



## Orterviraes: New Virus Order Unifying Five Families of Reverse-Transcribing Viruses

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1 ***Ortervirales*: A new viral order unifying five families of reverse-transcribing viruses**  
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57 **Text**

58 Reverse-transcribing viruses, which synthesize a copy of genomic DNA from an RNA template, are  
59 widespread in animals, plants, algae and fungi (1, 2). This broad distribution suggests ancient origin(s)  
60 of these viruses, possibly concomitant with the emergence of eukaryotes (3). Reverse-transcribing  
61 viruses include prominent human pathogens, such as human immunodeficiency viruses 1 and 2 (HIV-  
62 1/2) and hepatitis B virus, as well as plant pathogens that cause considerable economic losses (4).

63 The International Committee on Taxonomy of Viruses (ICTV) traditionally classified reverse-  
64 transcribing viruses into five families: *Caulimoviridae*, *Hepadnaviridae*, *Metaviridae*, *Pseudoviridae*,  
65 and *Retroviridae* (5). In 2018, the ICTV recognized an additional family, *Belpaoviridae*, which  
66 contains the genus *Semotivirus* (previously included in *Metaviridae* (6)). The infection cycles, nucleic  
67 acid types, genome organizations, and virion morphologies of these viruses are very diverse. Indeed,  
68 reverse-transcribing viruses are distributed between two Baltimore Classes of viruses. Belpaoviruses,  
69 metaviruses, pseudoviruses — better known as Bel/Pao, Ty3/Gypsy, and Ty1/Copia retrotransposons,  
70 respectively (1, 7) — and retroviruses typically have single-stranded RNA genomes (Table 1) and  
71 frequently integrate into the host genomes as part of their replication cycles (Baltimore Class VI). In  
72 contrast, members of the families *Caulimoviridae* and *Hepadnaviridae*, often referred to as  
73 “pararetroviruses” (8), encapsidate circular double-stranded DNA genomes and do not actively  
74 integrate into host chromosomes (Baltimore Class VII). However, capture of pararetroviral DNA in  
75 host genomes, presumably by illegitimate recombination, is commonplace, particularly in plants,  
76 giving rise to the corresponding endogenous elements (9, 10).

77 Mechanistic studies on the replication cycles of reverse-transcribing viruses of different  
78 families have revealed many similarities that have been reinforced by comparative genomics of the  
79 viral reverse transcriptases (RTs), the hallmark enzymes encoded by all reverse-transcribing viruses.  
80 Indeed, phylogenetic analyses support the monophyly of all viral RTs, to the exclusion of those  
81 encoded by non-viral retroelements from both eukaryotes and prokaryotes (11, 12). In addition to the  
82 evidence from the RT phylogeny, belpaoviruses, caulimoviruses, metaviruses, pseudoviruses, and  
83 retroviruses share several conserved features that hepadnaviruses lack (Table 1). In particular, the  
84 polymerase (Pol) polyproteins of belpaoviruses, metaviruses, pseudoviruses, and retroviruses possess

similar domain architectures. These Pol polyproteins contain an aspartate protease, which is responsible for the processing of viral polyproteins, and an integrase of the DDE recombinase superfamily. The genomes of these viruses also share long terminal repeats (LTRs) (13). Within certain clades, Pol polyproteins of retroviruses and metaviruses share additional features, such as a dUTPase domain (14-16) and the GPY/F subdomain of the integrase (17, 18). Caulimoviruses also possess a homologous aspartate protease domain in their Pol polyprotein (19), but lack an integrase and LTR. However, RT-based phylogenies consistently place these plant-infecting viruses as a sister clade to the metaviruses (Figure 1), suggesting that among “pararetroviruses”, encapsidation of a DNA genome is a homoplasious character and therefore not a reliable criterion for classification. The basal branches of the RT tree are not resolved and are presented as a multifurcation in Figure 1. This topology is at least compatible with placing the *Hepadnaviridae* clade outside the viral group that includes belpaoviruses, caulimoviruses, metaviruses, pseudoviruses, and retroviruses.

Belpaoviruses, caulimoviruses, metaviruses, pseudoviruses, and retroviruses share not only homologous proteins involved in genome replication and polyprotein processing, but also the two principal protein components of the virions, namely, the capsid and nucleocapsid proteins/domains (20-22), although the nucleocapsid domain appears to be absent in spumaretroviruses (family *Retroviridae*; Table 1). By contrast, hepadnaviruses encode an unrelated capsid protein (23). These findings suggest that belpaoviruses, caulimoviruses, metaviruses, pseudoviruses, and retroviruses have evolved from a common viral ancestor, rather than from distinct capsid-less retrotransposons (20).

Finally, similarities between belpaoviruses, caulimoviruses, metaviruses, pseudoviruses, and retroviruses extend to the mechanism of replication priming. All these viruses utilize host tRNA molecules as primers for genome replication by reverse transcription (24), whereas hepadnaviruses use a specific protein priming mechanism mediated by the polymerase terminal protein domain (25).

Taken together, the common complement of proteins required for genome replication, polyprotein processing, and virion formation, the topology of the RT phylogenetic tree, and mechanistic similarities in genome replication present strong evidence that belpaoviruses, caulimoviruses, metaviruses, pseudoviruses, and retroviruses share a common evolutionary origin. The hepadnaviruses, which typically branch out at the base of the viral RT clade (Figure 1), possess a

113 unique capsid protein and employ a distinct replication mechanism, appear to be more distantly related  
114 to all these virus families. In recognition of these relationships, the ICTV has recently regrouped the  
115 families *Belpaoviridae*, *Caulimoviridae*, *Metaviridae*, *Pseudoviridae* and *Retroviridae* into an order  
116 *Ortervirales* (*orter*: an inversion of *retro*, which was derived from reverse transcription; *virales*: suffix  
117 for an order). This change in taxonomy acknowledges and formalizes the long-proposed evolutionary  
118 relationship among most groups of reverse-transcribing viruses (26). We note that although  
119 hepadnaviruses are not included in the order, they might be unified with other reverse-transcribing  
120 viruses at a higher taxonomic level in the future.

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122

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- 198  
199  
200

201 **Figure legend**

202 **Figure 1.** Maximum likelihood phylogeny of viral reverse transcriptases. The tree includes sequences of 290 viruses belonging to all ICTV-  
203 recognized genera of reverse-transcribing viruses. The phylogeny was inferred using PhyML (30) with the LG+G+F substitution model and is  
204 rooted with sequences from non-viral retroelements (bacterial group II introns and eukaryotic LINE retroelements). Genomic organizations of  
205 selected representatives of reverse-transcribing viruses are shown next to the corresponding branches. Long terminal repeats (LTR) are shown as  
206 black triangles. Note that members of the virus families display considerable variation in gene/domain content (5), which is not captured in this  
207 figure. Abbreviations: 6, 6-kDa protein; ATF, aphid transmission factor; CA/CP, capsid protein; CHR, chromodomain (only present in the INT of  
208 particular clades of metaviruses of plants, fungi and several vertebrates); *gag*, group-specific antigen; *env*, envelope genes; SU, surface  
209 glycoprotein; TM, transmembrane glycoprotein; INT, integrase; MA, matrix protein; NC, MP, movement protein; nucleocapsid; *nef*, *tat*, *rev*, *vif*,  
210 *vpr*, and *vpu*, genes that express regulatory proteins via spliced mRNAs; TP, terminal protein domain; TT/SR, translation trans-activator/suppressor  
211 of RNA interference; P, polymerase; *pol*, polymerase gene; PR, protease; PreS, pre-surface protein (envelope); PX/TA, protein X/transcription  
212 activator; RH, RNase H; RT, reverse transcriptase; VAP, virion-associated protein.

**Table 1.** Features shared by reverse-transcribing viruses.

Family	<i>Retroviridae</i>		<i>Metaviridae</i>	<i>Pseudoviridae</i>	<i>Belpaoviridae</i>	<i>Caulimoviridae</i>	<i>Hepadnaviridae</i>
Subfamily	<i>Orthoretrovirinae</i>	<i>Spumaretrovirinae</i>					
Pol	RT-RH	+	+	+	+	+	+
	Protease	+	+	+	+	+	–
	Integrase	+	+	+	+	–	–
Gag	CA/CP	+	+	+	+	+	–
	NC	+	–	+	+	+	–
LTR		+	+	+	+	–\$	–#
Priming	tRNA	tRNA	tRNA	tRNA	tRNA	tRNA	TP
Genome type	ssRNA	ssRNA/dsDNA*	ssRNA	ssRNA	ssRNA	dsDNA	dsDNA

\* – Members of the subfamily *Spumaretrovirinae* contain both ssRNA and dsDNA in extracellular particles and reverse transcription occurs during virus assembly and disassembly.

\$ – In the genus *Petuvirus* (*Caulimoviridae*) an inactivated integrase-like domain and quasi (long) terminal repeats have been identified (27, 28), suggesting that certain ancestral elements have been lost during the evolution of caulimoviruses.

# – Upstream of the capsid protein gene, hepadnavirus genomes contain a sequence showing similarity to the U5 region of the retroviral LTR (29).

Abbreviations: CA/CP, capsid protein; Gag, group-specific antigen; LTR, long terminal repeats; NC, nucleocapsid protein; RH, RNase H; RT, reverse transcriptase; Pol, polymerase polyprotein; TP, terminal protein.

