This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

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.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.005S*** | | | | (to be completed by ICTV officers) |
| **Short title:** Create 2 new species, *Enterovirus K, Enterovirus L* in the genus *Enterovirus*  (e.g. 6 new species in the genus *Zetavirus*) | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Roland Zell, Eric Delwart, Alexander E. Gorbalenya, Tapani Hovi, Andrew M.Q. King, Nick J. Knowles, A. Michael Lindberg, Mark A. Pallansch, Ann C. Palmenberg, Gabor Reuter, Peter Simmonds, Tim Skern, Glyn Stanway and Teruo Yamashita | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Roland Zell ([roland.zell@med.uni-jena.de](mailto:roland.zell@med.uni-jena.de)) | | | | | |
| **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) | | | *Picornaviridae* Study Group | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | 02 June 2017 | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.005S.N.v1.Enterovirus\_2sp |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| **Rodent enteroviruses:**  Du J, Lu L, Liu F, Su H, Dong J, Sun L, Zhu Y, Ren X, Yang F, Guo F, Liu Q, Wu Z, Jin Q. 2016. Distribution and characteristics of rodent picornaviruses in China. Sci Rep 6:34381.  **Simian enterovirus from rhesus macaque:**  Ao Y, unpublished [Viral Diarrhea, Institute for Viral Disease Control and Prevention of China CDC, No. 100 Ying-Xin Street, Xuan-Wu District, Beijing 100052, China]. |

|  |
| --- |
| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

**Create 2 new species, *Enterovirus K, Enterovirus L* in the genus *Enterovirus***

Novel enteroviruses have been identified. Two rodent enteroviruses were detected in pharyngeal and anal swabs of unspecified rodents in Ning Xia and Tibet (Du et al. 2016). A simian enterovirus was detected in a sample of the rhesus maquaque. All three viruses exhibit the typical *Enterovirus* genome layout:

VPg+5'UTRIRES-I[1A-1B-1C-1D/2APro-2B-2CHel/3A-3BVPg-3CPro-3DPol]3'UTR-poly(A).

**Significant differences to the existing *Enterovirus* species are:**

(i) There is little sequence similarity with the known enterovirus species (amino acid identity of P1 protein <50%; amino acid identity of 3CD protein <60%; see attached Tables 1, 2). The amino acid identities of the rodent enteroviruses and the simian enterovirus are consistent with the assumption of distinct enterovirus species. Notably, the amino acid identities of P1 and 3CD proteins of the proposed EV-K1 and EV-K2 are similar (c. 33%) which is unusual. One explanation could be that either strain is a recombinant virus comprising sequences of the proposed EV-K and another yet unknown enterovirus species.

(ii) Both proposed species comprise distinct branches in phylogenetic trees (compare attached Figures 1, 2). The P1 tree (Fig. 2) indicates two EV-K types. The divergence of the P1 protein of the EV-K sequences is c. 33% which is consistent with the assumption of other enterovirus types (Table 1).



**Figure 1:** Phylogenetic analysis of the **enterovirus** **3CD** gene region using Bayesian tree inference (MrBayes 3.2). Twenty-eight enterovirus sequences plus sequences of raboviruses and sapeloviruses (serving as outgroup) were retrieved from GenBank. Presented are GenBank accession numbers, ***genus names***, *species names* and *types* (underlined). If available, designations of isolates are given in square brackets. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Figure 2:** Phylogenetic analysis of **enterovirus** **P1** gene region using Bayesian tree inference (MrBayes 3.2). Twenty-nine enterovirus sequences plus sequences of raboviruses and sapeloviruses (serving as outgroup) were retrieved from GenBank. Presented are GenBank accession numbers, ***genus names***, *species names* and *types* (underlined). If available, designations of isolates are given in square brackets. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 3,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

**Table 1. Estimates of Evolutionary Divergence of P1 Polyprotein between Sequences.**

[ 1] #KX156158\_Enterovirus\_EV-K1\_rodent/Ee/PicoV/NX2015

[ 2] #KX156159\_Enterovirus\_EV-K2\_rodent/Mc/PicoV/Tibet2015

[ 3] #KU587555\_Enterovirus\_EV-L1\_Macaca\_mulatta/SEV-gx/2014/China

[ 4] #U22521\_Enterovirus\_EV-A71\_BrCr

[ 5] #L28146\_Enterovirus\_EV-A\_CV-A2\_Fleetwood

[ 6] #M16560\_Enterovirus\_EV-B\_CV-B1\_Japan

[ 7] #M33854\_Enterovirus\_EV-B\_CV-B3\_Nancy

[ 8] #V01149\_Enterovirus\_EV-C\_PV-1\_Mahoney

[ 9] #D00538\_Enterovirus\_HEV-C\_CV-A21\_Coe

[10] #AY426531\_Enterovirus\_EV-D68\_Fermon

[11] #D00820\_Enterovirus\_EV-D70\_J670/71

[12] #DQ092769\_Enterovirus\_EV-E1\_BEV-1\_LC-R4

[13] #DQ092792\_Enterovirus\_EV-E2\_PS42

[14] #DQ092770\_Enterovirus\_EV-F1\_BEV-261\_RM2

[15] #DQ092795\_Enterovirus\_EV-F2\_PS89

[16] #AF363453\_Enterovirus\_EV-G1\_UKG-410-73

[17] #AF363455\_Enterovirus\_EV-G2\_LP54

[18] #AF201894\_Enterovirus\_EV-H1\_A-2\_plaque

[19] #AF326759\_Enterovirus\_EV-H1\_SV4-1715-UWB

[20] #KP345887\_Enterovirus\_EV-I1\_dromedary\_camel\_enterovirus\_1\_19CC

[21] #KP345888\_Enterovirus\_EV-I1\_Dromedary\_camel\_enterovirus\_2\_20CC

[22] #AF326766\_Enterovirus\_EV-J1\_SV6-1631

[23] #KT961657\_Enterovirus\_EV-J103\_isolate\_cg3697

[24] #FJ445177\_Enterovirus\_RV-A\_HRV-9\_211-CV13

[25] #L24917\_Enterovirus\_RV-A\_HRV-A16\_11757

[26] #DQ473485\_Enterovirus\_RV-B\_HRV-3\_FEB

[27] #K02121\_Enterovirus\_RV-B\_HRV-14\_1959

[28] #EF186077\_Enterovirus\_RV-C1\_HRV-QPM

[29] #EF077280\_Enterovirus\_HRV-C2\_NAT045

[30] #KP233897\_Rabovirus\_A\_isolate\_Berlin/Jan2011/0572

[31] #KJ950883\_Rabovirus\_A\_rat\_picornavirus\_isolate\_RPV/NYC-B10

[32] #AF406813\_Sapelovirus\_A1\_PSV\_strain\_V13

[33] #AY064708\_Sapelovirus\_B1\_SSV-1\_strain\_2383

[34] #AY563023\_Avian\_sapelovirus\_ASV-1\_Duck\_picornavirus\_TW90A

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 ]

[ 1]

[ 2] 0.324

[ 3] 0.522 0.552

[ 4] 0.591 0.602 0.538 -

[ 5] 0.603 0.604 0.543 0.333

[ 6] 0.582 0.584 0.532 0.554 0.537

[ 7] 0.569 0.582 0.532 0.543 0.541 0.182

[ 8] 0.604 0.606 0.562 0.564 0.555 0.464 0.467

[ 9] 0.591 0.586 0.571 0.551 0.553 0.460 0.452 0.321

[10] 0.602 0.601 0.549 0.523 0.505 0.522 0.543 0.549 0.532

[11] 0.595 0.609 0.562 0.511 0.509 0.533 0.538 0.558 0.552 0.249

[12] 0.602 0.612 0.547 0.496 0.490 0.544 0.544 0.561 0.563 0.502 0.490

[13] 0.608 0.618 0.549 0.498 0.496 0.537 0.547 0.556 0.558 0.509 0.492 0.131

[14] 0.585 0.602 0.543 0.492 0.476 0.505 0.509 0.527 0.525 0.492 0.474 0.339 0.338

[15] 0.587 0.600 0.538 0.490 0.471 0.513 0.506 0.536 0.534 0.487 0.481 0.343 0.340 0.152

[16] 0.621 0.620 0.573 0.493 0.484 0.548 0.549 0.572 0.567 0.501 0.510 0.401 0.399 0.393 0.395

[17] 0.617 0.621 0.556 0.501 0.487 0.531 0.539 0.561 0.552 0.494 0.499 0.412 0.408 0.398 0.394 0.265

[18] 0.589 0.571 0.546 0.515 0.509 0.515 0.517 0.519 0.535 0.525 0.521 0.513 0.512 0.482 0.484 0.504 0.506

[19] 0.586 0.570 0.549 0.519 0.507 0.510 0.518 0.520 0.529 0.522 0.518 0.508 0.508 0.479 0.482 0.502 0.505 0.042

[20] 0.598 0.602 0.551 0.471 0.473 0.525 0.527 0.540 0.532 0.481 0.477 0.356 0.351 0.287 0.274 0.398 0.385 0.495 0.492

[21] 0.598 0.602 0.551 0.470 0.473 0.525 0.525 0.541 0.533 0.483 0.475 0.356 0.349 0.286 0.276 0.401 0.382 0.495 0.492 0.010

[22] 0.609 0.596 0.550 0.449 0.434 0.531 0.530 0.557 0.542 0.473 0.480 0.454 0.461 0.440 0.442 0.478 0.461 0.480 0.482 0.425 0.425

[23] 0.578 0.589 0.529 0.440 0.432 0.513 0.509 0.536 0.522 0.486 0.476 0.448 0.445 0.442 0.445 0.469 0.451 0.498 0.492 0.443 0.441 0.361

[24] 0.597 0.607 0.569 0.565 0.560 0.507 0.528 0.537 0.511 0.544 0.556 0.557 0.564 0.543 0.540 0.557 0.545 0.552 0.550 0.536 0.536 0.572 0.541

[25] 0.596 0.607 0.558 0.571 0.554 0.511 0.520 0.533 0.525 0.552 0.561 0.541 0.543 0.529 0.533 0.556 0.537 0.546 0.546 0.531 0.529 0.573 0.530 0.222

[26] 0.608 0.607 0.585 0.552 0.547 0.510 0.524 0.525 0.505 0.525 0.557 0.548 0.555 0.535 0.545 0.549 0.540 0.572 0.572 0.540 0.540 0.562 0.552 0.485 0.486

[27] 0.624 0.627 0.592 0.563 0.558 0.524 0.529 0.530 0.514 0.538 0.560 0.563 0.571 0.538 0.548 0.556 0.539 0.573 0.578 0.543 0.543 0.569 0.563 0.487 0.492 0.131

[28] 0.612 0.640 0.602 0.585 0.587 0.541 0.548 0.571 0.551 0.581 0.581 0.582 0.577 0.562 0.567 0.583 0.564 0.578 0.580 0.560 0.560 0.590 0.567 0.490 0.501 0.528 0.527

[29] 0.613 0.627 0.610 0.584 0.589 0.549 0.559 0.567 0.542 0.561 0.573 0.563 0.567 0.555 0.559 0.581 0.555 0.582 0.583 0.551 0.551 0.593 0.575 0.515 0.502 0.525 0.529 0.313

[30] 0.601 0.598 0.608 0.634 0.633 0.631 0.626 0.636 0.650 0.627 0.641 0.624 0.625 0.616 0.602 0.645 0.638 0.603 0.604 0.607 0.605 0.620 0.614 0.651 0.648 0.647 0.646 0.647 0.645

[31] 0.619 0.622 0.630 0.646 0.653 0.635 0.635 0.654 0.660 0.634 0.643 0.634 0.627 0.612 0.603 0.650 0.646 0.627 0.625 0.624 0.625 0.632 0.619 0.661 0.658 0.663 0.664 0.657 0.650 0.142

[32] 0.620 0.631 0.596 0.621 0.640 0.627 0.625 0.662 0.644 0.628 0.642 0.637 0.629 0.625 0.629 0.644 0.644 0.635 0.634 0.638 0.638 0.640 0.609 0.657 0.658 0.659 0.659 0.653 0.659 0.582 0.588

[33] 0.624 0.624 0.602 0.636 0.631 0.619 0.614 0.660 0.657 0.645 0.658 0.636 0.632 0.636 0.631 0.641 0.648 0.644 0.641 0.637 0.637 0.642 0.622 0.664 0.661 0.662 0.667 0.662 0.668 0.584 0.591 0.382

[34] 0.642 0.647 0.629 0.640 0.644 0.664 0.657 0.654 0.664 0.654 0.649 0.619 0.626 0.621 0.634 0.644 0.653 0.619 0.623 0.625 0.625 0.632 0.623 0.681 0.662 0.664 0.673 0.696 0.687 0.621 0.615 0.578 0.573

The number of amino acid differences per site from between sequences are shown.

\_\_\_ within type comparison, \_\_\_ between types/within species comparison, \_\_\_ between species/within genus comparison, \_\_\_ between genera comparison

**Table 2. Estimates of Evolutionary Divergence of 3CD Protein between Sequences**

[ 1] #KX156158\_Enterovirus\_EV-K1\_rodent\_Ee\_PicoV\_NX2015

[ 2] #KX156159\_Enterovirus\_EV-K2\_rodent\_Mc\_PicoV\_Tibet2015

[ 3] #KU587555\_Enterovirus\_EV-L1\_Macaca\_mulatta/SEV-gx/2014/China

[ 4] #U22521\_Enterovirus\_EV-A71\_BrCr

[ 5] #AY421760\_Enterovirus\_EV-A2\_CV-A2\_Fleetwood

[ 6] #M16560\_Enterovirus\_EV-B\_CV-B1\_Japan

[ 7] #M33854\_Enterovirus\_EV-B\_CV-B3\_Nancy

[ 8] #V01149\_Enterovirus\_EV-C\_PV-1\_Mahoney

[ 9] #D00538\_Enterovirus\_EV-C\_CV-A21\_Coe

[10] #AY426531\_Enterovirus\_EV-D68\_Fermon

[11] #D00820\_Enterovirus\_EV-D70\_J670\_71

[12] #DQ092769\_Enterovirus\_EV-E1\_BEV-1\_LC-R4

[13] #DQ092792\_Enterovirus\_EV-E2\_PS42

[14] #DQ092795\_Enterovirus\_EV-F2\_PS89

[15] #DQ092770\_Enterovirus\_EV-F1\_BEV-261\_RM2

[16] #AF363453\_Enterovirus\_EV-G1\_UKG-410-73

[17] #AF363455\_Enterovirus\_EV-G2\_LP54

[18] #AF201894\_Enterovirus\_EV-H1\_A-2\_plaque

[19] #AF326766\_Enterovirus\_EV-J1\_SV6-1631

[20] #KT961657\_Enterovirus\_EV-J103\_cg3697

[21] #KP345887\_Enterovirus\_EV-I1\_dromedary\_camel\_enterov\_1\_19CC

[22] #KP345888\_Enterovirus\_EV-I1\_Dromedary\_camel\_enterov\_2\_20CC

[23] #FJ445177\_Enterovirus\_RV-A9\_HRV-9\_211-CV13

[24] #L24917\_L24917\_Enterovirus\_RV-A16\_HRV-A16\_11757

[25] #DQ473485\_Enterovirus\_RV-B3\_HRV-3\_FEB

[26] #K02121\_Enterovirus\_RV-B14\_HRV-14\_1959

[27] #EF186077\_Enterovirus\_RV-C1\_HRV-QPM

[28] #EF077280\_Enterovirus\_RV-C2\_NAT045

[29] #AF406813\_Sapelovirus\_A\_PSV-1\_PEV8-V13

[30] #AY064708\_Sapelovirus\_B\_SSV-1\_SV2-2383

[31] #AY563023\_Avian\_sapelovirus\_ASV-1\_TW90A

[32] #KP233897\_Rabovirus\_A1\_isolate\_Berlin/Jan2011/0572

[33] #KJ950883\_Rabovirus\_A1\_isolate\_RV-A\_rat/NYC-B10/USA/2010

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 ]

[ 1]

[ 2] 0.332

[ 3] 0.433 0.412

[ 4] 0.459 0.459 0.428

[ 5] 0.447 0.457 0.407 0.045

[ 6] 0.408 0.401 0.377 0.380 0.360

[ 7] 0.409 0.400 0.374 0.380 0.358 0.029

[ 8] 0.418 0.408 0.376 0.365 0.345 0.300 0.295

[ 9] 0.422 0.404 0.377 0.363 0.349 0.300 0.295 0.025

[10] 0.420 0.417 0.370 0.402 0.391 0.283 0.277 0.289 0.300

[11] 0.407 0.410 0.367 0.392 0.383 0.281 0.270 0.284 0.298 0.123

[12] 0.439 0.425 0.405 0.398 0.384 0.328 0.328 0.346 0.348 0.369 0.370

[13] 0.439 0.425 0.401 0.398 0.382 0.334 0.331 0.346 0.348 0.375 0.369 0.036

[14] 0.426 0.401 0.371 0.404 0.387 0.332 0.331 0.334 0.337 0.372 0.359 0.191 0.193

[15] 0.423 0.403 0.370 0.401 0.387 0.332 0.331 0.335 0.339 0.372 0.356 0.189 0.191 0.009

[16] 0.425 0.409 0.376 0.387 0.374 0.331 0.328 0.321 0.325 0.359 0.353 0.275 0.267 0.275 0.270

[17] 0.423 0.417 0.399 0.385 0.378 0.346 0.346 0.335 0.337 0.369 0.367 0.290 0.289 0.281 0.276 0.116

[18] 0.434 0.459 0.416 0.430 0.416 0.357 0.357 0.358 0.361 0.382 0.370 0.385 0.385 0.366 0.369 0.382 0.371

[19] 0.409 0.384 0.355 0.346 0.336 0.200 0.198 0.283 0.278 0.295 0.289 0.332 0.334 0.318 0.317 0.329 0.326 0.341

[20] 0.408 0.386 0.362 0.354 0.343 0.191 0.189 0.280 0.275 0.297 0.286 0.337 0.339 0.328 0.327 0.327 0.328 0.342 0.019

[21] 0.415 0.406 0.384 0.405 0.385 0.321 0.321 0.339 0.343 0.356 0.353 0.191 0.194 0.102 0.102 0.264 0.275 0.368 0.311 0.320

[22] 0.415 0.400 0.383 0.407 0.387 0.324 0.324 0.336 0.343 0.356 0.353 0.197 0.199 0.105 0.105 0.264 0.277 0.369 0.310 0.318 0.013

[23] 0.482 0.466 0.459 0.482 0.470 0.451 0.448 0.456 0.460 0.452 0.447 0.441 0.441 0.449 0.445 0.448 0.452 0.460 0.431 0.433 0.445 0.443

[24] 0.478 0.475 0.469 0.480 0.477 0.458 0.449 0.474 0.472 0.459 0.451 0.456 0.456 0.463 0.458 0.456 0.450 0.463 0.431 0.435 0.463 0.463 0.190

[25] 0.475 0.454 0.410 0.430 0.418 0.385 0.385 0.403 0.407 0.420 0.401 0.433 0.424 0.422 0.421 0.416 0.414 0.434 0.405 0.401 0.421 0.424 0.447 0.459

[26] 0.464 0.445 0.417 0.425 0.419 0.385 0.382 0.407 0.407 0.422 0.406 0.435 0.425 0.422 0.417 0.400 0.405 0.431 0.388 0.387 0.421 0.424 0.441 0.460 0.126

[27] 0.472 0.491 0.467 0.477 0.465 0.450 0.449 0.442 0.442 0.442 0.440 0.445 0.449 0.463 0.461 0.441 0.452 0.463 0.439 0.440 0.450 0.449 0.432 0.435 0.431 0.432

[28] 0.469 0.473 0.470 0.472 0.460 0.435 0.438 0.431 0.438 0.437 0.428 0.458 0.463 0.464 0.463 0.460 0.445 0.470 0.419 0.424 0.463 0.465 0.438 0.439 0.423 0.410 0.308

[29] 0.504 0.518 0.491 0.495 0.484 0.471 0.468 0.480 0.484 0.480 0.464 0.497 0.495 0.480 0.476 0.473 0.469 0.486 0.441 0.445 0.476 0.472 0.494 0.491 0.484 0.473 0.508 0.513

[30] 0.492 0.503 0.472 0.494 0.479 0.470 0.467 0.484 0.487 0.479 0.465 0.493 0.490 0.468 0.467 0.460 0.468 0.498 0.458 0.459 0.473 0.470 0.495 0.496 0.496 0.501 0.504 0.523 0.348

[31] 0.523 0.507 0.499 0.512 0.508 0.507 0.504 0.506 0.508 0.517 0.509 0.497 0.495 0.505 0.503 0.503 0.509 0.508 0.490 0.487 0.500 0.502 0.512 0.508 0.516 0.516 0.531 0.528 0.466 0.411

[32] 0.527 0.522 0.481 0.502 0.490 0.492 0.486 0.498 0.502 0.485 0.479 0.508 0.503 0.495 0.495 0.489 0.487 0.519 0.462 0.465 0.492 0.491 0.517 0.509 0.515 0.515 0.535 0.515 0.490 0.469 0.475

[33] 0.531 0.522 0.486 0.502 0.489 0.493 0.486 0.498 0.502 0.496 0.490 0.512 0.512 0.497 0.497 0.498 0.498 0.522 0.468 0.473 0.495 0.494 0.515 0.503 0.520 0.525 0.537 0.516 0.496 0.473 0.476 0.022

The number of amino acid differences per site from between sequences are shown. The analysis involved 33 amino acid sequences.

\_\_\_ within type comparison, \_\_\_ between types/within species comparison, \_\_\_ between species/within genus comparison, \_\_\_ between genera comparison