

PZOV-380**First genomic characterization of group D, F and G rotaviruses identifies terminal sequences conserved between different rotavirus groups**

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Rotaviruses are a leading cause of acute viral gastroenteritis in humans and animals. Currently, six different groups (A to E) have been defined based on antibody reactivity to the major structural protein VP6 and two additional putative rotavirus groups (F and G) have been recognized. Group A, B and C rotaviruses are found in humans and animals. In contrast, group D, F and G rotaviruses have only been detected in bird so far.

Here, the first complete genome sequence of a group D rotavirus (strain 05V0049) and nucleotide sequences of the VP6-encoding genome segment of group F (strain 03V0568) and group G (strain 03V0567) rotaviruses, all derived from chicken, are presented. The deduced amino acid (aa) sequence identities of rotavirus D varied between 12.3% and 51.7%, 11.0% and 23.1%, and 9.5% and 46.9% compared to those of group A, B and C rotaviruses, respectively. The group F rotavirus is most closely related to avian group A and D rotaviruses (36.5–39.0% aa sequence identity) and the group G rotavirus is most closely related to mammalian group B rotaviruses (48.2–49.9% aa sequence identity). Most interestingly, the terminal sequences of the genome segments are highly conserved between groups A, D and F, and between groups B and G. The findings indicate a long-term evolution of rotaviruses in two separated clades. As - among other factors - the terminal sequences determine specificity of genome segment packaging, the findings may indicate the possibility of intergroup reassortments.