

# Terminase large-subunit maximum-likelihood phylogeny of *Aeromonas* phages Hp3 and HJ05 (Figure 2)

Supporting file for the taxonomy proposal “Hapetrivirus” (Bacterial Viruses Subcommittee, 2026)

## Methods

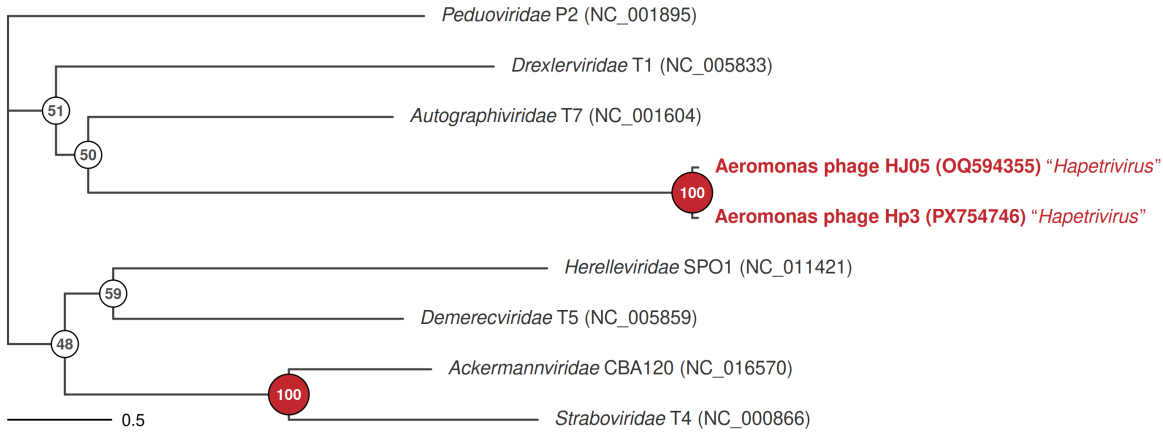
Terminase large-subunit (TerL) sequences of Hp3 (GenBank PX754746), HJ05 (OQ594355) and representatives of seven *Caudoviricetes* families were taken from the GenBank annotations (longest CDS annotated as a terminase other than the small subunit; for HJ05, the CDS identified by BLASTP with the Hp3 TerL). The *Schitoviridae* representative N4 (NC\_008720) has no terminase annotated in its GenBank record and is absent from the panel. Sequences were aligned with MAFFT v7.526 (--auto; Katoh and Standley 2013). The maximum-likelihood tree was inferred with IQ-TREE v3.1.2 (Wong et al. 2025) under the best-fit model LG+I+G4 selected by ModelFinder (BIC; Kalyaanamoorthy et al. 2017), with 1,000 ultrafast bootstrap replicates (UFBoot2; Hoang et al. 2018), random seed 843024. The tree is unrooted and drawn ladderized; the sampled TerL sequences include no suitable outgroup. Node values are UFBoot support and the scale bar is in substitutions per site. Sequence lengths are those of the GenBank protein records; the alignment has 1,081 columns.

## Sequences

| Tip label               | Virus                                          | ICTV family /<br>proposed taxon                    | Genome<br>accession | TerL protein                                                                                                | Length<br>(aa) |
|-------------------------|------------------------------------------------|----------------------------------------------------|---------------------|-------------------------------------------------------------------------------------------------------------|----------------|
| Hp3                     | <i>Aeromonas</i><br>phage Hp3<br>(vB_AhyM_Hp3) | unassigned;<br>proposed<br>“ <i>Hapetrivirus</i> ” | PX754746.1          | YCJ06451.1 (hp3_0001, terminase<br>large subunit)                                                           | 646            |
| HJ05                    | <i>Aeromonas</i><br>phage HJ05                 | unassigned;<br>proposed<br>“ <i>Hapetrivirus</i> ” | OQ594355.1          | WEV89306.1 (H10PHJ05_5,<br>annotated as hypothetical protein;<br>identified by BLASTP with the<br>Hp3 TerL) | 652            |
| Peduoviridae_P2         | <i>Escherichia</i><br>phage P2                 | <i>Peduoviridae</i>                                | NC_001895.1         | NP_046758.1 (P2p02)                                                                                         | 590            |
| Straboviridae_T4        | <i>Escherichia</i><br>phage T4                 | <i>Straboviridae</i>                               | NC_000866.4         | NP_049776.1 (T4p163, gp17)                                                                                  | 610            |
| Autographiviridae_T7    | <i>Escherichia</i><br>phage T7                 | <i>Autographiviridae</i>                           | NC_001604.1         | NP_042010.1 (T7p57)                                                                                         | 586            |
| Drexelviridae_T1        | <i>Escherichia</i><br>phage T1                 | <i>Drexelviridae</i>                               | NC_005833.1         | YP_003892.1 (ST53)                                                                                          | 527            |
| Demereciviridae_T5      | <i>Escherichia</i><br>phage T5                 | <i>Demereciviridae</i>                             | NC_005859.1         | YP_006983.1 (T5.155)                                                                                        | 438            |
| Herelleviridae_SPO1     | <i>Bacillus</i> phage<br>SPO1                  | <i>Herelleviridae</i>                              | NC_011421.1         | YP_002300330.1 (SPO1_54)                                                                                    | 547            |
| Ackermannviridae_CBA120 | <i>Escherichia</i><br>phage CBA120             | <i>Ackermannviridae</i>                            | NC_016570.1         | YP_004957856.1<br>(CBA120_gp154)                                                                            | 736            |

Figure 2

TerL maximum-likelihood phylogeny (unrooted; UFBoot support at nodes)



Hp3 and HJ05 form an exclusive clade (UFBoot 100) on a long stem; the internodes separating the family representatives from one another have UFBoot support of 43-60, apart from the T4-CBA120 pairing (100).

Newick tree (UFBoot support at nodes; labels as in the Sequences table; line breaks fall after commas only, so the text can be copied as a valid Newick string. Machine-readable copies of this tree, the alignment and the IQ-TREE report are in Hapetrivirus\_supporting\_tables.xlsx, sheets TerL\_Newick, TerL\_alignment and TerL\_IQTREE\_report)

```
(Peduoviridae_P2:1.9933954352,
(Straboviridae_T4:1.0798892491,
Ackermannviridae_CBA120:0.8093529881)100:0.8398476743,
(((Autographiviridae_T7:1.6022335206,
(Hp3:0.0452406278,
HJ05:0.0112012806)100:2.7821406100)43:0.0886034520,
Drexlerviridae_T1:2.0635635239)48:0.2803687791,
(Demerecviridae_T5:1.2674265600,
Herelleviridae_SPO1:1.9927136859)51:0.2073464845)60:0.4077921647);
```

## IQ-TREE report (excerpt)

```
IQ-TREE 3.1.2 built May 17 2026
IQ-TREE 3: Phylogenomic Inference Software using Complex Evolutionary Models.
Input data: 9 sequences with 1081 amino-acid sites
Number of constant sites: 330 (= 30.5273% of all sites)
Number of parsimony informative sites: 383
Number of distinct site patterns: 893
Best-fit model according to BIC: LG+I+G4
Model of substitution: LG+I+G4
Proportion of invariable sites: 0.0139
Gamma shape alpha: 2.9467
Log-likelihood of the tree: -12874.6295 (s.e. 253.5067)
```

Total tree length (sum of branch lengths): 15.4711  
Sum of internal branch lengths: 4.6061 (29.7722% of tree length)

## MAFFT alignment (FASTA)

>Peduoviridae\_P2

```
-----MTITTTDTLLHDPRRQAALLYWQGFSPQIAAMLQMKRPTVQSWKQRDG-----
-WDSVAPISRVEMSLEARLTQLIIKPQKTGGDFKEIDLLGRQIERLARVNRYSQTGNEAD
LNPVNANRNKGGRKPKKNFFSDEAIEKLEQ-----IFFEQS-----FD
YQLHWYRAGLE-----HRIRDILKSRQ-----
-----IGA-----
-----
-----TFYFSREALLRAL-KTGHNQIFLSA-SKTQAYVFREYIIA-----
-----FARLVDVLT-GDPIVLGNNGAK-----LIFLGTNSNTAQSH-----
NGDLYVDEIFWIPN-----FQVLRKVASGMASQSHLRSTYFSTPSTLAHDA
YPFWSGE-----LFNRGRASAAERVEIDVSHNALAGLLCADG-----
-----QWRQIVTIE-----DAL-KGGCTLF-----
----DIEQLKRE-----NSADDFKNLFMCEFV-----DDKASVFPFE--ELQRCMVDTL
-----EWEDEYAPFAANPFGSRPVWIGYDPSHR-GDSAG
CVVLAPP-VVAGGKFRILERH--QWKGMDFATQAES--IRKLTEKYN-----VEYIGIDA
TG-----LGVGVFQLVRSFYPAARDIRY-----PEMK
TAMVLKA-----KDVIRRGCLEYDVSATDITSSFMAIRKTM-TSSGRSAT
YEASRSEEASHADLA-----WATMHALLNE-----
-----PLTAGISTP-----LTSTILEF--
Y
```

>Straboviridae\_T4

```
-----MEQPIN--VLND-----FHPLNEAGKILIKHPSLAERKDEDGIHWIKS
QWDGKWYPEK--FSDYLRLHKIVKIPN----NSDKPELFQTYKDKNNKRSRYMGL-----
--PNL-----KRAIKTQWTREMVEEWKCRDDIVFYAETYCAITHIDYGVIVKQLRD
YQRDMLKIMSS-----KRMTVCNLSRQ-----
-----LGK-----
-----
-----TTVVAIFLAHFVCF-NKDKAVGILAH-KGSMSAEVLDRTKQAIELLP
D-----FLQPGIVEWN--KGSIELDNGSSIG-----AYASSPDAVRGNS-----
FAMIYIDECAPFIPNFHDS-----W---LAIQPVISSGRRSKIIITTPNGLNH-F
YDIWTAA-----VEGKSGFEPYTAIWNVSVKERLYNDEDIFDDG-----
-----W-----
----QWSIQTIN--GSSLAQFRQEHTAAFE-----GTSGTLISGMKLAVMDFIEVTP
-----DDHGFHQ-FKKPEPDRKYIATLDCSE--GRGQD
YHALHI--IDVTDDVWEQGV-LHSNTISHLILPDI--VMRYLVEYN-----ECPVYIEL
NST-----GVSVAKSLYMDLEYEGVICDSYTDL-----GMK
QTKRTKAVGCS-----TLKDLIEKDKLIIHHRAT-----IQEFR-TFSEKGV
WA--AEEGYHDDLVMVIFVGLSTQSKFIDYAD-----KDDMRL-----ASEVFS
KELQDMSDDYAPVIFVDSVHSAEYVPVSHGMSMV-----
-
```

>Autographiviridae\_T7

```
-----MSTQSN-----RNALVVAQLKGDFVAFLFV
LWKALNLPV-----
--P-----TK
CQIDMAKVLANG-----DNKKFILQAFRG-----
-----IGK-----
-----
-----SFITCAFVWVSLWRDPQLKILIVSA-SKERADANSIFIKNIIDLLP
-----FLSELKPRPGQRDSVISFDVGPANPDHSPSVKSGITGQLTGSR-----
ADIIIADDVEIPSNSATMGAREK---LWTLVQEFAALLKPLPSSRVYILGTPQTEMTLY
KELEDNRGYTTIIWPALYPRTREENLYYSQRLAPMLRAEYDENPEALAG-----
```

```

-----TPTDPVR
FDRDDLREERELE---YGKAGFTLQFMLNPN-----LSDAEKYPLRLRDAIVAALDLE
KAPMHYQWLPNRQNIIEDLPNVGLKGDDLHTYHDCSNNSGQYQQKILVIDPSGRGKDETG
YAVLYT----LNGYIYLMEAG--GFRDGYSDKTLEL--LAKKAKQWG-----VQTVVYES
NFG-----DGMFGKVFSPIILLKHHNCAMEEIRA-----RGMK
EMRICDT-----LEPVMQTHRLVIRDEVI-----RADYQSAR-----
-----DVDGKHD-----VKYSLFYQMTRITREKGALAHDDRLDALALGIEYLR
ESMQLDSVKVEGEVLADFLEEHRMPTVAATHIEMS VGGVDVYSEDDEGYGTSFIEW--
-
>Drexlerviridae_T1
-----MG-----
-----DLIMIQWEDLNATQKLAIK-----
-----KMSEANFEKMIR-----IWFQLMQA-----QQ
FQPNWHLHLYLC-----HEVEEIIAGRRCN-----
-----TIFN-----VTPGSGK-----
-----
-----TEVFSIHLVPYAMLKCKKVRNLNVSF-ADSLVKRNSKRVREIISSE
FQELWPCKFGTSKDEEMQ-----VLNEDGKVWF-----ELISAAAGGRITGSRGGYMPGF
SGMVMLDDIDKPDDMFSKVKR-----ERTHMLLKNTIRSRRMHNETPIIAIQQR
LHAQDSTWFMM-----NGMGIEFDQISIPALVT--EEYGKTLPD-----
-----WLQPYFER-----DVL-SSEYVELDGVKHYSFW--PSK
ESVHDLALLR---EADQYTFDSQYQQKPI-----ALGGSVFNSEWWTYYGSSLDAD
-----EPDPGKYDYRFITADTAQKTGELND
YTVFCLW-GKKNDKVYFIDGI--RGKWEAPDMERQFTAFVNQAWRHNSMGVLRKIYVED
KA-----SGTGLIQNLRKKTPI SITPLQR-----NKDK
VTRAMDA-----QPVIKAGRVVLP EEHPMLAE---IIAEHS-AFTY----
-----DDTHPHDDIVDNF-----MDAANIELLT
ID-----DPIERMKRLAGMVKR-----
-
>Demerecviridae_T5
-----MEVSRP-----
-----YVNTVDVI-----DFGIDKRFFRL-----
--P-----VSGILAQEGIT-----PNG
PQIAIINALEDP-----RHRFVTACVSRR-----
-----VGK-----
-----
-----SFIAYTLGFLKLL-EPNVKVLVVAP-NYSLANIGWSQIRGLIKKYG
-----LQTERENAKD--KEIELANGSLFK-----LASAAQADSAVGRS-----
YDFIIFDEAAISDVGGA-----F--RVQLRPTLDKPNKALFISTPRGGNW-F
KEFYA-----YGFDDTLPN-----
-----WVSI-----HGTYRDNPR
ADLNDIEEARRT---VSKNYFRQEYEADFS-----VFEGQIF-----DTFNAIDHVK
-----DLKGMRRHFFKDDEAF-ETLLGIDVGYR----DP
TAVLTIKYHYD TD TYVLEEY--QQA EKT TAQHAAY--IQHCIDRYK-----VDRIFVDS
AAA-----QFRQDLAYEHEIASAPAKK-----
--SVLDGLAC-----LQALFQQGKIIVDASCSSLIH--ALQNYKWDFQEGEEK
LS--REKPRHD-----ANSHL-CDALRYGIYS
ISR GK-----
-
>Herelleviridae_SP01
-----MTKYTK-----EQIQRALINRTPTL-----
-----YALRYRYIKG-----
--NP-----LTFKSTKNPIK-----HRP
WQIAI--LED-----QHPDKVVRKSRQ-----
-----LGL-----
-----

```

-----SEMAVTEFIWFLDTHPNVNGMYTFPRKEQMEDFSNTRIAPIFDESP  
 -----YLSSRLDKKMNNVRLKKLVNGSAMF-----LRSAGSALGEGQA-----  
 IDILGLDEYDRMKDGVELAFRESMKSSAYGLMRRWSTPTIPGRGVDMLFSDSDQRY---Y  
 HHKCDKCGHWQVI-----TLEDNIVCINEKGV-----NLVDETIDD-----GTYQF  
 QCQKCKQELNRW-----NKGEYVAK-----YPTRKDRRG  
 YHISQLDAVWISADEIMRNQFDYKVKQLFYNYVIGMPYASEGLIITDQ--DVLNCVAFPE  
 PI-----G-----YRDNskyVKIVAGIDWGYF-----NW  
 MVILGL---TEDNQVHLLDFHWVEDNPNRPLDCVNV--FTALLKPYD-----PDVIVADN  
 GF-----GADRNSYLIQFPGRTYACDWDTPRGRNMMVDQWNDNAAKVRVDKTVK  
 MKRTLYNIKAK-----ALKTFGQGEKLSM-----LTK---HLKNVR-TLME-----  
 -----EEEG-----EIFERVSRIGDDHG-----ACALTYGYIA  
 LDRILEAHKPKQDMNYDFI-----  
 -

>Ackermannviridae\_CBA120

-----MAYQKR-----  
 -----DIEYAPIKTG-----FKIDDVKLMDQTFMRK-----  
 --PSV-----RAPRVELMLTDEQEDEFVECSMDAHYFAANYKITTIDKGFILFDMHD  
 YQKQLFHFQD-----YRFNAVQARQSGKCVKGDTLTVTYDLSQEELLLTIGEL  
 HSRFEDVNHAUPLNTIGNHDKFVDSRFGKRYFVQSDSGWVPVIAAHKTKKYAEFVIVTVT  
 GRRINVADEHMFPTPDMKEIFAKDLNAGSYIMTTEGPEEIREIWQTGEYHHMYDLQVKSS  
 DQRYTNGFLSHNTTVAAFLWYAMF-HSDKEIAVLN-KEKQAEILDRIRKAYQDLP  
 F-----FLQQGCEKFG--STLIEFENGSKIY-----AYATSSDSIRGRS-----  
 VSLLYVDEVAFIENDFEF-----W---ESTFPAIASADTSRCILTSTPKGQRGLF  
 YDIVTKA-----DPRHPQYNDFHLTEVP-----  
 -----WYKV-----PAY  
 TKDPDWETKQRA--RLGDARFDQEFGIKFR-----GSVGLIPAKCLDKMTSKLYRE  
 PN-----EFTKI-YKEYDPQRLYFGIADTGK--GVEGD  
 YSVLTI--LDITEYPHVIAAK-YRNTTIPPMYAYT--IADMCTEYG----ECPVLVET  
 NNDV-----GGQVITILYQEIEYPEIIFTSTDNKGTKGRI-----GGRKPEPGIN  
 TNRKVRSIGCA-----NLKALIEKEMLVIEDQDT-----IDELS-TFVFKGAR  
 YE--ADDGCHDDCVMLPLVLYSAVKQEWFSDLTSTS----ISQDMR-----NRMS  
 STESQQVFPFGGLVVGDTPSETEHLPGGGIQVF-----NEMSGMTMDEWFK  
 N

>Hp3

-----MKSRA-----RMYSMALAKGLK-REAEVYHAANQLIEHDNS  
 LW-----FR-----AIGAMNKMPVTIDEFIESDEFLGHGGGLT  
 VWPTLRDDL--RAYNPDVFTGAEPVHEIVD--GGATGTGKTHKAI-----TQA  
 YQLYLLTCFDNPVTLFPNLSNNTTIVMLFQS-----  
 -----VQDRVTRRVIYD--PFRSAFLGMPY---SRRWV---NHDKNK-----  
 -----ESTLVISL-----GRSAKVEVAPALALQNLAMVGQAIIGGIIDEVN  
 -----FMAVVENSKN-----VPGSR-----  
 GGGGHYDQAEIIHSNITR-----RRKGRFQTPALSIGALSVLSSTRYRGDF  
 LDKRQAS-----IKENNEKNVVMRRRAQ-----YEVQPVYQD-----  
 -----CTEWFDLLVGNTDYPTTILKPVAKRGVDYP-EGGMVVKIPMSYYADFKRDPE  
 GALRDVCGIATD--VIAPYITQRHKITES--VMR---AAERGMRPFVLKQNVDTSVGL  
 PV-INPDWLPR-----DKDTPRYIHVDLSQT-GDRTG  
 IAMAKPD-----GYMDIVDEHTGLCTRLPRVAVEL  
 AVSIQSPAKPIDLPSVRAWILALKQVYGLNIAQVSY-----DGFDSRESVQLL  
 RKAGIQAVGLSVDMTTAPYDYLRLDALYDDRVDIIDNEL-----LRIELSNLEFDENKNK  
 VDH--PPKGSKD-----IADAVAGSVYSAATARGIRHG-----VGSSAAPTSS  
 QGEGEEDGQPS-----QPPRRGPTRRNVSRR-----  
 -

>HJ05

MNREQMKARAD-----RMYSMALARGLK-REAEVVYHAANQLIEHDNS  
 LW-----FR-----AIGAMNKMPVTIDEFIESDEFLGHGGGLT

VWPTLRDDL---RAYNPDVFTGAEPVHEIVD--GGATGTGKTHKAI-----TQA  
 YQLYLLTCFDNPVTLFPNLSNNTTIVMLFQS-----  
 -----VQDRVTRRVIYD--PFRAAFLGMPY----SRRWV---NYDKNK-----  
 -----  
 -----ESTLVLT-----GRSAKVEVAPALAQNLAMVGQAIIGGIIDEVN  
 -----FMSVVENSKN-----VPGSR-----  
 GQGGHYDQAEIIHSNITR-----RRKGRFHTPALSIGALSVLSSTRYRGDF  
 LDKRQAA-----IKENKEKNVVMRRRAQ-----YEVQPVYQD-----  
 -----CTEWFDLLVGNTDYPTTILKPVAKRGVDYP-DGATVLKIPMAYYADFMRDPE  
 GALRDVCGIATD---VIAPYITQRHKITEA--VMR---GTDRGLLPFVLKQNVDTSVGL  
 PV-INIDWLPK-----DKDTPRYIHVDLSQT-GDRTG  
 LAMSKPD-----GYMDIVDEHTGLCTRLPRIAVAL  
 AVSIQPSPAKPIDLPSVRAWILALKQVYGLNIAQVSY-----DGFDSRESVQLL  
 RKAGIQAVGLSVDMTTAPYDYLRLDALYDDRVDMDNEL-----LRIELSNLEFDENKNK  
 VDH--PPKGSKD-----IADAVAGSVYSAATARGIRHG-----VGSSAAQPSS  
 HGEGEDDGQPSQ-----QAPRRGPTRRSVSRR-----  
 -