

Figure 1a. Molecular Phylogenetic analysis of 135 partial RdRp.280nt HEV genomes by Maximum Likelihood method based on the Kimura 2-parameter model. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions with less than 95% site coverage were eliminated. There were a total of 280 positions in the final dataset. Evolutionary analyses were conducted in MEGA6. (Figure 1a) Global view of the unrooted tree, which correspond to Vina-Rodriguez, 2015.Fig.4 (b); (Figure 1b) Detailed view of the HEV-3 and "rabbit" clades. Some subtrees are collapsed and shown as ◀. (\*) - references sequences cited by Lu; (\*\*) strain used in the HEV RNA WHO standard; wb − wild boar.

**Figure 1b** . RdRp.280nt: 135 partial HEV-3 genome sequences spanning the region Burma.M73218 : 4284-4563 nt. Include the sequences obtained in this study (●)

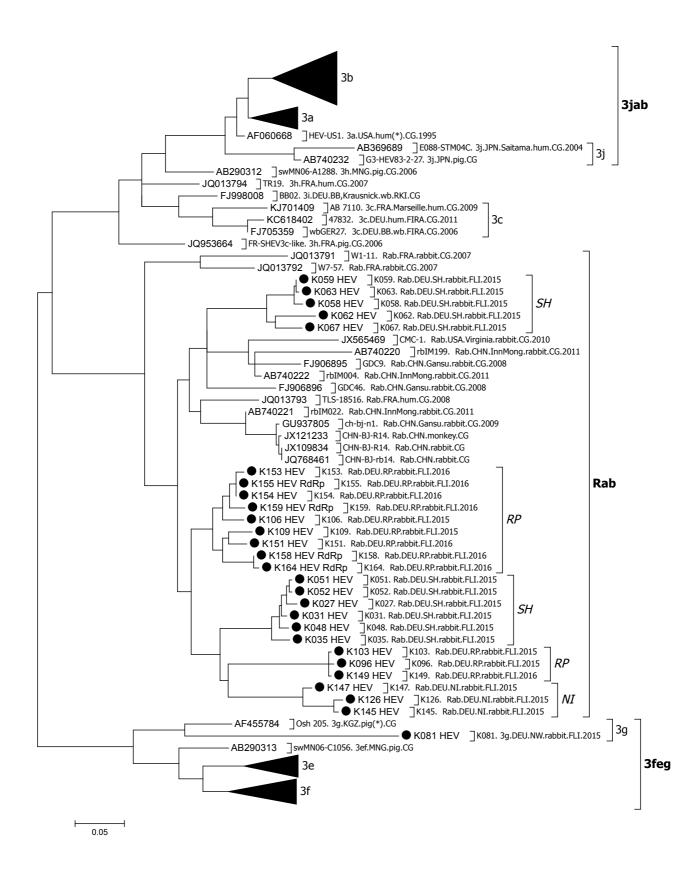


Figure 1c. Detailed view of the HEV-1, 4 and "rabbit" clades.

**Figure 1b** . RdRp.280nt: 135 partial HEV-3 genome sequences spanning the region Burma.M73218 : 4284-4563 nt. Include the sequences obtained in this study (●)

Hyo 3jab **CND** CHN **3**j 32 **3c** 3 3chi 31 3g **3e** 

93-1952 nt 96 sequences

ORF1.1860nt

**Figure 4.** Molecular phylogenetic analysis of: HVR.319nt (left): 126 partial HEV-3 genome sequences spanning the region Burma.M73218: 2094-2412 nt

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