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NDV

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Identification and genomic sequence analysis of an Avian Paramyxovirus serotype 4 (APMV-4) isolated from Egyptian geese (*Alopochen aegypticus*) in South Africa

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Ten serotypes of Avian Paramyxoviruses (APMV 1-10) have been described to date. Some of these, for example Newcastle disease (APMV-1) cause serious disease in poultry. APMV -2, -3, -6 and -7 have been associated with milder disease in poultry and APMV-5 is known to cause disease in wild birds, but APMV -4, -8, -9 and -10, isolated from healthy wild birds, have not been associated with disease in poultry thus far. A paramyxovirus isolated from wild Egyptian geese in South Africa was identified as APMV-4 by RT-PCR and sequence analysis. This is the first report of APMV-4 in Africa and we present results of genomic sequence analysis.

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Characterization of a Newcastle Disease Virus isolate from chicken in Mexico

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The Newcastle Disease Virus (NDV) belong to the genus Avulavirus in the family Paramyxoviridae. It is a highly infectious virus that affects birds, and causing great economic loss in the poultry industry. In Mexico, the disease is present in several regions, with a high incidence of velogenic strains. We report here the genome of a strain of NDV isolated in 2005 (APMV1/chicken/Mexico/P05/2005). The virus isolated was characterized by embryonic average mortality (36 h) and intracerebral pathogenicity index (ICPI) (1.99) and was identified as a velogenic virus. This was confirmed by analyzing the cleavage site of the F protein, which reveals a high content of basic amino acids. The RNA genome has a size of 15.192 nt, and phylogenetic analysis places it as a virus belonging to genotype V. This virus is related to other NDV isolated in Mexico and other countries in America.

