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PRIMER SET DESIGNING FOR THE COMPLETE GENOME SANGER - SEQUENCING OF NEWCASTLE DISEASE VIRUS

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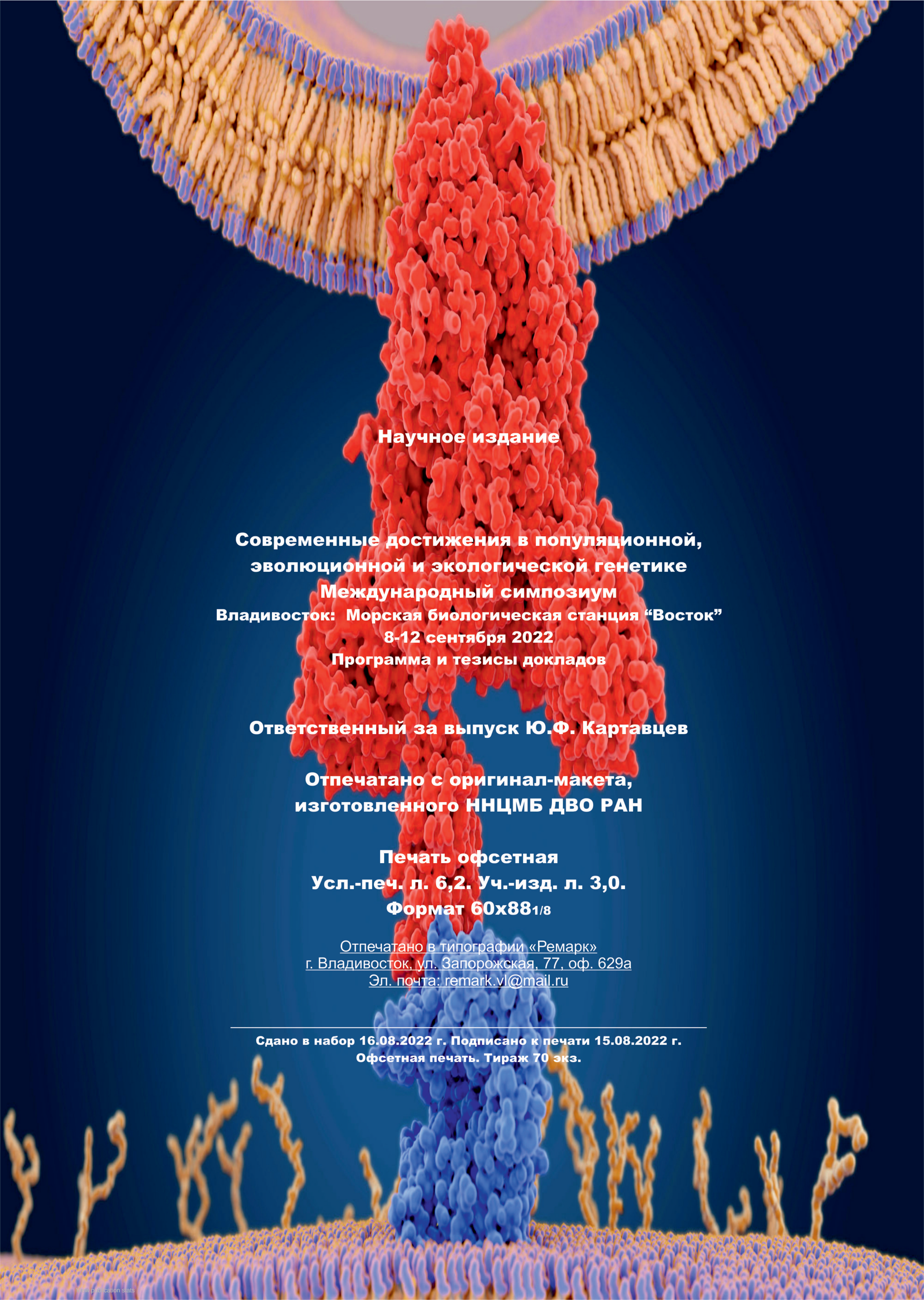
Newcastle disease virus (NDV), or Avian paramyxovirus type 1 (Paramyxoviridae, Avulavirinae: *Orthoavulavirus*, Newcastle antigenic complex), is the etiological agent of the disease of the same name, causing epizootics with a high mortality rate in bird populations. The NDV genome is represented by single-stranded RNA (15 kb) of negative polarity and is divided into 18 genotypes and a number of subgenotypes (Ia-c, II, III, IV, Va-d, VIa-h, VIIa-i, VIII, IX, X, XI, XII, XIIIa-c, XIVa-b, XV, XVI, XVIIa-b, XVIIIa-b), which differ in nucleotide sequences in the genome, virulence level and geographical distribution. The natural reservoir of NDV are wild birds of both aquatic and terrestrial ecological complex. From wild populations, NDV penetrates into poultry populations. The virus is transmitted by droplet-air and oral-fecal route.

Genome sequencing is the most reliable method for identifying, determining some biological properties and forming hypotheses about the origin of pathogenic microorganisms. At the same time, Sanger sequencing, which requires a system of primers that flank overlapping nucleotide sequences, remains the most technologically and economically accessible approach to viral sequencing. Several sequencing schemes are known for NDV, but it should be taken into account that the high degree of genetic variability of this virus requires the development of region-specific primer systems. This paper describes such a system verified for NDV strains isolated from agricultural and wild birds in Primorsky Krai.



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