

Characterization and genomic study of “phiKMV-Like” phage

PAXYB1 infecting *Pseudomonas aeruginosa*

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Supplementary Fig. S1

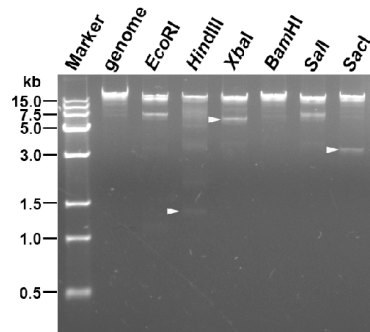
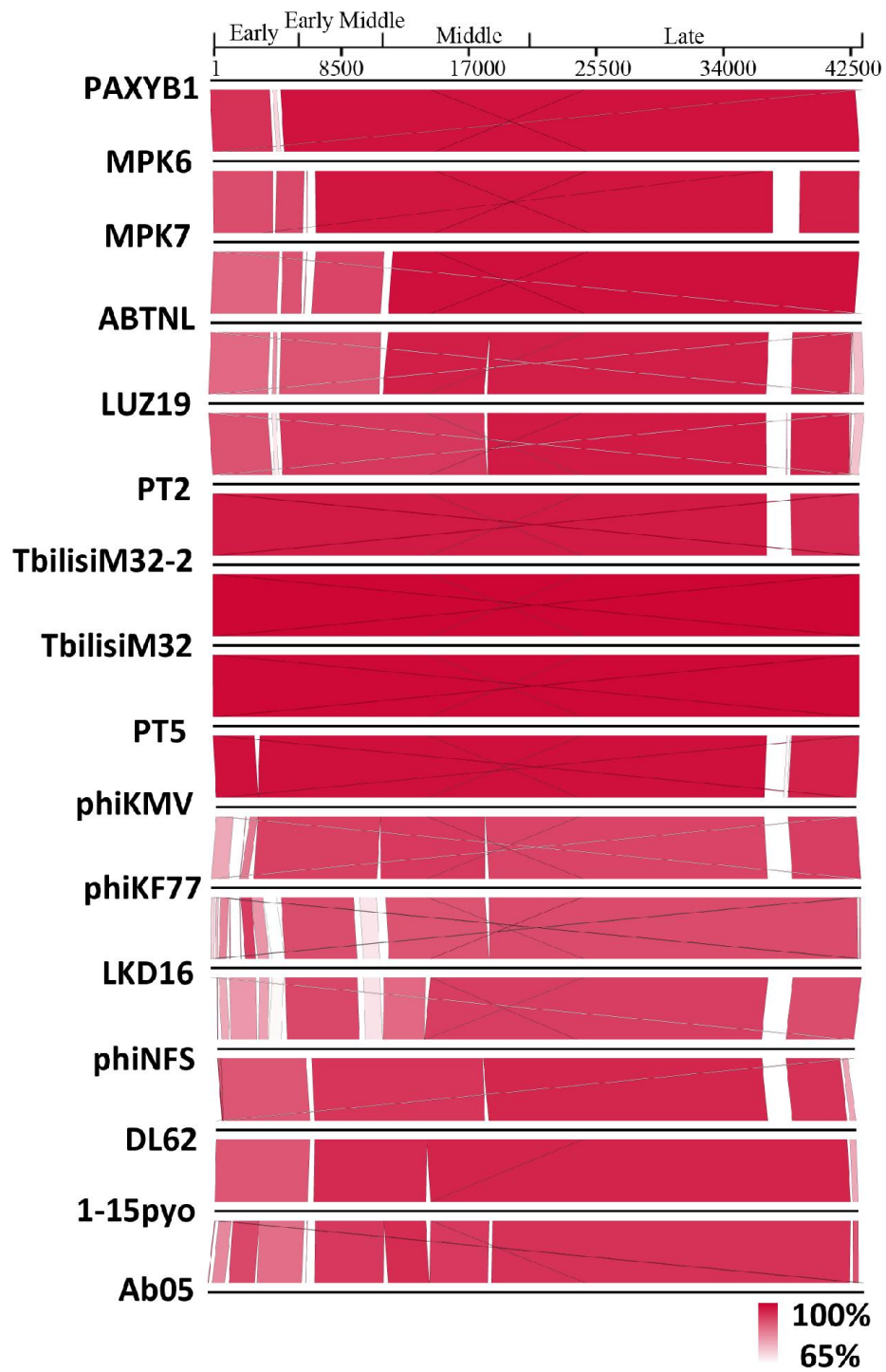


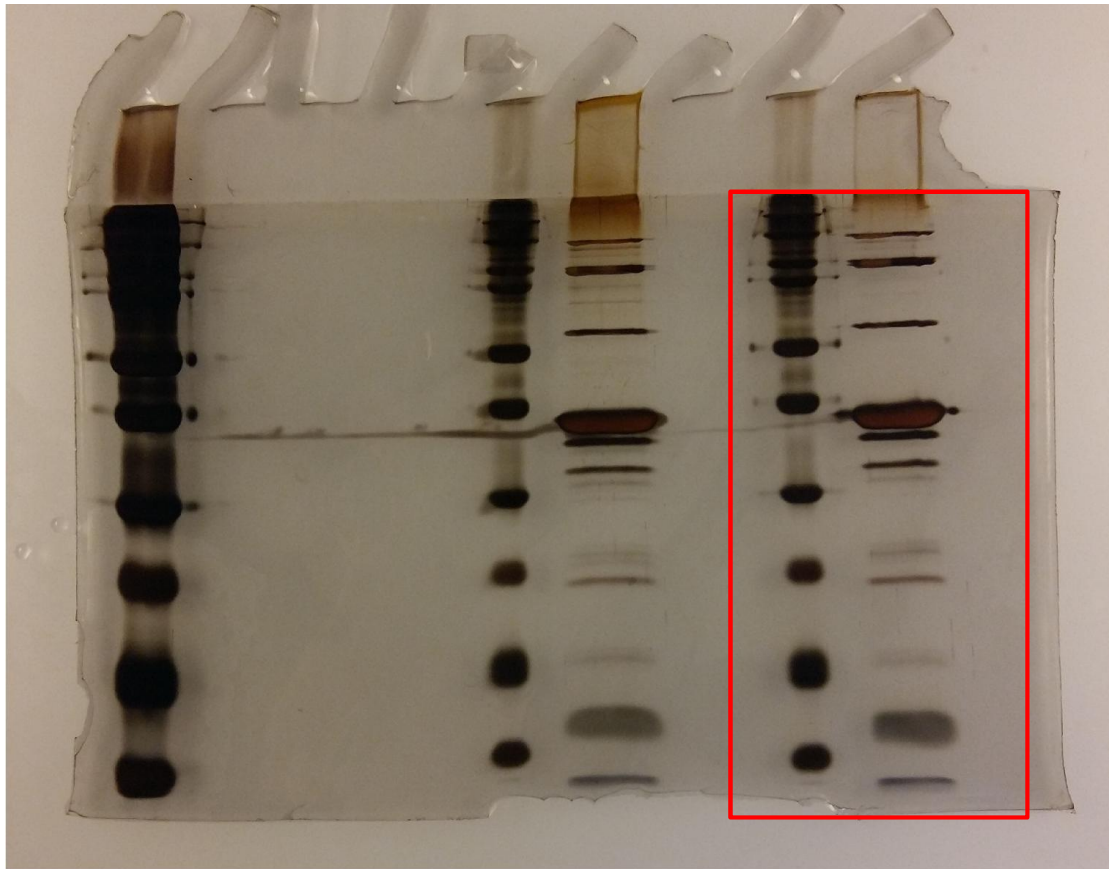
Fig. S1. Restriction digestion analysis of the PAXYB1 genome. The PAXYB1 genomic DNA was digested with *EcoRI* (2), *HindIII* (3), *XbaI* (4), *BamHI* (5), *SalI* (6) and *SacI* (7), with the genome without digestion as a control (1). 15 kb DNA ladder marker was used as the standard (M).

Supplementary Fig. S2



Supplementary Fig. S2. Whole-genome comparisons of all phiKMV-Like family phages using EasyFig. TbilisimM32-2 is Modified TbilisiM32.

Supplementary Fig. S3



Supplementary Fig. S3. Original image for the silver staining of the purified PAXYB1 particles separated by SDS-PAGE (**Related to Fig. 5**). The area marked in red frame indicating the part shown in Fig.5.

Supplementary Table S1. Overview of ϕ KMV-like phages included in this study.

| Phage | Accession | Isolation site | Genome size (bp) | GC% | ORFs | tRNAs (n) | DTR (bp) | Query Coverage (%) | Identity (%) |
|---------------------|------------|------------------------|------------------|------|------|-----------|----------|--------------------|--------------|
| PAXYB1 | KY618819 | Nanjing, China | 43,337 | 62.3 | 60 | 0 | 468 | 100 | 100 |
| Φ KMV | AJ505558 | Moscow, Russia | 42,519 | 62.3 | 48 | 0 | 414 | 93 | 94 |
| LKD16 | AM265638 | Leuven, Belgium | 43,200 | 62.6 | 54 | 0 | 428 | 86 | 91 |
| LUZ19 | AM910651 | Leuven, Belgium | 43,548 | 62.3 | 54 | 0 | 472 | 96 | 97 |
| Φ KF77 | FN263372 | Moscow, Russia | 43,152 | 62.9 | 53 | 0 | 452 | 96 | 92 |
| PT2 | EU236438 | Tbilisi, Georgia | 42,961 | 62.2 | 54 | 0 | 488 | 94 | 95 |
| PT5 | EU056923 | Tbilisi, Georgia | 42,954 | 62.3 | 52 | 0 | 413 | 97 | 94 |
| ABTNL | KM067278 | Dalian, China | 43,227 | 62.4 | 54 | 0 | 453 | 92 | 98 |
| Modified TbilisiM32 | KX711710.1 | Dalian, China | 42965 | 62.3 | 54 | 0 | ND | 97 | 95 |
| TbilisiM32 | JQ307386 | San Antonio, USA | 42,966 | 62.3 | 51 | 0 | 423 | 97 | 94 |
| Ab05 | LN610574 | Abidjan, Côte d'Ivoire | 43,639 | 62.3 | 54 | 0 | 431 | 94 | 94 |
| 1-15pyo | LN610580 | Orsay, France | 42,750 | 62.2 | 49 | 0 | ND | 96 | 95 |
| DL62 | KR054031 | Somerset, UK | 42,508 | 62.2 | 55 | 0 | ND | 95 | 96 |
| phiNFS | KU743887 | Belfast, UK | 42,351 | 62.3 | 49 | 0 | ND | 93 | 94 |
| MPK6 | JX997978 | Seongnam-si, Korea | 42,957 | 62.3 | 50 | 0 | ND | 97 | 98 |
| MPK7 | JX501340 | Seongnam-si, Korea | 42,874 | 62.1 | 53 | 0 | ND | 93 | 99 |

Supplementary Table S2. Comparison of genes encoding tail fiber proteins between PAXYB1 and other ϕ KMV-like phages.

| Phage | ORF49 | ORF50 | ORF51 | ORF52 |
|-------------------|--------------|--------------|--------------|--------------|
| PAXYB1 49-52 | 100 (251aa) | 100 (152aa) | 100 (301aa) | 100 (201aa) |
| MPK6 38-41 | 99.2 (251aa) | 99.3 (152aa) | 100 (301aa) | 100 (201aa) |
| Φ KF77 38-41 | 100 (251aa) | 98.7 (152aa) | 98.7 (301aa) | 100 (201aa) |
| LUZ19 38-41 | 100 (251aa) | 98.7 (152aa) | 98.3 (301aa) | 100 (201aa) |
| LKD16 38-41 | 97.6 (251aa) | 56.6 (152aa) | 73.5 (302aa) | 88.1 (201aa) |
| TbilisiM32 38-41 | 94.4 (251aa) | 50.0 (152aa) | 71.2 (302aa) | 98.0 (201aa) |
| DL62 59.1-62.1 | 99.6 (251aa) | 50.0 (152aa) | 70.9 (302aa) | 88.6 (201aa) |
| Ab05 43-46 | 99.6 (251aa) | 50.0 (152aa) | 70.5 (302aa) | 88.6 (201aa) |
| PT5 38-41 | 94.4 (251aa) | 50.0 (152aa) | 66.6 (281aa) | 97.5 (201aa) |
| 1-15pyo 39-41 | 83.7 (225aa) | 46.6 (163aa) | 71.2 (302aa) | ND |
| MPK7 43-46 | 96.8 (251aa) | 30.0 (146aa) | 27.3 (292aa) | 47.3 (196aa) |
| ABTNL 44-47 | 96.8 (251aa) | 28.8 (146aa) | 26.3 (292aa) | 47.3 (196aa) |
| phiNFS 39-42 | 95.2 (251aa) | 28.1 (146aa) | 24.9 (291aa) | 50.2 (196aa) |
| PT2 38-41 | 95.2 (251aa) | 28.1 (146aa) | 25.3 (292aa) | 34.3 (130aa) |
| Φ KMV 38-41 | 95.2 (251aa) | 28.1 (146aa) | 24.9 (292aa) | 34.3 (139aa) |

The homologues of the four assumed tail fiber proteins of PAXYB1 and other phages are searched using BLASTp analysis. The homologues of gp52 in MPK7, ABTNL, ϕ KF77, PT2 and KMV are not found using BLASTp, and obtained throughout analysis of the genomes. The global identity values between amino acid sequences are determined by EMBOSS Needle tool at EMBL-EBI.