who also emphasized the influence of additive gene action on key horticultural traits in cucumber. High broad-sense heritability recorded for all traits implies strong genetic control. Furthermore, traits such as vine length, fruit weight, node to first male and female flower, and fruit yield per plant exhibited both high heritability and high genetic advance as a percentage of the mean. This combination indicates additive gene action and suggests that these traits can be improved through direct selection. Similar conclusions were previously reported by Kumar (2006) [11], Munshi *et al.* (2007) [16], and Kandasamy (2017) [9]. The correlation analysis demonstrated that fruit yield per plant was significantly and positively associated with fruit weight, fruit diameter, fruit length, vine length, node to first female

flower, and number of fruits per plant. These relationships indicate that simultaneous improvement of these component traits would likely enhance overall productivity. Conversely, the negative association between yield and days to first flowering and the node number of the first female flower underscores the importance of earliness in achieving higher yield potential. These trends corroborate earlier reports by Rao *et al.* (2004) [21], Kumar *et al.* (2011), and Pal *et al.* (2017) [19]. Mahalanobis D²-based genetic divergence analysis grouped the 100 genotypes into four distinct clusters, with Cluster II being the largest, followed by Cluster I. The substantial inter-cluster distances, particularly between Clusters I and II, indicate considerable genetic divergence that can be exploited in hybridization to generate transgressive segregants. The weak correspondence between the cluster pattern and geographical origin suggests that cucumber diversity may be shaped more by selection pressure, localized adaptation, and gene flow than by geographic separation. Similar conclusions were drawn by Sharma and Sharma (2006) [24] and Hossain *et al.* (2010) [8]. Molecular characterization using 59 polymorphic SSR markers revealed substantial allelic richness, with 295 alleles identified (3-8 alleles per locus). The high mean PIC value, coupled with moderate to high gene diversity and heterozygosity, confirms the effectiveness of SSRs in capturing genetic variation in cucumber. These results are in agreement with previous SSR-based diversity studies in cucumber reported by Chiba *et al.* (2003) [1]. Screening for ToLCNDV resistance identified three genotypes, DC-61, DC-70 and DC-91, with consistently low vulnerability index (VI) values (18.75-25.35%), indicating a high degree of resistance. Seven genotypes exhibited moderate resistance, whereas the remaining accessions ranged from moderately susceptible to susceptible. The observed variation in disease response reveals substantial genetic diversity for ToLCNDV resistance within the indigenous germplasm. Notably, the resistant genotypes identified in this study represent valuable and novel sources of resistance in cucumber. These results are consistent with global observations that cucurbit germplasm showing resistance to ToLCNDV and related begomoviruses often originates from the Indian subcontinent

Table 1: Genetic parameter of nine important horticultural traits in cucumber

SL.NO	Characters	σ^2_g	σ^2_p	GCV (%)	PCV (%)	h^2 (b.s.) (%)	G.A	G.A as % of Mean
1	Node to first male flower	5.74	5.88	50.12	50.76	0.97	4.87	101.94
2	Node to first female flower	4.92	5.41	31.62	33.15	0.90	4.35	62.13
3	Days to first female flower anthesis	13.83	14.74	9.80	10.12	0.93	7.42	19.56
4	Numbers of fruits per plant	1.93	2.17	29.30	31.09	0.88	2.69	56.87
5	Fruit length	3.32	3.73	16.94	17.96	0.88	3.54	32.90
6	Fruit diameter	0.40	0.50	18.46	20.68	0.79	1.16	33.96
7	Average fruit weight	1265.04	1370.11	37.80	39.34	0.92	70.40	74.83
8	Vine length	3631.94	3657.21	43.28	43.43	0.99	123.71	88.86
9	Yield	35046.02	38453.06	44.00	46.09	0.91	368.16	86.55

Table 2: Genotypes and their vulnerability index of cucumber (*Cucumis sativus* L.) used in this study

SL.NO	Genotypes	17-09-2020	27-09-2020	07-10-2020	V.I (%) AVG	Category
1	769	74.67	100.00	100.00	91.56	S
2	AZMC-1	50.00	93.75	93.75	79.17	S
3	BARO PATTA	60.00	72.50	95.00	75.83	MS
4	BARSATI-1	48.33	57.22	65.00	56.85	MS
5	BARSATI LOCAL	71.88	84.38	90.63	82.29	S
6	BARSHA RANI	45.00	52.50	80.00	59.17	MS
7	CHAITALI	25.00	65.00	80.00	56.67	MS
8	DAMPET LOCAL	31.25	50.00	56.25	45.83	MR

9	DARL-106	35.42	76.39	86.11	65.97	MS
10	DC-1-1	35.00	67.50	85.00	62.50	MS
11	DC-166	50.00	91.67	95.83	79.17	S
12	DC-175	50.00	75.00	100.00	75.00	MS
13	DC-201	56.25	81.25	87.50	75.00	MS
14	DC-202	37.50	81.25	100.00	72.92	MS
15	DC-204	50.83	89.15	95.83	78.60	S
16	DC-205	52.08	68.75	75.00	65.28	MS
17	DC-206	100.00	90.63	100.00	96.88	S
18	DC-207	50.00	79.17	89.58	72.92	MS
19	DC-208	75.00	75.00	100.00	83.33	S
20	DC-209	71.88	97.50	100.00	89.79	S
21	Dc-2091	62.50	67.50	70.00	66.67	MS
22	DC-301	42.71	81.98	91.35	72.01	MS
23	DC-40	29.17	58.33	62.50	50.00	MR
24	DC-48	53.13	68.75	78.13	66.67	MS
25	DC-505	25.00	75.00	75.00	58.33	MS
26	DC-55	60.42	83.33	83.33	75.69	S
27	DC-61	0.00	28.13	28.13	18.75	R
28	DC-70	12.50	31.25	31.25	25.00	R
29	DC-70-26-1	50.00	100.00	100.00	83.33	S
30	DC-70-26-2	43.75	87.50	100.00	77.08	S
31	DC-70-26-3	72.50	100.00	100.00	90.83	S
32	DC-746	71.88	100.00	100.00	90.63	S
33	DC-748	93.75	100.00	100.00	97.92	S
34	DC-758	81.25	100.00	100.00	93.75	S
35	DC-77	16.88	38.75	41.25	32.29	MR
36	DC-773	43.75	100.00	100.00	81.25	S
37	DC-83	52.50	63.75	72.50	62.92	MS
38	DC-91	4.17	31.25	40.63	25.35	R
39	DC-921	50.00	66.66	79.17	65.27	MS
40	DC-92-2	29.15	53.13	70.80	51.03	MS
41	DGC-102	37.78	72.22	92.36	67.45	MS
42	DGC-103	62.50	93.75	100.00	85.42	S
43	DGC-104	25.00	50.00	75.00	50.00	MR
44	DGC-114	40.63	75.00	84.38	66.67	MS
45	DGC-15	50.00	72.50	81.67	68.06	MR
46	DGC-15-1	37.50	87.50	87.50	70.83	MS
47	DGC-21	52.08	70.83	75.00	65.97	MS
48	DGC-22	66.67	83.33	87.50	79.17	S
49	DGC-27	42.50	81.25	97.50	73.75	S
50	DGPC-58	50.00	87.50	100.00	79.17	S
51	DGPC-59	83.33	100.00	100.00	94.44	S
52	DGPC-60	87.50	100.00	100.00	95.83	S
53	DPAC-21	75.00	100.00	100.00	91.67	S
54	DPaC-6	70.83	100.00	100.00	90.28	S
55	DPAC-9-3	81.67	100.00	100.00	93.89	S
56	GS-2	53.13	71.88	81.25	68.75	MS
57	GYCL-10-1	50.00	68.75	75.00	64.58	MS
58	GYCL-11-5	43.75	81.25	90.63	71.88	MS
59	HS-5	59.38	75.00	96.88	77.08	S
60	HS-8	37.78	63.47	82.50	61.25	MS
61	IC-410617	37.50	65.63	68.75	57.29	MS
62	IC-410657	37.50	65.63	68.75	57.29	MS
63	IC-410658	35.00	81.25	86.25	67.50	MS
64	IC-538137	50.00	68.75	84.38	67.71	MS
65	JLG	71.88	100.00	100.00	90.63	S
66	KALYANPUR GREEN	43.75	62.50	75.00	60.42	MS
67	KP-1134	66.63	100.00	100.00	88.88	S
68	KP-1291	75.00	100.00	100.00	91.67	S
69	KSP-1301	75.00	91.67	91.67	86.11	S
70	LOM-400	91.66	100.00	100.00	97.22	S
71	PAHARI LOCAL	87.50	100.00	100.00	95.83	S
72	PANIPAT LOCAL	33.33	58.33	66.66	52.77	MS
73	PCUC-8	37.50	68.75	75.00	60.42	MS
74	Pragya-3	66.66	95.83	100.00	87.50	S
75	PUNJAB NAVEEEN	34.38	63.54	85.42	61.11	MS
76	PUSA BARKHA	34.92	67.88	85.40	62.73	MS
77	PUSA UDAY	31.25	66.88	76.25	58.13	MS
78	RUSSIAN PICKLING	58.33	83.33	95.83	79.16	S
79	SL-749	75.00	100.00	100.00	91.67	S

80	SWARNA AGETHI	77.50	85.00	97.50	86.67	S
81	SWARNA SHEETAL	62.50	68.75	90.63	73.96	MS
82	WBC-10	47.50	66.67	70.83	61.67	MS
83	WBC-11	35.80	73.30	85.80	64.97	MS
84	WBC-13	43.75	62.50	66.67	57.64	MS
85	WBC-17	45.83	71.88	87.50	68.40	MS
86	WBC-21	46.88	55.63	77.50	60.00	MS
87	WBC-22	28.75	68.33	79.38	58.82	MS
88	WBC-2-2	20.00	65.00	75.00	53.33	MS
89	WBC-22-2	33.33	90.63	96.88	73.61	MS
90	WBC-231	25.00	62.50	87.50	58.33	MS
91	WBC-232	37.50	54.16	58.33	50.00	MR
92	WBC-24	54.17	72.92	72.92	66.67	MS
93	WBC-26	37.50	56.25	68.75	54.17	MS
94	WBC-27-1	46.88	65.63	87.50	66.67	MS
95	WBC-27-2	28.13	75.00	87.50	63.54	MS
96	WBC-352	32.50	60.00	65.00	52.50	MS
97	WBC-391	25.00	75.00	75.00	58.33	MS
98	WBC-41	30.00	55.00	80.00	55.00	MS
99	WBC-5	10.00	52.50	57.50	40.00	MR
100	WBC-9	37.50	65.63	68.75	57.29	MS



Fig 1: Disease scoring based on the symptoms

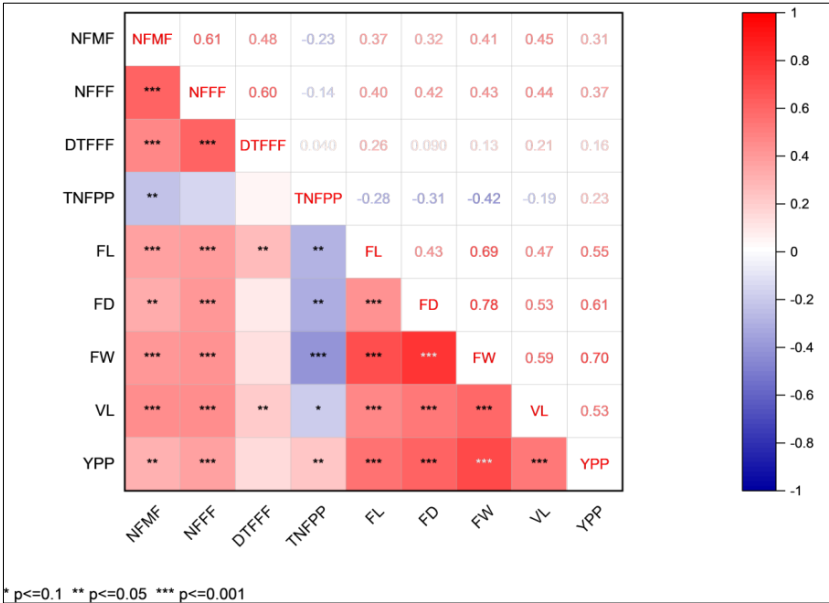


Fig 2: Corplot based on Pearson's correlation coefficient depicting inter-relationship between different variables used for this study

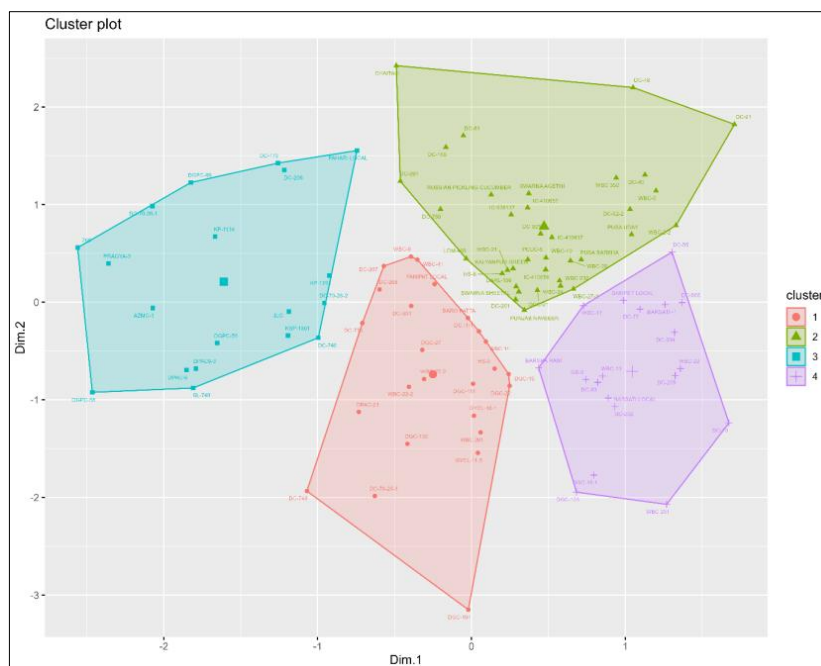


Fig 3: Dendrogram of 100 cucumber genotypes-based neighbour joining clustering

Conclusion

The present investigation revealed substantial agro-morphological, molecular, and pathological variability among the 100 cucumber genotypes, underscoring considerable potential for genetic enhancement. The high heritability estimates, coupled with strong positive associations among key yield components, indicate that traits such as fruit weight, fruit length, fruit diameter, and vine length constitute robust and efficient selection indices for yield improvement. Both genetic divergence analysis and SSR-based molecular profiling confirmed the presence of broad genetic diversity, offering valuable opportunities for identifying complementary parental lines in breeding programmes. Notably, the discovery of three highly resistant genotypes DC-61, DC-70, and DC-91 against Tomato leaf curl New Delhi Virus (ToLCNDV) represents a significant advancement, as these accessions serve as promising donor lines for incorporating durable virus resistance into elite cucumber cultivars through conventional breeding and marker-assisted selection strategies.

CRedit authorship contribution statement

Malatesha kenchikoppa: Methodology, writing – original draft. Maheebub: Data curation, writing – review & editing and software work. Anjan das: Methodology & data curation. Shyam sundarney: Conceptualization, Resources, Writing – review & editing; A. D. Munshi: writing – review & editing. Amalendu Ghosh: writing – review & editing. Haritha Bollinedi: writing – review & editing. Veerendra Kumar Verma: writing – review & editing. Md Yeasin Data curation, software work, writing – review & editing

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Declaration of competing interest

The authors declare that they have no conflict of interest.

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References

1. Chiba N, Suwabe K, Nunome T, Hirai M. Development of microsatellite marker in melon (*Cucumis melo* L.) and their application to major cucurbit crops. *Breed Sci.* 2003;53(1):21-27.
2. Czosnek H, Laterrot H. A worldwide survey of tomato yellow leaf curl viruses. *Arch Virol.* 1997;142(7):1391-1406.
3. De Candolle A. Origin of cultivated plants. 2nd ed. London: Kegan Paul, Trench & Co.; 1886.
4. Deepa SK, Hadimani HP, Hanchinamani CN, Shet R, Koulgi S, Ashok. Estimation of genetic variability in cucumber (*Cucumis sativus* L.). *Int J Chem Stud.* 2018;6(6):115-118.
5. Doyle J, Doyle JL. Isolation of plant DNA from fresh tissue. *Focus.* 1990;12(1):13-15.
6. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza. *Agron J.* 1956;48(6):268-272.
7. Havey MJ. CMV resistance in three sources of cucumber. *Cucurbit Genet Coop.* 1996;19:32-33.
8. Hossain MD, Rabbani MG, Hakim MA, Amanullah ASM. Study on variability, character association and yield performance of cucumber (*Cucumis sativus* L.). *Bangladesh Res Publ J.* 2010;4(3):297-311.
9. Kandasamy R. Variability studies in cucumber (*Cucumis sativus* L.). *Asian J Hort.* 2017;12(1):84-87.
10. Kendall M. Multivariate analysis. London: Charles Griffin and Co.; 1980.
11. Kumar A. Studies on heterosis and inheritance of resistance to fruit fly in cucumber (*Cucumis sativus* L.) [doctoral thesis]. Nauni, Solan: Dr. YS Parmar University of Horticulture and Forestry; 2006.
12. Kumar JS, Pandit MK, Pathy TL. Genetic variability, diversity and character association in sponge gourd

- [*Luffa cylindrica* (Roem.) L.]. Int J Curr Microbiol App Sci. 2019;8(3):278-290.
13. Kumar PJ, Syed S, Reddy SS, Lakshmi LM, Reddy DS. Studies on correlation and path coefficient analysis for yield and its contributing characters in cucumber (*Cucumis sativus* L.). Int J Chem Stud. 2018;6(6):1649-1653.
 14. Liu K, Muse SV. PowerMarker: an integrated analysis environment for genetic marker analysis. Bioinformatics. 2005;21(9):2128-2129.
 15. Mnari-Hattab M, Zammouri S, Belkadi M, Doña DB, Ben Nahia E, Hajlaoui M. First report of tomato leaf curl New Delhi virus infecting cucurbits in Tunisia. New Dis Rep. 2015;31:21.
 16. Munshi AD, Panda B, Behera TK, Kumar R. Genetic variability in *Cucumis sativus* var. *hardwickii* R. (Alef.) germplasm. Cucurbit Genet Coop Rep. 2007;30:5-10.
 17. Nei M, Li WH. Mathematical model for studying genetic variation in terms of restriction endonucleases. Proc Natl Acad Sci U S A. 1979;76(10):5269-5273.
 18. Padidam M, Beachy RN, Fauquet CM. Tomato leaf curl geminivirus from India has a bipartite genome and coat protein is not essential for infectivity. J Gen Virol. 1995;76(1):25-35.
 19. Pal S, Sharma HR, Rai AK, Bhardwaj RK, Das A. Estimation of genetic divergence for yield and quality traits in cucumber (*Cucumis sativus* L.). Green Farm. 2017;8(2):296-300.
 20. Panno S, Iacono G, Davino M, Marchione S, Zappardo V, Bella P, *et al.* First report of tomato leaf curl New Delhi virus affecting zucchini squash in an important horticultural area of southern Italy. New Dis Rep. 2016;33:6.
 21. Rao ES, Munshi AD, Verma VK. Genetic association and interrelationship of yield and its components in cucumber (*Cucumis sativus* L.). Indian J Hort. 2004;61(4):315-318.
 22. Sáez C, Ambrosio LG, Miguel SM, Valcárcel JV, Díez MJ, Picó B, *et al.* Resistant sources and genetic control of resistance to ToLCNDV in cucumber. Microorganisms. 2021;9(5):913.
 23. Sáez C, Esteras C, Martínez C, Ferriol M, Singh NPSD, López C, *et al.* Resistance to tomato leaf curl New Delhi virus in melon is controlled by a major QTL located in chromosome 11. Plant Cell Rep. 2017;36(10):1571-1584.
 24. Sharma HR, Sharma D. Genetic divergence for yield and yield contributing traits in cucumber (*Cucumis sativus* L.). J Hort Sci. 2006;1(2):141-143.
 25. Singh SK, Singh SV, Srivastava JP. Genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.). Agriways. 2013;1(1):46-48.
 26. Zaidi SSS, Martin DP, Amin I, Farooq M, Mansoor S. Tomato leaf curl New Delhi virus: a widespread bipartite begomovirus in the territory of monopartite begomoviruses. Mol Plant Pathol. 2017;18(7):901-911.