

Genome Sequences of Three Turkey Orthoreovirus Strains Isolated in Hungary

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We have investigated the genomic properties of three turkey reovirus strains—19831M09, D1246, and D1104—isolated in Hungary in 2009. Sequence identity values and phylogenetic calculations indicated genetic conservativeness among the studied Hungarian strains and a close relationship with strains isolated in the United States.

Received 25 September 2015 Accepted 8 October 2015 Published 19 November 2015

Citation Dandár E, Fehér E, Bálint Á, Kísfali P, Melegh B, Mató T, Kecskeméti S, Palya V, Bányai K, Farkas SL. 2015. Genome sequences of three turkey orthoreovirus strains isolated in Hungary. *Genome Announc* 3(6):e01333-15. doi:10.1128/genomeA.01333-15.

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Avian orthoreoviruses (ARVs) belong to the genus *Orthoreovirus* in the *Reoviridae* virus family. Their genome consists of 10 double-stranded RNA segments classified into three sizes: L (large, L1 to L3), M (medium, M1 to M3), and S (small, S1 to S4). With the exception of the S1 or S4, which encode two or three partially overlapping open reading frames, all genomic segments are monocistronic (1).

ARVs and reovirus associated diseases have been detected worldwide since the middle of the last century in commercial poultry and also in different wild-living or captive-bred bird species (2–9). Turkey reovirus (TRV) infections are usually associated with different disease manifestations including arthritis, tenosynovitis, myocarditis, and/or enteric symptoms (6, 10–13).

In this study we investigated the genomic properties of three TRV field strains isolated in Hungary in 2009. The strain 19831M was isolated from a young, 14-day-old turkey with ruffled feather, pericarditis, and enteritis, while the strains D1246 and D1104 were isolated from 35-day-old and 42-week-old healthy animals, respectively. Genome sequences of strains D1246 and 19831M09 were determined with next-generation sequencing using an Ion Torrent PGM (Life Technologies), whereas Sanger sequencing was applied in the case of strain D1104. Complete genome sequences were assembled using the CLC Genomics Workbench software (<http://www.clcbio.com>). Phylogenetic analysis was performed using the MEGA6 package (14).

The genomic organization of the three Hungarian TRV strains was similar and corresponded with that of the strain Reo/PA/Turkey/22342/13 isolated in the United States. The complete genome of D1104 was 23,484 bp long. Sequence termini could be determined for most of the segments except for L2 of 19831M and S3 and S4 of D1246. Each of the Hungarian TRVs encoded 12 proteins (λ A, 1,293 amino acids (aa) in length; λ B, 1,259 aa; λ C, 1,285 aa; μ A, 732 aa; μ B, 676 aa; μ NS, 635 aa; σ A, 416 aa; σ B, 367 aa; σ C, 326 aa; σ NS, 367 aa; p10, 99 aa; and p17, 150 aa).

The genome sequences of the three strains were most similar to

each other (99.2 to 100% nucleotide and 98.2 to 100% aa identity) and were closely related to turkey strains isolated in the United States. In all gene phylogenies, the three reovirus strains were most closely related to each other and belonged to the same monophyletic group. In most gene phylogenies, the host specific evolution of the turkey, chicken, and waterfowl ARVs was evident; the only apparent exception was the gene-encoding protein μ B, where chicken and turkey origin ARVs and also waterfowl origin “novel” reovirus strains clustered together, suggesting possible reassortment events in the past. In the μ B gene phylogeny, the Hungarian turkey origin reovirus strains grouped together with the AVS-B (chicken) and TARV-MN4 and TERV-MN5 (turkey) strains.

As far as we know, 19831M09, D1246, and D1104 are the first characterized near-complete genomic TRV sequences from Europe. Further studies are needed to uncover the evolution and diversity of TRVs.

Nucleotide sequence accession numbers. The genome sequences of TRV strains 19831M09, D1246, and D1104 have been deposited in GenBank under accession numbers [KR997899](https://www.ncbi.nlm.nih.gov/nuccore/KR997899) to [KR997908](https://www.ncbi.nlm.nih.gov/nuccore/KR997908), [KR997909](https://www.ncbi.nlm.nih.gov/nuccore/KR997909) to [KR997918](https://www.ncbi.nlm.nih.gov/nuccore/KR997918), and [KR997919](https://www.ncbi.nlm.nih.gov/nuccore/KR997919) to [KR997928](https://www.ncbi.nlm.nih.gov/nuccore/KR997928), respectively.

ACKNOWLEDGMENTS

Our work was supported by the Momentum Program of the Hungarian Academy of Sciences and the OTKA K108727 grant of the National Scientific Research Fund of Hungary. E.F. was supported by the Bolyai Scholarship Programme.

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