



Picornaviridae to Picornavirales: Taxonomy and Comparative Genomics

Nick J. Knowles

Institute for Animal Health, Pirbright Laboratory, Ash Road, Pirbright, Woking, Surrey, GU24 0NF, UK.

ABSTRACT

The increasing number of new picornavirus genome sequences shows the genetic diversity of this virus family. Currently the *Picornaviridae* consists of nine genera, however, this is likely to increase to at least 13 in the near future, despite the joining of the enteroviruses and rhinoviruses to form a single genus (with the name *Enterovirus*). It is now becoming possible to map genetic and phenotypic characters onto a phylogenetic tree of the family to show how particular genes may have evolved or been derived. Of particular interest are the Internal Ribosome Entry Site (IRES), the leader polypeptide (L) and 2A, since they are particularly variable between the genera. Additionally, proteolytic processing (or lack of it) of VP0 combined with the presence or absence of myristic acid attached to its N-terminus may also be informative about the evolution of the picornaviruses. The position of a new picornavirus on the family tree (even if only based on a small amount of sequence data) can be used to make predictions about the characteristics of these variable genome regions. On a larger perspective, the recent proposal to create a new virus order, *Picornavirales*, may encourage wider comparisons of picornaviruses with the other related families. At the other end of the spectrum, virus sequences are now being used to define new picornavirus types, based on comparisons of the sequences of existing serotypes. However, some anomalies have been encountered with the human parechoviruses and erboviruses. These and other issues will be presented.

Much of my presentation will be based on other work presented at this meeting and I refer you to the following posters:

Hollister, J.R., Vagnozzi, A., Knowles, N.J. and Rieder, E. Molecular analysis of bovine rhinovirus type 2 shows a close relationship to the aphthoviruses.

Knowles, N.J., Hovi, T., Hyypiä, T., King, A.M.Q., Lindberg, A.M., Minor, P.D., Pallansch, M.A., Palmenberg, A.C., Skern, T., Stanway, G., Yamashita, T. and Zell, R. Taxonomy of *Picornaviridae*: current situation and future proposals.

Knowles, N.J., Oberste, M.S., Pallansch, M.A., Stanway, G. and Hovi, T. Picornavirus classification below the level of species: new serotypes or types.

Le Gall, O., Christian, P., Fauquet, C., Gorbalenya, A.E., King, A., Knowles, N.J., Nakashima, N. and Stanway, G. *Picornavirales*, an order of positive-sense single-stranded RNA viruses with a pseudo-T=3 virion architecture.

Tseng, C.-H., Knowles, N.J. and Tsai, H.-J. Molecular analysis of duck hepatitis virus type 1 indicates that it should be assigned to a new picornavirus genus.

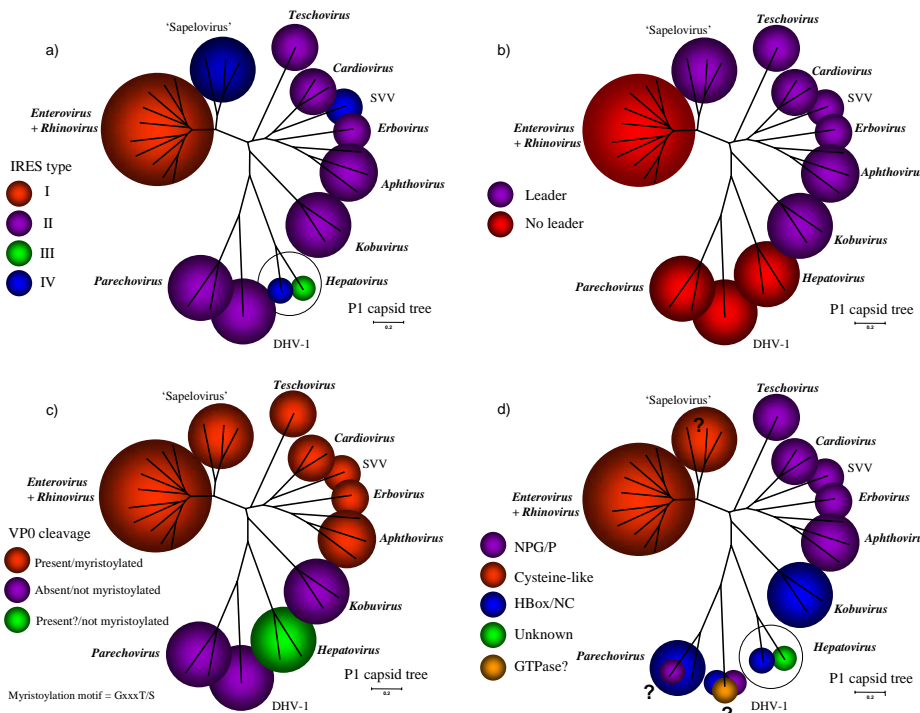


Fig. 1. Unrooted Neighbor-joining trees (produced with MEGA 3.1) of the P1 capsid showing the relationships between virus species in the different picornavirus genera. Overlaid on each are various characteristics or properties: a) type of internal ribosome entry site; b) presence or absence of a leader polypeptide; c) presence or absence of a VP0 maturation cleavage; d) type of 2A protein(s).

The above figure shows how different characteristics or properties of picornaviruses may be represented and used to give clues about how particular genome features have evolved. This type of analysis may prove more useful as more and more picornaviruses are discovered. However, it can already be used to predict certain features in genomes where only a small amount of sequence data is available.

For example, a small amount of sequence at the 3' end of the genome of a newly identified picornavirus of sheep indicates a relationship to the *Aphthovirus*, *Cardiovirus*, *Erbovirus* and *Teschovirus* genera (Fig. 2). It could be predicted that this new virus might i) have a Type II IRES; ii) possess a leader polypeptide; iii) possess at VP0 which is both myristoylated and undergoes a maturation cleavage; and iv) has a 2A with a NPG/P motif at its carboxy-joinment with 2B.

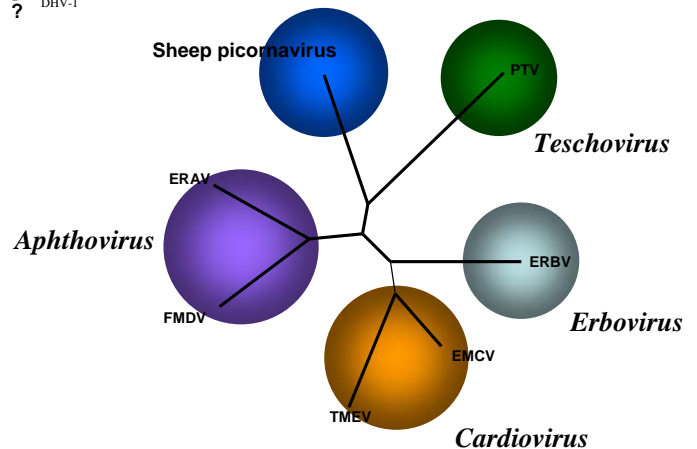


Fig. 2. Neighbor-joining tree based on a comparison of ~110 amino acids of the 3D polymerase showing the relationships of a newly identified picornavirus of sheep to existing genera.