



Genetic characterization of the HA and NA gene segments of a HPAI H5N8 virus identified in Bulgaria in June 2020

Phylogenetic analysis

The HPAI H5N8 virus A/chicken/Bulgaria/380-1_20VIR3542-1/2020 was collected in Bulgaria on 03/06/2020 in Plovdiv region.

The HA and NA gene segments of this H5N8 virus cluster together and with H5N8 viruses circulating in Bulgaria in 2017-2020. In particular, it is highly related (99.7% and 99.4% similarity for the HA and NA genes, respectively) to the H5N8 virus A/chicken/Bulgaria/217_20VIR1724-1/2020 from outbreak 7 (layer hens) collected from Plovdiv in March 2020 (Figures 1-2).

Molecular analysis

A potential additional glycosylation site was identified in the NA protein of the H5N8 virus A/chicken/Bulgaria/380-1_20VIR3542-1/2020 in position 411-413 (ELS to NLS) as previously observed for A/chicken/Bulgaria/217_20VIR1724-1/2020 (outbreak 7).



Fig.1. Maximum Likelihood phylogenetic tree of the **HA gene** (IQ-TREE v.1.6.8). The new Bulgarian sequence is marked in blue, the other H5N8/H5N2 viruses from Bulgaria are marked in pink. Ultra-fast bootstrap supports higher than 80% are indicated next to the nodes.

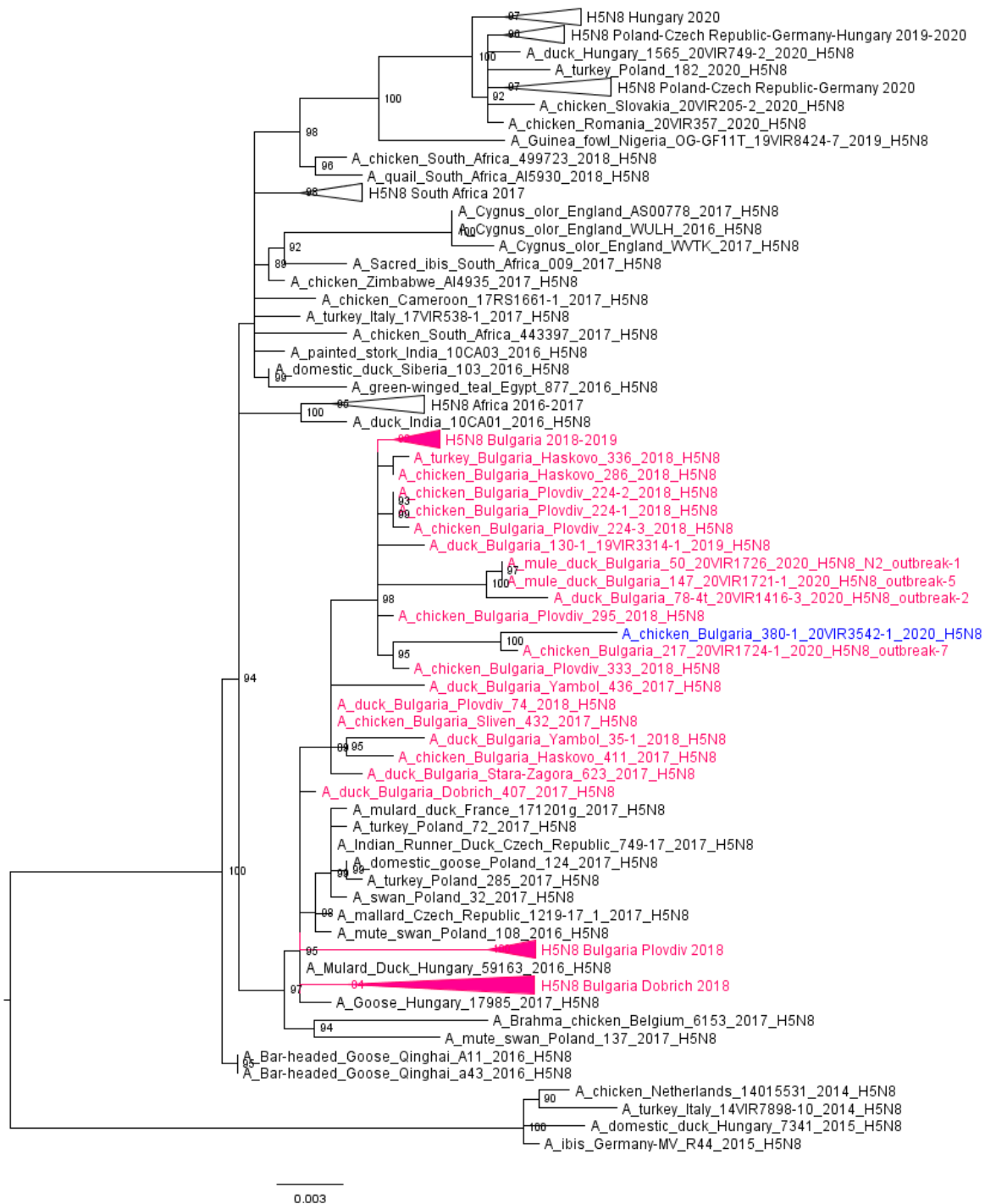


Fig.2. Maximum Likelihood phylogenetic tree of the **N8 gene** (IQ-TREE v.1.6.8). The new Bulgarian sequence is marked in blue, the other H5N8/H5N2 viruses from Bulgaria are marked in pink. Ultra-fast bootstrap supports higher than 80% are indicated next to the nodes.