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The family *Picornaviridae* currently consists of 28 species classified into 12 genera (*Enterovirus*, *Cardiovirus*, *Aphthovirus*, *Hepatovirus*, *Parechovirus*, *Erbovirus*, *Kobuvirus*, *Teschovirus*, *Sapelovirus*, *Senecavirus*, *Tremovirus* and *Avihepatovirus*). In the past two years the genome sequences of 18 novel unclassified picornaviruses have been reported. These include three viruses which are the first confirmed picornaviruses in reptiles and fish.

TAXONOMIC PROPOSALS UNDER DISCUSSION OR IN PREPARATION

- 1) the species *Bovine enterovirus* is to be divided into two species, "*Bovine enterovirus A*" and "*Bovine enterovirus B*";
- 2) the genome sequences of three unassigned simian enteroviruses types (SV6, EV-103 & EV-108) suggest their placement in one or more new species in the *Enterovirus* genus.

Two **seal picornaviruses** form a candidate species in a novel genus (Kapoor *et al.*, 2008a; Knowles & Wadsworth, this meeting).

The first confirmed picornaviruses of fish:

Eel picornavirus forms a candidate species in a novel genus (Philipps *et al.*, this meeting).

Bluegill picornavirus forms a candidate species in a novel genus (Barbknecht, 2009; MSc Thesis, University of Wisconsin-La Crosse; M.A. Hoffman, personal communication, 2010).

Porcine kobuvirus a new candidate species in the genus *Kobuvirus* (Reuter *et al.*, 2009, Arch Virol 154: 101-108).

Human klassevirus (Greninger *et al.*, 2009; Holtz *et al.*, 2009) and **salivirus** (Li *et al.*, 2009) are closely related to each other and would form a single candidate species in another potential new genus.

Turdivirus (TV) 1, TV-2, TV-3, isolated from wild birds, have been suggested to form three species in two new genera (TV-1 in "*Orthoturdivirus*" and TV-2 and TV-3 in "*Paraturdivirus*") (Woo *et al.*, 2010).

Bovine rhinovirus (BRV) 1 and BRV-3 together form a new candidate species ("*Bovine rhinitis A virus*") in the genus *Aphthovirus* (Piccone *et al.*, this meeting)

OTHER NEW PICORNAVIRUSES

Although only a partial genome sequence exists for **bat kobu-like virus** (Li *et al.*, 2010), this suggests it may be another novel virus distantly related to the kobuviruses. Another picornavirus isolated from turkeys with hepatitis also appears to be distinct from other picornaviruses and may form a new species in a novel genus (W.I. Lipkin, personal communication, 2010).

**Your opinions are important to us:
If you have any views on the classification/taxonomy of the *Picornaviridae* please contact one of the Study Group members.**

Figure 1. Unrooted Neighbor-joining tree of the *Picornaviridae* based on a comparison of the P1 capsid region. The 12 current genera are shown in italics.

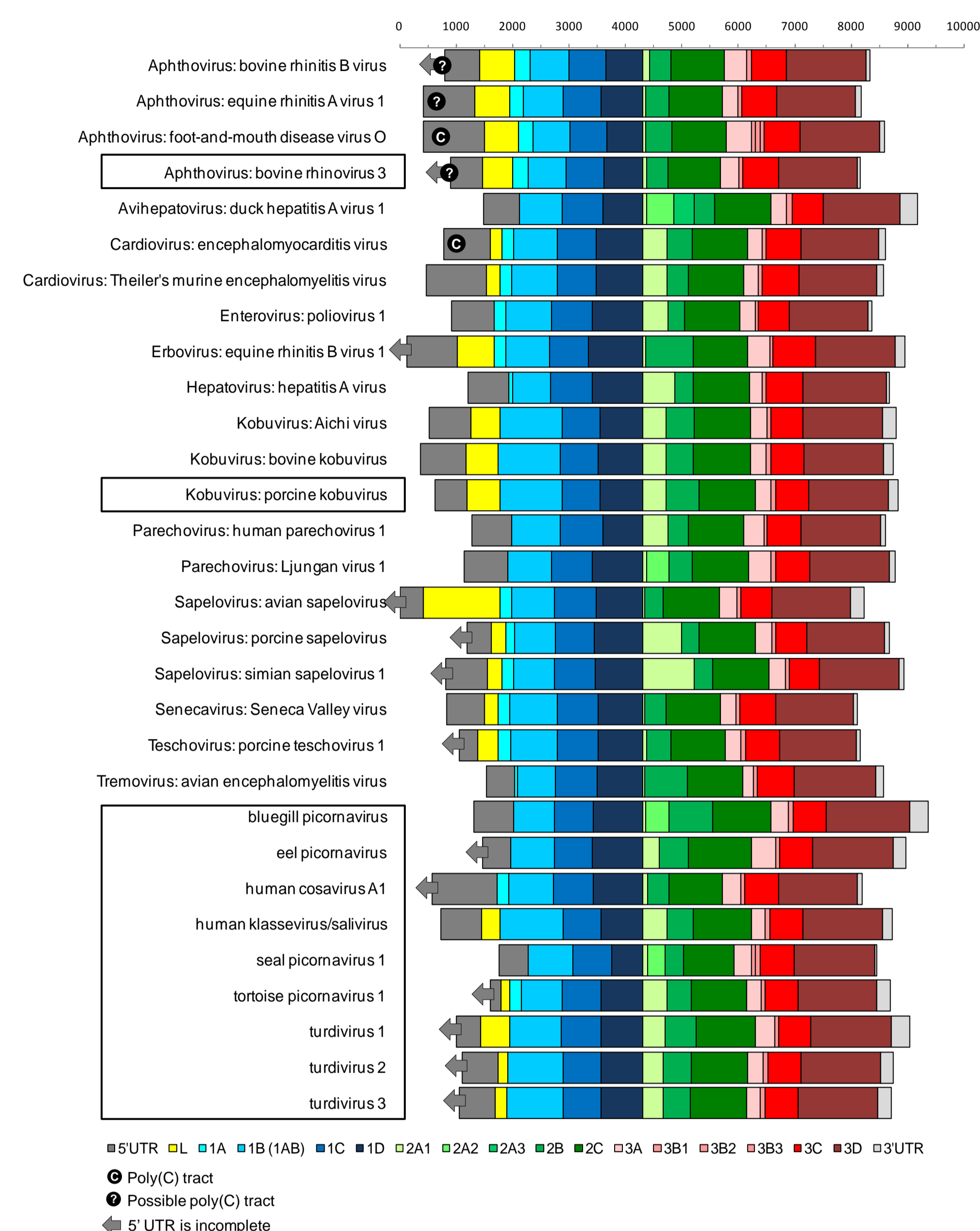
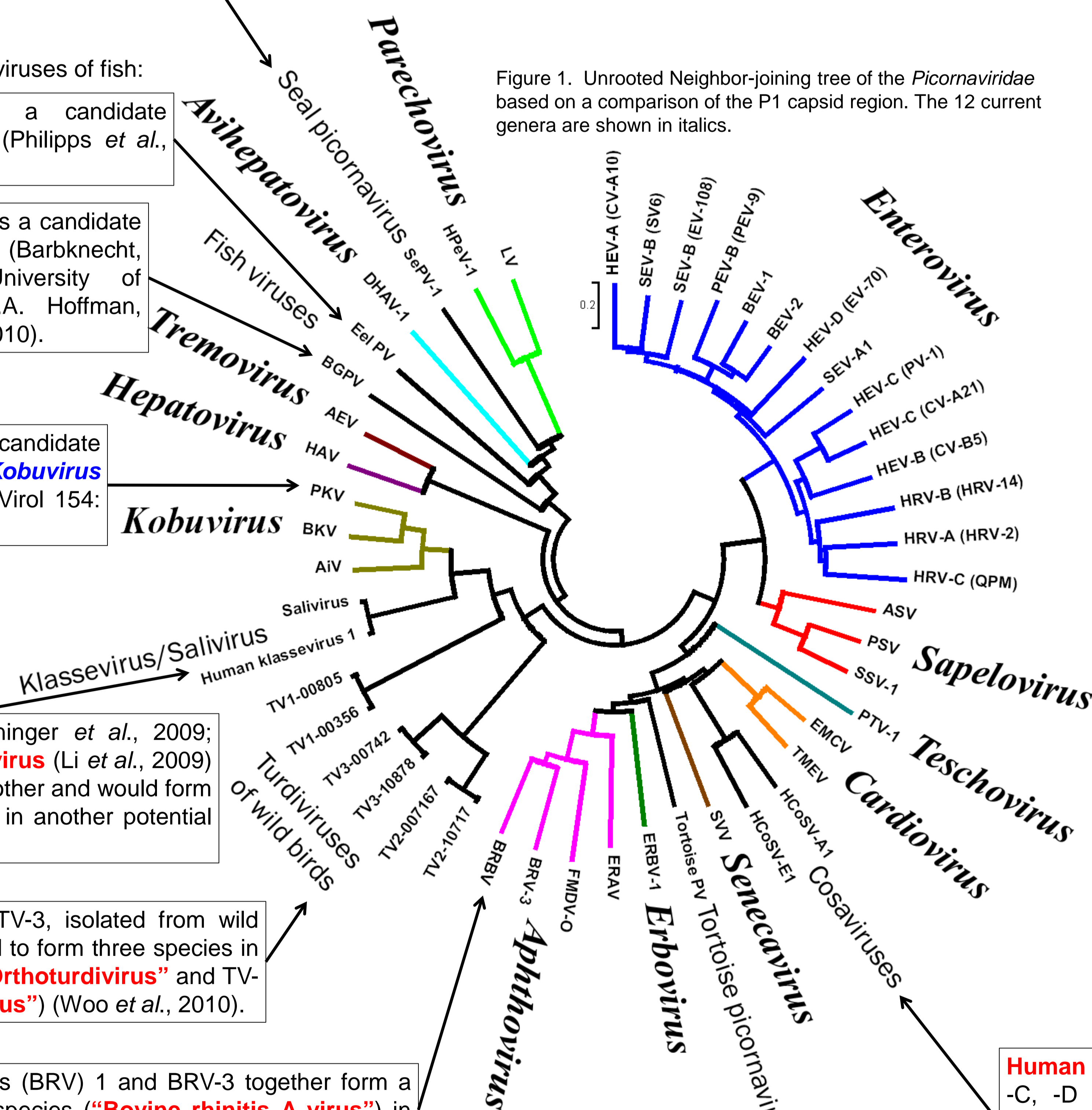


Figure 2. Genome maps of the 12 current genera and some newly sequenced picornaviruses. The new candidate taxa are boxed.

THE FUTURE

As well as being phylogenetically distinct, each of the viruses described have distinguishing features which differentiate them from existing taxa.

If all these changes are eventually approved by the ICTV, the *Picornaviridae* will comprise some 45 species in 22 genera and it is expected that these numbers will steadily increase as new picornaviruses are discovered.

The latest classification and proposals may be viewed on the *Picornaviridae* Study Group website: <http://www.picornastudygroup.com> and on the ICTV website: <http://talk.ictvonline.org>.

Human cosavirus A (HCoV-A), -B, -C, -D and -E form five candidate species in a potential new genus ("*Cosavirus*") (Kapoor *et al.*, 2008b; Holtz *et al.*, 2008).

Tortoise picornavirus (aka virus "X"), the first confirmed picornavirus isolated from reptiles (Heuser *et al.*, this meeting).

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