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Putative avian/mammalian reassortant rotavirus isolated from a pheasant (*phasanus colchicus*)E. Trojnar¹, J. Sachsenröder¹, S. Twardziok², J. Reetz¹, P. H. Otto³, R. Johne¹¹Federal Institute for Risk Assessment, Berlin, Germany²Institute for Molecular Biology and Bioinformatic, Charite, Berlin, Germany³Freidrich Loeffler Institute, Jena, Germany

Group A rotaviruses (RVAs) are an important cause of diarrhoeal illness in humans as well as in mammalian and avian animal species. Previous sequence analyses indicated that avian RVAs are only distantly related to mammalian RVAs thus reflecting some degree of host specificity. However, the genome sequences of only two avian rotavirus strains were available so far.

Here, the complete genomes of RVA strain 03V0002E10 from turkey and RVA strain 10V0112H5 from pheasant were analyzed using 454 FLX deep sequencing. Most of the genome segments were closely related to avian RVAs; however, the VP4 gene of the pheasant RVA represents a novel genotype with highest sequence identities to RVAs from pigs, dogs, and humans. This grouping is also confirmed by the branching of this gene in phylogenetic trees, thus suggesting a reassortment event between a turkey rotavirus and a so far unknown mammalian rotavirus.

Avian rotaviruses have been previously detected in mammals and vice versa, and experimental creation of a reassortant turkey RVA strain containing a VP4-gene of a simian RVA has been described earlier. However, the analysis of the pheasant strain provides the first evidence for such reassortment under field conditions. The findings suggest that avian and mammalian RVAs are capable of exchanging genetic material under certain circumstances; thereby broadening the potential of genetic and antigenic variability among RVAs.

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