

Sugar beet yellowing viruses in Belgium: insights from two complementary field surveys

Ellen A. Everaert (0000-0001-8504-3517)¹, Pierre Hellin (0000-0003-4777-6036)², Isabelle Stockmans (0009-0003-3557-7192)³, Annelies Haegeman (0000-0002-8192-5368)¹, Margot Beelaert (0009-0007-3685-0313)², Louis Hautier (0000-0002-6390-300X)², Yoika Foucart¹, Thomas Goedefroit¹, Maaïke Heyneman¹, Chloé Dufrane (0009-0002-2715-7043)³, André Wauters (0009-0009-6312-8064)³, Stéphan Steyer (0000-0001-6679-1296)², Kris De Jonghe (0000-0003-1763-5654)¹

¹Flanders Research Institute for Agriculture, Fisheries and Food (ILVO), Plant Sciences Unit, Merelbeke-Melle, 9820, Belgium

²Walloon Agricultural Research Center (CRA-W) - Life Sciences Department – Plant and Forest Health Unit, Rue de Liroux 2-4, Gembloux, 5030, Belgium

³Royal Belgian Institute for Beet Improvement (IRBAB-KBIVB), Tienen, 3300, Belgium

*Corresponding author: E.A. Everaert; E-mail: ellen.everaert@ilvo.vlaanderen.be

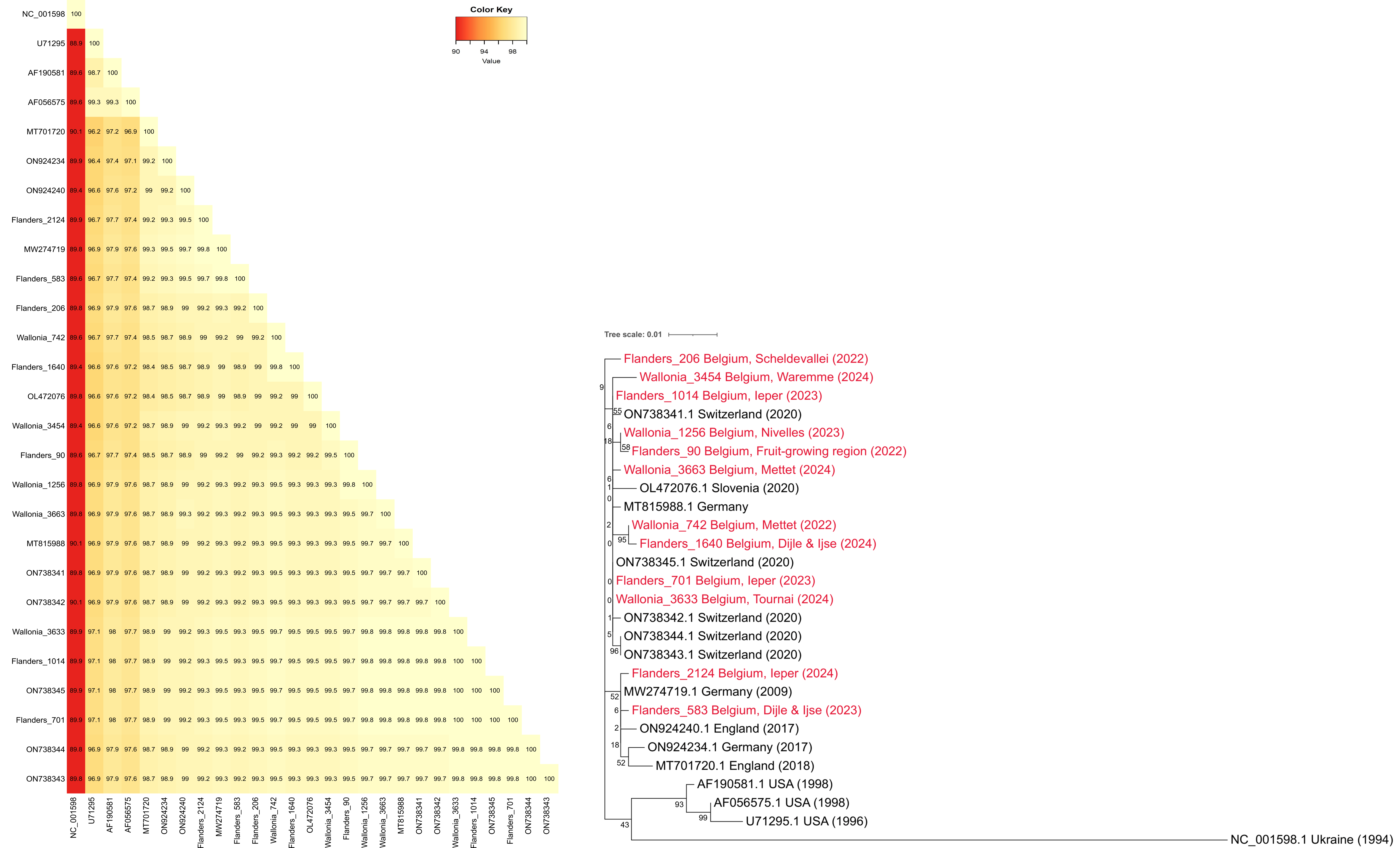


Fig 1. Pairwise identity matrix (left) and phylogenetic tree (right) based on coat protein (CP) sequences of Belgian beet yellows virus (BYV) isolates and isolates retrieved from public databases. The phylogenetic tree was constructed using the HKY+I nucleotide substitution model. Branch support was assessed using 1,000 bootstrap replicates. Bootstrap support values are indicated at the nodes. Belgian isolates are highlighted in red.

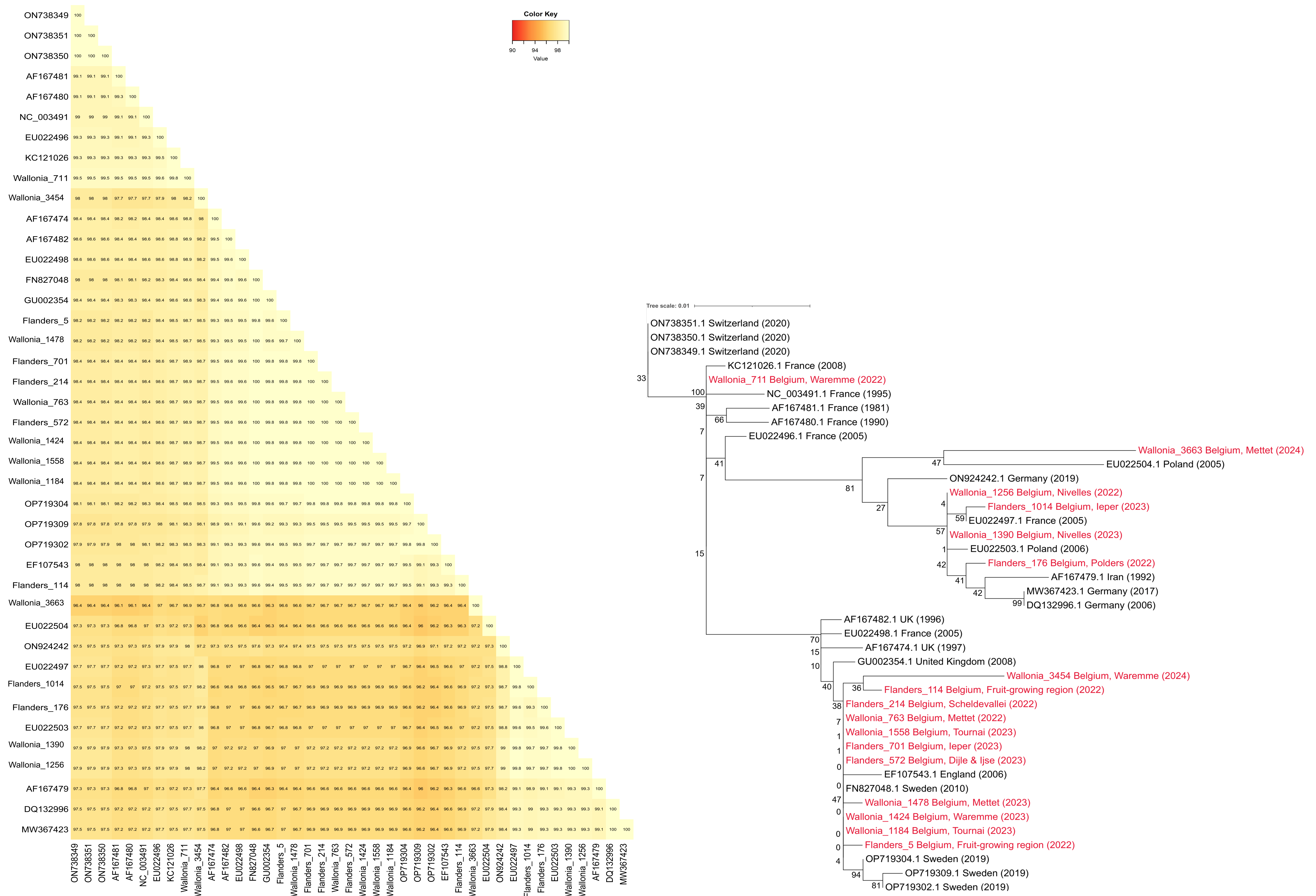


Fig 2. Pairwise identity matrix (left) and phylogenetic tree (right) based on coat protein (CP) sequences of Belgian beet mild yellowing virus (BMV) isolates and isolates retrieved from public databases. The phylogenetic tree was constructed using the HKY+I nucleotide substitution model. Branch support was assessed using 1,000 bootstrap replicates. Bootstrap support values are indicated at the nodes. Belgian isolates are highlighted in red.

