

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2020.004D** |  |
| **Short title:** Create one new species in the genus *Lymphocystivirus* (*Pimascovirales*: *Iridoviridae*) | | |
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**Author(s) and email address(es)**

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| Doszpoly A, Kaján GL, Puentes R, Perretta A | [andor.doszpoly@gmail.com](mailto:andor.doszpoly@gmail.com); [gykajan@gmail.com](mailto:gykajan@gmail.com); [rodrigopuentes2011@gmail.com](mailto:rodrigopuentes2011@gmail.com); [aleperretta@gmail.com](mailto:aleperretta@gmail.com) |

**Author(s) institutional address(es) (optional)**

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| Institute for Veterinary Medical Research, Centre for Agricultural Research [AD, GLK]  Instituto de Patobiología, Facultad de Veterinaria, Universidad de la República [RP]  Instituto de Investigaciones Pesqueras, Facultad de Veterinaria, Universidad de la República [AP] |

**Corresponding author**

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| Andor Doszpoly |

**List the ICTV Study Group(s) that have seen this proposal**

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| *Iridoviridae* Study Group |

**ICTV study group comments and response of proposer**

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| Seven of seven responding members of the SG support this proposal. Species demarcation criteria should be explicitly mentioned. The “number of genes shared by ALL iridovirids” should be lowered to 24. The 10th Report on *Iridoviridae* should be cited. It would be nice to also have a table showing the pairwise identities.  Response of proposer: Requested corrections and additions done. |

**Authority to use the name of a living person**

|  |  |  |
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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | July 29, 2020 |
| Date of this revision (if different to above) | August 13, 2020 |

**ICTV-EC comments and response of the proposer**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.004D.R.Iridoviridae\_1nsp |

**Abstract**

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| A novel lymphocystivirus (LCDV-WC) has been detected and described recently at the coast of Uruguay in whitemouth croaker (*Micropogonias furnieri*) causing the typical signs of the lymphocystis virus disease [1]. The whole genome of the above mentioned virus has been sequenced and analysed [2]. Considering the actual species demarcation criteria for the family *Iridoviridae*, the establishment of a novel species (*Lymphocystis disease virus 4*) in the genus *Lymphocystivirus* issuggested [2]. |

**Text of proposal**

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| |  | | --- | | The complete genome of the LCDV-WC (MN803438) was found to be 211,086 bp. The G+C content of the whole genome proved to be 26.0%. Comparing the genome of the LCDV-WC to that of the formerly described LCDVs, the genome size of the LCDV-WC is the longest, and its G+C content is the lowest (LCDV-1: 29.1%, LCDV-2: 27.2% and LCDV-3: 33.0%) [2-5]. The genome organization of the LCDV-WC shows similarity to that of the LCDV-2 and -3, but major rearrangements were also observed (Figure 1). 148 predicted ORFs were determined in LCDV-WC genome. The majority of the ORFs (102) showed clear homology to the genes of all three other LCDVs. Twenty six core genes, which are conserved in most sequenced iridoviruses, were also identified in the genome [6]. Nine ORFs lacked similarity to any known viral genes. The rest of the putative genes showed homology only to genes of one or two of the LCDVs. The protein product concatenate of the core genes showed 67.1–85.1% amino acid identity to their LCDV counterparts (Figure 2). The phylogenetic tree reconstruction illustrates that the LCDV-WC undoubtedly clusters into the genus *Lymphocystivirus* and shows the clear separation of the LCDV-WC from the other LCDVs (Figure 3).  There are 26 well conserved core genes in the genomes of most known and completely sequenced iridoviruses (6). The products of these genes are associated with a variety of viral activities, like DNA metabolism, transcriptional regulation, protein modification, and viral structure [7]. According to species demarcation criteria for the members of the family *Iridoviridae*, 10th Report of the ICTV [6], viruses sharing 95% or greater amino acid identity (core genes) will be considered as belonging to the same virus species. Moreover, members of the same species should possess similar genome sizes, G+C content and display a collinear arrangement of viral genes. Furthermore, members of the same species should show phylogenetic relatedness. The analysis of the complete genome of the LCDV-WC indicates that LCDV-WC is a distinct virus species in the genus *Lymphocystivirus* based on differences in genome size, gene order, amino acid sequence identity, and phylogenetic analysis. The authors propose the *Lymphocystis disease virus 4* to be considered as the species designation. Thus the virus could be called lymphoystis disease virus 4 and abbreviated as LCDV-4. | |

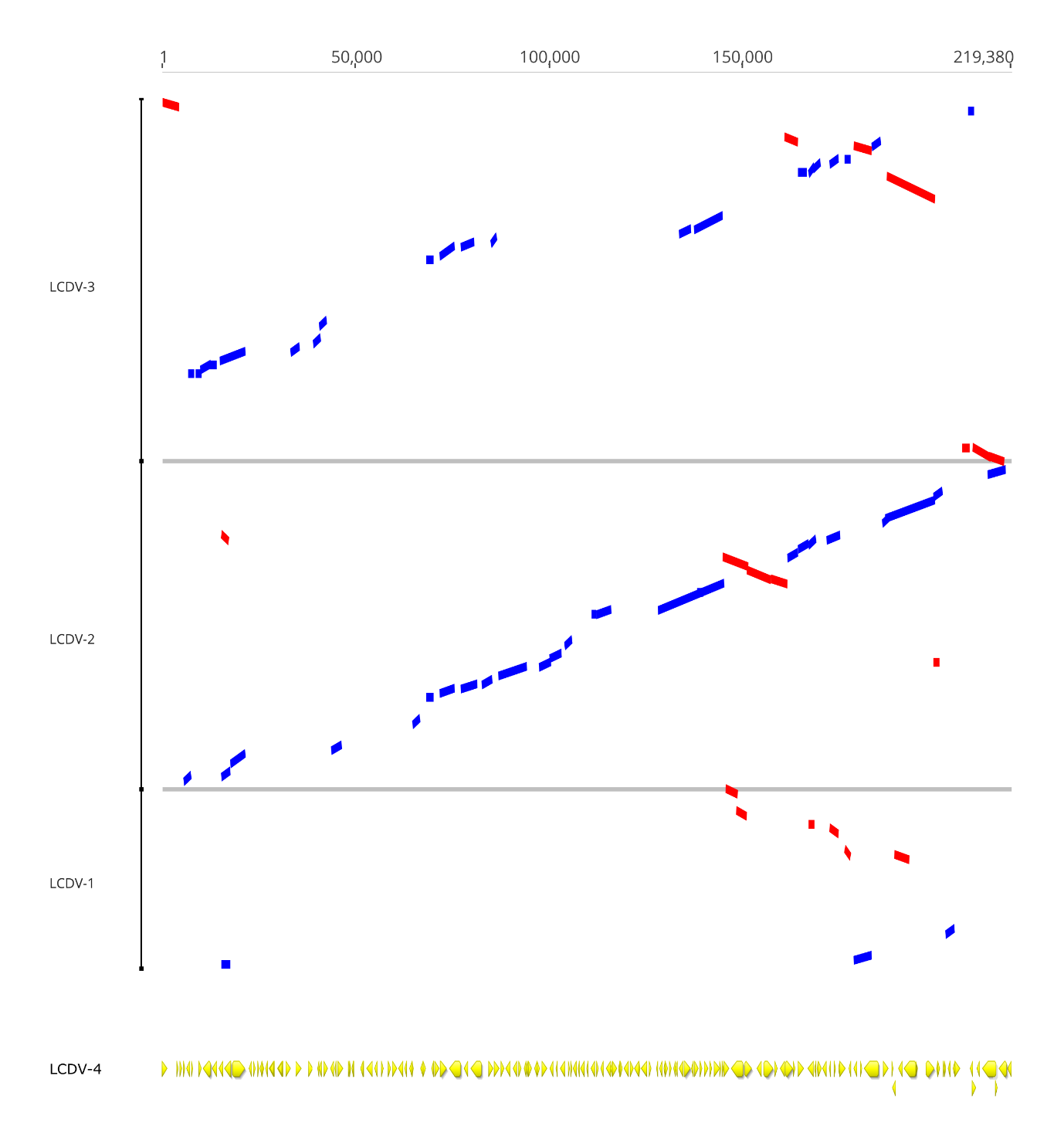
**Supporting evidence**

All figures are found in [2] and are open access.

**Table 1:** Genomic characteristics of lymphocystivirus isolates

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| **Virus** | **Genome size (kbp)** | **No. of ORFsa** | **G+C%** | **Hostb** | **GenBank Acc. No.** |
| LCDV-1 | 102 | 108 | 29% | *Platichthys flesus* (European flounder) | L63545 |
| LCDV-2 | 186 | 176 | 27% | *Paralichthys olivaceus* (Japanese flounder) | AY380826 |
| LCDV-3 | 208 | 183 | 33% | *Sparus aurata (*gilthead seabream) | KX643370 |
| LCDV-4 | 211 | 148 | 26% | *Micropogonias furnieri* (whitemouth croaker) | MN803438 |

a This value represent the number of putative genes, i.e., non-overlapping open reading frames. b. The indicated host is the source of this isolate.

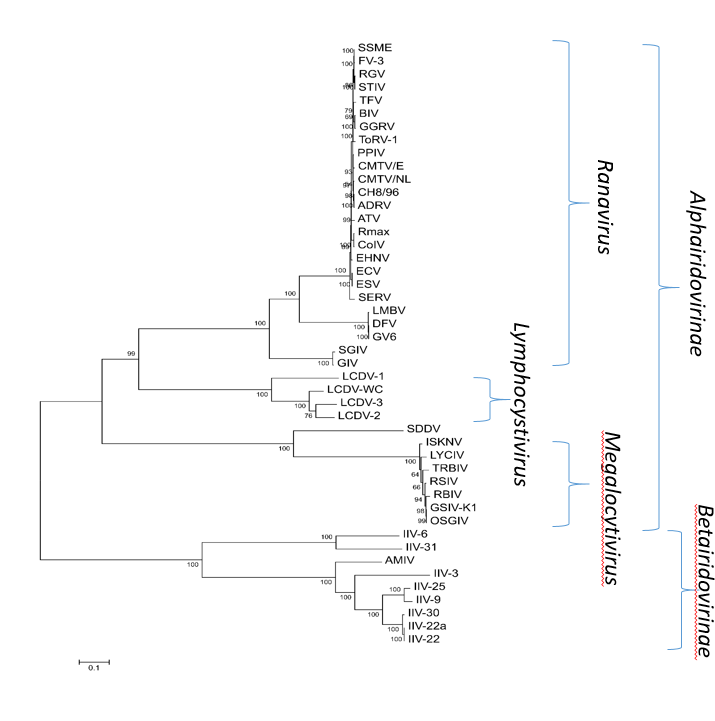
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**Figure. 1.** Comparison of thewhitemouth croaker lymphocystis disease virus (LCDV-WC) genome to the genomes of lymphocystis disease virus 1 to 3. The genome sequence of the LCDV-WC was placed on the abscissa (all CDSs of LCDV-4 is showed in the figure), whereas lymphocystis disease virus 1–3 genome sequences are placed on the ordinate in separate sections. Blue bars represent homologous high-scoring segment pairs in codirectional orientation, whereas red bars represent reversed pairs. The figure was conducted using LASTZ which does not simply make a whole genome alignment: genomic regions of LCDV-1, -2 and -3 were aligned against any possible match in the LCDV-4 genome. Thus the long gaps in the LCDV-1 and -3 parts of the figure mean that there was no significant match from these genomes to these genomic loci of LCDV-4 [2]. LCDV: Lymphocystis disease virus.

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|  | **LCDV-4** | **LCDV-2** | **LCDV-3** | **LCDV-1** |
| **LCDV-4** | X | 85.10% | 84.30% | 67.10% |
| **LCDV-2** | 85.10% | X | 85.20% | 66.30% |
| **LCDV-3** | 84.30% | 85.20% | X | 66.10% |
| **LCDV-1** | 67.10% | 66.30% | 66.10% | X |

**Figure. 2a.** Pairwise sequence identity analysis of the 26 core gene amino acid sequence concatenates of lymphocystis disease virus 1–3and whitemouth croaker lymphocystis disease virus. LCDV: lymphocystis disease virus; LCDV-WC: whitemouth croaker lymphocystis disease virus. Pairwise sequence identity percentages are represented using different colours. Cut-off values: 85% and 95%. Blue squares represent similarity below 85%, green squares 85-95%, red ≥95% [2]. **2b.** The same pairwise sequence identity matrix showing the precise percentages.



**Figure. 3.** Phylogenetic analysis of iridoviruses. Maximum likelihood analysis of 26 core gene amino acid sequence concatenates (8178 aa). The tree was rooted on midpoint. Bootstrap values are given as percentages. ADRV: Andrias davidianus ranavirus; AMIV: Anopholes minimus iridovirus; ATV: Ambystoma tigrinum virus; BIV: Bohle iridovirus; CH: Testudo hermanii ranavirus; CMTV: common midwife toad virus; CoIV: cod iridovirus; DFV: doctor fish virus; ECV: European catfish virus; EHNV: epizootic haematopoietic necrosis virus; ESV: European sheatfish virus; FV: frog virus; GGRV: German gecko ranavirus; GIV: grouper iridovirus; GSIV: giant seaperch iridovirus; GV: guppy virus; IIV: invertebrate iridescent virus; ISKNV: infectious skin and kidney necrosis virus; LCDV: lymphocystis disease virus; LMBV: largemouth bass virus; LYCIV: lemon yellow croaker iridovirus; OSGIV: orange-spotted grouper iridovirus; PPIV: pike perch iridovirus; RBIV: rock bream iridovirus; RGV: Rana grylio virus; Rmax: Rana maxima virus; RSIV: red seabream iridovirus; SDDV: scale drop disease virus; SERV: short-finned eel ranavirus; SGIV: Singapore grouper iridovirus; SSME: spotted salamander Maine virus; STIV: soft-shelled turtle iridovirus; TFV: tiger frog virus; ToRV: tortoise ranavirus; TRBIV: turbot reddish body iridovirus [2].

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