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:** | ***2016.005aD*** | (to be completed by ICTV officers) |

**Short title:** Six new species in genus *Betabaculovirus*
(e.g. 6 new species in the genus *Zetavirus*)

| | |
|---|---|
| **Modules attached**<br>(modules 1 and 11 are required) | **2** ☒ **3** ☐ **4** ☐ **5** ☐<br>**6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐ |

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**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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses) | Baculoviridae/Nudiviridae Study Group |

**ICTV Study Group comments (if any) and response of the proposer:**

| | |
|---|---|
| Date first submitted to ICTV: | July 15, 2016 |
| 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 | ***2016.005aD*** | (assigned by ICTV officers) |

**To create 6 new species within:**

| | |
|---|---|
| Genus: | ***Betabaculovirus*** |
| Subfamily: | |
| Family: | ***Baculoviridae*** |
| Order: | |

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.

| **Name of new species:** | **Representative isolate: (only 1 per species please)** | **GenBank sequence accession number(s)** |
|---|---|---|
| *Clostera anachoreta granulovirus* | Clostera anachoreta granulovirus HBHN | HQ116624 |
| *Clostera anastomosis granulovirus A* | Clostera anastomosis granulovirus Henan | KC179784 |
| *Clostera anastomosis granulovirus B* | Clostera anastomosis granulovirus B | KR091910 |
| *Diatraea saccharalis granulovirus* | Diatraea saccharalis granulovirus Parana-2009 | KP296186 |
| *Epinotia aporema granulovirus* | Epinotia aporema granulovirus Oliveros.Santa Fe | JN408834 |
| *Spodoptera litura granulovirus* | Spodoptera litura granulovirus K1 | DQ288858 |

**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

Isolates of the above proposed species can be identified as belonging to the genus *Betabaculovirus* of family *Baculoviridae* on the basis of three or more of the following criteria (Herniou et al., 2011):

- host species of the insect order Lepidoptera;
- circular double-stranded DNA genome ranging in size from 100 – 180 kbp with a gene content characteristic of other betabaculoviruses;
- relationships to other baculoviruses as inferred by molecular phylogeny;
- occlusion bodies formed within the nucleus with a characteristic shape and size

(ovocylindrical, approximately 0.13 x 0.50 µm);
- rod-shaped virions consisting of a single enveloped nucleocapsid, with a single virion contained in each occlusion body.

Figure 1 shows the relationships of representative isolates of the proposed species to representative isolates of other recognized species in the genus *Betabaculovirus* (Table 1), as well as a selection of representative isolates for the other three genera of *Baculoviridae* (*Alphabaculovirus*, *Gammabaculovirus*, and *Deltabaculovirus*), determined from the concatenated alignment of the predicted amino acid sequences of 37 baculovirus core genes (Garavaglia et al., 2012). The tree shows that all six representatives of the proposed *Betabaculovirus* species group with other betabaculoviruses.

Distinctions among species of the *Baculoviridae* have been based on host range, DNA restriction endonuclease fragment patterns, and comparisons of nucleotide and predicted amino acid sequences from various genes. In addition, species demarcation criteria for baculoviruses have been proposed that rely upon pairwise nucleotide distances estimated with the Kimura-2-parameter substitution model from partial sequences of three conserved baculovirus genes: *lef-8* and *lef-9* (encoding viral RNA polymerase subunits), and *granulin* (*polh*) (encoding the viral occlusion body matrix protein) (Jehle et al., 2006). If nucleotide distances between two viruses are less than 0.015 substitutions/site, the two baculoviruses are considered to be the same species. If nucleotide distances between two viruses are greater than 0.05 substitutions/site, the viruses are considered to be different species. If the nucleotide distances lie between 0.015 and 0.050 substitutions/site, additional characteristics of the two viruses (*i.e.* host range) must be considered to make a decision about their taxonomic status. The proposed criterion was originally based on an alignment of sequences from 117 separate baculovirus isolates and the phylogeny inferred from this alignment. Researchers have applied this criterion to other isolates to identify many new baculovirus species and variants of currently recognized species.

Pairwise nucleotide distances for *lef*-8, *lef*-9, and *granulin* (*polh*) are shown in Tables 2 and 3. The distances between the sequences of the proposed species' representative isolates and other betabaculovirus isolates are >0.05 substitutions/site for each locus, indicating that the isolates under consideration are representatives of new, previously unrecognized species and not variants of currently existing species.

## MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

**_*Baculoviridae* core genes, *Betabaculovirus* characteristics, and proposed species demarcation criterion_**

Jehle, J.A., Lange, M., Wang, H., Hu, Z., Wang, Y., Hauschild, R., 2006. Molecular identification and phylogenetic analysis of baculoviruses from Lepidoptera. Virology 346, 180-193.

Garavaglia, M.J., Miele, S.A., Iserte, J.A., Belaich, M.N., Ghiringhelli, P.D., 2012. The ac53, ac78, ac101, and ac103 genes are newly discovered core genes in the family *Baculoviridae*. J Virol 86, 12069-12079.

Herniou, E.A., Arif, B.M., Becnel, J.J., Blissard, G.W., Bonning, B., Harrison, R.L., Jehle, J.A., Theilmann, D.A., Vlak, J.M., 2011. Baculoviridae, in: King, A.M.Q., Adams, M.J., Carstens, E.B., Lefkowitz, E.J. (Eds.), Virus Taxonomy: Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier, Oxford, pp. 163-174.

**_*Clostera anachoreta granulovirus*_**

Zhang, X.X., Liang, Z.P., Peng, H.Y., Zhang, Z.X., Tang, X.C., Liu, T.Q., 2005. Characterization and partial genome sequence analysis of Clostera anachoreta granulovirus. Virus Res 113, 36–43

Liang, Z., Zhang, X., Yin, X., Cao, S. and Xu, F., 2011. Genomic sequencing and analysis of Clostera anachoreta granulovirus. Arch Virol 156, 1185-1198.

**_*Clostera anastomosis granulovirus A*_**

Liang, Z., Zhang, X., Yin, X., Song, X., Shao, X., Wang, L., 2013. Comparative analysis of the genomes of Clostera anastomosis (L.) granulovirus and Clostera anachoreta granulovirus. Arch Virol 158, 2109-2114.

**_*Clostera anastomosis granulovirus B*_**

Tang, X., Peng, H., Zhang, X., Zhao, S., Xiao, Y., 2004. Analysis on morphology and restriction endonucleases of *Clostera anastomosis* (L.) granulosis virus. J Huazhong Agri 23, 616–619.

Yin, F., Zhu, Z., Liu, X., Hou, D., Wang, J., Zhang, L., Wang, M., Kou, Z., Wang, H., Deng, F., Hu, Z., 2015. The complete genome of a new betabaculovirus from *Clostera anastomosis*. PLoS One 10, e0132792.

**_*Diatraea saccharalis granulovirus*_**

Ardisson-Araújo, D.M., Pereira, B.T., Melo, .FL., Ribeiro, B.M., Báo, S.N., Zanotto, P.M. de A., Moscardi, F., Kitajima, E.W., Sosa-Gomez, D.R., Wolff, J.L., 2016. A betabaculovirus encoding a gp64 homolog. BMC Genomics 17, 94.

**_*Epinotia aporema granulovirus*_**

Sciocco-Cap A., Parola A.D., Goldberg A.V., Ghiringhelli P.D., Romanowski V., 2001. Characterization of a granulovirus isolated from *Epinotia aporema* Wals. (Lepidoptera: Tortricidae) larvae. Appl Environ Microbiol 67, 3702-3706.

Ferrelli, M.L., Salvador, R., Biedma, M.E., Berretta, M.F., Haase, S., Sciocco-Cap, A., Ghiringhelli, P.D. and Romanowski, V., 2012. Genome of Epinotia aporema granulovirus (EpapGV), a polyorganotropic fast killing betabaculovirus with a novel

additional material in support of this proposal

## References:

thymidylate kinase gene. BMC Genomics 13, 548.

***Spodoptera litura granulovirus***

Wang,Y., Choi, J.Y., Roh, J.Y., Woo, S.D., Jin, B.R., Je,Y.H., 2008. Molecular and phylogenetic characterization of Spodoptera litura granulovirus. J Microbiol 46, 704-708.

Wang, Y, Choi, J.Y., Roh, J.Y., Liu, Q., Tao, X.Y., Park, J.B., Kim, J.S., Je, Y.H., 2011. Genomic sequence analysis of granulovirus isolated from the tobacco cutworm, *Spodoptera litura*. PLoS One 6, e28163.

## 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. Betabaculovirus isolates used in core gene phylogeny and pairwise distance estimation. Isolates for newly proposed species are indicated in bold type.

| Isolate | Species | Accession no. | Abbreviation |
|---|---|---|---|
| Adoxophyes orana granulovirus-English | *Adoxophyes orana granulovirus* | AF547984 | AdorGV-English |
| Agrotis segetum granulovirus Darmstadt | *Agrotis segetum granulovirus* | KR584663 | AgseGV-DA |
| Choristoneura occidentalis granulovirus | *Choristoneura fumiferana granulovirus* | DQ333351 | ChocGV |
| **Clostera anachoreta granulovirus HBHN** | ***Clostera anachoreta granulovirus*** | **HQ116624** | **ClanGV-HBHN** |
| **Clostera anastomosis granulovirus Henan** | ***Clostera anastomosis granulovirus A*** | **KC179784** | **CalGV-Henan (ClasGV-A)** |
| **Clostera anastomosis granulovirus B** | ***Clostera anastomosis granulovirus B*** | **KR091910** | **ClasGV-B** |
| Cryptophlebia leucotreta granulovirus CV3 | *Cryptophlebia leucotreta granulovirus* | AY229987 | CrleGV-CV3 |
| Cydia pomonella granulovirus M1 | *Cydia pomonella granulovirus* | U53466 | CpGV-M1 |
| **Diatraea saccharalis granulovirus Parana-2009** | ***Diatraea saccharalis granulovirus*** | **KP296186** | **DisaGV-Parana-2009** |
| **Epinotia aporema granulovirus Oliveros.Santa Fe** | ***Epinotia aporema granulovirus*** | **JN408834** | **EpapGV-Oliveros.Santa Fe** |
| Erinnyis ello granulovirus S68 | *Erinnyis ello granulovirus* | KJ406702 | ErelGV-S68 |
| Helicoverpa armigera granulovirus | *Helicoverpa armigera granulovirus* | EU255577 | HearGV |
| Mocis sp. granulovirus | - | KR011718 | MospGV |
| Phthorimaea operculella granulovirus Tunisian | *Phthorimaea operculella granulovirus* | AF499596 | PhopGV-T |
| Pieris rapae granulovirus-Wuhan | *Artogeia rapae granulovirus* | GQ884143 | PiraGV-Wuhan |
| Plutella xylostella granulovirus K1 | *Plutella xylostella granulovirus* | AF270937 | PlxyGV-K1 |
| Pseudalatia unipuncta granulovirus Hawaiian | *Pseudalatia unipuncta granulovirus* | EU678671 | PsunGV-H |
| Spodoptera frugiperda granulovirus VG008 | *Spodoptera frugiperda granulovirus* | KM371112 | SpfrGV-VG008 |
| **Spodoptera litura granulovirus K1** | ***Spodoptera litura granulovirus*** | **DQ288858** | **SpltGV-K1** |
| Trichoplusia ni granulovirus M10-5 | *Trichoplusia ni granulovirus* | AY519201-AY519203 | TnGV M10-5 |
| Xestia c-nigrum granulovirus α4 | *Xestia c-nigrum granulovirus* | AF162221 | XecnGV-α4 |

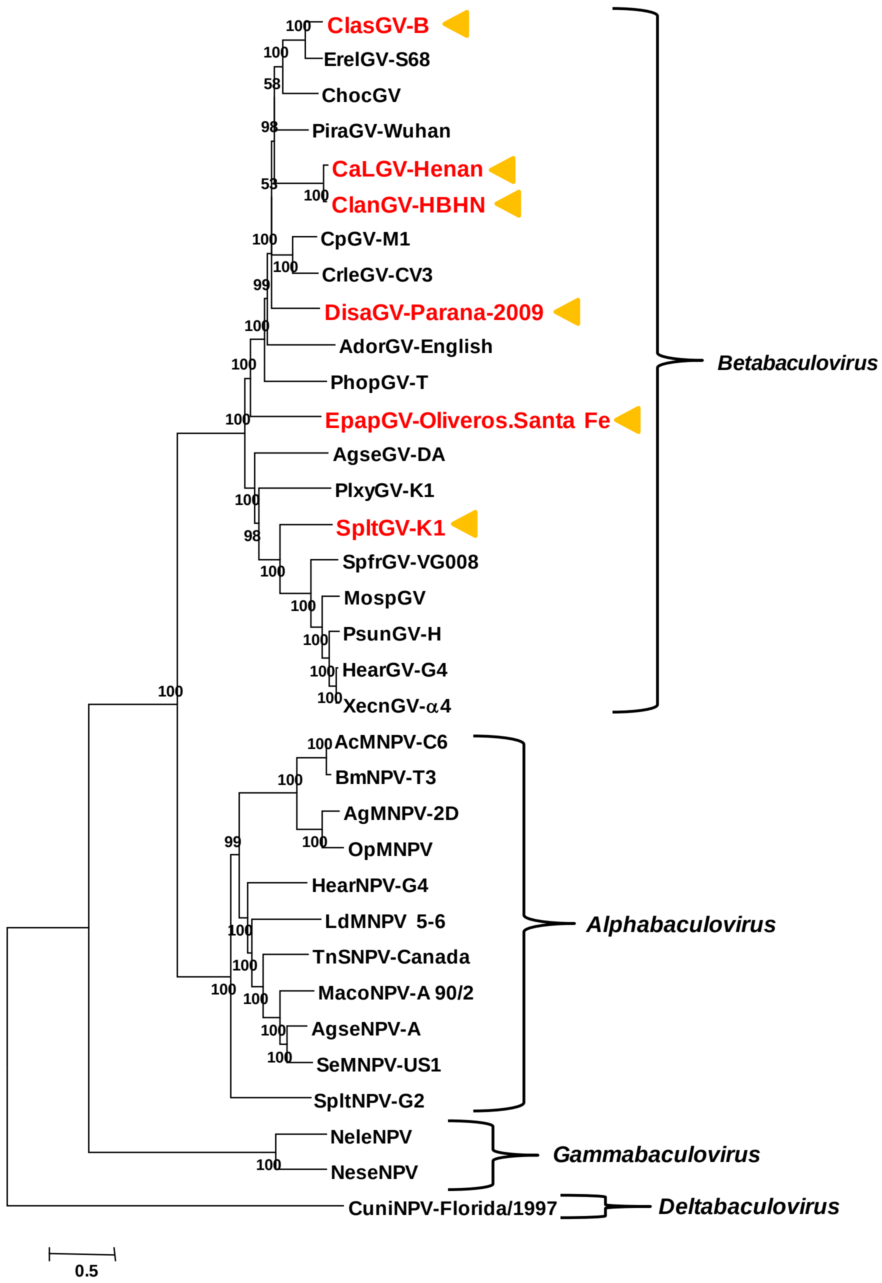

Figure 1. Relationships of betabaculovirus isolates (Table 1) and other baculovirus isolates, inferred from the predicted amino acid sequences of baculovirus core genes. The phylogenetic tree was constructed from the concatenated alignments of 37 baculovirus core gene amino acid sequences using the minimum-evolution method using the James-Taylor-Thornton substitution model. Bootstrap values are shown for each node. Clades corresponding to the four genera of *Baculoviridae* are indicated. Representative isolates of the proposed species are listed in red font and denoted with a yellow arrow. In addition to betabaculoviruses listed in Table 1, taxa from the other baculovirus genera are included in the analysis, including Agrotis segetum nucleopolyhedrovirus A (AgseNPV-A), Anticarsia gemmatalis multiple nucleopolyhedrovirus 2D (AgMNPV-2D), Autographa californica multiple nucleopolyhedrovirus C6 (AcMNPV-C6), Bombyx mori nucleopolyhedrovirus T3 (BmNPV-T3), Culex nigripalpus nucleopolyhedrovirus Florida/1997 (CuniNPV-Florida/1997), Helicoverpa armigera nucleopolyhedrovirus G4 (HearNPV-G4), Lymantria dispar multiple nucleopolyhedrovirus 5-6 (LdMNPV 5-6), Mamestra configurata nucleopolyhedroviruses A 90/2 (MacoNPV-A 90/2), Neodiprion lecontei nucleopolyhedrovirus (NeleNPV), Neodiprion sertifer nucleopolyhedrovirus (NeseNPV), Spodoptera exigua multiple nucleopolyhedrovirus US1 (SeMNPV-US1), Spodoptera litura nucleopolyhedrovirus G2 (SpltNPV-G2), Trichoplusia ni single nucleopolyhedrovirus Canada (TnSNPV-Canada).

Table 2. Pairwise nucleotide distances calculated from partial *lef-8* and *lef-9* sequence alignments*

| *lef-9* | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *lef-8* | **1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** | **10** | **11** | **12** | **13** | **14** | **15** | **16** | **17** | **18** | **19** | **20** | **21** |
| **1.** AdorGV-English | | 0.563 | 0.297 | **0.419** | 0.386 | **0.406** | **0.445** | 0.433 | 0.361 | **0.426** | **0.423** | 0.428 | 0.632 | 0.475 | 0.467 | 0.461 | 0.640 | 0.551 | **0.516** | 0.632 | 0.614 |
| **2.** AgseGV-DA | 0.794 | | 0.500 | **0.680** | 0.489 | **0.421** | **0.680** | 0.504 | 0.404 | **0.560** | **0.507** | 0.504 | 0.469 | 0.469 | 0.575 | 0.631 | 0.526 | 0.453 | **0.498** | 0.548 | 0.477 |
| **3.** PiraGV-Wuhan | 0.577 | 0.655 | | **0.481** | 0.438 | **0.331** | **0.454** | 0.404 | 0.419 | **0.429** | **0.414** | 0.380 | 0.508 | 0.479 | 0.390 | 0.506 | 0.569 | 0.484 | **0.482** | 0.577 | 0.508 |
| **4.** CalGV-Henan (ClasGV-A) | **0.939** | **0.947** | **0.961** | | **0.442** | **0.435** | **0.090** | **0.317** | **0.526** | **0.478** | **0.467** | **0.428** | **0.597** | **0.675** | **0.433** | **0.414** | **0.723** | **0.484** | **0.566** | **0.696** | **0.605** |
| **5.** ChocGV | 0.568 | 0.738 | 0.375 | **1.053** | | **0.374** | **0.474** | 0.441 | 0.319 | **0.433** | **0.473** | 0.314 | 0.490 | 0.465 | 0.435 | 0.488 | 0.610 | 0.627 | **0.463** | 0.624 | 0.504 |
| **6.** ClasGV-B | **0.751** | **0.813** | **0.453** | **0.996** | **0.463** | | **0.447** | **0.384** | **0.346** | **0.484** | **0.348** | **0.279** | **0.395** | **0.513** | **0.395** | **0.511** | **0.614** | **0.459** | **0.478** | **0.624** | **0.408** |
| **7.** ClanGV-HBHN | **0.891** | **0.866** | **0.892** | **0.079** | **0.972** | **0.970** | | **0.355** | **0.554** | **0.414** | **0.488** | **0.440** | **0.623** | **0.713** | **0.490** | **0.475** | **0.753** | **0.484** | **0.598** | **0.766** | **0.614** |
| **8.** CpGV-M1 | 0.721 | 0.867 | 0.597 | **0.850** | 0.547 | **0.569** | **0.868** | | 0.342 | **0.414** | **0.335** | 0.345 | 0.499 | 0.624 | 0.396 | 0.561 | 0.565 | 0.365 | **0.450** | 0.546 | 0.465 |
| **9.** CrleGV-CV3 | 0.628 | 0.825 | 0.448 | **0.911** | 0.441 | **0.593** | **0.841** | 0.482 | | **0.482** | **0.441** | 0.327 | 0.539 | 0.465 | 0.443 | 0.484 | 0.699 | 0.435 | **0.538** | 0.716 | 0.526 |
| **10.** DisaGV-Parana-2009 | **0.647** | **0.730** | **0.573** | **0.724** | **0.777** | **0.779** | **0.735** | **0.630** | **0.674** | | **0.529** | **0.543** | **0.606** | **0.713** | **0.402** | **0.429** | **0.666** | **0.560** | **0.645** | **0.696** | **0.631** |
| **11.** EpapGV-Oliveros.Santa Fe | **0.734** | **0.890** | **0.709** | **0.782** | **0.804** | **0.713** | **0.778** | **0.775** | **0.832** | **0.802** | | **0.452** | **0.484** | **0.520** | **0.437** | **0.426** | **0.520** | **0.463** | **0.434** | **0.499** | **0.492** |
| **12.** ErelGV-S68 | 0.787 | 0.740 | 0.481 | **1.222** | 0.423 | **0.351** | **1.222** | 0.583 | 0.632 | **0.800** | **0.844** | | 0.566 | 0.535 | 0.371 | 0.572 | 0.723 | 0.472 | **0.593** | 0.740 | 0.558 |
| **13.** HearGV | 0.773 | 0.844 | 0.719 | **0.993** | 0.839 | **0.786** | **0.973** | 0.872 | 0.859 | **0.791** | **0.778** | 0.920 | | 0.316 | 0.582 | 0.578 | 0.232 | 0.310 | **0.389** | 0.226 | 0.025 |
| **14.** MospGV | 0.719 | 0.782 | 0.735 | **0.926** | 0.813 | **0.842** | **0.914** | 0.905 | 0.780 | **0.767** | **0.742** | 0.879 | 0.363 | | 0.661 | 0.594 | 0.318 | 0.452 | **0.495** | 0.312 | 0.316 |
| **15.** PhopGV-T | 0.652 | 0.803 | 0.598 | **0.746** | 0.685 | **0.627** | **0.756** | 0.607 | 0.687 | **0.686** | **0.623** | 0.696 | 0.599 | 0.665 | | 0.512 | 0.653 | 0.530 | **0.576** | 0.682 | 0.597 |
| **16.** PlxyGV-K1 | 0.633 | 0.788 | 0.772 | **0.879** | 0.784 | **0.837** | **0.871** | 0.814 | 0.754 | **0.662** | **0.585** | 0.910 | 0.674 | 0.665 | 0.726 | | 0.636 | 0.388 | **0.455** | 0.629 | 0.585 |
| **17.** PsunGV-H | 0.742 | 0.942 | 0.706 | **0.877** | 0.784 | **0.829** | **0.899** | 0.950 | 0.771 | **0.775** | **0.876** | 0.940 | 0.186 | 0.322 | 0.659 | 0.746 | | 0.345 | **0.417** | 0.004 | 0.221 |
| **18.** SpfrGV-VG008 | 0.819 | 1.001 | 0.856 | **0.852** | 0.925 | **0.917** | **0.896** | 0.731 | 0.902 | **0.923** | **0.817** | 0.943 | 0.429 | 0.552 | 0.732 | 0.754 | 0.470 | | **0.378** | 0.359 | 0.313 |
| **19.** SpltGV-K1 | **0.823** | **0.807** | **0.686** | **0.888** | **0.827** | **0.981** | **0.888** | **0.938** | **0.739** | **0.723** | **0.817** | **0.961** | **0.629** | **0.701** | **0.829** | **0.809** | **0.613** | **0.666** | | **0.398** | **0.382** |
| **20.** TnGV-M10-5 | 0.749 | 0.942 | 0.713 | **0.877** | 0.792 | **0.837** | **0.899** | 0.960 | 0.778 | **0.775** | **0.886** | 0.951 | 0.189 | 0.326 | 0.665 | 0.753 | 0.002 | 0.475 | **0.619** | | 0.216 |
| **21.** XecnGV-α4 | 0.783 | 0.856 | 0.730 | **1.003** | 0.865 | **0.808** | **0.983** | 0.891 | 0.838 | **0.767** | **0.813** | 0.918 | 0.017 | 0.376 | 0.628 | 0.706 | 0.191 | 0.416 | **0.615** | 0.194 | |

*The number of base substitutions per site between pairs of sequences are shown. Abbrevations of the taxa are as listed for Table 1. Analyses were conducted using the Kimura 2-parameter model in MEGA6. Pairwise distances for *lef-8* sequences are listed below the diagonal lines, and *lef-9* distances are listed above the diagonal lines. Values for the proposed species are in red bold type.

Table 3. Pairwise nucleotide distances calculated from partial *gran* (*polh*) sequence alignments*

| *granulin* (*polh*) | **1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** | **10** | **11** | **12** | **13** | **14** | **15** | **16** | **17** | **18** | **19** | **20** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1.** AdorGV-English | | | | | | | | | | | | | | | | | | | | |
| **2.** AgseGV-DA | 0.509 | | | | | | | | | | | | | | | | | | | |
| **3.** PiraGV-Wuhan | 0.630 | 0.886 | | | | | | | | | | | | | | | | | | |
| **4.** CalGV-Henan (ClasGV-A) | **0.419** | **0.628** | **0.733** | | | | | | | | | | | | | | | | | |
| **5.** ChocGV | 0.549 | 0.640 | 0.648 | **0.451** | | | | | | | | | | | | | | | | |
| **6.** ClasGV-B | **0.472** | **0.535** | **0.648** | **0.533** | **0.467** | | | | | | | | | | | | | | | |
| **7.** ClanGV-HBHN | **0.393** | **0.702** | **0.597** | **0.083** | **0.440** | **0.463** | | | | | | | | | | | | | | |
| **8.** CpGV-M1 | 0.443 | 0.520 | 0.554 | **0.459** | 0.530 | **0.463** | **0.411** | | | | | | | | | | | | | |
| **9.** CrleGV-CV3 | 0.547 | 0.489 | 0.660 | **0.592** | 0.512 | **0.377** | **0.561** | 0.351 | | | | | | | | | | | | |
| **10.** DisaGV-Parana-2009 | **0.829** | **0.918** | **0.886** | **0.751** | **0.607** | **0.463** | **0.772** | **0.667** | **0.652** | | | | | | | | | | | |
| **11.** EpapGV-Oliveros.Santa Fe | **0.501** | **0.447** | **0.570** | **0.493** | **0.539** | **0.553** | **0.479** | **0.308** | **0.404** | **0.955** | | | | | | | | | | |
| **12.** ErelGV-S68 | 0.389 | 0.513 | 0.730 | **0.388** | 0.440 | **0.353** | **0.424** | 0.329 | 0.443 | **0.581** | **0.524** | | | | | | | | | |
| **13.** HearGV | 0.551 | 0.575 | 0.942 | **0.504** | 0.803 | **0.617** | **0.563** | 0.524 | 0.683 | **0.969** | **0.489** | 0.501 | | | | | | | | |
| **14.** MospGV | 0.715 | 0.794 | 1.066 | **0.809** | 0.561 | **0.520** | **0.788** | 0.688 | 0.833 | **0.759** | **0.881** | 0.623 | 0.367 | | | | | | | |
| **15.** PhopGV-T | 0.607 | 0.507 | 0.568 | **0.740** | 0.612 | **0.510** | **0.557** | 0.392 | 0.463 | **0.746** | **0.623** | 0.505 | 0.721 | 0.779 | | | | | | |
| **16.** PlxyGV-K1 | 0.768 | 0.774 | 1.158 | **0.766** | 0.967 | **0.959** | **0.736** | 0.558 | 0.774 | **1.637** | **0.617** | 0.858 | 0.746 | 1.278 | 0.708 | | | | | |
| **17.** PsunGV-H | 0.557 | 0.579 | 0.871 | **0.602** | 0.892 | **0.628** | **0.650** | 0.494 | 0.651 | **0.896** | **0.601** | 0.547 | 0.175 | 0.380 | 0.582 | 0.774 | | | | |
| **18.** SpfrGV-VG008 | 0.547 | 0.653 | 1.111 | **0.553** | 0.806 | **0.731** | **0.526** | 0.411 | 0.656 | **1.417** | **0.474** | 0.557 | 0.309 | 0.451 | 0.715 | 0.629 | 0.295 | | | |
| **19.** SpltGV-K1 | **0.656** | **0.736** | **1.083** | **0.807** | **0.917** | **0.696** | **0.779** | **0.729** | **0.780** | **0.850** | **0.667** | **0.559** | **0.457** | **0.509** | **0.733** | **1.151** | **0.561** | **0.715** | | |
| **20.** TnGV M10-5 | 0.546 | 0.581 | 0.876 | **0.590** | 0.873 | **0.615** | **0.637** | 0.484 | 0.637 | **0.877** | **0.604** | 0.536 | 0.176 | 0.382 | 0.584 | 0.778 | 0.000 | 0.288 | **0.564** | |
| **21.** XecnGV-α4 | 0.551 | 0.589 | 0.893 | **0.516** | 0.782 | **0.668** | **0.549** | 0.498 | 0.630 | **0.969** | **0.454** | 0.476 | 0.010 | 0.398 | 0.668 | 0.691 | 0.170 | 0.293 | **0.446** | 0.170 |

*The number of base substitutions per site between pairs of sequences are shown. Abbrevations of the taxa are as listed for Table 1. Analyses were conducted using the Kimura 2-parameter model in MEGA6. Pairwise distances for *granulin* (*polh* homologue) sequences are listed below the diagonal lines. Values for the proposed species are in red bold type.