



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:	2012.012V	(to be completed by ICTV officers)			
Short title: Naming convention for human metapneumovirus strains (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/>	2 <input type="checkbox"/>	3 <input 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)

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 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	2012.012V	(assigned by ICTV officers)
Title of proposal: <i>Naming convention for human metapneumovirus strains</i>		

Text of proposal:

Human metapneumovirus (HMPV) is a member of Subfamily *Pneumovirinae* of Family *Paramyxoviridae* that was discovered in 2001 (van den Hoogen et al., 2001). There are four genetic lineages of HMPV, designated as A1, A2, B1, and B2 that segregate into two antigenic subgroups (A and B), (Biacchesi et al., 2003; Piyaratna et al., 2011; van den Hoogen et al., 2004). Numerous strains of HMPV from diverse global locations have been isolated and partially or fully sequenced. A standardized naming convention will facilitate the identification, analysis, and comparison of HMPV strains. We propose the following standard described below, which is similar to the standard for influenza strains. In instances where information such as the antigenic subgroup or genetic lineage is not known, it would be omitted.

SPECIES: "HMPV"

STRAIN: "<Site (ISO 3166 alpha-2 country code)>/<Lab strain ID>/<Year>/<Major subgroup (A or B) optional>"

Examples:

Current GenBank name	Proposed nomenclature
Human metapneumovirus isolate 00-1	HMPV NL/1/00/A1
Human metapneumovirus isolate NL/00/17 type A2	HMPV NL/17/00/A2
Human metapneumovirus strain TN982-42	HMPV US/242/98/B1
Human metapneumovirus isolate CAN98-75	HMPV CA/75/98/B2

References:

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Annex:

HMPV sequences have been extensively analyzed by multiple investigators (Agrawal et al., 2011; Bastien et al., 2004; Bastien et al., 2003; Biacchesi et al., 2003; Boivin et al., 2004; de Graaf et al., 2008; Galiano et al., 2006; Gaunt et al., 2011; Ishiguro et al., 2004; Mackay et al., 2006; Mackay et al., 2004; Peret et al., 2004; Piyaratna et al., 2011; van den Hoogen et al., 2004; Yang et al., 2009). These analyses have shown that there are four distinct genetic lineages and that these lineages remain distinct over time (Figure).

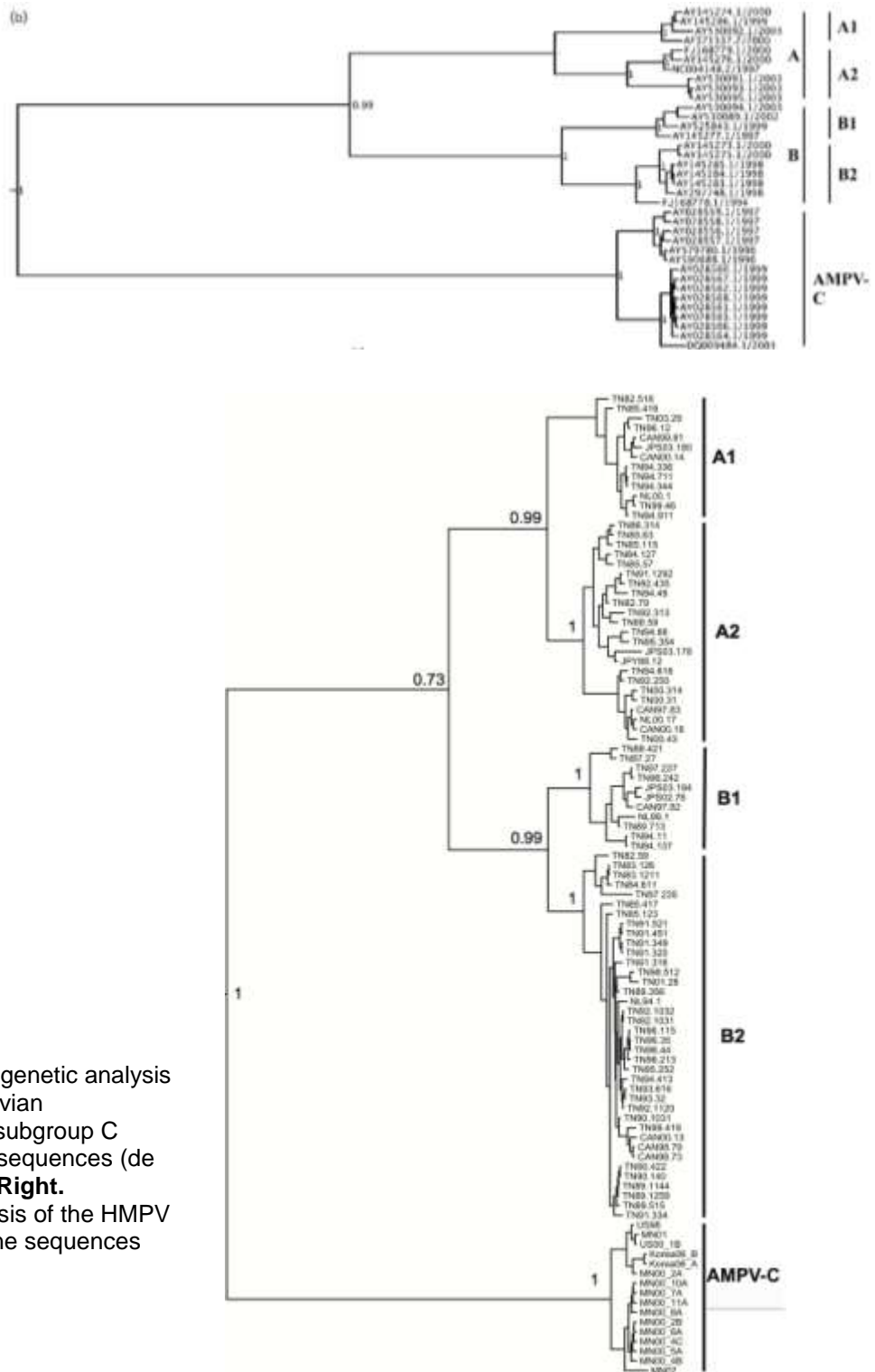


Figure. Top. Phylogenetic analysis of the HMPV and avian metapneumovirus subgroup C (AMPV-C) N gene sequences (de Graaf et al, 2008). **Right.** Phylogenetic analysis of the HMPV and AMPV-C F gene sequences (Yang et al, 2009).