

Família *Iridoviridae*

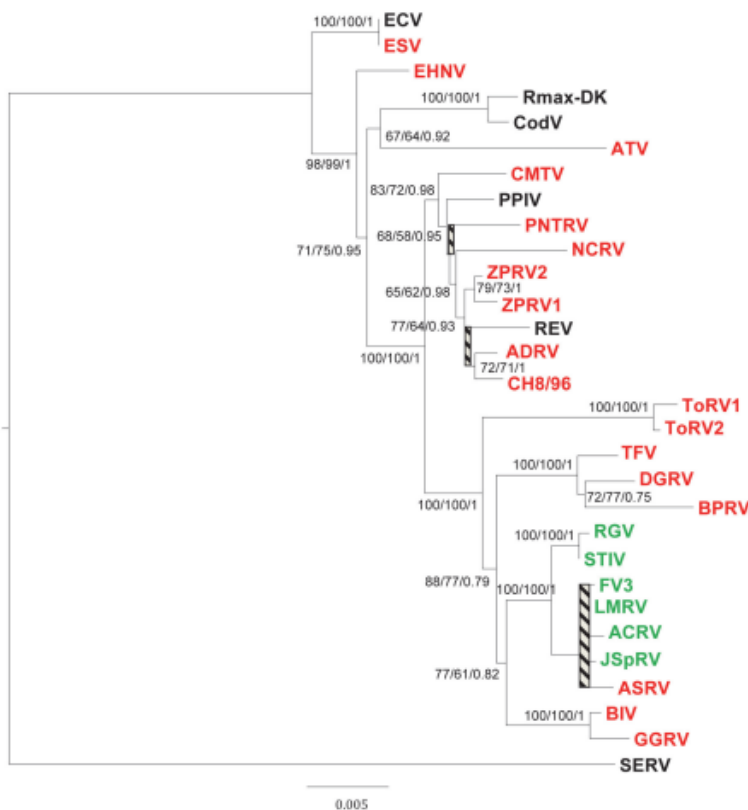
Género *Ranavirus*

Stöhr AC, López-Bueno A, Blahak S, Caeiro MF, Rosa GM, Alves de Matos AP, et al. (2015) Phylogeny and Differentiation of Reptilian and Amphibian Ranaviruses Detected in Europe. PLoS ONE 10(2): e0118633. doi:10.1371/journal.pone.0118633

Table 1

Table 2

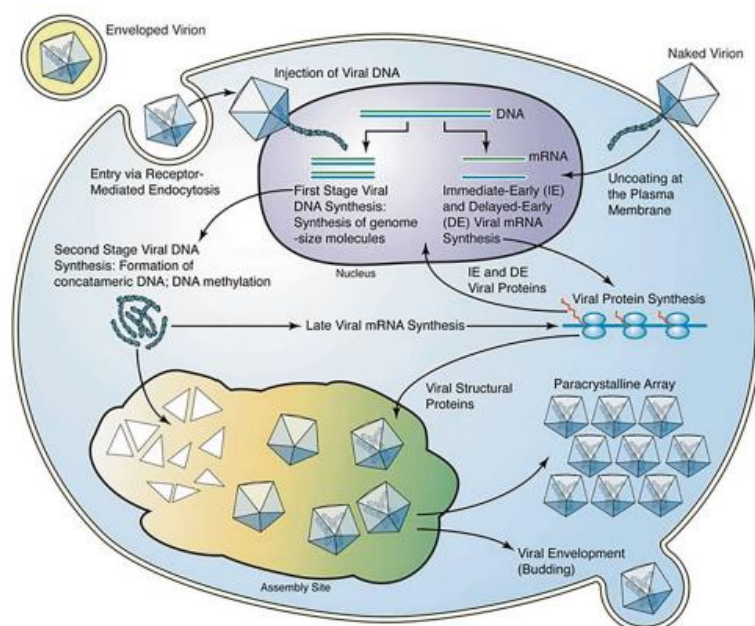
Table 5



**Fig 3. Ranavirus DNA distance tree of concatenated sequences (3223 bp) of MCP, DNAPol, RNR-α and RNR-β genes.** Partial nucleotide sequences of the different ranaviruses characterized in this study and ALRV sequences available in GenBank are included. Numbers at the nodes of the tree indicate bootstrap values of 1000 replicates in DNAdist-Fitch, maximum likelihood calculations, and MrBayes posterior probabilities. Branches with less than 60% support or variant clustering on the obtained trees were shaded. All calculated trees showed similar topologies. Ranaviruses with a full-length vIF-2α gene are indicated in red, truncated vIF-2α genes are in green, and those isolates for which this gene has not been sequenced are in black. GenBank accession numbers of the sequences used in the analysis: *Andrias davidianus* ranavirus isolate 1201 (ADRV) (KC865735), *Ambystoma tigrinum* virus (ATV) (AY150217), *Bohle iridovirus* (BIV) (AY187046, FJ374280, GU391286, GU391264), common midwife toad virus (CMTV) (JQ231222), cod ranavirus (CodV) (GU391284, GU391282, GU391287, GU391265), *European catfish virus* (ECV) (FJ358608, FJ374277, GU391288, GU391266), *Epizootic haematopoietic necrosis virus* (EHN) (FJ433873, FJ374274, GU391289, GU391267), *European sheatfish virus* (ESV) (FJ358609, FJ374278, GU391290, GU391268), *Frog virus 3* (FV3) (AY548484), pike-perch iridovirus (PPIV) (FJ358610, FJ374276, GU391292, GU391269), *Rana esculenta* virus Italy 282/02 (REV) (FJ358611, FJ374275, GU391293, GU391271), *Rana grylio* virus (RGV) (JQ654586), *Ranavirus maxima* (Rmax) (GU391285, GU391283, GU391291, GU391270), short-finned eel ranavirus (SERV) (FJ358612, FJ374279, GU391294, GU391272), soft-shelled turtle iridovirus (STIV) (EU627010), tiger frog virus (TFV) (AF389451), Zuerich Pelophylax collection ranavirus 1 (ZPRV1) (KC440841, KC440843, KC440845, KC440846), Zuerich Pelophylax collection ranavirus 2 (ZPRV2) (KC440842, KC440844, KC440845, KC440847).

**Ranavirus Replication: New Studies Provide Answers to Old Questions. James K. Jancovich, Qi-Ya Zhang, and V. Gregory Chinchar, 2025**

([https://link.springer.com/chapter/10.1007/978-3-031-64973-8\\_3](https://link.springer.com/chapter/10.1007/978-3-031-64973-8_3))



**Fig. 2** Schematic diagram of ranavirus replication. Virions enter cells by one of several routes, two of which are shown here. Initial events in virus replication (early viral transcription and the synthesis of unit length genomes) take place within the nucleus. Viral genomes are subsequently transported into the cytoplasm where they are methylated and serve as templates for concatemer formation. Viral assembly sites contain viral DNA and a number of virus-encoded proteins and serve as the loci of virion formation. Newly synthesized virions are found free within the cytoplasm or as members of paracrystalline arrays, or seen budding from the plasma membrane and in the process acquiring an envelope

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HyperLadder 1Kb (Bioline)

