

# Molecular characterization of *Nerine latent carlavirus* (NeLV)

Khanh Pham<sup>1</sup>, Miriam Lemmers<sup>1</sup>, Chin-An Chang<sup>2</sup>, Ellis Meekes<sup>3</sup> and Maarten de Kock<sup>1</sup>

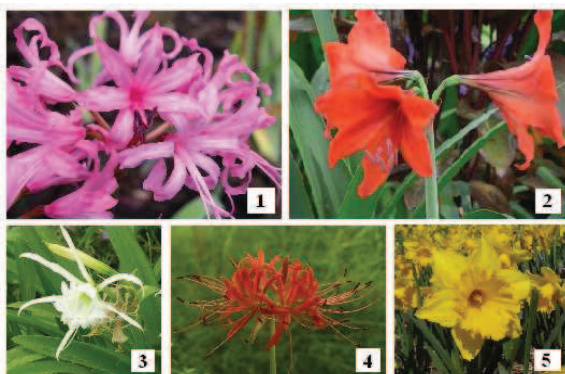
<sup>1</sup> Wageningen UR - Applied Plant Research, P.O. Box 85, 2160 AB Lisse, The Netherlands

<sup>2</sup> Chaoyang Technology University, Wufeng, Taichung 413, Taiwan

<sup>3</sup> Netherlands Inspection Service for Horticulture, P.O. Box 40, 2370 AA Roelofarendsveen, The Netherlands

## Introduction

*Nerine latent virus* (NeLV) was first identified in *Nerine bowdenii* and subsequently described by the ICTV. NeLV was also reported in other *Nerine* and *Hippeastrum* species (Figure 1). The synonym for *Nerine latent virus* is *Hippeastrum latent virus*. Antiserum against this virus was prepared by IPO-Wageningen and has been used for diagnostic purposes by different institutes in The Netherlands and over the world.



**Figure 1:** Bulbous ornamentals which are host species for NLV: *Nerine* (1), *Hippeastrum* (2), *Ismene* (3), *Lycoris* (4) and *Narcissus* (5).

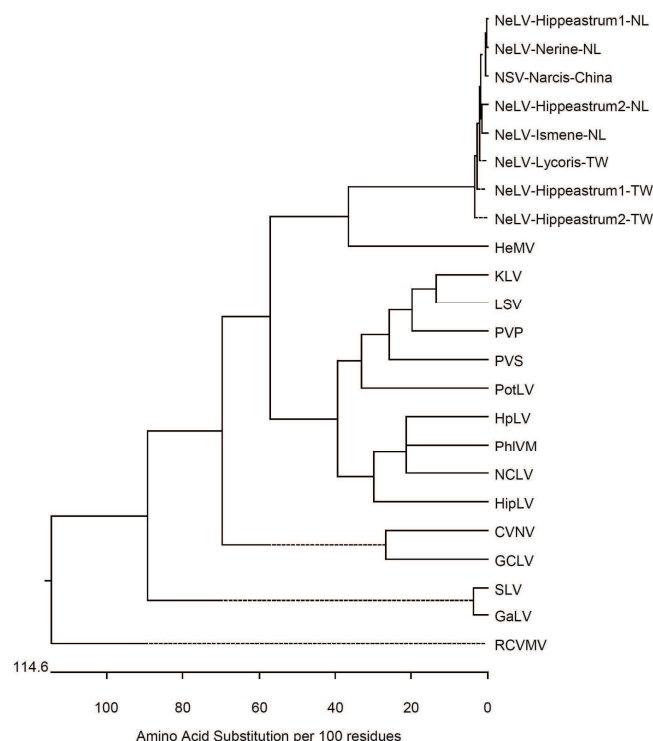
## Characterization of Dutch isolates

Generic carlavirus primers were used in RT-PCR to amplify the partial viral replicase gene of several NeLV isolates from *Nerine*, *Hippeastrum* and *Ismene*. The nucleotide sequences of the fragments have been determined and were compared with carlavirus sequences present in the NCBI database. Nucleotide sequence and phylogenetic analyses showed that no significant variations exist between the three NeLV isolates that have been found. The NeLV isolates that were studied shared more than 92% identity with *Narcissus symptomless virus* (NSV, Genbank NC\_008552) from *Narcissus pseudonarcissus* from China and only 70% with *Hippeastrum latent virus* (HipLV, Genbank NC\_011540) from *Hippeastrum*.

Using specific primers based on the sequence of the NSV, the complete Cp gene of Dutch NeLV isolates have been amplified. The sequences of the amplified fragments showed more than 97% homology with NSV whereas significant homology with *Hippeastrum latent virus* was absent.

## Characterization of Taiwanese isolates

Additionally, several Taiwanese carlavirus isolates from *Lycoris* and *Hippeastrum* were characterized based on their coat protein sequences. Also these isolates were almost identical to the Dutch NeLV isolates and the published NSV sequence (Figure 2).



**Figure 2:** Phylogenetic relationship of Dutch (NL) and Taiwanese (TW) *Nerine latent virus* isolates and other viruses of the genus Carlavirus based on the ORF5 (coat protein). Multiple sequence alignment and phylogenetic tree was generated using DNASTAR Lasergene 8 software.

## Conclusion

Based on high identity of both the partial replicase gene and the complete coat protein gene sequences, we can conclude that the *Narcissus symptomless virus* (NSV) that was identified in *Narcissus* in China should be considered as an isolate of NeLV. The carlavirus from *Hippeastrum* (NC\_011540) is probably a distinct carlavirus that is not related to the NeLV isolates from *Hippeastrum* which were studied.