

**Genetic structure and evolution of Tobamoviruses infecting a variety of
agriculturally important plants in Azerbaijan**

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**Genetic structure and evolution of *Tobamoviruses* infecting a variety of
agriculturally important plants in Azerbaijan**

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Tobamoviruses, plant-infecting viruses with an ancient origin dating back to the Cretaceous period around 145–66 million years ago, are known for their remarkable resilience. These viruses, characterized by tough rod-shaped virions, have persisted for centuries in dried leaf material and have been found to remain viable for at least 140,000 years in ice cores from Greenland. Among the approximately forty known species, several pose significant threats to primary producers of specific crops, particularly those belonging to the solanaceous, brassicaceous, and cucurbitaceous families. The *Tobacco mosaic virus* (TMV), the first virus identified in this genus, evolved alongside its solanaceous hosts in the Americas. Its global dissemination was facilitated by the widespread cultivation of solanaceous plants driven by nicotine addiction and the popularity of New World crops like tomatoes and chilies. Presently, various tobamoviruses are spreading globally, causing substantial losses in agricultural production and necessitating significant biosecurity measures for containment.

New tobamoviruses continue to emerge, with some originating from wild flora and subsequently infecting cultivated plants. Tobamoviruses, a genus of plant viruses, exhibit a noteworthy impact on various crops globally, including Azerbaijan. The genetic structure of tobamoviruses comprises singlestranded, positive-sense RNA genomes. This linear genome is characterized by its simplicity, comprising approximately 6,400 to 6,700 nucleotides, encapsidated in ridged cylindrical particles about 18 nm in diameter and 300 nm long, and encodes essential proteins for the virus's replication and assembly. Their transmission mechanisms encompass modes such as seed transmission, mechanical contact, and vectors like insects. These viruses exhibit a broad host range, infecting vegetables, ornamental plants, and other essential crops crucial to Azerbaijan's agricultural sector. Noteworthy species of tobamoviruses include *Tobacco mosaic virus* (TMV), *Pepper mild mottle virus* (PMMoV), and *Tomato mosaic virus* (ToMV). Investigation of tobamoviruses at the molecular level, and understanding their modes of reproduction, transmission, and geographical distribution stands as a primary challenge in global scientific endeavors. The investigation into biodiverse tobamoviruses and pests damaging crops, diminishing their productivity and market value, holds significant importance for predicting future disease spread dynamics. The recent coronavirus pandemic has underscored the global susceptibility to rapid viral dissemination, emphasizing the formidable challenges associated with controlling and combatting such outbreaks. The evolutionary trajectory of tobamoviruses involves genetic mutations and recombination events, shaping the emergence of novel viral strains. This evolutionary process is influenced by factors such as host plants, environmental conditions, and agricultural

practices unique to the regions of Azerbaijan. Over the past few years, the convergence of genomic analysis and the advent of artificial intelligence (AI) have resulted in a substantial change in our comprehension of infectious diseases. This synergy has enhanced our ability to predict viral mutations, potentially foreseeing developments that could lead to future pandemics. These resources can offer a deeper understanding of the implications of tobamovirus infections on various plants in Azerbaijan.

This work was supported by the Azerbaijan Science Foundation-Grant AEF-MCG-2022-1(42)-12/07/3-M-07.