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Genetic Characteristics of the Avian Paramyxovirus Type 4 Strain Isolated from *Uria Aalge* on the Tyuleniy Island (Okhotsk Sea)

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Abstract: As a part of the monitoring and studying influenza viruses Program we collect samples of cloaca swabs of waterfowl in the Far East. In 2015, during the expedition to the Tyuleniy Island (Okhotsk Sea) we collected a sample that contained Avian paramyxovirus type 4 (APMV-4) (*Mononegavirales*, *Paramyxoviridae*, *Avulavirus*) strain. This virus has been isolated from a seabird Common guillemot (*Uria aalge*) (*Charadriiformes*, *Alcidae*). Isolated strain APMV-4/*Uria aalge*/Russia/Tyuleniy Island/115/2015 was deposited into Russian Collection of East Asia Viruses and investigated by various laboratory methods. Genetic and laboratory tests showed that the strain we identified was apathogenic. The nucleotide sequence of complete genome was obtained applying the *Illumina* platform and deposited in GenBank database (KU601399.1).

APMV-4/*Uria aalge*/Russia/Tyuleniy Island/115/2015 has molecular characteristics usual for other avuloviruses: enveloped virion with negative sense single-stranded RNA genome containing 15 054 nucleotides. The proteins are encoded in a certain order: 3'-NP-P-M-F-HN-L. The array of the RNA nucleotide chain, in which the protein-coding regions are noted, is as follows: NP (nucleocapsid protein) is recorded in coding sequence (CDS) 116..1489 with transcribed length 457 aa; P (phosphoprotein) CDS 1662..2843 with 393 aa; M (matrix protein) CDS 3091..4203 with 370 aa; F (fusion protein) CDS 4394..6094 with 566 aa; HN (hemagglutinin-neuraminidase) CDS 6329..8026 with 565 aa; L (large polymerase protein) CDS 8299..14934 with 2211 aa. The F-protein of the isolated strain contains a restriction site on the segment ¹¹⁶DIQPR¹²⁰ ↓, which is typical for all Avian avulavirus 4 strains.

Comparison with other 13th full-length sequences that are currently available in GenBank showed the close relationship of the isolated strain with the strain APMV-4/Egyptian goose/South Africa/N1468/2010. Statistical data comparing the nucleotide sequences of the F-protein with other APMV-4 strains also revealed the affinity of the APMV-4/*Uria aalge*/Russia/Tyuleniy Island/115/2015 with APMV-4 strains isolated in Ukraine, Japan, China and Korea.

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