This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.015P*** | | | | (to be completed by ICTV officers) |
| **Short title:** A new species in the genus *Polerovirus*: *Pepo aphid-borne yellows virus*  (e.g. 6 new species in the genus *Zetavirus*) | | | | | |
| **Modules attached**  (modules 1 and 11 are required) | | **2** **⌧ 3  4  5**  **6  7  8  9  10** | | | |
| **Author(s):** | | | | | |
| Jacques Davy Ibaba Augustine Gubba  Mark D. Laing | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Jacques Davy Ibaba; davy\_i@hotmail.com | | | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | *Luteoviridae* | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | |  | |
| Date of this revision (if different to above): | | | |  | |

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

MODULE 2: **NEW SPECIES**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| creating and naming one or more new species.  If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed. | | | | | | | |
| Code |  | | | (assigned by ICTV officers) | | | |
| **To create a new species within:**  **Please see the accompanying Excel module <2017.015P.N.v1.Polerovirus\_sp>, which displays the taxonomic change in spreadsheet format** | | | | | | | |
|  | |  | | |  | Fill in all that apply.   * If the higher taxon has yet to be created (in a later module, below) write “**(new)**” after its proposed name. * If no genus is specified, enter “**unassigned**” in the genus box. | |
| Genus: | | ***Polerovirus*** | | |  |
| Subfamily: | |  | | |  |
| Family: | | ***Luteoviridae*** | | |  |
| Order: | |  | | |  |
| **Name of new species:** | | | **Representative isolate: (only 1 per species please)** | | | | **GenBank sequence accession number(s)** |
| *Pepo aphid-borne yellows virus* | | | RSA\_Pattypan | | | | KU315177 |
|  | | |  | | | |  |
|  | | | | | | | |
| **Reasons to justify the creation and assignment of the new species:**   * Explain how the proposed species differ(s) from all existing species.   + If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.   + If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria. * Further material in support of this proposal may be presented in the Appendix, Module 11 | | | | | | | |
| Pepo aphid-borne yellows virus (PABYV) genome consists of 5813 nucleotides and displays an organization typical of poleroviruses (Table 1). Blast results indicated that PABYV is related to other cucurbit-infecting poleroviruses. The highest nt and amino acid (aa) sequence identities, between 64 and 86%, were recorded with the ORFs 3a, 3, 4 and 5 (Table 2 and 3). The presence of both ORF0 and ORF4 on the genome is a distinguishing feature of the genus *Polerovirus*. Therefore, PABYV should be considered as a member of the genus *Polerovirus* based on the presence of these two ORFs on its genome. The species demarcation criterion in the family *Luteoviridae* is a 10% threshold difference in the aa identity in any of the viral proteins. All PABYV proteins have a difference in aa identity greater than 10% to known poleroviruses, thereby, confirming PABYV as a distinct species. The phylogenetic analysis showed that PABYV shared distant relationships with cucurbit aphid-borne yellows virus and Suakwa aphid-borne yellows virus for the coat protein and the RNA dependent RNA polymerase genes respectively (Fig. 1). | | | | | | | |

MODULE 11: **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| Ibaba, J. D., Laing, M. D. & Gubba, A. *Pepo aphid-borne yellows virus*: a new species in the genus *Polerovirus*. *Virus Genes* **53,** 134–136 (2017).  Knierim, D., Tsai, W. S., Maiss, E. & Kenyon, L. Molecular diversity of poleroviruses infecting cucurbit crops in four countries reveals the presence of members of six distinct species. *Arch. Virol.* **159,** 1459–1465 (2014). |

|  |
| --- |
| **Annex:**  Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

**Table 1.** Genome organization of SA PABYV

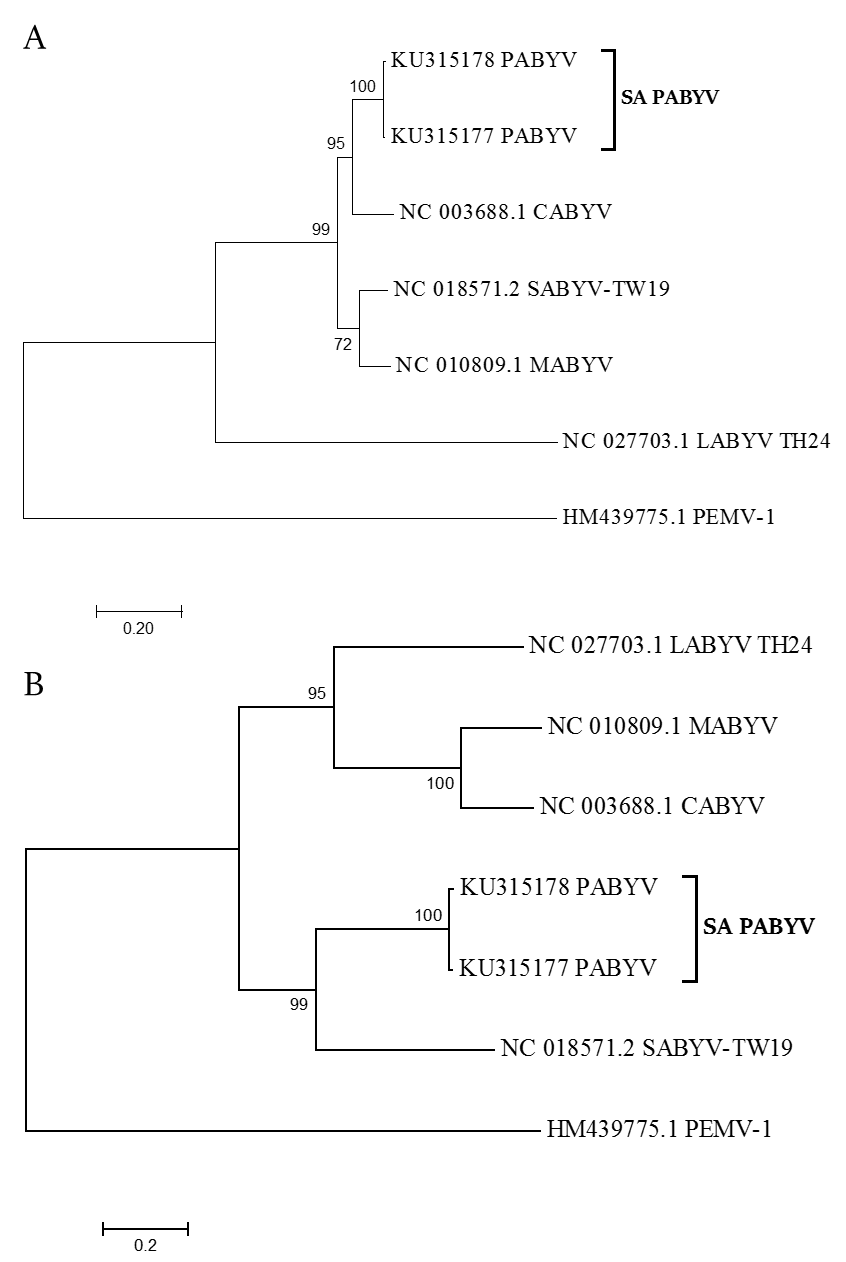
|  |  |
| --- | --- |
| Genome features | Position |
| 5’ Non-coding region (NCR) | 1-55 |
| ORF0 | 56-847 |
| ORF1 | 210-2081 |
| ORF2 | 210-1655, 1655-3343 |
| Intergenic region | 3344-3449 |
| ORF3a | 3450- 3587 |
| ORF3 | 3568-4167 |
| ORF4 | 3596-4171 |
| ORF5 | 3568-5619 |
| 3’NCR | 5620-5813 |

**Table 2.** Nucleotide sequence identities between the genomes of the SA PABYV isolate and the other cucurbit-infecting poleroviruses

|  |  |  |
| --- | --- | --- |
| Genome features | Polerovirus infecting cucurbits | PABYV patty pan |
| 5’NCR | CABYV NC003688.1 | 30.0% |
| LABYV NC027703.1 | 41.8% |
| MABYV NC010809.1 | 30.0% |
| SABYV NC 018571.2 | 42.6% |
| ORF0 | CABYV NC003688.1 | 40.7% |
| LABYV NC027703.1 | 36.0% |
| MABYV NC010809.1 | 40.6% |
| SABYV NC 018571.2 | 35.8% |
| OFR1 | CABYV NC003688.1 | 42.8% |
| LABYV NC027703.1 | 42.4% |
| MABYV NC010809.1 | 42.0% |
| SABYV NC 018571.2 | 49.8% |
| ORF2 | CABYV NC003688.1 | 48.9% |
| LABYV NC027703.1 | 49.8% |
| MABYV NC010809.1 | 50.2% |
| SABYV NC 018571.2 | 56.5% |
| ORF3a | CABYV NC003688.1 | 74.6% |
| LABYV NC027703.1 | 75.4% |
| MABYV NC010809.1 | 74.6% |
| SABYV NC 018571.2 | 73.9% |
| ORF3 | CABYV NC003688.1 | 85.7% |
| LABYV NC027703.1 | 51.8% |
| MABYV NC010809.1 | 83.2% |
| SABYV NC 018571.2 | 82.5% |
| ORF4 | CABYV NC003688.1 | 86.1% |
| LABYV NC027703.1 | 25.7% |
| MABYV NC010809.1 | 74.8% |
| SABYV NC 018571.2 | 83.8% |
| ORF5 | CABYV NC003688.1 | 64.1% |
| LABYV NC027703.1 | 38.5% |
| MABYV NC010809.1 | 59.6% |
| SABYV NC 018571.2 | 60.4% |
| 3’NCR | CABYV NC003688.1 | 42.2% |
| LABYV NC027703.1 | 53.6% |
| MABYV NC010809.1 | 41.3% |
| SABYV NC 018571.2 | 52.1% |

**Table 3.** Amino-acid sequence identities between the proteins of the SA PABYV isolate and the other cucurbit-infecting poleroviruses

|  |  |  |
| --- | --- | --- |
| Proteins | Polerovirus infecting cucurbits | PABYV patty pan |
| P0 | CABYV NC003688.1 | 21.3% |
| LABYV NC027703.1 | 17.9% |
| MABYV NC010809.1 | 22.7% |
| SABYV NC 018571.2 | 20.5% |
| P1 | CABYV NC003688.1 | 28.5% |
| LABYV NC027703.1 | 26.4% |
| MABYV NC010809.1 | 28.5% |
| SABYV NC 018571.2 | 38.0% |
| P1-P2 | CABYV NC003688.1 | 41.5% |
| LABYV NC027703.1 | 41.3% |
| MABYV NC010809.1 | 43.6% |
| SABYV NC 018571.2 | 51.7% |
| P3a | CABYV NC003688.1 | 78.3% |
| LABYV NC027703.1 | 78.3% |
| MABYV NC010809.1 | 78.3% |
| SABYV NC 018571.2 | 76.1% |
| P3 | CABYV NC003688.1 | 82.5% |
| LABYV NC027703.1 | 43.5% |
| MABYV NC010809.1 | 82.5% |
| SABYV NC 018571.2 | 84.0% |
| P4 | CABYV NC003688.1 | 76.6% |
| LABYV NC027703.1 | 28.6% |
| MABYV NC010809.1 | 71.9% |
| SABYV NC 018571.2 | 72.4% |
| P3-P5 | CABYV NC003688.1 | 64.5% |
| LABYV NC027703.1 | 25.7% |
| MABYV NC010809.1 | 58.7% |
| SABYV NC 018571.2 | 58.9% |

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**Fig. 1.** Maximum likelihood relationships of the South African Pepo aphid-borne yellows virus (SA PABYV) isolates to poleroviruses infecting cucurbits reported to date based on the general time reversible model with a discrete gamma distribution and evolutionarily invariable sites for the coat protein (A) and the RNA dependent RNA polymerase (B). The trees were generated using MEGA 7 with 1000 replicates. Bootstrap values are indicated next to the branches. The branch scale represents the number of substitutions per site. CABYV: cucurbit aphid-borne yellows virus; LABYV: Luffa aphid-borne yellows virus; MABYV: melon aphid-borne yellows virus; SABYV: Suakwa aphid-borne yellows virus; PEMV-1: pea enation mosaic virus 1 was used to root the trees.