

Novel Variants of *Avian Paramyxoviruses 13* in Wild Migratory Waterfowl Reveals 2 Low Evolutionary Rate

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Research Article

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Abstract

Avian paramyxovirus 13 (APMV-13), formerly known as Avian orthoavulavirus 13, is found scatteredly in wild birds around the world. Although four complete genome sequences of APMV-13 had been identified since the first discovery in Japan in 2003, the information available on the genetic variation and biological characteristics of APMV-13 is still limited. In the present study, we isolated six APMV-13 strains from fecal samples of wild migratory waterfowls during annual (2013-2018) viral surveillance of wild bird populations from wetland in China. The phylogenetic analyses showed that they had very close relationship in HN and F genes. The molecular clock estimations also showed a low evolutionary rate of APMV-13. However, there are obvious sequence differences among these strains. Bean goose/Hubei/V97-1/2015 is 1,953 nt in size (ORF, 1, 776 nt), which is a unique size and longer than other reported APMV-13 strains. Additionally, Swan goose/Hubei/VI49-1/2016 has four repeats of conserved sequences "AAAAAT" in the 5'-end trailer, which is unprecedented in the APMV-13. These findings reveal the existence of novel variants within APMV-13, which highlights the importance of continuous monitoring the specific species of APMVs.

Full Text

This preprint is available for [download as a PDF](#).

Figures

▲ APMV-13/Wild goose/Hubei/2015/V93-1	15781	CTATATTTTTAAAACACTGTAAGTTTATAAAAAAATAAAAAATAAAAAATAAAAAACAGGGAT	15840
▲ APMV-13/Swan goose/Hubei/2015/V104-2	15781	CTATATTTTTAAAACACTGTAAGTTTATAA-----AAAAATAAAAAATAAAAAATAAAAAACAGGGAT	15840
▲ APMV-13/Bean goose/Hubei/2015/V85-1	15781	CTATATTTTTAAAACACTGTAAGTTTATAA-----AAAAATAAAAAATAAAAAATAAAAAACAGGGAT	15840
▲ APMV-13/Bean goose/Hubei/2015/V97-1	15781	CTATATTTTTAAAACACTGTAAGTTTATAA-----AAAAATAAAAAATAAAAAATAAAAAACAGGGAT	15840
▲ APMV-13/Bar-headed goose/Hubei/VI82-1	15781	CTATATTTTTAAAACACTGTAAGTTTATAA-----AAAAATAAAAAATAAAAAATAAAAAACAGGGAT	15840
▲ APMV-13/Goose/Kazakhstan/5751/2013	15781	CTATATTTTTAAAACACTGTAAGTTTATAA-----AAAAATAAAAAATAAACCCAGGGAT	15834
▲ APMV-13/White-fronted goose/Ukraine/2011	15781	CTATATTTTTAAAACACTGTAAGTTTATAA-----AAAAATAAAAAACAGGGAC	15828
▲ APMV-13/Goose/Shimane/67/2000	15781	CTATATTTTTAAAACACTGTAAGTTTATAA-----AAAAATAAAAAACAGGGGA	15828
		*****	***** ****

Figure 1

Alignment of the trailer regions of APMV-13 isolates. The asterisks indicate identities and short-terms indicate difference. The triangles indicate the existing known sequences.

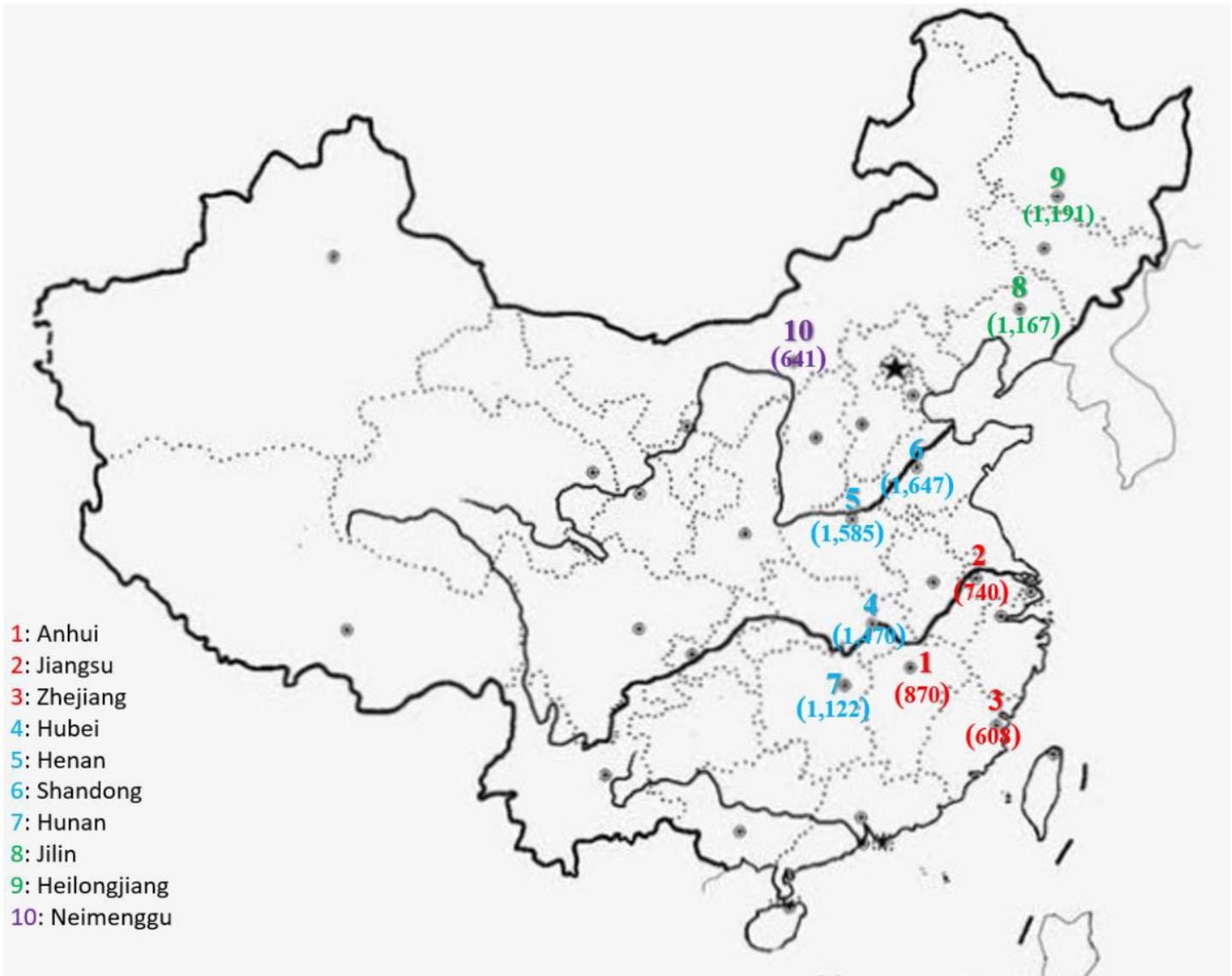
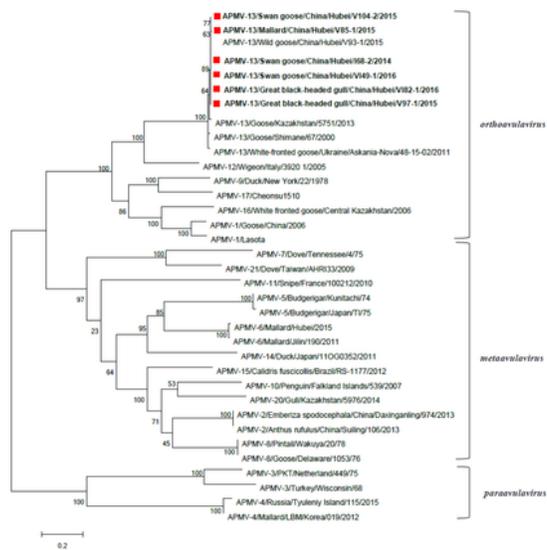
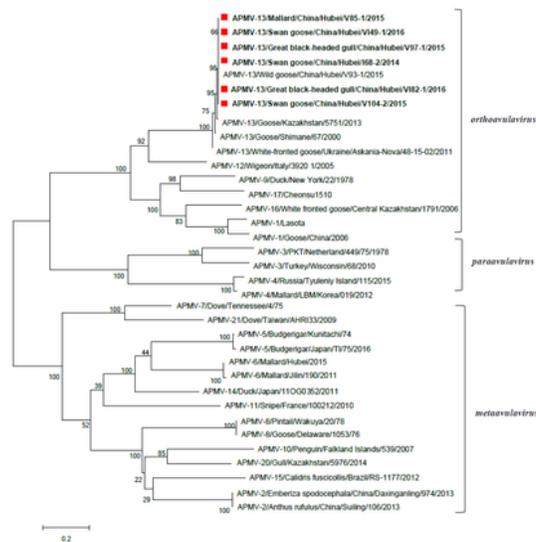


Figure 2

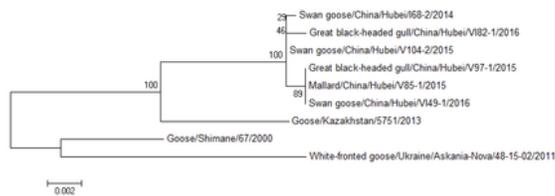
Sample collection sites in China. Sampled provinces are indicated by colors. Different colors represent the different regions of sample collection. The number of samples for each region have been shown in parentheses. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.



A



B



C

Figure 3

Phylogenetic analysis of the entire F genes (A) and HN genes of APMV-13 and other viruses of species. Three genera (Metaavulavirus, Orthoavulavirus, and Paraavulavirus) exist in the Avulavirinae subfamily, including 21 described species (1 to 20), as revealed by genetic relationship of the entire F genes (A) and HN genes (B) of all viruses within Avulavirinae. The red solid squares represent the isolates in this study. And the genetic relationship of HN genes (C) of all APMV-13 isolates are shown in figure 3C.

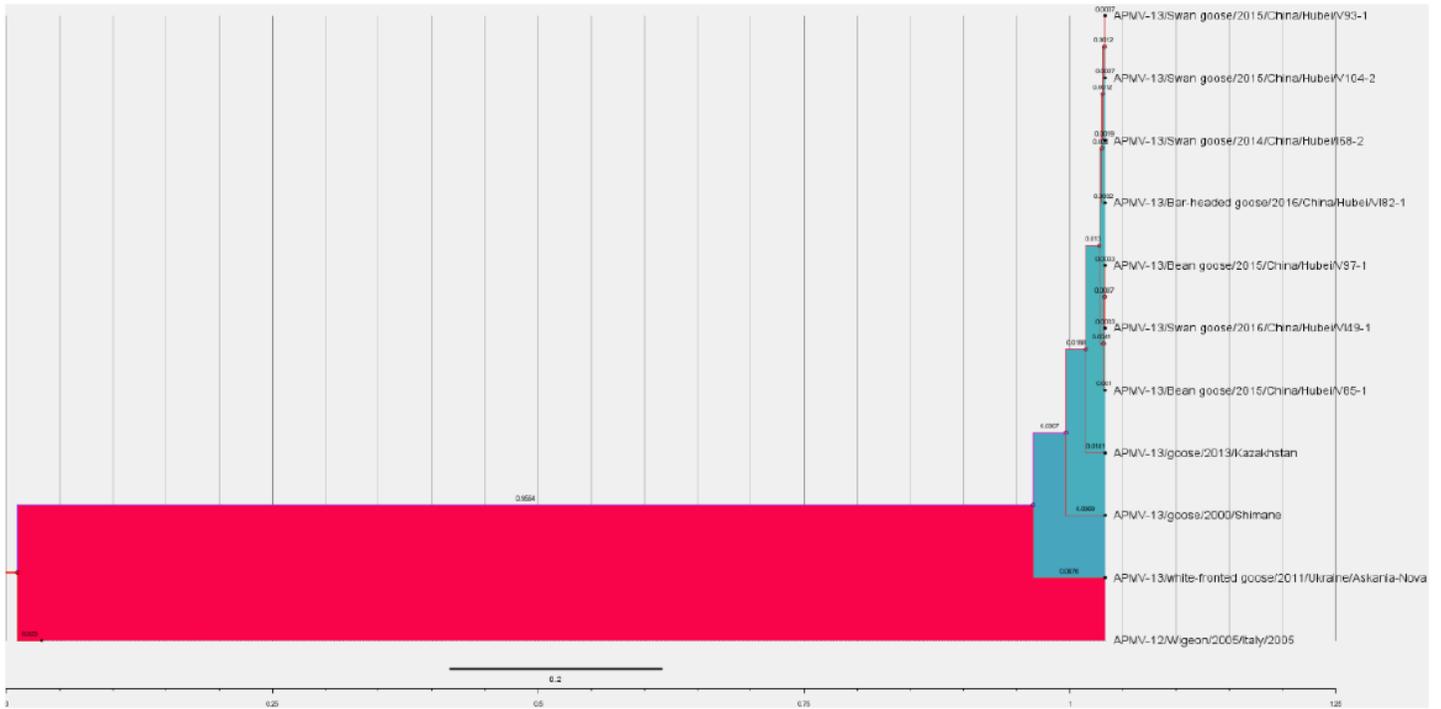


Figure 4

Bayesian phylogenetic trees of APMV-12 and APMV-13 isolates based on the HN genes. The Bayesian posterior probabilities and maximum likelihood bootstrap are indicated above the branches (Bayesian posterior/bootstrap). The distance unit is substitutions/site.