



PHYLOGENETIC ANALYSIS OF POTYVIRUSES FROM ALLIUM PLANTS IN UKRAINE

Kyrylo Taher¹, Tetiana Shevchenko¹, Prevor Dmytro¹

¹ Virology Department, ESC «Institute of Biology and Medicine», Taras Shevchenko National University of Kyiv, 64/13 Volodymyrska str., Kyiv 01601, Ukraine

INTRODUCTION

Garlic and onion are crucial agricultural crops in Ukraine. However, they are threatened by viral pathogens, specifically Leek yellow stripe virus (LYSV) and Onion yellow dwarf virus (OYDV). Comprehensive understanding of the genetic diversity of these viruses, in relation to their host specificity and geographical distribution, is vital for developing robust strategies for their control and prevention [1].

METHODS

In this study, samples of garlic, onion, and other types of Allium plants from Vinnytsia, Kyiv, Cherkasy, Zaporizhzhya, and Poltava regions were analyzed using DAS-ELISA and RT-PCR, employing primer sets to coat protein [2]. For the phylogenetic analysis, nucleotide sequences of the coat protein of the viruses from various countries were acquired from the Genbank "NCBI Virus" database. Sequence alignment was performed using the MAFFT algorithm (version 7.520). Sequence editing, alignment analysis, and the determination of the optimal nucleotide substitution model were conducted in MEGA XI software. The construction of the phylogenetic tree utilized the Neighbor Joining method in MEGA XI. Sequence gaps were treated as missing data. Tree topology was validated through bootstrap analysis based on 10,000 replicates, and graphical editing of the trees was also done in MEGA XI.

RESULTS AND CONCLUSION

Our phylogenetic analysis revealed that the Ukrainian OYDV isolates formed a distinct clade, closely related to Italian isolates and specifically infecting onions, indicating the possible existence of a unique Ukrainian strain or variant of OYDV. The LYSV isolates were found to belong to the geographically diverse N-type LYSV, which is commonly associated with garlic crops [3]. Interestingly, these LYSV isolates were more closely related to isolates from geographically distant countries like China, USA, Italy, and Serbia than to those from neighboring regions, potentially indicating virus transmission from other continents via extensive trade.

The study highlights the presence of LYSV and OYDV in garlic and onion crops across multiple regions in Ukraine, revealing potential geographical and host-specific variations of these viruses. These findings will serve as a foundation for future studies, aiding in the development of effective strategies to control and prevent these diseases. They will also contribute to preserving the productivity of Ukraine's critical Allium crops, supporting economic stability and food security in the country.

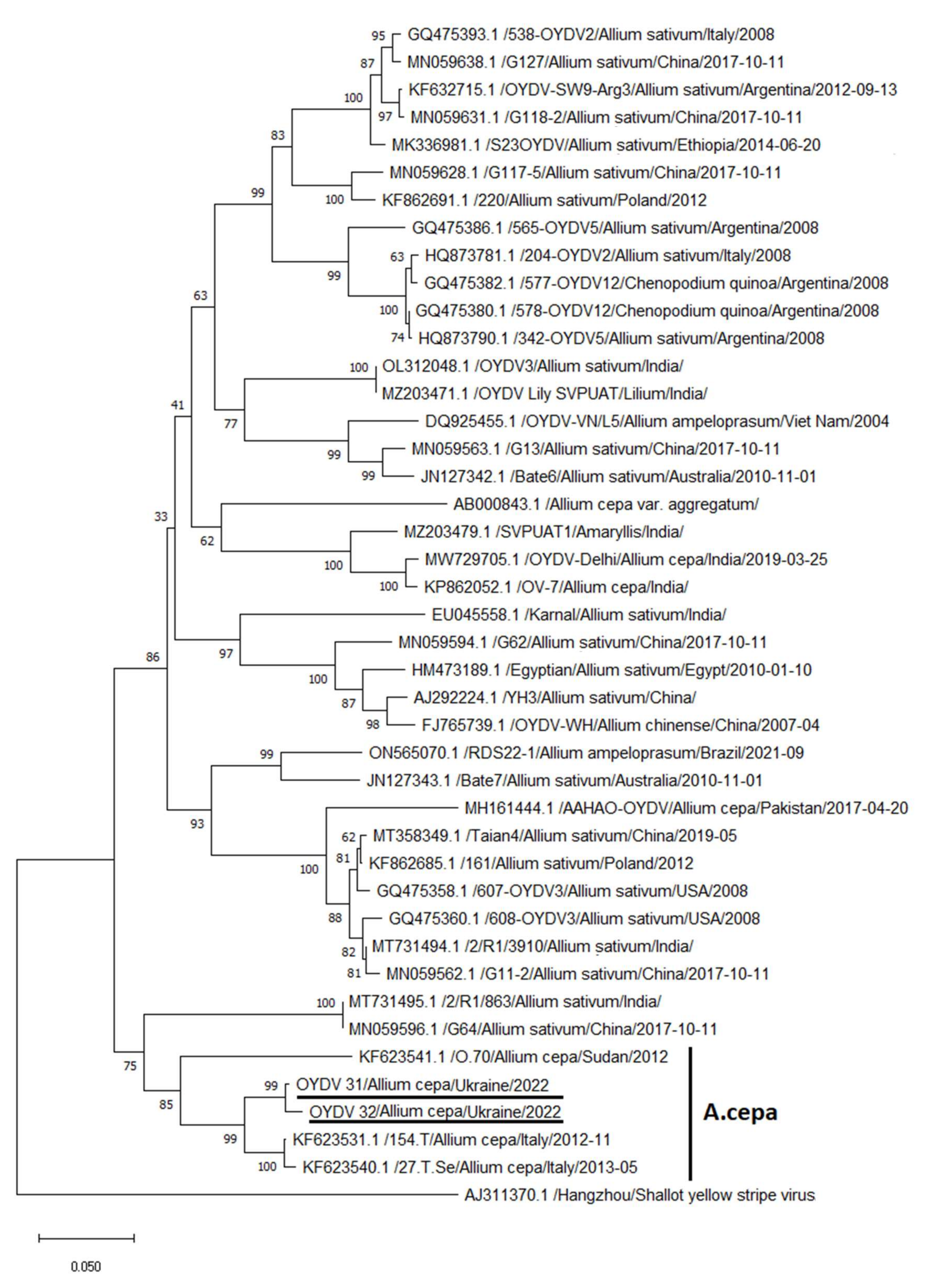
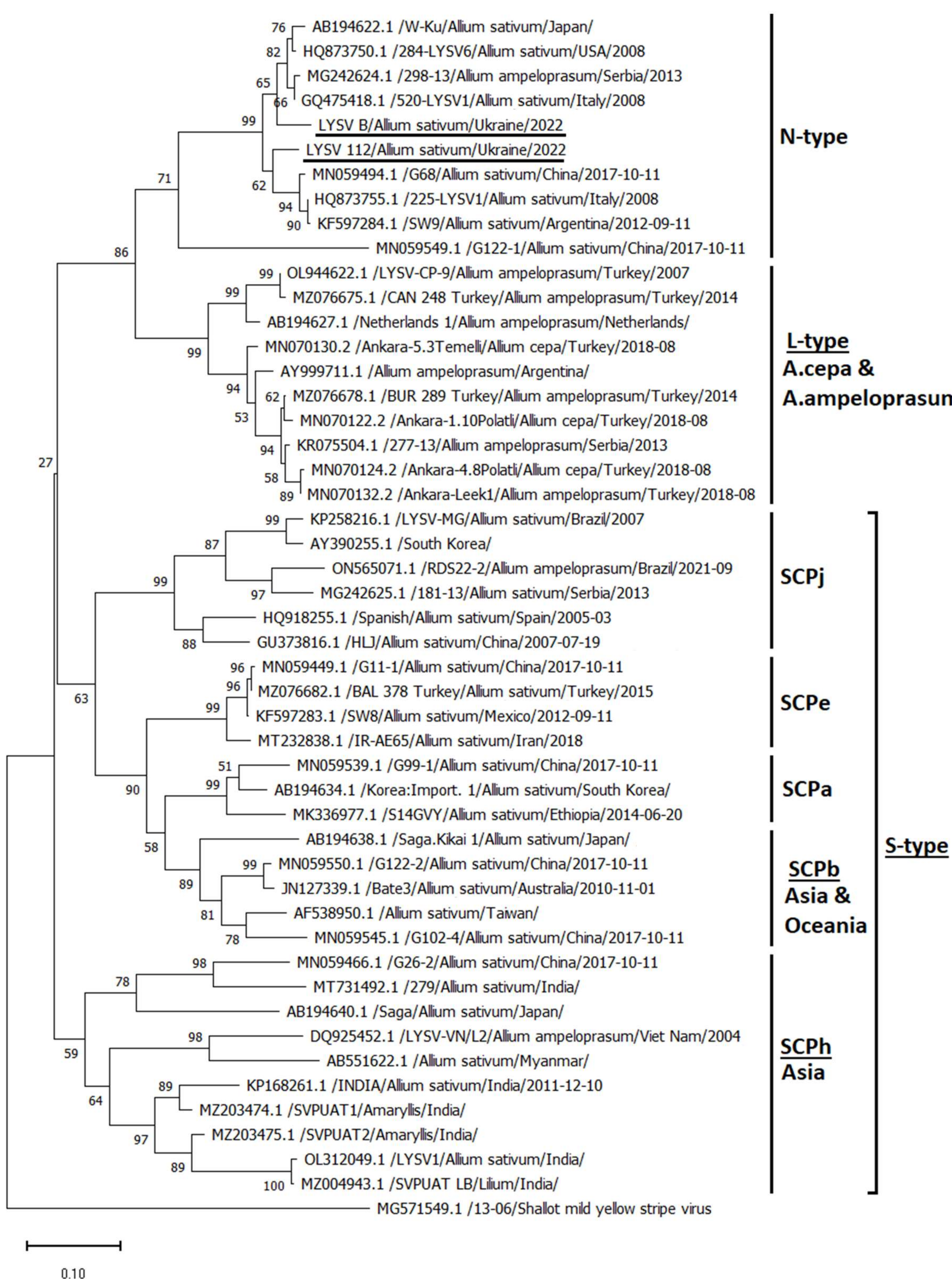


Fig. 1. Phylogenetic analysis of the nucleotide sequence of the LYSV coat protein gene. The Shallot mild yellow stripe virus isolate was used as an outgroup.

Fig. 2. Phylogenetic analysis of the nucleotide sequence of the OYDV coat protein gene. The Shallot yellow stripe virus isolate served as an outgroup.

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