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Influence of pigeon paramyxovirus type 1 (PPMV-1) surface proteins on the pathogenicity of Newcastle disease virus

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The recombinant Newcastle Disease virus (NDV) CH4 expresses the fusion (F) and hemagglutinin-neuraminidase (HN) protein of the mesogenic PPMV-1 isolate M5 in the genome background of the lentogenic NDV strain Clone 30. Despite presence of a polybasic F cleavage site motif ^{112}RRKKR*F^{117}, which is typical for virulent (mesogenic or velogenic) NDV, the intracerebral pathogenicity index (ICPI) was 0.1, unexpectedly indicating a lentogenic pathotype. Four new recombinant NDV were generated by reverse genetics to assess whether this is caused by the M5 surface proteins or parts of them within the lentogenic Clone 30 background. In two recombinants the Clone 30 surface proteins (F or HN) were substituted singly with the corresponding protein of PPMV-1 isolate M5, whereas two others express a Clone 30 F protein with the M5 polybasic cleavage site in the presence or absence of the M5 HN protein. Recombinant NDV expressing a Clone 30 F protein with the M5 cleavage site exhibited an ICPI of 1.36 which was even higher than that of the mesogenic PPMV-1 M5 (ICPI 0.9). However, recombinant NDV expressing M5 F or M5 HN proteins within the NDV Clone 30 backbone exhibited a lentogenic pathotype. These results demonstrate that lentogenic NDV can specify a polybasic F cleavage site and indicate presence of virulence determinants beyond the polybasic F cleavage site in either F and/or HN.