

Occurrence and diversity of apple mosaic ilarvirus in apple and hazelnut in Serbia

Zastupljenost i genetička raznovrsnost virusa mozaika jabuke na jabuci i lešniku u Srbiji

Bojana VASILJIJEVIĆ (✉), Vera KATANIĆ, Darko JEVREMOVIĆ

Fruit Research Institute, Kralja Petra I nr. 9, 32102 Čačak, Serbia

✉ Corresponding author: bvasilijevic@institut-cacak.org

Received: July 8, 2025; accepted: December 27, 2025

ABSTRACT

Two hundred and twenty trees (150 apples and 70 hazelnuts) from seven locations in Serbia were tested for the presence of ilarvirus ApMV (apple mosaic virus). ELISA test confirmed the presence of ApMV in 11 apples (7.3%) and six hazelnuts (8.5%) samples, with typical and severe mosaic symptoms on the leaves. ELISA-positive samples were further tested by RT-PCR with two different primer pairs. One primer pair was efficient for the RT-PCR detection of ApMV isolates from apple, and the other one for isolates from hazelnut. Sequence analysis of amplified PCR fragments of the selected isolates confirmed that Serbian ApMV isolates from apple share the highest nucleotide identity (98.66 – 99.02%) with isolates from India and Canada.

Keywords: *Malus × domestica* Borkh., *Corylus avellana* L., double antibody sandwich enzyme-linked immunosorbent assay, reverse transcription polymerase chain reaction, sequencing

APSTRAKT

Ukupno 220 stabala (150 jabuka i 70 lešnika) sa sedam lokaliteta u Srbiji, testirano je na prisustvo ilarvirusa ApMV (virus mozaika jabuke). ELISA test potvrdio je prisustvo ApMV na 11 uzoraka jabuke (7,3%) i šest uzoraka lešnika (8,5%) koji su pokazivali tipične i izražene simptome mozaika na listovima. Pozitivni uzorci dobijeni u ELISA testu, dalje su analizirani metodom RT-PCR, koristeći dva različita para prajmera. Jedan par prajmera bio je efikasan za detekciju ApMV izolata sa jabuke, dok je drugi bio uspešan za izolate sa lešnika. Analiza sekvence umnoženih PCR fragmenata odabranih izolata potvrdilo je da srpski izolati ApMV sa jabuke pokazuju najviši stepen identičnosti (98,66-99,02%) sa izolatima iz Indije i Kanade.

Ključne reči: *Malus × domestica* Borkh., *Corylus avellana* L., enzimski imunoadsorbicioni test, lančana reakcija polimeraze, sekvenciranje

INTRODUCTION

Apple (*Malus × domestica* Borkh.) is one of the most economically important fruit crops grown in Serbia, where favourable climatic and soil conditions support its widespread cultivation. Serbia is a notable apple producer in the Balkan region and Eastern Europe, with increasing export potential in recent years (Pavlović et al.,

2020). Apples are grown on more than 27,000 hectares. Commonly cultivated varieties include 'Idared', 'Golden Delicious', 'Red Delicious', 'Granny Smith', 'Fuji', 'Braeburn', and 'Gala' (Magazin et al., 2022), along with several autochthonous cultivars.

Hazelnut (*Corylus avellana* L.) is also cultivated in Serbia, particularly in regions with suitable microclimates, such as the western and southern parts of the country. Although Serbia is not a global leader in hazelnut production, it has been expanding its hazelnut orchards, partly due to increasing demand from the confectionery industry. The area under hazelnut cultivation has risen rapidly in the last decade, reaching approximately 9,000 hectares, which accounts for about 1.8% of the total fruit orchard area in Serbia (Džankić et al., 2024).

Both crops are susceptible to numerous pathogens that challenge their production. Apple trees are affected by over 20 viruses and virus-like agents, while only three viruses are known to infect hazelnuts. One of the viruses that can limit apple and hazelnut production in Serbia is *Ilarvirus* ApMV (apple mosaic virus, ApMV). This virus belongs to the family *Bromoviridae*, genus *Ilarvirus*, and was initially described in apple. ApMV affects over 65 plant species within the *Rosaceae* family and represents a serious threat to sensitive apple cultivars by reducing tree growth, fruit yield, and overall fruit quality (Grimová et al., 2016). In apples, typical leaf symptoms include irregular pale-yellow to bright cream spots or bands along the main veins on spring foliage, often forming mosaic patterns. On severely affected leaves, these spots may become necrotic following exposure to summer heat and sunlight. Such symptomatic leaves tend to drop prematurely. The distribution of symptoms may be uneven across the tree or confined to just one branch. Fruits do not show specific symptoms (Barba et al., 2015). ApMV is also the most important virus affecting hazelnuts, where it can lead to reduced growth and decreased yields. Infected hazelnut leaves often display chlorotic and yellow patterns, rings, and mosaic symptoms.

ApMV is an isometric virus with relatively unstable virions, measuring approximately 30 nm in diameter. The ApMV genome comprises three RNA segments (RNA 1–3) and a sub-genomic RNA 4. RNA 1 and RNA 2 encode the replication-related proteins P1 and P2, containing methyltransferase (MT) and RNA-dependent RNA polymerase (RdRP) domains, respectively. RNA 3 encodes the movement protein (MP) and the coat protein

(CP), with CP expressed from RNA 4 (Akbaş et al., 2025). It is serologically related to *Ilarvirus* PNRSV (prunus necrotic ringspot virus, PNRSV) and may have been mistakenly identified as PNRSV in serological tests (Petrzik and Lenz, 2011). ApMV is commonly detected in mixed infections with PNRSV and *Ilarvirus* PDV (prune dwarf virus, PDV) on their shared stone fruit hosts and infects a wide range of woody plants. In apple trees, it is often found alongside other viruses such as *Trichovirus mali* (apple chlorotic leafspot virus, ACLSV), *Foveavirus mali* (apple stem pitting virus, ASPV), *Capillovirus mali* (apple stem grooving virus, ASGV), and additional apple-infecting viruses. ApMV is a major causal agent of apple mosaic disease, widely distributed in apple-growing regions worldwide, causing significant qualitative and quantitative losses. The recent identification of Apple necrotic mosaic virus (ApNMV) as a closely related pathogen indicates that the epidemiology of apple mosaic disease should be reconsidered. As highlighted in a comprehensive review, disease incidence, spread, and symptom expression may also be influenced by these newly recognized viruses (Manzoor et al., 2023). ApMV is transmitted only through vegetative propagation and grafting, and slowly via root grafting in nurseries, with no known insect vector and no transmission through pollen (Grimová et al., 2016). In other words, transmission occurs when a virus-infected scion bud is grafted onto a healthy rootstock, or onto a rootstock that is already infected. Consequently, the virus can move from the infected scion to a healthy rootstock, or from an infected rootstock to a healthy scion, resulting in infected and declining trees.

Although ApMV is one of the most common viruses infecting apples and hazelnuts in Serbia, no studies have investigated its incidence on these hosts in the country. ApMV was not confirmed in *Prunus* species in Serbia (Jevremović and Vasilijević, 2021), and it is listed on the List IA part I – Harmful organisms not known to be present in the territory of the Republic of Serbia and whose introduction and spread into the Republic of Serbia is prohibited, as a pathogen of *Rubus* species (Official Gazette of the Republic of Serbia, Nos. 7/2010, 22/2012, 57/2015).

This research was conducted to assess the incidence of ApMV in apples and hazelnuts in Serbia using serological and molecular methods, and to examine the genetic diversity of selected isolates.

MATERIAL AND METHODS

During a survey from 2010 to 2022, a total of 150 apple and 70 hazelnut samples were collected from the orchards in Serbia. Samples were collected in the localities: Čačak, Deč, Kruševac, Mladenovac, Sombor, Šabac and Trstenik. The majority of leaf samples were asymptomatic; however, a small proportion showed chlorotic and yellow patterns and mosaic, both on apple and hazelnut.

All samples were initially analyzed for the ApMV presence using a double antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) using the reagents of BIOREBA AG, Switzerland, according to manufacturers' recommendations. Fresh leaf samples were prepared at a 1:10 ratio in the extraction buffer. Color development was measured at 405 nm on an ELISA MULTISKAN MCC/340 reader (Labsystems, Finland) after 60-120 min. Samples were considered positive when optical density (OD) values were at least two times higher than the OD values of the negative control.

All ELISA-positive samples were further tested by reverse transcription polymerase chain reaction (RT-PCR). RNA was extracted from fresh young leaves with the RNeasy mini kit (Qiagen, Germany) following the recommended protocol. RT was performed using random hexamer primers (ThermoFisher Scientific, USA). The obtained cDNA was used for PCRs with two specific primer pairs. A primer pair 87e5/87e6 (92D9up/92E0re) spanning the coat protein (CP) gene was used for the amplification of the 821 bp fragment (Petřík and Lenz, 2002; Petřík, 2005). The program for PCR was as follows: 94 °C for 3 min, followed by 35 cycles at 94 °C for 30 s, 50 °C for 30 s and 68 °C for 90 s, followed by a final extension step at 68 °C for 10 min. A primer pair 1F/1R that amplifies a fragment of the 312 bp in the CP gene (Massart et al., 2009) was used for the second PCR that was done according to the program: 95 °C for 3 min,

followed by 40 cycles at 95 °C for 45 s, 55 °C for 45 s and 72 °C for 60 s, and a final extension step at 72 °C for 10 min. PCR products were analyzed by 1.5% agarose gel electrophoresis and ethidium bromide staining. The visualization of the products was done in the Gel Doc EZ System using a UV tray (Bio-Rad Laboratories, USA).

To further examine the diversity of the isolates, 10 isolates were purified and custom sequenced (Macrogen Europe Laboratory, the Netherlands). BioEdit software was used to assemble raw sequences (Hall, 1999). Phylogenetic analyses were conducted using MEGA software version 12 (Kumar et al., 2024). Phylogenetic trees were created using the Maximum Likelihood (ML) method with 1000 bootstrap replications.

RESULTS AND DISCUSSION

Apple mosaic virus is considered an economically important virus infecting apple and hazelnut. During survey and visual inspection, a great majority of plants in apple and hazelnut plantations did not show any symptoms indicating virus presence. Symptoms typical of apple mosaic disease were observed on the leaves of 11 apple trees and six hazelnut bushes. These plants showed typical whitish and pale-yellow chlorotic spots and mosaic patterns (Figures 1 and 2).



Figure 1. Whitish and yellow chlorotic spots on apple leaves caused by ApMV



Figure 2. Mosaic symptoms on hazelnut leaves induced by ApMV

ELISA tests confirmed ApMV presence in 17 out of 220 tested samples (7.7%). ApMV was detected in all 11 symptomatic apple and six hazelnut samples, with OD values at least 3 times higher than the value for the negative control (data not shown). ApMV was not detected in asymptomatic samples. This study confirmed a low incidence of ApMV in the analyzed apple and hazelnut samples, 7.3% and 8.5%, respectively. ApMV was confirmed in apple samples from Čačak, Kruševac, Trstenik and Šabac, and in hazelnut samples from the locality Deč and Sombor. In apples, ApMV was confirmed in cultivars 'Granny Smith', 'Golden Delicious' and 'Jonathan'. These cultivars are described as sensitive and express severe mosaic symptoms on the leaves (Wood et al., 1975), as it was confirmed in our study. In hazelnut, ApMV was confirmed in cultivars 'Tonda Gentile delle Langhe' and 'Hall's Giant'.

ApMV is distributed worldwide, and its incidence varies widely. ApMV incidence in most countries is low to moderate, depending on the host, cultivar and region (Valasevich et al., 2014). A high ApMV incidence (68.3%) was reported in apple orchards in the central Anatolia Region of Turkey (Akbaş and İlhan, 2005), while the incidence in hazelnut was low (13.6%), resulting in significant yield losses (Akbaş and Değirmenci, 2009).

The RT-PCR analysis with the 87e5/87e6 primer pair revealed the presence of the expected 821 bp fragment in 11 ELISA-positive apple samples. This primer pair

failed to detect ApMV isolates from hazelnut. Ertunc et al. (2014) also reported that this primer pair was ineffective for the detection of ApMV in hazelnut in Turkey. According to the results of Ertunç (2016), hazelnut isolates were distinct from other ApMV strains. The sequences obtained from hazelnut showed slightly different nucleic acid and amino acid compositions compared to those obtained from apples in Turkey and from various locations around the world. These findings suggest that ApMV strains may co-evolve with their host plants, leading to heterogeneity in the CP. Phylogenetic analysis of the CP gene showed that hazelnut isolates from Poland grouped separately from virus strains infecting other plant species, including apple, pear, *Prunus* spp., and rose (Cieślińska and Valasevich, 2016). These Polish isolates also differed genetically from the hazelnut isolate of ApMV reported from the Czech Republic (Grimová et al., 2013). Together, these studies provide clear evidence that ApMV exhibits genetic heterogeneity across host species, particularly in the CP and movement protein (MP) genes. This divergence can affect PCR-based detection, especially when primers are designed based on apple-specific viral sequences. This may explain the failure of the 87e5/87e6 primer pair to detect ApMV in hazelnut, despite confirmed infection.

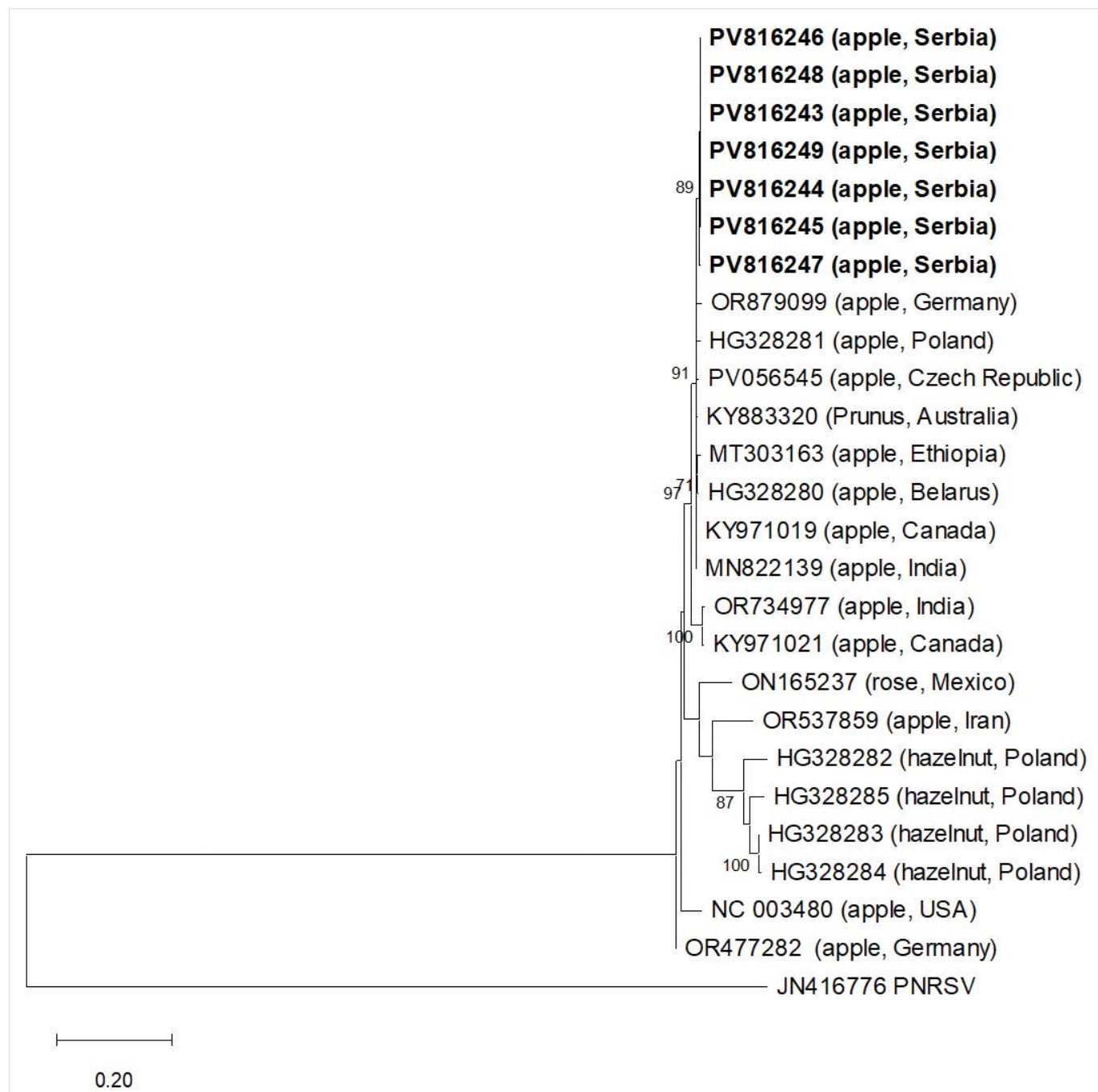
To further evaluate detected isolates, seven isolates from apple were sequenced (Table 1). When compared, Serbian ApMV isolates showed 99.5–100% nucleotide (nt) sequence identity. The sequences of these isolates were compared with the sequences of other ApMV isolates available in the NCBI GenBank. Serbian isolates RS-ApMV-10, RS-ApMV-11, RS-ApMV-18, and RS-ApMV-20 have identical sequences and share the highest nt identity (98.66%) with apple isolate CITH GD from India (MN822139) and apple isolate 13TF151 from Canada (KY971019). Our isolates RS-ApMV-12 and RS-ApMV-13 share 98.78% nt identity with isolates CITH GD and 13TF151, whereas isolate RS-ApMV-14 shares the highest nt identity (99.02%) with isolate 13TF151.

Table 1. ApMV isolates characterized in this study

Isolate	Host	Cultivar	Locality	Year	NCBI Accession No.
RS-ApMV-10	<i>Malus x domestica</i>	Granny Smith	Serbia	2012	PV816243
RS-ApMV-11	<i>Malus x domestica</i>	Granny Smith	Serbia	2012	PV816244
RS-ApMV-12	<i>Malus x domestica</i>	Golden Delicious	Serbia	2018	PV816245
RS-ApMV-13	<i>Malus x domestica</i>	Granny Smith	Serbia	2018	PV816246
RS-ApMV-14	<i>Malus x domestica</i>	Golden Delicious	Serbia	2020	PV816247
RS-ApMV-18	<i>Malus x domestica</i>	Jonathan	Serbia	2020	PV816248
RS-ApMV-20	<i>Malus x domestica</i>	Granny Smith	Serbia	2020	PV816249
DSMZ PV-0994	<i>Malus sylvestris</i>	-	Germany	-	OR879099
26XII7	<i>Malus domestica</i>	-	Poland	-	HG328281
S1	<i>Malus domestica</i>	Taborita	Czechia	2023	PV056545
K75R3	<i>Prunus</i> sp.	-	Australia	2015	KY883320
Eth3	<i>Malus domestica</i>	Fuji	Ethiopia	2017	MT303163
Zaslavskoje	<i>Malus domestica</i>	-	Belarus	-	HG328280
13TF151	<i>Malus</i> sp.	-	Canada	2013	KY971019
CITH GD	apple	Golden Delicious	India	2019	MN822139
A2	<i>Malus domestica</i>	Red Fuji	India	2022	OR734977
13TF160	<i>Malus</i> sp.	-	Canada	2013	KY971021
Temix-Mor-3	<i>Rosa</i> sp.	-	Mexico	2021	ON165237
Alborz-A2	<i>Malus domestica</i>	-	Iran	2020	OR537859
Negret 7	<i>Corylus avellana</i>	-	Poland	-	HG328282
Negret 2	<i>Corylus avellana</i>	-	Poland	-	HG328285
Trapez 4	<i>Corylus avellana</i>	-	Poland	-	HG328283
Trapez 6	<i>Corylus avellana</i>	-	Poland	-	HG328284
-	<i>Malus domestica</i>	-	USA	-	NC_003480
DSMZ PV-0742	<i>Rubus</i> sp.	-	Germany	-	OR477282
Pch12	peach	-	Canada	2011	JN416776

The evaluation of phylogenetic relationships of seven Serbian and 23 ApMV isolates from other countries (Australia, Belarus, Canada, the Czech Republic, Ethiopia, Germany, India, Iran, Mexico, Poland, and the USA)

was performed with MEGA12 (Kumar et al., 2024). Serbian isolates were clustered with other ApMV isolates, grouped together in a separate branch (Figure 3).



Isolates from GenBank are reported with their accession numbers, host and country of origin given in parentheses. Serbian isolates from this study are marked in bold. Phylogeny was inferred after 1000 bootstrap replications. Bootstrap values $\geq 70\%$ are shown. PNRSV isolate Pch12 (JN416776) was used as an outgroup.

Figure 3. The phylogenetic tree was reconstructed using partial ApMV sequences

In the second PCR with the 1F/1R primer pair, no positive reactions were obtained in ApMV-infected apple samples. This primer pair is targeting the fragment of 312 bp of the CP gene, within the fragment amplified with primers 87e5/87e6. This primer pair was evaluated with other primers for the detection of pome fruit viruses in the study of Massart et al. (2009). The method has been carefully validated, but it is important to evaluate primers with a wide range of isolates from different hosts and geographic origins for their recommendation in charge of phytosanitary certification. Analyzing the obtained sequences (Table 1), we confirmed that the reverse primer does not match the target sequence, and the PCRs did not show any amplification. This study confirmed that the 1F/1R primer pair failed to detect Serbian ApMV isolates from apples, but yielded amplicons of the expected size with isolates from hazelnut that were sequenced. The BLASTn analysis of the obtained sequences confirmed that amplified fragments showed very high similarity (99,26%) with the sequence of the *Corylus avellana* genome (accession XM_059587490). The result indicated that the used primers are not specific enough, binding to the plant's DNA and amplifying it instead of the virus.

Several studies on ApMV diversity were focused on the MP and CP gene (Grimová et al., 2013; Lakshmi et al., 2011; Petrzik, 2005; Petrzik and Lenz, 2002). Gene sequences of ApMV isolates from different hosts and geographic origins were investigated, and the results confirmed significant diversity of the studied isolates. A high variability of the ApMV capsid protein gene after nucleotide position 141 was demonstrated by Petrzik and Lenz (2002). High diversity of the targeted genomic region makes it difficult to properly select primers for reliable detection. Furthermore, the development and application of modern diagnostic methods, including RT-qPCR, have significantly improved the accuracy and sensitivity of epidemiological assessments of ApMV infections (Nabi et al., 2023).

CONCLUSIONS

This is the first comprehensive study on the ApMV presence in apples and hazelnuts in Serbia. The presented results confirmed a low incidence of ApMV in both fruit species. The ELISA test proved to be a reliable method for ApMV detection from apple and hazelnut leaf samples. On the contrary, reliable RT-PCR diagnosis is highly dependent on the primers used and should be further evaluated with a range of other primer pairs before recommendation for wider use.

ACKNOWLEDGEMENTS

This research was funded by the Ministry of Science, Technological Development, and Innovation of the Republic of Serbia, grant number 451-03-136/2025-03/200215.

REFERENCES

- Akbaş, B., Değirmenci, K. (2009) Incidence and natural spread of apple mosaic virus on hazelnut in the west black sea coast of Turkey and its effect on yield. *Journal of Plant Pathology*, 91 (3), 767-771. DOI: <https://www.jstor.org/stable/41998703>
- Akbaş, B., İlhan, D. (2005) Widespread distribution of Apple mosaic virus on apple in Turkey. *Plant Disease*, 89 (9), 1010. DOI: <https://doi.org/10.1094/PD-89-1010C>
- Akbaş, B., Morca, A. F., Coşkan, S., Şahin-Taylan, Z., Taylan, E., Güler, E., Çelik, A. (2025) Strengthening hazelnut certification systems through sensitive detection of apple mosaic virus (ApMV). *Journal of Plant Diseases and Protection*, 132 (3), 102. DOI: <https://doi.org/10.1007/s41348-025-01098-x>
- Barba, M., Ilardi, V., Pasquini, G. (2015) Control of pome and stone fruit virus diseases. In: Loebenstein, G., Nikolaos, I., eds. *Advances in virus research*. Burlington, VT: Academic Press, pp. 47-83.
- Cieślińska, M., Valasevich, N. (2016) Characterization of Apple mosaic virus isolates detected in hazelnut in Poland. *Journal of Plant Diseases and Protection*, 123 (4), 187-192. DOI: <https://link.springer.com/article/10.1007/s41348-016-0021-4>
- Džankić, S., Bijelić, S., Bogdanović, B., Jaćimović, G., Ünver, H. (2024) Grafting success and quality of hazelnut plants: impact of grafting methods, clones and bonding materials. *Turkish Journal of Agriculture and Forestry*, 48 (6), 1023-1033. DOI: <https://doi.org/10.55730/1300-011X.3238>
- Ertunç F. (2016) Genomic conformation of apple mosaic virus Turkish isolates coat protein gene regions. *Journal of Applied Biological Sciences*, 10 (2), 35-40.
- Ertunç, F., Topkaya, S., Sezer, A. (2014) Distribution and molecular detection of apple mosaic virus in apple and hazelnut in Turkey. *African Journal of Biotechnology*, 13 (31), 3144-3149. DOI: <https://doi.org/10.5897/AJB2013.13154>
- Grimova, L., Winkowska, L., Konrady, M., Ryšánek, P. (2016) Apple mosaic virus. *Phytopathologia Mediterranea*, 55 (1), 1-19. DOI: https://doi.org/10.14601/Phytopathol_Mediterr-16295

- Grimová, L., Winkowska, L., Ryšánek, P., Svoboda, P., Petrzik, K. (2013) Reflects the coat protein variability of apple mosaic virus host preference? *Virus Genes*, 47, 119-125.
DOI: <http://dx.doi.org/10.1007/s11262-013-0925-z>
- Hall, T.A. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acid Symposium Series*, 41, 95-98.
- Jevremović, D., Vasiljević, B. (2021) Monitoring of stone fruit viruses in Serbia. *Voćarstvo*, 55 (209-210), 55-61.
- Kumar, S., Stecher, G., Suleski, M., Sanderford, M., Sharma, S., Tamura, K. (2024) Molecular Evolutionary Genetics Analysis Version 12 for adaptive and green computing. *Molecular Biology and Evolution*, 41, 1-9. DOI: <https://doi.org/10.1093/molbev/msae263>
- Lakshmi, V., Hallan, V., Ram, R., Ahmed, N., Zaidi, A., Varma, A. (2011) Diversity of apple mosaic virus isolates in India based on coat protein and movement protein genes. *Indian Journal of Virology*, 22, 44-49. DOI: <https://doi.org/10.1007/s13337-011-0036-1>
- Magazin, N., Milić, B., Keserović, Z. (2022) Production and assortment of apple in Serbia. *Plant doctor*, 50 (6), 411-426.
DOI: <https://doi.org/10.5937/BiljLek2206411M>
- Massart, S., Brostaux, Y., Barbarossa, L., Batlle, A., Cesar, V., Dutrecq, O., Fonseca, F., Guillem, R., Komorowska, B., Olmos, A., Steyer, S., Wetzel, T., Kummert, J., Jijakli, M.H. (2009) Interlaboratory evaluation of two Reverse-transcriptase Polymerase Chain Reaction-based methods for detection of four fruit tree viruses. *Annals of Applied Biology*, 154 (1), 133-141.
DOI: <https://doi.org/10.1111/j.1744-7348.2008.00281.x>
- Manzoor, S., Nabi, S. U., Baranwal, V. K., Verma, M. K., Parveen, S., Rather, T. R., Raja, W. H., Shafi, M. (2023). Overview on century progress in research on mosaic disease of apple (*Malus domestica* Borkh) incited by apple mosaic virus/apple necrotic mosaic virus. *Virology*, 587, 109846. DOI: <https://doi.org/10.1016/j.virol.2023.109846>
- Nabi, S. U., Mir, J. I., Yasmin, S., Din, A., Raja, W. H., Madhu, G. S., Parveen, S., Mansoor, S., Chung, Y. S., Sharma, O. C., Sheikh, M. A., Al-Misned, F., Serehy, H. A. (2023) Tissue and time optimization for real-time detection of apple mosaic virus and apple necrotic mosaic virus associated with mosaic disease of apple (*Malus domestica*). *Viruses*, 15(3), 795. DOI: <https://doi.org/10.3390/v15030795>
- Pavlović, M., Radoičić, J., Milanović, M. (2020) Profitability analysis of apple production in the Republic of Serbia. *Ekonomika poljoprivrede*, 67 (3), 817-830. DOI: <https://doi.org/10.5937/ekoPolj2003817P>
- Petrzik, K. (2005) Capsid protein sequence gene analysis of Apple mosaic virus infecting pears. *European Journal of Plant Pathology*, 111, 355-360. DOI: <https://doi.org/10.1007/s10658-004-4889-7>
- Petrzik, K., Lenz, O. (2002) Remarkable variability of apple mosaic virus capsid protein gene after nucleotide position 141. *Archives of Virology*, 147 (7), 1275-1285.
DOI: <https://doi.org/10.1007/s00705-002-0819-1>
- Petrzik, K., Lenz, O. (2011) Apple mosaic virus in Pome Fruits. In: Hadidi, A., Barba, M., Candresse, T., Jelkmann, W., eds. *Virus and virus-like diseases of pome and stone fruits*. St Paul, AB: The American Phytopathological Society, pp. 25-28.
- Official Gazette of the Republic of Serbia (Nos. 7/2010, 22/2012, 57/2015) Rulebook on Lists of harmful organisms and the Lists of plants, plant products and regulated objects.
- Valasevich, N., Cieślińska, M., Kolbanova, E. (2015) Molecular characterization of Apple mosaic virus isolates from apple and rose. *European Journal of Plant Pathology*, 141, 839-845.
DOI: <https://doi.org/10.1007/s10658-014-0580-9>
- Wood, G. A., Chamberlain, E. E., Atkinson, J. D., Hunter, J.A. (1975) Field studies with apple mosaic virus. *New Zealand Journal of Agricultural Research*, 18 (4), 99-404.
DOI: <https://doi.org/10.1080/00288233.1975.10421067>