

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2020.011S** |  |
| **Short title:** Create two new species and rename one species in genus *Rubivirus* (*Hepelivirales*: *Matonaviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Due to the absence of an ICTV *Matonaviridae* Study Group, this is a direct submission to the ICTV Animal ssRNA+ Viruses Subcommittee Chair. |

**ICTV study group comments and response of proposer**

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**Submission dates**

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| Date first submitted to SC Chair | July 31, 2020 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.011S.R.Rubivirus\_nspp.xlsx |

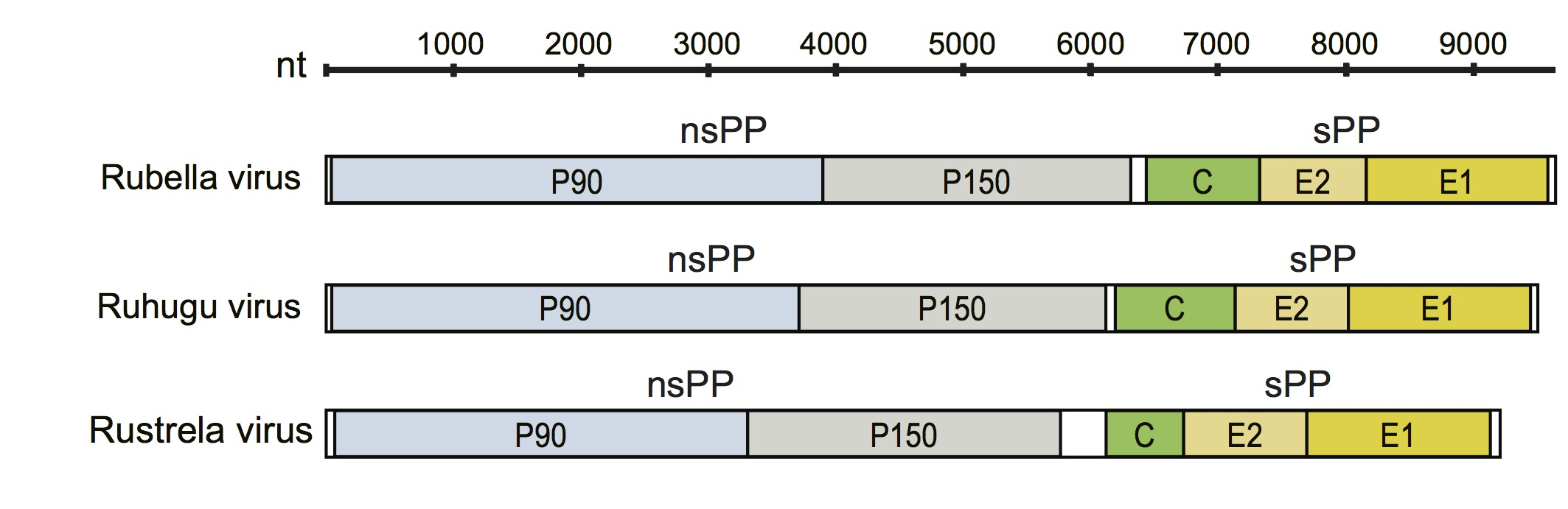
**Abstract**

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| Two new species in genus *Rubivirus* are proposed for ruhugu virus (RuhV), detected in cyclops leaf-nosed bats (*Hipposideros cyclops*) sampled in Ruteete Subcounty, Uganda, and rustrela virus (RusV), detected in a donkey (*Equus asinus*) and a Bennett’s tree kangaroo (*Dendrolagus bennettianus*) sampled in Strela Sound, Germany [unpublished]. Based on the helicase, RNA-directed RNA polymerase, and envelope protein sequences, RuhV and RusV cluster phylogenetically with rubella virus (RuV), currently the sole member of genus *Rubivirus* and family *Matonaviridae*. Species and genus demarcation criteria are not set for viruses of family *Matonaviridae*. Based on the standard set for family *Hepeviridae*, a sister family of *Matonaviridae* in order *Hepelivirales* and the most closely related speciose family of animal viruses in that order, RuhV and RusV meet the demarcation criteria for new rubivirus species. |

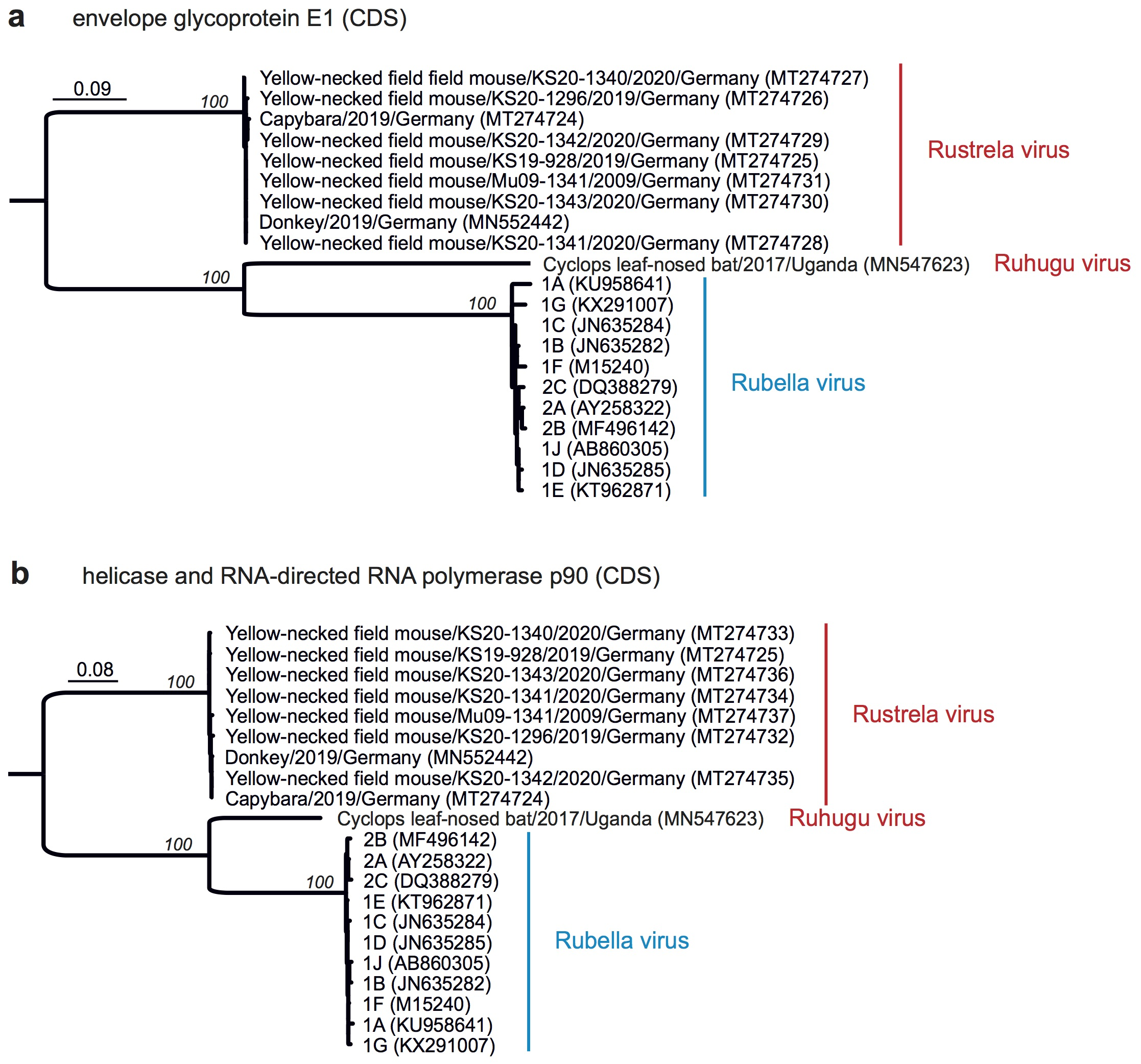
**Text of proposal**

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| |  | | --- | | The complete genome sequence for RuhV (9,621 nt) and RusV (9,322 nt) have been determined [unpublished]. Both are structurally similar to the genome of RuV: they contain the two open reading frames (ORFs) encoding the non-structural polyprotein (nsPP; P200) and structural polyprotein (sPP), which in RuV are post-translationally cleaved to produce non-structural (P150 and P90) and structural proteins (C, E2, E1) (**Figure 1**).  Based on ML trees generated from coding sequence of P90 replication complex protein (non-structural protein containing helicase and RNA-directed RNA polymerase domains) and the E1 envelope glycoprotein, RuhV represents a sister taxon to the species established for RuV, with RusV being the outgroup (**Figure 2**). Amino acid sequence identities estimated from pair-wise alignments confirm that RuhV is most closely related to RuV (75.7% identity for P90 and 56.3% identity for E1), whereas RusV is more distantly related (65.5% identity for P90 and 51.0% identity for E1) (**Table 1**).  Neither RuhV nor RusV could be isolated in culture thus far.  **Species demarcation criteria**  Until now, RuV was the lone member of genus *Rubivirus* and of family *Matonaviridae.* Consequently,species and genus demarcation criteria have not been set. The nearest speciose family of animal viruses is family *Hepeviridae*. Genus demarcation for family *Hepeviridae* is governed by amino acid p-distances of at conserved sites within ORF1. *Hepevirid* ORF1 is organized similarly to matonavirid P200, and replicative enzymes of hepeviruses(i.e., hepatitis E virus [HEV]) shows highest, if limited, amino acid sequence similarity to RuV P90. For *Hepeviridae*, inter-genus amino p-distances at these conserved ORF1 sites are greater than 0.6, whereas intra-genus amino p-distances are less than 0.5 [1]. Drawing analogy to these demarcation criteria, RuhV and RusV should join RuV as members of genus *Rubivirus* given the percent amino acid identity of the P90 replication complex described above. Species demarcation for genus *Orthohepevirus* of family *Hepeviridae* is decided by monophyly of isolates from unique hosts [1]. Given the unique host ecologies of RuhV (bats), RusV (equids, marsupials), and RuV (humans) and the amino p-distance across the genome these three viruses should be considered as representatives of distinct species.  **Etymology**  We propose to introduce binomial species names for the entire genus *Rubivirus* in family *Matonaviridae*:   * establish species *Rubivirus ruteetense* (a reference to Ruteete Subcounty, Uganda, where RuhV was discovered); * establish species *Rubivirus strelense* (a reference to Strela Sound, Germany, where RusV was discovered); and * to rename species *Rubella virus* to *Rubivirus rubellae* (a reference to rubella, the disease caused by the species member, rubella virus). | |

**Supporting evidence**

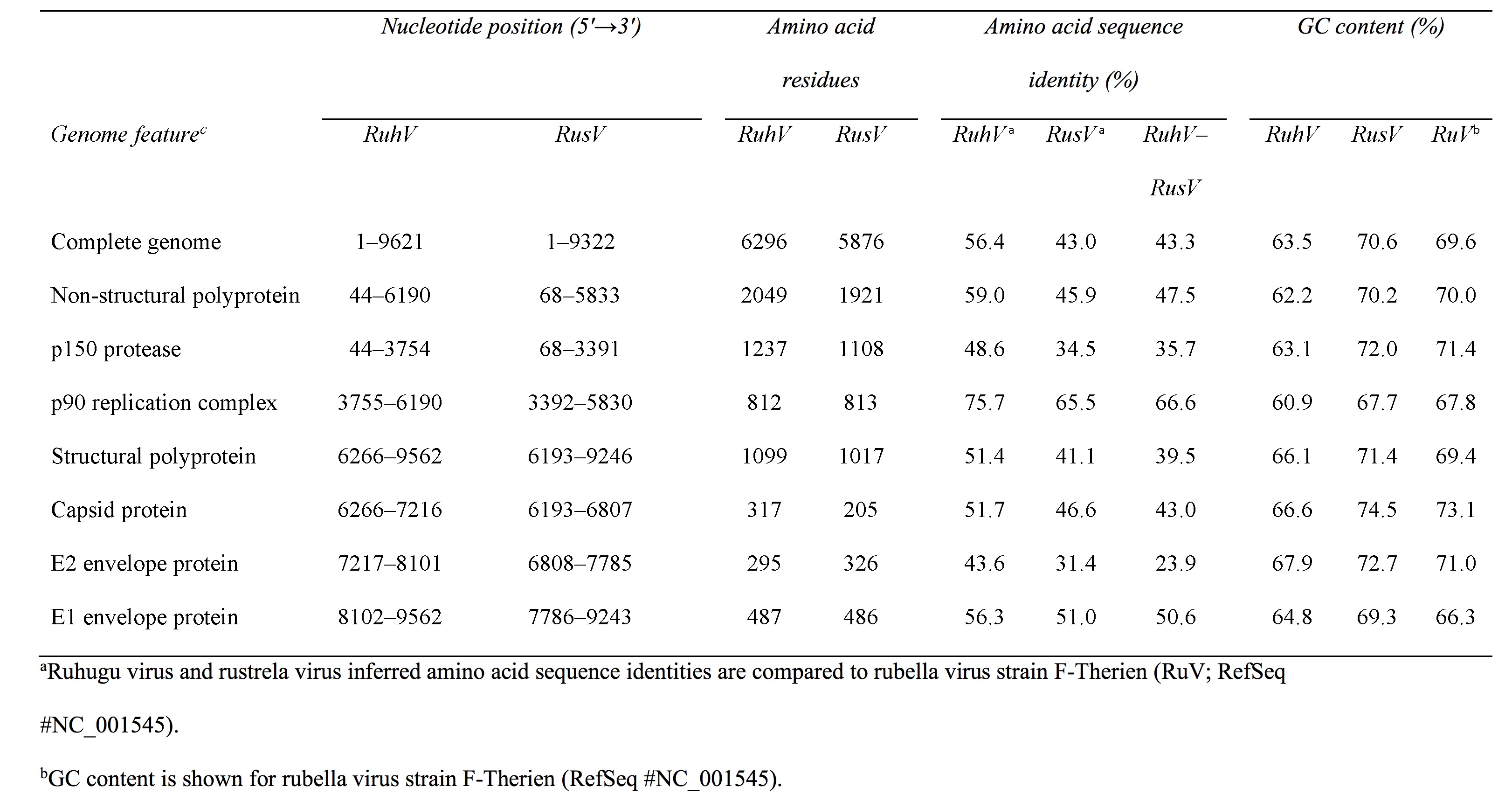
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**Figure 1.** Comparative genome architecture of RuV, RuhV, and RusV, showing two open reading frames (colored), two untranslated regions at the 5′ and 3′ termini (white), and an intergenic region (white) between the ORFs encoding the non-structural (nsPP) and structural (sPP) polyproteins.

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**Figure 2.** Phylogenetic analyses of the coding sequences of envelope glycoprotein E1 (a) and helicase and RNA-directed RNA polymerase p90 (b) of RusV and RuhV and RusV, including all sequences obtained. Numbers above branches represent bootstrap values; scale bars indicate amino acid substitutions per site.

**Table 1.** Genomic features of ruhugu virus (RuhV; GenBank #MN547623) and rustrela virus (RusV; GenBank #MN552442).

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**References**

1. Smith DB, Simmonds P, Jameel S, Emerson SU, Harrison TJ, Meng XJ, Okamoto H, Van der Poel WHM, and Purdy MA (2014) Consensus proposals for classificiation of the family *Hepeviridae*. J Gen Virol 95: 2223-2232. PMID: 24989172 DOI: 10.1099/vir.0.068429-0