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Complete Genome Characterization and Phylogenetic Analysis of Jasmine Virus H (JaVH) Infecting Jasminum sambac in Türkiye

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Research Article

Keywords: (HTS), Pelarspovirus, Virus Detection, Plant virology, ornamental, İskenderun

Posted Date: February 2nd, 2026

DOI: https://doi.org/10.21203/rs.3.rs-8460044/v1

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Abstract

This study represents the first identification and complete genome characterization of *Jasmine virus H (JaVH)* infecting *Jasminum sambac in Türkiye* belongs to the genus Pelarspovirus, family *Tombusviridae* and was first reported in *Jasminum sambac* in China before it was found in other countries. This paper presents an initial disease outbreak and full genome characterization of JaVH in plants of the genus *J. sambac* with observed yellow mosaics and leaf deformation symptoms reported in İskenderun, Hatay Province, southern Turkey. High-throughput sequencing (HTS) was performed on the infected samples and the de novo assembly produced a complete genome of 3,867 nucleotides of virus. Genome annotation showed five open reading frames (ORFs) encoding for the replication related proteins, p27 and p87, two movement proteins (p7 and p9), and the coating protein p37, as expected with other members of *pellarspovir*. The analysis of the nucleotide revealed the maximum identity (91–93%) of the isolate with JaVH isolates described in China and the United States, which proved the identity of the Turkish isolate. Full-length genome phylogenetic analysis and MEGA-based analysis of the replicase and coat protein sequences placed the Turkish JaVH isolate in their well-substantiated clade with other JaVH isolates, separate to that of Jasmine mosaic-associated virus (JMaV) and Jasmine virus C (JaVC). This distinct genetic clustering to the point of classifying it as a separate JaVH isolate, as opposed to a separate species. This is the first case of JaVH to be reported in Turkey and adds to extant coverage of the wide geographic distribution of Pelarspovirus species in relation to jasmine infection across the globe.

1. Introduction

Jasmine (*Jasmine Sambac* L.) is an essential oils and fragrant flower crop of the family Oleaceae that is grown globally and used as an ornamental crop. Jasmine is an economically and culturally important plant in Turkey especially in the southern Mediterranean area where it is widely cultivated in residential gardens and nurseries(Sudheera et al., 2014). Viral infections however, have become a rising threat to the production of jasmine and lead to mosaic, leaf, deformation, chlorosis, and reduction of the level of plant vigor(Addae et al., 2017; Garg & Garg, 2023).

Jasmine diseases in various locations have been linked to a number of viruses. *J. multiflorum* was reported to be infected by tomato mosaic virus (genus *Tobamovirus*) in Florida (Fillmer et al., 2015) and was shown to be infected by Tobacco streak virus (genus *Ilarvirus*) in Jasmine sambac in India (Goud et al., 2013), and by Jasmine Virus C (JaVC) in *Jasmine officinale* in Italy (Amoia et al., 2022). Recently, a new virus, Jasmine virus H (JaVH), was initially described in J. sambac that showed yellow mosaic symptoms in Fujian Province, China (Zhuo et al., 2018). Genomic and phylogenetic studies showed that JaVH is a positive-sense single-stranded RNA virus that belongs to the genus Pelarspovirus (family *Tombusviridae*). Several plant viruses are now classified in this genus, including Pelargonium line pattern virus, Rosa rugosa leaf distortion virus, and Clematis chlorotic mottle virus which have a similar genome organization and replication behavior(Usharani et al., 2016; Widowati et al., 2018).

After its identification in China, Jasmine virus H (JaVH) and the associated pelarspoviruses were later identified in jasmine plants in Hawaii and Washington, DC (Dey et al., 2018). Recently, JaVH was reported once more in the United States, in both single and mixed infections with Jasmine mosaic-associated virus (JMaV) in Florida (Dey et al., 2024). The latter paper was the first report of these two viruses infecting jasmine in Florida and increased the existing diversity and geographic range of *Pelarspovirus* species known to infect jasmine.

Irrespective of these findings, there has been the unavailability of the occurrence and any molecular characterization of JaVH in the eastern Mediterranean basin. We present the initial identification and molecular characterization of the first case of a *Jasmine virus H* (JaVH) in plants of *J. sambac* with characteristic mosaic and chlorotic ring spot symptoms in south Turkey, Iskenderun. This discovery offers new data on JaVH presence in the Mediterranean area and adds to the general knowledge on the epidemiology and genetic variability of ornamental crops(Srivastava et al., 2021).

2. Method and material

2.1. Field Survey and Sampling

During a field survey conducted in April 2024, *Jasminum sambac* (L.) plants exhibiting mosaic, leaf curling, and chlorotic mottling symptoms were observed in ornamental plantings in İskenderun, Hatay Province, southern Turkey. Symptomatic leaf samples were collected, cryopreserved in liquid nitrogen, and stored at − 80°C until further analysis(Al-Waeli et al., 2024).

2.2. RNA Extraction and cDNA Synthesis

Total RNA was extracted from 100 mg of symptomatic leaf tissue using the **RNeasy Plant Mini Kit** (Qiagen, Hilden, Germany) following the manufacturer's instructions. RNA concentration and purity were measured with a **NanoDrop 2000 spectrophotometer** (Thermo Fisher Scientific, USA), and RNA integrity was evaluated using an **Agilent 2100 Bioanalyzer** (Agilent Technologies, USA). Samples exhibiting RNA integrity number (RIN) greater than 7.0 were selected for downstream applications.

Residual genomic DNA was eliminated using **DNase I** (Thermo Fisher Scientific, USA). First-strand cDNA synthesis was performed using **Superscript IV Reverse Transcriptase** (Thermo Fisher Scientific, USA) and random hexamer primers according to the manufacturer's protocol.

2.3. High-Throughput Sequencing (HTS) and Assembly

Purified RNA was subjected to **high-throughput sequencing (HTS)** by **Gen Era, Türkiye**. The sequencing library was constructed using the **NEBNext Ultra II RNA Library Prep Kit** (New England Biolabs, USA), and paired-end (2 × 150 bp) reads were generated on an **Illumina NovaSeq 6000** platform.

Raw reads were quality-assessed using **FastQC v0.11.9**, and low-quality bases and adapters were trimmed with **Trimmomatic v0.39**. To remove host-derived reads, sequences mapping to plant ribosomal

and chloroplast sequences were filtered out using **BWA-MEM v0.7.17**. The remaining reads were assembled de novo with **Trinity v2.15.1** using default parameters.

Assembled contigs were compared against the NCBI non-redundant (nr) protein database via **BLASTx**. Contigs showing significant similarity to members of the **family Tombusviridae**, genus **Pelarspovirus**, were identified as *Jasmine virus H* (JaVH). The complete viral genome was reconstructed, validated through read mapping with **BWA v0.7.17**, and visualized using **Integrative Genomics Viewer (IGV v2.14.1)** to confirm genome coverage and uniformity.

2.4. Genome Annotation and Comparative Analysis

Open reading frames (ORFs) were predicted using **NCBI ORF Finder** and verified manually by alignment with reference pelarspovirus genomes. Pairwise nucleotide identity was calculated using **SDT v1.2 (Sequence Demarcation Tool)**.

Multiple sequence alignment of complete JaVH genomes was performed using **MAFFT v7**, and phylogenetic relationships were inferred with **MEGA X** (Kumar et al., 2018) employing the **maximum likelihood** method under the **Tamura–Nei** model with 1,000 bootstrap replicates.

2.5. Genetic and Phylogenetic Characterization

To determine the genetic relationship of the Turkish JaVH isolate (JaVH-TR) with other reported JaVH genomes from China and the United States, complete genome sequences retrieved from GenBank were compared using pairwise identity matrices and phylogenetic clustering. Since only a single JaVH isolate was obtained in this study, population-level diversity indices (e.g., Tajima's D, Fu's Fs) were not computed.

The complete genome of JaVH-TR has been submitted to the **NCBI GenBank** under accession number PX531343.

2.6. Visualization of Symptoms and Phylogeny

Photographs of symptomatic *Jasminum sambac* plants and the corresponding phylogenetic tree were compiled and formatted for publication using Adobe Illustrator CC 2024.

3. Results

3.1. Symptom observation

Jasmine plants (*Jasminum sambac*) exhibiting pronounced leaf mottling, yellow mosaic, and chlorotic patches were observed in home gardens in İskenderun, Hatay Province, southern Turkey (Fig. 1). The affected leaves showed variable degrees of deformation and discoloration, while adjacent plants displayed mild or no symptoms. The observed symptoms were consistent with those previously reported for *Jasmine virus H* (JaVH) and other *Pelarspovirus* infections in jasmine.

3.2. Genome characterization and sequence analysis

High-throughput sequencing of total RNA from symptomatic jasmine leaves yielded a complete viral genome of approximately 3,870 nucleotides. BLASTn analysis of the assembled sequence revealed the highest nucleotide identity (97.4–99.1%) with *Jasmine virus H* (JaVH) isolates previously reported from China (Zhuo et al., 2018). The genome organization follows the characteristic structure of members of the genus *Pelarspovirus* (family *Tombusviridae*), containing open reading frames encoding the replication-associated protein (Rep), movement protein (MP), and coat protein (CP).

3.3. Phylogenetic analysis

Phylogenetic analysis based on the complete genome sequence placed the Turkish JaVH isolate within the *Pelarspovirus* clade, clustering closely with Chinese JaVH isolates from Yunnan (MH231182), Guangxi (MH231176) and Guangdong (MH231175), (Fig. 2). The JaVH İskenderun isolate (PX531343) formed a distinct yet well-supported subclade, clearly separated from *Jasmine mosaic-associated virus* (JMaV) and *Jasmine virus C* (JaVC). This grouping confirms that the Turkish isolate belongs to *JaVH* and represents the first record of this virus in Turkey.

3.4. Pairwise nucleotide identity

Pairwise nucleotide identity comparisons among JaVH and related *Pelarspovirus* species were calculated using SDT v1.2 (Fig. 3). The JaVH İskenderun isolate showed 97–99% identity with Chinese JaVH sequences, 70–73% identity with JMaV isolates, and less than 50% identity with *JaVC* and *Rosa rugosa leaf distortion virus* (RrLDV). These results support the phylogenetic findings and confirm that the detected virus is a distinct isolate of *Jasmine virus H*.

4. Discussion

Here, we describe the identification and molecular identification of the *Jasmine virus H* (JaVH) as a pathogen of *J. sambac* in İskenderun, Hatay Province, Turkey. This is a new geographic reference of JaVH and extends the distribution of known species of *Pelarspovirus* with jasmine to areas outside East Asia, Europe and United States.

The mosaic and chlorotic spots that are identified on infected leaves are similar to those reported in China (Zhuo et al., 2018) and the United States (Dey et al., 2024, 2018) and indicate that the symptoms described may be comparable among distinct geographies of the various isolates. The entire genome sequence that was obtained in the current study exhibited a genome structure and arrangement of genes which is characteristic of the representatives of the genus *Pelarspovirus* of the family *Tombusviridae*.

Phylogenetic and pair-wise (Fig. 2), (Fig. 3), identity analyses verified that the Turkish isolate was of JaVH with a nucleotide identity of over 97% with previously described Chinese isolates and a well-

supported clade in the Pelarspovirus lineage. Its distinct separation against Jasmine mosaic-associated virus and *Jasmine virus C* (JaVC) support its existence as a separate JaVH isolate but not as another species.

The JaVH threat in Turkey is especially crucial, as it links the known instances of this virus between Asia (China and India) and Europe (Italy) and the eastern Mediterranean area, now. This pattern of distribution indicates that JaVH could have been transferred due to the transportation of infected planting material, which is in line with vegetative propagation methods that are predominantly applied in growing jasmine. This has been attributed to similar mechanisms that have been implicated in the spread of JMaV and related *pelarspoviruses* (Dey et al., 2024).

In terms of epidemiology, JaVH naturally present in Turkish jasmine highlights the importance of regional monitoring and diagnostics screening of nursery and ornamental stock to avoid further transmission. Considering the economic and cultural significance of jasmine in Turkey and adjacent nations, identification of reliable molecular means of detecting any disease and enactment of phytosanitary mechanisms will be very necessary in managing the disease(Abou Kubaa et al., 2023; Raj et al., 2021).

Finally, the current study extends the global spread of *Jasmine virus H* to the eastern Mediterranean and offers a full genomic resource in the future to compare and evolutionary studies. Subsequent research must be done to examine potential co-infections and host range, and the dynamics of transmission of JaVH to understand its epidemiology and potential influence on jasmine production.

Declarations

Funding

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Competing Interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Author Contributions

G. Koç: Conceptualization, Investigation.

B.B. Arpacı: Data curation.

B. Özgören: Sample collection, Laboratory analysis.
A. Alsalmo: Writing – original draft.
All authors reviewed and approved the final manuscript.

Acknowledgement

Thanks to Assoc. Prof. Dr. Hakan Fidan for critical reviews of this article.

References

1. Abou Kubaa, R., Amoia, S.S., Altamura, G., Minafra, A., Chiumenti, M., Cillo, F., 2023. Nanopore Technology Applied to Targeted Detection of Tomato Brown Rugose Fruit Virus Allows Sequencing of Related Viruses and the Diagnosis of Mixed Infections. Plants 12, 999. https://doi.org/10.3390/plants12050999
2. Addae, J.I., Pingal, R., Walkins, K., Cruickshank, R., Youssef, F.F., Nayak, S.B., 2017. Effects of Jasminum multiflorum leaf extract on rodent models of epilepsy, motor coordination and anxiety. Epilepsy Res. 131, 58–63. https://doi.org/10.1016/j.eplepsyres.2017.02.012
3. Al-Waeli, M., Shahmohammadi, N., Tavakoli, S., Dizadji, A., Kvarnheden, A., 2024. Infection of tomato in Iraq with tomato leaf curl Palampur virus and multiple variants of tomato yellow leaf curl virus. J. Plant Pathol. 106, 1283–1294. https://doi.org/10.1007/s42161-024-01682-4
4. Amoia, S.S., Minafra, A., Nicoloso, V., Loconsole, G., Chiumenti, M., 2022. A New Jasmine Virus C Isolate Identified by Nanopore Sequencing Is Associated to Yellow Mosaic Symptoms of Jasminum officinale in Italy. Plants 11. https://doi.org/10.3390/plants11030309
5. Dey, K.K., Leite, M., Hu, J.S., Jordan, R., Melzer, M.J., 2018. Detection of Jasmine virus H and characterization of a second pelarspovirus infecting star jasmine (Jasminum multiflorum) and angelwing jasmine (J. nitidum) plants displaying virus-like symptoms. Arch. Virol. 163, 3051–3058. https://doi.org/10.1007/s00705-018-3947-y
6. Dey, K.K., Velez-Climent, M., Soria, P., McVay, J., Adkins, S., 2024. First Report of Mixed Infection of Jasmine Mosaic-Associated Virus (JMaV) and Jasmine Virus H (JaVH) in Jasmine Species in Florida, United States. Plant Health Prog. 25, 210–211. https://doi.org/10.1094/PHP-08-23-0073-BR
7. Fillmer, K., Adkins, S., Pongam, P., D'Elia, T., 2015. Complete Genome Sequence of Tomato Mosaic Virus Isolated from Jasmine in the United States. Genome Announc. 3, e00706-15. https://doi.org/10.1128/genomeA.00706-15
8. Garg, P., Garg, V., 2023. Bibliometric Analysis of the Genus Jasminum: Global Status, Research and Trends. J. Herb. Med. https://doi.org/10.1016/j.hermed.2023.100711
9. Goud, T.E.S., Vemana, K., Reddy, D.L., Khureshee, C.S.M., Padma, J.G., Shabbir, S., Venkateswarlu, N.C., Naik, K.S.S., Kumar, D.S., Johnson, A.M.A., Subramanyam, K., 2013. First report of Tobacco streak ilarvirus infecting jasmine and horse gram. New Dis. Rep. 28, 7–7. https://doi.org/10.5197/j.2044-0588.2013.028.007
10. Raj, S.K., Gaur, R.K., Yin, Z. (Eds.), 2021. Virus Diseases of Ornamental Plants: Characterization, Identification, Diagnosis and Management. Springer Singapore, Singapore. https://doi.org/10.1007/978-981-16-3919-7

11. Srivastava, A., Verma, S., Singhal, T., Raj, S.K., 2021. Molecular Characterization of Viruses Occurring on Some Ornamental Shrubs Grown in India, in: Raj, S. K., Gaur, R.K., Yin, Z. (Eds.), Virus Diseases of Ornamental Plants: Characterization, Identification, Diagnosis and Management. Springer Singapore, Singapore, pp. 165–179. https://doi.org/10.1007/978-981-16-3919-7_9
12. Sudheera, Y., Vardhan, G.P.V., Hema, M., Reddy, M.K., Sreenivasulu, P., 2014. Characterization of a potyvirus associated with yellow mosaic disease of jasmine (Jasminum sambac L.) in Andhra Pradesh, India. VirusDisease 25, 394–397. https://doi.org/10.1007/s13337-014-0193-0
13. Usharani, T.R., Jalali, S., Manasa, M., Samuel, D.K., Krishnareddy, M., 2016. Identification of mixed infection caused by Badnavirus and CMV in Jasmine (Jasminum multiflorum Roth), Indian Journal of Biotechnology.
14. Widowati, W., Janeva, W.B., Nadya, S., Amalia, A., Arumwardana, S., Kusuma, H.W.S., Arinta, Y., Author, C., 2018. Jasminum sambac as an antioxidant and antiaging Antioxidant and Antiaging Activities of Jasminum Sambac Extract, and its Compounds, Medical Sciences Journal of Reports in Pharmaceutical Sciences.
15. Zhuo, T., Zhu, L.J., Lu, C.C., Jiang, C.Y., Chen, Z.Y., Zhang, G., Wang, Z.H., Jovel, J., Han, Y.H., 2018. Complete nucleotide sequence of jasmine virus H, a new member of the family Tombusviridae. Arch. Virol. 163, 731–735. https://doi.org/10.1007/s00705-017-3663-z

Figures

Figure 1

Mosaic and chlorotic symptoms on *Jasminum sambac*leaves naturally infected with Jasmine virus H (JaVH) collected from İskenderun, Hatay Province, Turkey. Affected leaves display distinct patterns of light and dark green mottling, mosaic, and chlorotic patches indicative of viral infection.

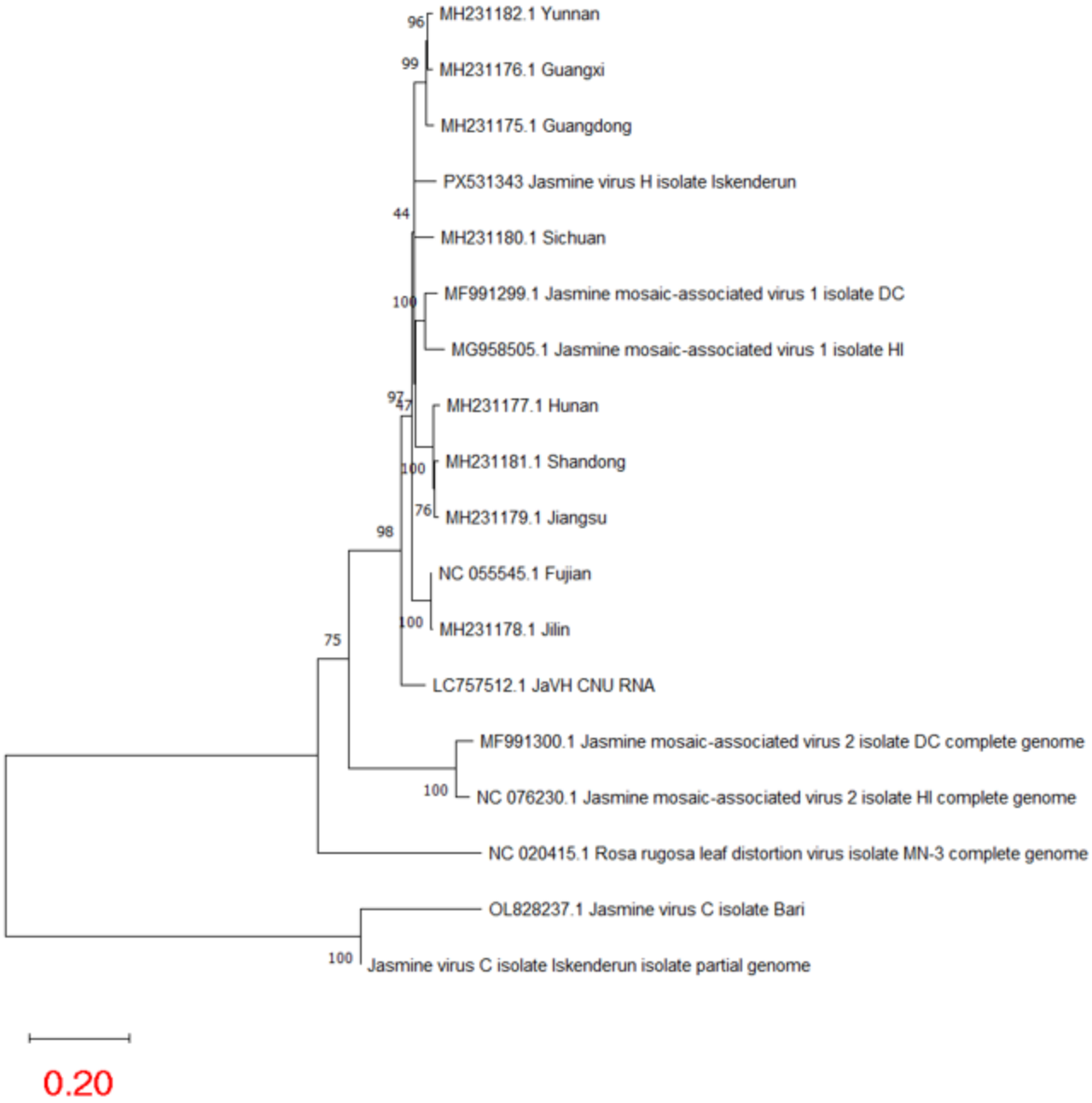

Figure 2

Phylogenetic analysis of *Jasmine virus H* (JaVH) isolate from İskenderun, Hatay Province, Turkey, based on the complete genome sequence. The isolate clusters closely with JaVH isolates from China, forming a distinct clade within the *Pelarspovirus* genus (family *Tombusviridae*). The scale bar represents 0.20 nucleotide substitutions per site.

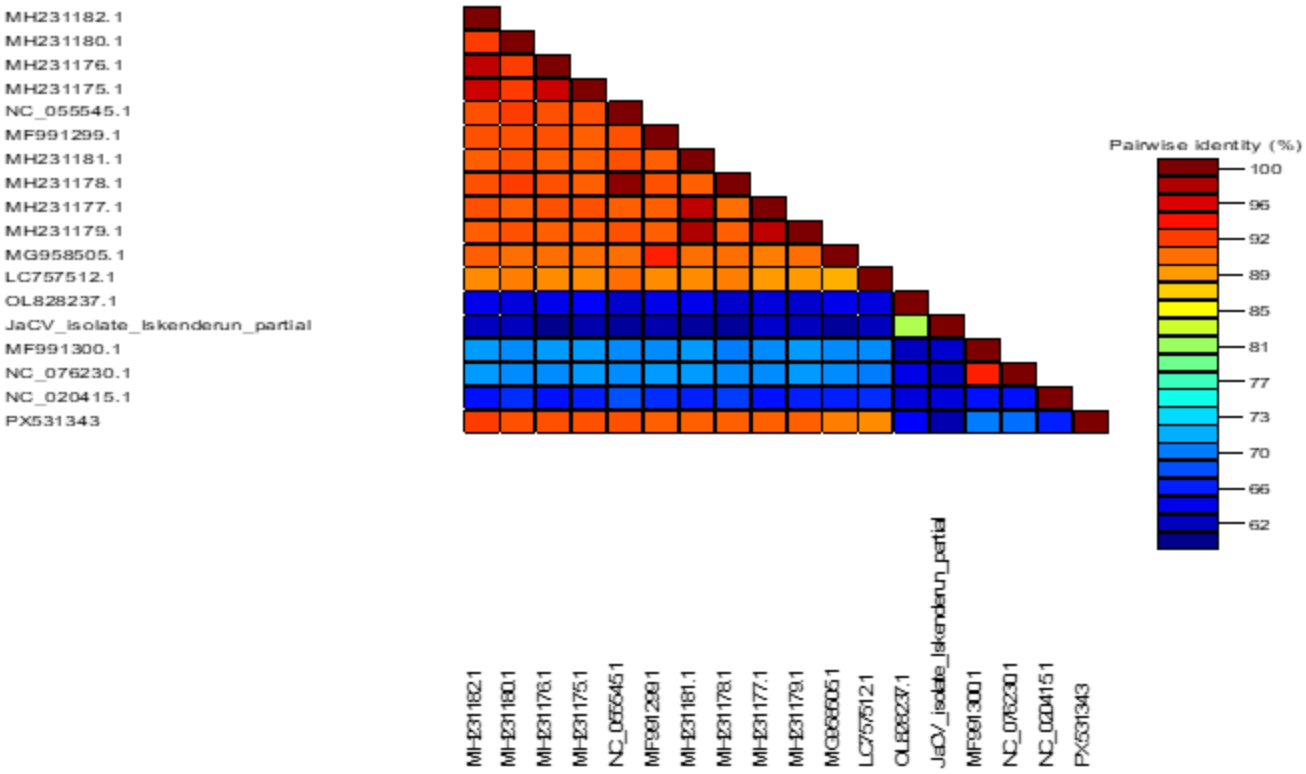

Figure 3

Pairwise nucleotide identity matrix of *Jasmine virus H*(JaVH) isolate from İskenderun, Turkey, and representative members of the genus (family *Tombusviridae*). The heatmap was generated using SDT v1.2, based on complete or partial genome sequences. red–orange indicate lower nucleotide identity, whereas green–blue indicate higher identity values. The JaVH İskenderun isolate shows the highest nucleotide similarity (≈97–99%) to Chinese JaVH isolates, supporting their close phylogenetic relationship.