

ICTV Virus Taxonomy Profile: Matonaviridae 2022

Annette Mankertz^{1,*}, Min-Hsin Chen², Tony L. Goldberg³, Judith M. Hübschen⁴, Florian Pfaff⁵, Rainer G. Ulrich⁶ and ICTV Report Consortium

Abstract

The family *Matonaviridae* comprises enveloped viruses with positive-sense RNA genomes of 9.6–10kb. The genus *Rubivirus* includes rubella virus (species *Rubivirus rubellae*) infecting humans, ruhugu virus (species *Rubivirus ruteetense*) infecting bats and rustrela virus (species *Rubivirus strelense*) infecting rodents and zoo animals. Rubella virus is spread via droplets. Postnatal infection leads to benign disease with rash and fever. Infection of seronegative women with rubella virus during the first trimester of pregnancy will often result in severe foetal malformations, known as congenital rubella syndrome. Vaccines are globally available. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Matonaviridae*, which is available at ictv.global/report/matonaviridae.

Table 1. Characteristics of members of the family Matonaviridae

Example:	rubella virus (JN635296), species Rubivirus rubellae, genus Rubivirus
Virion	Enveloped, 50–90 nm pleomorphic virions, spherical to tube-like, with a single capsid protein and two envelope glycoproteins
Genome	9.6–10 kb of positive-sense, non-segmented RNA
Replication	Cytoplasmic
Translation	Non-structural proteins are translated from genomic RNA, and structural proteins from subgenomic RNA
Host range	Humans (rubella virus), bats (ruhugu virus), rodents and zoo animals (rustrela virus)
Taxonomy	Realm Riboviria, kingdom Orthornavirae, phylum Kitrinovircota, class Alsuviricetes, order Hepelivirales: the genus Rubivirus includes several species

VIRION

Particles of rubella virus are heterogenous, ranging from spherical to tube-like in shape (Table 1, Fig. 1). Particles range between 50 and 90 nm in length and width, with a nucle-ocapsid core, a lipid bilayer and surface glycoproteins [1].

GENOME

Members of the family *Matonaviridae* have positive-sense RNA genomes of 9.6–10kb with high G+C contents – 69%

in rubella virus. Genomes possess two open reading frames encoding non-structural proteins and structural proteins (Fig. 2). In addition to the genome RNA, a subgenomic RNA encoding the structural proteins is synthesized during replication. Both the genomic and subgenomic RNAs have a viral type 0 ^{7me}GpppA cap at their 5'-terminus and a 3'-non-coding region with poly-A tail at their 3'-terminus [2, 3].

*Correspondence: Annette Mankertz, MankertzA@rki.de

Keywords: ICTV Report; Matonaviridae; rubella virus; taxonomy.

001817 © 2022 The Authors

This is an open-access article distributed under the terms of the Creative Commons Attribution License.

Received 09 November 2022; Accepted 15 November 2022; Published 20 December 2022

Author affiliations: ¹Department of Infectious Diseases, Robert Koch-Institute, 13353 Berlin, Germany; ²Viral Vaccine Preventable Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA; ³Department of Pathobiological Sciences, University of Wisconsin-Madison, Madison WI 53706, USA; ⁴Department of Infection and Immunity, Luxembourg Institute of Health, L-4354 Esch-sur-Alzette, Luxembourg; ⁵Institute of Diagnostic Virology, Friedrich-Loeffler-Institute, 17493 Greifswald-Insel Riems, Germany; ⁶Institute of Novel and Emerging Infectious Diseases, Friedrich-Loeffler-Institute, 17493 Greifswald-Insel Riems, Germany.



Fig. 1. Images and structures of rubella virus particles. (left) Purified rubella virus flash frozen in vitreous ice. (right) Representation of three different rubella virions, each determined using cryo-electron tomography without averaging procedures. Bars: 100 Å. The resolution of the reconstructions are not absolute but are estimated to be better than 50 Å (reproduced from [1]).

REPLICATION

Rubella virus induces a persistent infection in human foetal endothelial cells [4]. Replication is comparatively slow and, even at a high multiplicity of infection, cells are not uniformly infected after 24 h. Viral replication occurs in association with cellular membranes leading to formation of viral replication factory complexes. For rubella virus, genome replication



Fig. 2. Comparative genome architecture of rubella virus, rustrela virus and ruhugu virus showing the ORFs encoding the non-structural polyprotein (nsPP, pink), the structural polyprotein (sPP, blue), and the boundaries of processed products.

References

- Mangala Prasad V, Klose T, Rossmann MG. Assembly, maturation and three-dimensional helical structure of the teratogenic rubella virus. *PLoS Pathog* 2017;13:e1006377.
- Ahola T, Kääriäinen L. Reaction in alphavirus mRNA capping: formation of a covalent complex of nonstructural protein nsP1 with 7-methyl-GMP. *Proc Natl Acad Sci* 1995;92:507–511.
- Oker-Blom C, Ulmanen I, Kääriäinen L, Pettersson RF. Rubella virus 40S genome RNA specifies a 24S subgenomic mRNA that codes for a precursor to structural proteins. *J Virol* 1984;49:403–408.

initiates from the synthesis of negative-sense RNA that is complementary to the genomic sequence. This RNA serves as a template for both genomic and subgenomic RNA synthesis, the latter driven by the subgenomic RNA promoter present in the intergenic region [5]. Two non-structural proteins (p90 and p150) are expressed from the viral genome, while the three structural proteins C, E1 and E2 are expressed from the subgenomic RNA.

PATHOGENICITY

The illness produced in humans by rubella virus infection, known as rubella, is generally associated with fever and rash; complications such as arthralgia and arthritis are rare. However, infection of a seronegative woman with rubella virus during the first trimester of pregnancy leads to a >80% risk of the foetus developing birth defects known as congenital rubella syndrome, including deafness, cataracts and heart defects. Rubella virus is endemic worldwide and is vaccine-preventable [6].

TAXONOMY

Current taxonomy: ictv.global/taxonomy. The genus *Rubivirus* includes the species *Rubivirus rubellae*, *Rubivirus ruteetense* and *Rubivirus strelense* [7, 8]. Rubella virus was previously classified in the family *Togaviridae*.

RESOURCES

Full ICTV Report on the family *Matonaviridae*: ictv.global/report/matonaviridae

Funding information

Production of this Profile, the ICTV Report and associated resources was supported by the Microbiology Society.

Acknowledgements

Members of the ICTV (10th) Report Consortium are Stuart G. Siddell, Elliot J. Lefkowitz, Sead Sabanadzovic, F. Murilo Zerbini, Donald B. Smith and Peter Simmonds.

Conflicts of interest

The authors declare that there are no conflicts of interest

- Perelygina L, Zheng Q, Metcalfe M, Icenogle J. Persistent infection of human fetal endothelial cells with rubella virus. *PLoS One* 2013;8:e73014.
- 5. Tzeng WP, Frey TK. Mapping the rubella virus subgenomic promoter. *J Virol* 2002;76:3189–3201.
- 6. Best JM. Rubella. Semin Fetal Neonatal Med 2007;12:182–192.
- 7. Bennett AJ, Paskey AC, Ebinger A, Pfaff F, Priemer G, et al. Relatives of rubella virus in diverse mammals. *Nature* 2020;586:424–428.
- 8. **Pfaff F, Breithaupt A, Rubbenstroth D, Nippert S, Baumbach C**, *et al.* Revisiting rustrela virus: new cases of Encephalitis and a solution to the capsid enigma. *Microbiol Spectr* 2022;10:e0010322.