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## Corrigendum



Corrigendum to 'A new tetra-segmented splipalmivirus with divided RdRP domains from *Cryphonectria naterciae*, a fungus found on chestnut and cork oak trees in Europe' [Virus Research 307 (2022) 198606]

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The authors regret that although the original sequence data were correct, there were errors in the frame of CnSpV1 RNA3 ORF3-2 relative to ORF3-1 in Figs. 2 and S3, and associated text. Modified versions of the figures, legends and text are below.

The authors would like to apologise for any inconvenience caused. **Corrected text** 

The second open reading frame, ORF3-2, relative to the first one ORF3-1 on Cryphonectria naterciae splipalmivirus 1 (CnSpV1)

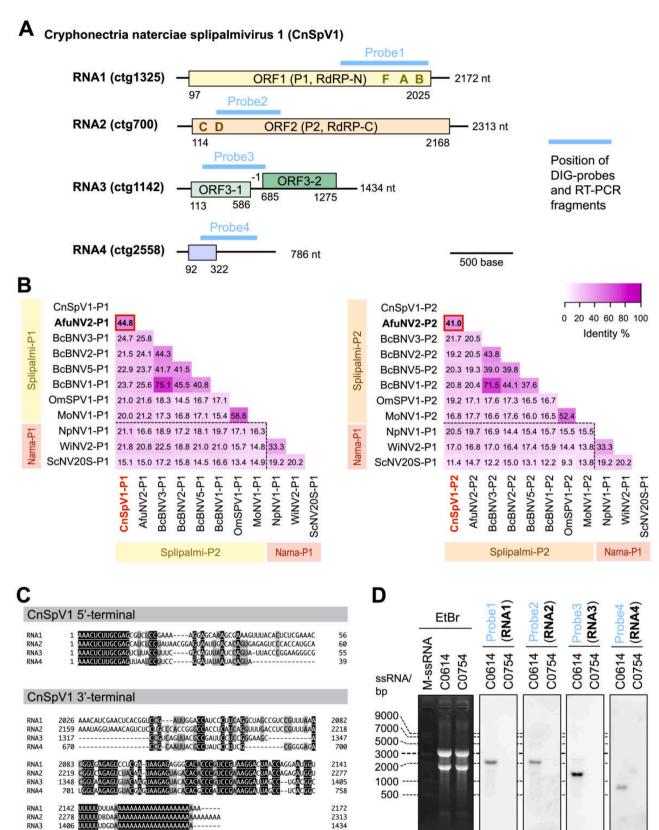
(GenBank: LC634421.1) should be situated "-1" not "-2" (Figs. 2 and Fig. S3). For RNA3 of Aspergillus fumigatus narnavirus 2 (AfuNV2) (GenBank: LC553686.1), the relative frame for ORF5 to ORF3 should be "-2" not "-1" (Fig. S3). Consistently, a hypothetical slippery sequence for -1 frameshifting [X\_XXY\_YYZ (Atkins et al., 2016)], C\_CCA\_AAT at nucleotide position 559-565, upstream of the stop codon of ORF3-1 on CnSpV1-RNA3 is observed (Fig. S3A). A prediction of RNA secondary structure by SPOT-RNA (Singh et al., 2019) suggests that this putative

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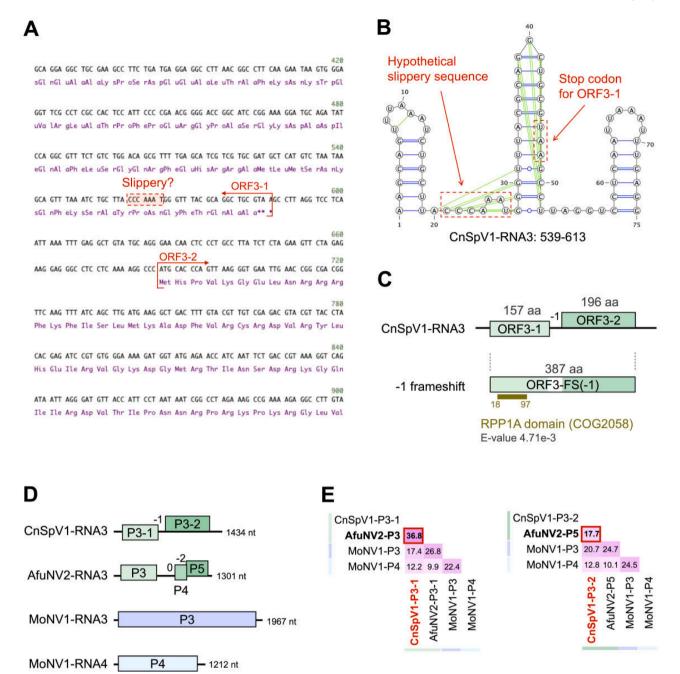
DOI of original article: https://doi.org/10.1016/j.virusres.2021.198606.

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Corrected Fig. 2. Genome organization of Cryphonectria naterciae splipalmivirus 1 (CnSpV1). See <a href="https://doi.org/10.1016/j.virusres.2021.198606">https://doi.org/10.1016/j.virusres.2021.198606</a> for the figure legend.

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Corrected Fig. S3. Hypothetical proteins encoded by CnSpV1-RNA3. (A) The nucleotide sequence around the intergenic region of the two hypothetical ORFs on CnSpV1 RNA3. The sequence was visualized in GENETYX-MAC version 20.1.0. (B) A putative secondary structure around the ORF3-1 stop codon on CnSpV1-RNA3 (nucleotide position 539-613). The structure was predicted by the stand-alone version of SPOT-RNA (https://github.com/jaswindersingh2/SPOT-RNA). (C) A hypothetical frameshift product encoded by CnSpV1-RNA3. The schematic diagram for the putative -1 frameshift products from CnSpV1-RNA3 was shown below its genome map. The hypothetical frameshift products contained the RPP1A (ribosomal protein L12E/L44/L45/RPP1/RPP2, COG2058) domain at the amino acid positions 18-97 with an e-value 4.71e<sup>-3</sup>. The conserved domain was predicted by DELTA-BLAST search of non-redundant protein sequences (nr) provided by NCBI. (D) Schematic representation of the splipalmiviruses non-RdRP-encoding segments. (E) Pairwise percent identity matrix of the non-RdRP-proteins of splipalmiviruses. Virus full names and accession numbers of the proteins are listed in Table S2. The analysis was performed as described in the legend for Fig. 2B. The left panel shows the comparison between CnSpV1-P3-2 and AfuNV2-P5 with MoNV1 proteins.

0 20 40 60 80 100 Identity %

500 base

slippery and following sequence could form a pseudoknot-like structure (Fig. S3B). The -1 frameshift at this site could generate a fusion protein from ORF3-1 and ORF3-2 (Fig. S3C). This fusion protein product contains a putative ribosomal protein domain at the N-terminal part (Fig. S3C).

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