



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	2011.012a-dV	(to be completed by ICTV officers)			
Short title: create 2 new species in the proposed new genus <i>Quaranjavirus</i>					
Modules attached	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input checked="" type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input checked="" type="checkbox"/>	

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

Orthomyxovirus study group

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:

Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

Code	<i>2011.012a</i>		
To create a new species within:			
Genus:	<i>Quaranjavirus</i> (new)		
Subfamily:			
Family:	<i>Orthomyxoviridae</i>		
Order:			
And name the new species:		GenBank sequence accession number(s) of reference isolate:	
<i>Quaranfil virus</i>		[FJ861695, FJ861694, GQ499304, JN412853, GQ499303, GQ499302];	
<i>Johnston Atoll virus</i>		[FJ861697.1, FJ861696.1]	

Reasons to justify the creation and assignment of the new species:

Proposed species differ both antigenically and genetically from other members of the Orthomyxovirus family.

Proposed criteria for demarcating species:

1. Species must meet criteria to be members of the family *Orthomyxoviridae*.
2. Species must share conserved terminal sequence at 5' (AGCAAUCACAA) and 3' (UCGUUAGUGUWR) ends. Both Quaranfil and Johnston Atoll virus share these sequences.
3. Species must cluster with Quaranfil virus when compared phylogenetically with other orthomyxoviruses. Please see phylogenetic analysis in the annex and in Presti et al, J. Virol 83, 11599-11606, 2009
4. Species must be antigenically distinct. The two proposed strains also do not cross react in standard serologic assays. Complement fixation data and hemagglutination inhibition data (presented in Presti RM et al, *ibid*) shown clear differences from other viruses from the family Orthomyxoviridae. Johnston Atoll virus and Quaranfil virus were readily distinguished as distinct viruses by complement fixation. Johnston Atoll virus does not agglutinate goose red blood cells and could not be assessed by hemagglutination inhibition assays.

This is to be the type species for the proposed new genus below: *Quaranjavirus*

MODULE 3: **NEW GENUS**

creating a new genus

Code	2011.012b
To create a new genus within:	
Subfamily:	
Family:	<i>Orthomyxoviridae</i>
Order:	

naming a new genus

Code	2011.012c
To name the new genus: <i>Quaranjavirus</i>	

Assigning the type species and other species to a new genus

Code	2011.012d
To designate the following as the type species of the new genus	
<i>Quaranfil virus</i>	
Please enter here the TOTAL number of species (including the type species) that the genus will contain: 2	

Reasons to justify the creation of a new genus:

We propose that Quarafil virus represents a novel genus in the family *Orthomyxoviridae* (Presti et al, J. Virol 83, 11599-11606, 2009). The virus was originally isolated from two children with febrile illness from the villages of Quarafil and Sindbis in Egypt in 1953 (Taylor et al., Am. J. Trop. Med. Hyg. 15:76-86, 1966). Several strains of Quarafil virus have been isolated from ticks and seabirds in multiple countries throughout Africa and the Middle East (see references).

- Morphology and morphogenesis of these viruses show similarities with the influenzaviruses.
- Quarafil virions contain at least 6 segments of linear, negative sense ssRNA which have been completely sequenced.
- Sequences of the ends of vRNA are partially complementary and resemble those of influenzaviruses. The conserved end sequences of both Quarafil and Johnston Atoll viral RNAs are 5'-AGCAAUCACAA and 3'- UCGUUAGUGU(A/U)(A/G).
- Quarafil RNA segments 1-3 (2421 nt, 2404 nt, and 2386 nt) encode single open reading frames that exhibit protein domain homology to the respective influenzavirus polymerase proteins PB2, PA and PB1.
- The fourth segment (1726 nt) contains one single predicted open reading frame of 527 aa but does not share significant sequence homology with any protein currently in the GenBank database.
- The fifth segment (1616 nt) is unrelated to any influenzavirus protein but shows distant amino acid sequence similarity with the glycoprotein of the thogotoviruses and with the glycoprotein

(gp64) of baculoviruses.

- The sixth segment of 898 nt contains one predicted open reading frame of 266 aa which does not share sequence homology with any known protein. (It is unclear which segments encode the nucleoprotein or matrix protein of the Quaranfil viruses.)
- There is no significant antigenic relationship between Quaranfil and either the thogotoviruses or the influenzaviruses. Johnston Atoll virus (JAV) and Lake Chad virus (LCV) are additional viruses within the genus.
- Comparatively low levels of hemagglutination occur at acidic pH and not at physiological pH for Quaranfil viruses against goose red blood cells, but Johnston Atoll virus does not agglutinate goose red blood cells in the range of pH 5.75-7.0.
- Quaranfil and Johnston Atoll are transmitted between vertebrates by ticks.

Origin of the new genus name:

Quaranja from the village of Qaranfil, Al - Qanatir Al - Khayreya, Qulubiya, near Cairo, Egypt, [combined with Johnston Atoll, North Pacific, an unincorporated territory of the United States.](#)

Reasons to justify the choice of type species:

All six genome segments of this virus have been sequenced.

Species demarcation criteria in the new genus:

Proposed criteria for demarcating species:

1. Species must meet criteria to be members of the family *Orthomyxoviridae*.
2. Species must share conserved terminal sequence at 5' (AGCAAUCACAA) and 3' (UCGUUAGUGUWR) ends.
3. Species must cluster with Quaranfil virus when compared phylogenetically with other orthomyxoviruses.
4. Species must be antigenically distinct.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Presti, R.M., G. Zhao, W.L. Beatty, K.A. Mihindukulasuriya, A.P.A. Travassos da Rosa, V.L. Popov, R.B. Tesh, H.W. Virgin, D. Wang.** 2009. Quaranfil, Johnston Atoll, and Lake Chad Viruses Are Novel Members of the Family Orthomyxoviridae. *J. Virol.* **83**(22): 11599-11606.
- Taylor, R. M., H. S. Hurlbut, T. H. Work, J. R. Kingston, and H. Hoogstraal.** 1966. Arboviruses isolated from Argas ticks in Egypt: Quaranfil, Chenuda, and Nyamanini. *Am. J. Trop. Med. Hyg.* **15**:76-86.
- Zeller, H. G., N. Karabatsos, C. H. Calisher, J. P. Digoutte, F. A. Murphy, and R. E. Shope.** 1989. Electron microscopy and antigenic studies of uncharacterized viruses. I. Evidence suggesting the placement of viruses in families Arenaviridae, Paramyxoviridae, or Poxviridae. *Arch. Virol.* **108**:191-209.
- Clifford, C. M., L. A. Thomas, L. E. Hughes, G. M. Kohls, and C. B. Philip.** 1968. Identification and comparison of two viruses isolated from ticks of the genus *Ornithodoros*. *Am. J. Trop. Med. Hyg.* **17**:881-885.
- Al-Khalifa, M. S., F. M. Diab, and G. M. Khalil.** 2007. Man-threatening viruses isolated from ticks in Saudi Arabia. *Saudi Med. J.* **28**:1864-1867.
- Converse, J. D., and M. I. Moussa.** 1982. Quaranfil virus from *Hyalomma dromedarii* (Acari: Ixodoidea) collected in Kuwait, Iraq and Yemen. *J. Med. Entomol.* **19**:209-210.
- Kemp, G. E., V. H. Lee, and D. L. Moore.** 1975. Isolation of Nyamanini and Quaranfil viruses from Argas (*Persicargas*) arboreal ticks in Nigeria. *J. Med. Entomol.* **12**:535-537.
- Sang, R., C. Onyango, J. Gachoya, E. Mabinda, S. Konongoi, V. Ofula, L. Dunster, F. Okoth, R. Coldren, R. Tesh, A. T. da Rosa, S. Finkbeiner, D. Wang, M. Crabtree, and B. Miller.** 2006. Tickborne arbovirus surveillance in market livestock, Nairobi, Kenya. *Emerg. Infect. Dis.* **12**:1074-1080.
- Sureau, P., and J. M. Klein.** 1980. Arboviruses in Iran. *Med. Trop. (Mars.)* **40**:549-554.

Annex:

A phylogenetic tree of viruses within the family *Orthomyxoviridae*. Established genera are shown with the proposed genus containing Quaranfil virus and Johnston Atoll virus. Nucleotide sequences of the polymerase basic 1 proteins (PB1) were aligned using transAlign and CLUSTAL W, and their phylogenetic relationships were determined by the neighbor-joining method (HKY model) using PAUP* (version 4.0b) by Dr. Gavin Smith, a member of the committee. The tree was mid-point rooted and bootstrap values (1,000 replicates) are indicated on the branches. The GenBank accession numbers for the sequences used for comparison were (top to bottom) AF404346, GU830904, FJ861695, FJ861697, AF004985, M65866, M28060, AF170575, CY018763, CY018771, GU053121, CY044267 and FJ966080. The figure was prepared for the forthcoming edition of ICTV Virus Taxonomy.

