frontiers

*Supplementary Material*

# Interaction of bacteriophage P1 with an epiphytic *Pantoea agglomerans* strain - the role of the interplay between various mobilome elements

**Katarzyna Giermasińska-Buczek[1,2], Jan Gawor[2], Emil Stefańczyk[2], Urszula Gągała[1], Karolina Żuchniewicz[2], Hanna Rekosz-Burlaga[1], Robert Gromadka[2] and Małgorzata Łobocka[2]**

[1]Department of Biochemistry and Microbiology, Institute of Biology, Warsaw University of Life Sciences (SGGW-WULS), Warsaw, Poland

[2] Institute of Biochemistry and Biophysics of the Polish Academy of Sciences, Warsaw, Poland

* **Correspondence: Małgorzata Łobocka:** lobocka@ibb.waw.pl

## 1 Supplementary Experimental Procedures

### 1.1. Phage adsorption

Phage adsorption experiments were carried out as described previously (Głowacka-Rutkowska et al., 2019) with some modifications. Overnight cultures of *E. coli* N99 and *P. agglomerans* L15 cells grown in LB liquid medium, at 30°C were refreshed in similar medium and grown with shaking to the optical density ($OD_{600}$) of about 0.4. Aliquots of each culture (500 µl) were supplemented with 250 µl of 20 mM CaCl2, 250 µl 20 mM MgSO, and 500 µl of lysate containing phages to obtain the multiplicity of infection (M.O.I.) £ 1, and incubated at room temperate for various 5, 10, and 15 min. without shaking. At the end of a given incubation time samples were immediately filtered through 0.20 µm syringe filters (Filtropur S, cat. no. 83.1825.001; Sarstedt, Nümbrecht, Germany) and used to determine the titer of unadsorbed phages by the double layer agar method (Adams, 1959). The fraction of adsorbed phages (in %) was calculated by the subtraction of the titer of unadsorbed phages from the initial titer of infecting phages, relative to the phage initial titer.

### 1.2. Optimization of P1-mediated plasmid transduction from *E. coli* to *P. agglomerans* L15

The region of P1 *c1-100* Tn*9* genome permissible for the insertion of about 12 kb plasmid without compromisig phage functionality was selected based on the ability of P1 *c1-100* Tn*9* obtained by the induction of lysogens of *E. coli* containing derivatives of a wide-host range pRK2

plasmid with cloned fragments of various P1 genome regions, to transduce these plasmids (see Table S1 and S3). In the first step, the *E. coli* C600 cells with any of these plasmids were lysogenized with P1 *c1-100* Tn*9*. Lysogens obtained as able to grow on solid medium with chloramphenicol (selective for P1 *c1-100* Tn*9)*, and tetracycline (selective for the pRK2-derived plasmids), were used to inoculate LB medium with chloramphenicol and tetracycline to induce the lytic development of prophage P1 *c1-100* Tn*9*. The phages ($10^8$ and $10^6$ pfu/mL) obtained through the thermal induction of lysogens served to infect cells of the *E. coli* C600 strain. Infected cells that could form colonies on LA medium with tetracycline, but without chloramphenicol at 30 °C, served to isolate plasmid DNA and verify, by restriction digestion, the identity of obtained plasmid with the plasmid present in the donor cells (Table S3, Figure S2). Only in the case of phage that was propagated in cells with the pKGI5 (*phddoc*$^+$) plasmid single $Tc^RCm^S$ colonies were obtained and they carried the pKGI5 plasmid. Thus, a cell infected with this phage and likely to contain a hybrid of P1 *c1-100* Tn*9* prophage and pKGI5 plasmid, as verified by its ability to grow on medium with chloramphenicol and tetracycline, and by restriction digestion of its plasmid DNA (Figure S2) was used to induce the lytic development of hybrid P1. Phages of the obtained lysate were used for transduction of the *E. coli* C600 cells from cultures of different optical densities ($OD_{600}$ 1.4 and 0.3) and with the use of different MOIs. Conditions optimal for the transduction of pKGI5 plasmid to *E. coli* cells (OD600 of recipient cell culture of about 0.3, MOI of about $10^5$) were used for transduction of *P. agglomerans* L15 (Table S4). The presence of pKGI5 plasmid in L15 transformants grown on LA medium with tetracycline, but sensitive to chloramphenicol was verified based on the restriction digestion pattern of plasmid DNA isolated from them and by testing whether plasmid DNA isolated from them can serve as a template for PCR amplification with primers specific for various regions of pKGI5 (Figure S3).

### 1.3. Shotgun diagnostic WGS sequencing

Diagnostic long-read sequencing of selected isolates of *P. agglomerans* L15 or its derivatives cured from plasmids or lysogenized with P1 *c1-100* Tn*9* IS*1*::$km^R$ was performed using MinION instrument (Oxford Nanopore Technologies, Oxford, UK). Nanopore libraries were constructed using Rapid Barcoding SQK-RBK004 kit and sequenced on MinION R9.4.1 flowcell. Raw nanopore reads were basecalled using guppy v.6.5.7 (Oxford Nanopore Technologies, Oxford, UK). Sequencing adapter removal was performed using Porechop (https://github.com/rrwick/Porechop) and quality filtering was done (mean read quality of 10 and read length of 1kb) using filtlong (https://github.com/rrwick/Filtlong). Cleaned nanopore reads were mapped to reference sequences set consisting of L15 strain plasmids sequences and P1 bacteriophage genome using minimap2 (Li, 2018). Alignment files were converted to sorted and indexed bam alignment files using samtools v1.6 (Danecek et al., 2021). Coverage statistics were calculated using Qualimap bamqc tool (http://qualimap.conesalab.org/).

### 1.4. Assembly of bacteriophage P1 genome from long nanopore reads.

Nanopore reads from L15 strains containing bacteriophage P1 replicon were merged into one fastq file and mapped to P1 reference sequence using minimap2. Sequence coverage statistics were

calculated using Qualimap bamqc tool. All reads that uniquely mapped to reference sequence were extracted from bam alignment file using samtools v1.6 (Danecek et al., 2021). Obtained long reads were then used for *de novo* assembly of P1 *c1-100* Tn*9* IS*1*::km$^R$ genome using flye assembler (Kolomogorov, 2019).

## 2 Supplementary Figures and Tables

### 2.1. Tables

**Supplementary Table 1.** Plasmids used in this study

| Plasmid[a] | Cloned genes | Description (comments) | Replication origin /Selective marker | Source or reference |
|---|---|---|---|---|
| pUC4K | km$^R$ | A multicopy *E. coli* vector containing the kanamycin resistance cassette of Tn*903* | pMB1/ap$^R$, km$^R$ | Taylor and Rose,1988 |
| pUC18 | - | Standard *E. coli* vector with a multiple cloning site (MCS) for DNA cloning | pMB1/ap$^R$ | Vieira and Messing, 1982 |
| pUCP1/270 | IS*1* | A derivative of pUC18 plasmid vector with a cloned fragment of P1 genomic library containing the 3' fragment *isaA* gene, and the 5' fragment of IS*1* sequence (pos. 22011+/-10- do 23306+/-10 of the P1 genome) | pMB1/ap$^R$ | Plasmid collection of IBB PAS; Łobocka et al., 2004 |
| pRK415 | tc$^R$ | A mini-RK2 derived low copy number vector containing the tcracycline resistance cassette | RK2/tc$^R$ | (Keen et al., 1988) |
| pKGI2 | *pdcB* ::km$^R$ | A derivative of pUC18 plasmid with cloned *pdcB* gene of bacteriophage P1 inactivated by the insertion of kanamycin resistance cassette | pMB1/ap$^R$ | Bednarek et al., 2023 |
| pPagL15_1 | - | Natural plasmid of *P. agglomerans* L15 | | This study |
| pPagL15_2 | - | Natural plasmid of *P. agglomerans* L15 | | This study |
| pPagL15_3 | - | Natural plasmid of *P. agglomerans* L15 | | This study |
| pKGI5 | *phd doc* | A derivartive of pRK415 in which the PstI-PstI fragment (pos. 893-1759) was replaced with a 512-bp fragment containing the *phd* and *doc* genes of bacteriophage P1. The P1 DNA fragment containing the *phd* and *doc* genes was amplified with the use of OMLO755 and OMLO756 primers and bacteriophage P1 DNA as a template. | RK2/tc$^R$ | This study |
| pKGI6 | *mod* | A derivartive of pRK415 in which the HindIII-HindIII fragment (pos. 901-1743) was replaced with a 649-bp fragment containing the *mod* gene of bacteriophage P1. The P1 DNA fragment containing the *mod* gene was amplified with the use of OMLO757 and OMLO758 primers and bacteriophage P1 DNA as a template. | RK2/tc$^R$ | This study |

| | | | | |
|---|---|---|---|---|
| pKGI7 | IS*1* | A derivartive of pRK415 in which the HindIII-HindIII fragment (pos. 901-1743) was replaced with a 570-bp fragment containing the IS*1* sequence of bacteriophage P1. The P1 DNA fragment containing the IS*1* sequence was amplified with the use of OMLO759 and OMLO760 primers and bacteriophage P1 DNA as a template. | RK2/tc$^R$ | This study |
| pKGI10 | km$^R$, IS*1* | A derivartive of pUCP1/270 containing the km$^R$ cassette in the IS*1* sequence of bacteriophage P1 (at pos. 322 of IS*1*). obtained by the insertion of the km$^R$ cassette of pUC4K plasmid amplified with OMLO623 and OMLO797 primers and digested with MluII into the MluI site of pUCP1/270 IS*1* sequence. | pMB1/ap$^R$, km$^R$ | This study |
| pKGI12 | *ccdA* | A derivartive of pUCP1/270 containing the *ccdA* gene of the *P. agglomerans* L15 pPagL15_3 plasmid inserted in the IS*1* sequence of bacteriophage P1 (pos. 322), and obtained by the insertion of *ccdA* gene amplified with OMLO806 and OMLO807 primers and digested with MluII in the MluI site of the pUCP1/270 IS*1* sequence. | pMB1/ap$^R$ | This study |

**Supplementary Table 2.** Oligonucleotides used in this work

| Name | Sequence 5'-3' | Types of primers | Complementary region | Aim of use | Product length (bp) | Tm [°C] |
|---|---|---|---|---|---|---|
| OMLO 531 | GCGTAAGCGCCCGGGTATGT | F | *P. agglomerans* L15 genome, pos. 4334-4354 | Amplification of *gyrB* gene of *P. agglomerans* (species identification) | 417 | 60°C |
| OMLO 532 | CCGTCGACGTCCGCATCGGTCAT | R | *P. agglomerans* L15 genome, pos. 5819-5841 | | | |
| OMLO 533 | GATGTGGCGTGTTACGGTGAA | F | Transposon Tn*9*, pos.1298-1318 | Amplification of *cat* gene of Tn*9* (verification of the transposon Tn*9* presence in the genome of P1 and *P. agglomerans*) | 282 | 55°C |
| OMLO 534 | CTGCCACTCATCGCAGTACTGTT | R | Transposon Tn*9*, pos. 1557-1579 | | | |
| OMLO 738 | ATCGGCACGTAAGAGGTTCCAACTTTC | F | Transposon Tn*9*, pos. 831-857 | Confirmation of the transposon Tn*9* presence in a phage P1 and *P. agglomerans* L15 genome (after infection with phage P1) by sequencing | 1000 | 55°C |
| OMLO 739 | CGGTATCAACAGGGACACCAGGATTTA | R | Transposon Tn*9*, pos. 765-791 | | | |
| OMLO 755 | ATTCTGCAGGCAATCCATTAACTTCCGTA | F | Phage P1 *c1-100 mod749*::IS*5* IS*1*::Tn*9* genome, pos. 88048-88067 | Amplification of *phd* and *doc* genes of phage P1 and addition of PstI recognition sites at its flanks | 512 | 55°C |
| OMLO 756 | ATTCTGCAGGCCAGTTCAGGTGAATCAA | R | Phage P1 *c1-100 mod749*::IS*5* IS*1*::Tn*9* genome, | | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | pos. 88541-88559 | | | |
| OMLO 757 | ATTAAGCTTCTCGGCTG ACTCAGTCATTTCA | F | Phage P1 *c1-100 mod749*::IS*5* IS*1*::Tn*9* genome, pos. 7681-7702 | Amplification of *mod* gene of phage P1 and addition of HindIII recognition sites at its flanks | 649 | 57,5°C |
| OMLO 758 | ATTAAGCTTCAGCTC-GACCAAGAACAAAGAG | R | Phage P1 *c1-100 mod749*::IS*5* IS*1*::Tn*9* genome, pos. 8308-8329 | | | |
| OMLO 759 | ATTAAGCTTTGCCAGGT GGTGCCTCAGATTC | F | Phage P1 *c1-100 mod749*::IS*5* IS*1*::Tn*9* genome, pos. 22734-22755 | Amplification of IS*1* sequence of phage P1 and addition of HindIII recognition sites at its flanks | 570 | 60°C |
| OMLO 760 | ATTAAGCTTAGCTACTG ACGGGGTGGTGCGTA | R | Phage P1 *c1-100 mod749*::IS*5* IS*1*::Tn*9* genome, pos. 23281-23303 | | | |
| OMLO 763 | AACTTTTGGCGAAAATG AGACGTTGATCGG | F | Transposon Tn*9*, pos. 806-835 | The region preceding the *cat* gene of the transposon Tn*9*. Identification of the location of the transposon Tn*9* in the genome of phage P1 by sequencing | - | 65°C |
| *trfAF* | GTGAAGATCACCTACAC CGGC | F | pRK415 plasmid, pos. 3500-3520 | Amplification of *trfA* and *trfB* genes of pRK415 plasmid | 130 | 55°C |
| *trfAR* | TGGCAAAGCTCGTAGA ACGTG | R | pRK415 plasmid, pos. 3390-3410 | | | |
| OMLO 623 | ATTACGCGTGCGCTGAG GTCTGCCTCGTGAAGA | F | pUC4K plasmid, pos. 1-24 | Amplification of $Kan^R$ cassette of pUC4K plasmid and addition of MluI recognition sites at its flanks | 1213 | 54°C |
| OMLO 797 | ATTACGCGTAAAGCCAC GTTGTGTCTCAAAATC | R | pUC4K plasmid, pos. 1190-1213 | | | |
| OMLO 806 | ATTACGCGTTCCGTGTG ATTGGCAGTGTTAGT | F | pPagL15_3 plasmid of *P. agglomerans* L15, pos. 22085-22107 | Amplification of *ccdA* gene of pPagL15_3 plasmid and addition of MluI recognition sites at its flanks | 353 | 56,5°C |
| OMLO 807 | ATTACGCGTGTAACATC GAGCAGGGGATA | R | pPagL15_3 plasmid of *P. agglomerans* L15, pos. 21755-21777 | | | |
| OMLO 919 | AATAGCTAGCGTGCTTA AACAGAGAATGCC | F | Phage P1 *c1-100 mod749*::IS*5* IS*1*::Tn*9* genome, pos. 88799-88818 | Amplification of *pdcB* gene of phage P1 and addition of NheI and XhoI recognition sites at its flanks | 1109 | 54,6 °C |
| OMLO 920 | ATACTCGAGCAATTTTAT CTAACACTCGACG | R | Phage P1 *c1-100 mod749*::IS*5* IS*1*::Tn*9* genome, pos. 89886-89907 | | | |
| OMLO 921 | GAAAATGATGAGTGAG TCTGAC | F | pPagL15_3 plasmid of *P. agglomerans* L15, pos. 2271- | Amplification of *parB* gene of pPagL15_3 plasmid | 928 | 54,4°C |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | 2292 | | | |
| OMLO 922 | GTCTTTTTCATTCACAA CCA | R | pPagL15_3 plasmid of *P. agglomerans* L15, pos. 1365-1384 | | | |
| OMLO 952 | ATTAAGCTTACTGCATT CTTAAAATGTCC | F | pPagL15_3 plasmid of *P. agglomerans* L15, pos. 21813-21832 | Amplification of *ccdA* gene of pPagL15_3 plasmid and addition of HindIII and SalI recognition site at its flanks | 407 | 56°C |
| OMLO 934 | ATTGTCGACGTAGTTCC TGTATTTCCATCA | R | pPagL15_3 plasmid of *P. agglomerans* L15, pos. 22199-22219 | | | |

[a]Positions in the genomes of plasmid pUC4K, pPagL15_3 and phage P1 *c1-100 mod749*::IS*5* IS*1*::Tn*9* refer to the sequences deposited in GenBank under the accession numbers X06404.1, CP034151, AF234172.1, respectively.

**Supplementary Table 3.** The number of *E. coli* C600 colonies grown on media with various antibiotics after infection with phages obtained by induction of P1 *c1-100* Tn*9* lysogens of *E. coli* N99 cells carrying plasmids with various fragments of the P1 genome

| **Plasmid present in a phage propagation host (P1 genome region cloned)** | **Phage titer in lysate** | **Number of colonies* grown in LA medium with:** | | |
|---|---|---|---|---|
| | | **Cm** | **Tc** | **Cm Tc** |
| **pKGI5 (*phddoc*)** | $10^8$ | uncountable | 23 | 6 |
| | $10^6$ | uncountable | 4 | 0 |
| **pKGI6 (*mod*)** | $10^8$ | uncountable | 0 | 0 |
| | $10^6$ | uncountable | 0 | 0 |
| **pKGI7 (IS*1*)** | $10^8$ | uncountable | 0 | 0 |
| | $10^6$ | uncountable | 0 | 0 |

* The numbers shown represent the average number of colonies obtained in four independent biological repetitions of each experiment.

**Supplementary Table 4.** The number of *E. coli* C600 or *P. agglomerans* L15 colonies grown on media with various antibiotics after infection with phages obtained by the induction of *E. coli* C600 lysogen carrying the P1 *c1-100* Tn*9*-pKGI5 hybrid prophage

| **Target cells** | **Culture density of infected cells** | **Phage titer in lysate** | **Number of colonies grown on LA medium with:** | | |
|---|---|---|---|---|---|
| | | | **Cm** | **Tc** | **Cm Tc** |
| *E. coli* C600 | 1.4 | $10^7$ | uncountable | 40 | 0 |
| | | $10^5$ | uncountable | 134 | 5 |
| | 0.3 | $10^7$ | uncountable | 156 | 2 |
| | | $10^5$ | uncountable | 432 | 5 |
| *P. agglomerans* L15* | | $10^7$ | uncountable | 0 | 0 |
| | | $10^5$ | 492 | 2 | 0 |

*Phage infection of *P. agglomerans* L15 was performed with the use of 10 times increased volumes of the culture and the lysate as compared to those used for the infection of *E. coli* C600.

**Supplementary Table 5.** *P. agglomerans* L15 genes encoding proteins significantly similar to the proteins of known bacterial anti-phage defense systems

| L15 genome part (GenBank acc . no) | System ID[1] | Type/ subtype | Start coord. | End coord. | Num-ber of genes | Protein coding gene starts coord. in the system | N-terminal protein sequences | Profile name in the system |
|---|---|---|---|---|---|---|---|---|
| chromosome( CP034148) | Mokosh_TypeII_1 | Mokosh/ Mokosh_TypeII | 541254 | 541254 | 1 | 541254 | MDSNTQGFTS | Mokosh_TypeII_MkoC |
| | Shango_2 | Shango/ Shango | 3084537 | 3088052I | 3 | 3084537<br>3086732,<br>3088052 | MSSAYDSLDP<br>MSLTRIRVKE<br>MELWLFLAAI | Shango_SngC,<br>Shango_SngB,<br>Shango__SngA |
| | RloC_1 | RloC/RloC | 2830219 | 2830219 | 1 | 2830219 | MSQLEIRGVR | RloC__RloC |
| | RM_Type_I_1 | RM/ RM_Type_I | 530103 | 537360 | 4 | 530103,<br>531608,<br>534220,<br>537360 | MTLINLKDLE<br>MSNKKLEEIL<br>MFNEQTVTEN<br>MNTSLFEDLL | RM_Type_I_Mtases,<br>RM_Type_I_Mtases,<br>RM_Type_I_Reases,<br>RM_Type_I_MTases |
| | MazEF | TA | 1722182 | 1722766 | 2 | 1722182<br>1722518 | MVSRFVPDAG<br>MIHGNVKRWG | MazE antitoxin<br>MazF toxin |
| pPagL15_1 (CP034149) | RM_Type_II_1 | RM/ RM_Type_II | 481968 | 483943 | 2 | 481968,<br>483943 | MVNKLYLNFH<br>MKAIDLFCGA | RM_Type_II_Type_II_ Reases,<br>RM_Type_II_Type_II_ MTases |
| pPagL15_3 (CP034151) | Gao_Ppl_1 | Gao_Ppl/ Gao_Ppl | 11414 | 11414 | 1 | 11414 | MSVGSRWYKF | Gao_Ppl__PplA |

**Supplementary Table 6.** Predicted proteins of *P. agglomerans* L15 significantly similar to bacteriophage P1 proteins

| P1 protein | Number of amino acid residues | Predicted product of L15 chromosome (number of amino acid residues), protein ID | % coverage/ % identity | Predicted product of pPagL15_1 plasmid (number of amino acid residues), protein ID | % coverage/% identity | Predicted product of pPagL15_2 plasmid (number of amino acid residues), protein ID | % coverage/ % identity | Predicted product of pPagL15_3 plasmid (number of amino acid residues) , protein ID | % coverage/% identity |
|---|---|---|---|---|---|---|---|---|---|
| Ssb | 162 | 549.44.peg.3044 (187) AZI52200.1 | 100/60 | | | | | | |
| HrdC | 301 | 549.44.peg.2480 (303) AZI51656.1 | 98/59 | | | | | | |
| Ban | 454 | 549.44.peg.3052 (468) AZI52206.1 | 97/78 | | | | | | |
| Ppp | 230 | 549.44.peg.1190 (215) AZI50471.1 | 93/48 | | | | | | |
| Hot | 87 | 549.44.peg.1161 (95) AZI50444.1 | 80/60 | | | | | | |
| HumD | 129 | 549.44.peg.1603 (139) AZI50853.1 | 89/46 | | | | | | |
| ParB | 333 | | | 549.45.peg.568 (323) WP_124890719.1 | 98/53 | 549.46.peg.69 (323) WP_124890785.1 | 94/42 | 549.47.peg.4 (324) WP_124890853.1 | 95/43 |
| ParA | 398 | | | 549.45.peg.569 (399) WP_010246822.1 | 99/78 | 549.46.peg.70 (400) WP_124890787.1 | 97/58 | 549.47.peg.5 (402) WP_069026998.1 | 97/54 |
| RepA | 286 | | | 549.45.peg.571 (309) WP_010246820.1 | 91/49 | 549.46.peg.71 (316) WP_010256943.1 | 88/47 | 549.47.peg.9 WP_124890855.1 | 98/73 |

*Only proteins with over 40% identity to P1 proteins over at least 80% of their length were considered as significantly similar.

**Supplementary Table 7.** Detection of plasmid or prophage DNA by diagnosting long-read WGS sequencing in cells of *P. agglomerans* L15 or its derivatives cured of particular plasmids or lysogenized with bacteriophage P1 *c1-100* Tn*9* IS*1*::km$^R$

| Strain | Reference sequence | Length (bp) | Mapped bases | Mean coverage | Standard deviation | Match to reference |
|---|---|---|---|---|---|---|
| ***P. agglomerans* L15** | PpagL15_1 | 583571 | 4515151 | 7.7371 | 3.5398 | YES |
| | PpagL15_2 | 179590 | 1076018 | 5.9915 | 2.6126 | YES |
| | PpagL15_3 | 66484 | 275114 | 4.138 | 1.2644 | YES |
| | Bacteriophage P1 | 94800 | 0 | 0 | 0 | NO |
| ***P. agglomerans* IPAG312** | PpagL15_1 | 583571 | 31188 | 0.0534 | 0.7287 | NO* |
| | PpagL15_2 | 179590 | 516105 | 2.8738 | 1.476 | YES |
| | PpagL15_3 | 66484 | 145246 | 2.1847 | 1.3995 | YES |
| | Bacteriophage P1 | 94800 | 0 | 0 | 0 | NO |
| ***P. agglomerans* IPAG312 cured of pPagL15_3 using P1 *c1-100* Tn*9* IS*1*::km$^R$ -mediated replication incompatibility** | PpagL15_1 | 583571 | 35863 | 0.0615 | 0.7753 | NO* |
| | PpagL15_2 | 179590 | 796824 | 4.4369 | 1.8461 | YES |
| | PpagL15_3 | 66484 | 0 | 0 | 0 | NO |
| | Bacteriophage P1 | 94800 | 265315 | 2.7987 | 1.5473 | YES |
| ***P. agglomerans* L15 cured of pPagL15_1 and pPagL15_3 using P1 *c1-100* Tn*9* IS*1*::km$^R$ -mediated partition and replication incompatibility, respectively** | PpagL15_1 | 583571 | 68320 | 0.1171 | 1.2518 | NO* |
| | PpagL15_2 | 179590 | 705034 | 3.9258 | 2.2059 | YES |
| | PpagL15_3 | 66484 | 0 | 0 | 0 | NO |
| | Bacteriophage P1 | 94800 | 499866 | 5.1 | 1.7937 | YES |
| **Bacteriophage P1 *c1-100* Tn*9* IS*1*::km$^R$ de novo assembly from the L15 derivatives cured of pPagL15_1 and pPagL15_3** | NA | 97417 | 876048 | 8.9928 | 2.6203 | NA |

*Matches to the reference pPagL15_1 sequence are slightly above 0 due to the presence of homologs of certain chromosomal genes in the sequence of pPagL15_1;
NA - not applicable

**Supplementary Table 8.** *Pantoea* sp. plasmids partitionally incompatible with P1, by prediction, based on the similarity of their ParB proteins to ParB of pPagL15_1 and P1, and on the conservation of ParB amino acid residues essential for specific interaction with P1 ParB.

| Description | Scientific name | Max score | Total score | Query cove-rage | E -value | Identity (%) | Acc. length | Accession |
|---|---|---|---|---|---|---|---|---|
| Pantoea agglomerans strain L15 plasmid pPagL15_1 | Pantoea agglomerans | 658 | 658 | 100% | 0.0 | 100.00% | 583567 | CP034149.1 |
| Pantoea agglomerans strain ASB05 plasmid pASB05p1 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 563807 | CP046723.1 |
| Pantoea agglomerans strain AR5 plasmid pAR5_A | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 555257 | CP134754.1 |
| Pantoea agglomerans strain AR8b plasmid pAR8b_A | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 575199 | CP134750.1 |
| Pantoea agglomerans strain BH6c plasmid pBH6cv2_A | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 569248 | CP134745.1 |
| Pantoea agglomerans strain FC61912-B plasmid pFC61912-B_A | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 547579 | CP134738.1 |
| Pantoea agglomerans strain MMD61212-C plasmid pMMD61212-C | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 612559 | CP134734.1 |
| Pantoea agglomerans strain ROTS050421 plasmid pROTS050421_A | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 519021 | CP134729.1 |
| Pantoea agglomerans strain SUH1 plasmid pSUH1_A | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 574725 | CP134725.1 |
| Pantoea agglomerans strain T88c plasmid pT88c_A | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 555281 | CP134720.1 |
| Pantoea agglomerans strain NBBC-01 plasmid pNBBC01-1 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 531583 | CP099729.1 |
| Pantoea agglomerans strain CB1 plasmid pCB1A | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 569555 | CP084198.1 |
| Pantoea agglomerans strain AB378 plasmid unnamed1 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 555125 | CP113086.1 |
| Pantoea agglomerans strain DAPP-PG734 genome assembly, plasmid: P1 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 530328 | OW970316.1 |
| Pantoea agglomerans strain CHTF15 plasmid unnamed1 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 514938 | CP103402.1 |
| Pantoea agglomerans strain CPHN 2 plasmid unnamed1 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 583238 | CP098412.1 |
| Pantoea agglomerans strain Pa58 plasmid p1 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 554101 | CP091097.1 |
| Pantoea agglomerans strain PSV1-7 plasmid unnamed1 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 621667 | CP091190.1 |
| Pantoea agglomerans strain DBM 3797 plasmid pPA_DBM3797_1 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 555522 | CP086134.1 |
| Pantoea agglomerans strain FDAARGOS 1447 plasmid unnamed2 | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 511735 | CP077368.1 |
| Pantoea agglomerans strain AR1a plasmid pAR1aA | Pantoea agglomerans | 656 | 656 | 100% | 0.0 | 99.69% | 557771 | CP059091.1 |
| Pantoea agglomerans strain UAEU18 plasmid unnamed1 | Pantoea agglomerans | 655 | 655 | 100% | 0.0 | 99.38% | 513383 | CP048034.1 |
| Pantoea agglomerans strain TH81 plasmid unnamed1 | Pantoea agglomerans | 654 | 654 | 99% | 0.0 | 99.69% | 520959 | CP031650.1 |
| Pantoea agglomerans strain CFSAN047153 plasmid pCFSAN047153_1 | Pantoea agglomerans | 654 | 654 | 100% | 0.0 | 99.38% | 613013 | CP034470.1 |
| Pantoea agglomerans strain CFSAN047154 plasmid pCFSAN047154_1 | Pantoea agglomerans | 654 | 654 | 100% | 0.0 | 99.38% | 613013 | CP034475.1 |
| Pantoea agglomerans strain C410P1 plasmid unnamed1 | Pantoea agglomerans | 654 | 654 | 100% | 0.0 | 99.38% | 543504 | CP016890.1 |
| Pantoea agglomerans strain AR24 plasmid pAR24_A | Pantoea agglomerans | 654 | 654 | 100% | 0.0 | 99.38% | 537957 | CP134758.1 |
| Pantoea agglomerans strain ZJU23 plasmid unnamed3 | Pantoea agglomerans | 654 | 654 | 100% | 0.0 | 99.38% | 567588 | CP068443.1 |
| Pantoea agglomerans strain AJ2b plasmid pAJ2b_A | Pantoea agglomerans | 653 | 653 | 100% | 0.0 | 99.38% | 571710 | CP134762.1 |
| Pantoea agglomerans pv. gypsophilae strain 824-1 plasmid pPAG02 | Pantoea agglomerans pv. gypsophilae | 653 | 653 | 100% | 0.0 | 99.38% | 582658 | CP122321.1 |
| Pantoea agglomerans pv. betae strain 4188 plasmid pPAB02 | Pantoea agglomerans pv. betae | 652 | 652 | 100% | 0.0 | 99.07% | 541337 | CP122325.1 |
| Pantoea agglomerans strain 1.2.4 plasmid unnamed | Pantoea agglomerans | 651 | 651 | 100% | 0.0 | 99.07% | 598453 | CP134150.1 |
| Pantoea vagans strain PV989 plasmid pPV989-508 | Pantoea vagans | 647 | 647 | 100% | 0.0 | 97.52% | 507680 | CP028350.1 |
| Pantoea vagans C9-1 plasmid pPag3 | Pantoea vagans C9-1 | 645 | 645 | 100% | 0.0 | 97.21% | 529676 | CP001895.1 |
| Pantoea vagans strain LMG 24199 plasmid pVag1 | Pantoea vagans | 644 | 644 | 100% | 0.0 | 96.90% | 559692 | CP038854.1 |
| Pantoea vagans strain FDAARGOS_160 plasmid unnamed2 | Pantoea vagans | 644 | 644 | 100% | 0.0 | 97.21% | 470309 | CP014127.2 |
| Pantoea alfalfae strain CQ10 plasmid p1_CQ10 | Pantoea alfalfae | 644 | 644 | 100% | 0.0 | 97.21% | 235469 | CP082293.1 |
| Pantoea agglomerans strain FL1 plasmid unnamed1 | Pantoea agglomerans | 644 | 644 | 100% | 0.0 | 97.21% | 504646 | CP126682.1 |
| Pantoea sp. Lij88 plasmid unnamed1 | Pantoea sp. Lij88 | 637 | 637 | 99% | 0.0 | 96.58% | 634148 | CP118267.1 |
| Pantoea vagans strain FBS135 plasmid pPant1 | Pantoea vagans | 632 | 707 | 100% | 0.0 | 95.98% | 526773 | CP022517.1 |
| Pantoea jilinensis strain D25 plasmid plas2 | Pantoea jilinensis | 632 | 706 | 100% | 0.0 | 95.98% | 483571 | CP077748.1 |
| Pantoea sp. MT58 plasmid unnamed1 | Pantoea sp. MT58 | 632 | 707 | 100% | 0.0 | 95.98% | 522095 | CP061084.1 |
| Pantoea eucalypti strain LMG 24197 plasmid pEuc1 | Pantoea eucalypti | 630 | 707 | 100% | 0.0 | 95.67% | 529303 | CP045721.1 |
| Pantoea deleyi strain LMG24200 plasmid Plas2 | Pantoea deleyi | 625 | 625 | 100% | 0.0 | 93.81% | 450383 | CP071407.1 |
| Pantoea anthophila strain CL1 plasmid unnamed1 | Pantoea anthophila | 619 | 619 | 100% | 0.0 | 93.19% | 454539 | CP110471.1 |
| Pantoea agglomerans strain HJS002 plasmid unnamed1 | Pantoea agglomerans | 617 | 617 | 100% | 0.0 | 92.57% | 548340 | CP090208.1 |
| Pantoea ananatis strain YJ76 plasmid p_unamed1 sequenced | Pantoea ananatis | 573 | 573 | 100% | 0.0 | 86.38% | 328324 | CP022429.1 |
| Pantoea ananatis strain JBR-LB3-16 plasmid unnamed | Pantoea ananatis | 573 | 573 | 100% | 0.0 | 86.38% | 338834 | CP090357.1 |
| Pantoea ananatis strain R100 plasmid | Pantoea ananatis | 572 | 572 | 100% | 0.0 | 86.07% | 331058 | CP014208.1 |
| Pantoea ananatis strain NN08200 plasmid unnamed2 | Pantoea ananatis | 572 | 572 | 100% | 0.0 | 86.38% | 307670 | CP035036.1 |
| Pantoea ananatis strain SGAir0210 plasmid pSGAir0210_2 | Pantoea ananatis | 572 | 572 | 100% | 0.0 | 86.38% | 304029 | CP028034.2 |
| Pantoea ananatis strain JT8-6 plasmid unnamed | Pantoea ananatis | 572 | 572 | 100% | 0.0 | 86.38% | 272048 | CP099543.1 |
| Pantoea ananatis strain JT1-188 plasmid unnamed1 | Pantoea ananatis | 572 | 572 | 100% | 0.0 | 86.38% | 286165 | CP099536.1 |
| Pantoea ananatis strain Lstri plasmid pLs | Pantoea ananatis | 572 | 572 | 100% | 0.0 | 86.38% | 267898 | CP060819.1 |
| Pantoea ananatis strain VY148 plasmid unnamed | Pantoea ananatis | 572 | 572 | 100% | 0.0 | 86.38% | 302727 | CP086008.1 |
| Pantoea ananatis strain TZ39 plasmid plas2 | Pantoea ananatis | 572 | 572 | 100% | 0.0 | 86.38% | 276579 | CP081344.1 |
| Pantoea ananatis LMG 5342 plasmid pPANA10 | Pantoea ananatis LMG 5342 | 572 | 572 | 100% | 0.0 | 86.38% | 302599 | HE617161.1 |
| Pantoea ananatis PA13 plasmid PAGR_p | Pantoea ananatis PA13 | 572 | 572 | 100% | 0.0 | 86.38% | 280753 | CP003086.1 |
| Pantoea ananatis AJ13355 plasmid pEA320 DNA | Pantoea ananatis AJ13355 | 572 | 572 | 100% | 0.0 | 86.38% | 321744 | AP012033.1 |
| Pantoea ananatis LMG 20103, complete genome | Pantoea ananatis LMG 20103 | 572 | 572 | 100% | 0.0 | 86.38% | 4703373 | CP001875.2 |
| Pantoea ananatis strain FDAARGOS_680 plasmid unnamed1 | Pantoea ananatis | 571 | 571 | 100% | 0.0 | 86.38% | 283516 | CP054909.1 |
| Pantoea ananatis strain PNA 97-1R plasmid pPNA97-1RA | Pantoea ananatis | 571 | 571 | 100% | 0.0 | 86.07% | 273809 | CP020944.2 |
| Pantoea ananatis FU-01 plasmid pPaFU01 DNA | Pantoea ananatis | 571 | 571 | 100% | 0.0 | 86.07% | 281268 | AP019754.1 |
| Pantoea ananatis strain OC5a plasmid pOC5aA | Pantoea ananatis | 570 | 570 | 100% | 0.0 | 86.07% | 305982 | CP059083.1 |

| Description | Scientific name | Max score | Total score | Query cove-rage | E -value | Identity (%) | Acc. length | Accession |
|---|---|---|---|---|---|---|---|---|
| Pantoea stewartii strain ZJ-FGZX1 plasmid unnamed1 | Pantoea stewartii | 562 | 562 | 100% | 0.0 | 84.52% | 326337 | CP049116.1 |
| Pantoea stewartii subsp. stewartii DC283 plasmid pDSJ10 | Pantoea stewartii subsp. stewartii DC283 | 562 | 562 | 100% | 0.0 | 84.52% | 304641 | CP017591.1 |
| Pantoea stewartii strain HR3-48 plasmid unnamed | Pantoea stewartii | 561 | 561 | 100% | 0.0 | 84.52% | 333832 | CP099541.1 |
| Pantoea stewartii isolate RON18713 plasmid pPSbnut | Pantoea stewartii | 560 | 560 | 100% | 0.0 | 84.52% | 262265 | CP116286.1 |
| Pantoea phytobeneficialis strain MSR2 plasmid pMSR2A | Pantoea phytobeneficialis | 541 | 541 | 100% | 6e-175 | 78.95% | 656860 | CP024637.1 |
| Pantoea cypripedii strain NE1 plasmid pNE1A | Pantoea cypripedii | 540 | 540 | 100% | 8e-175 | 79.26% | 673450 | CP024769.1 |
| Pantoea sp. At-9b plasmid pPAT9B01 | Pantoea sp. At-9b | 538 | 538 | 100% | 4e-174 | 78.95% | 793953 | CP002434.1 |
| Pantoea sp. SOD02 plasmid pSOD02 | Pantoea sp. SOD02 | 536 | 536 | 100% | 4e-173 | 79.26% | 926844 | CP102605.1 |
| Pantoea sp. SO10 plasmid unnamed1 | Pantoea sp. SO10 | 535 | 535 | 99% | 4e-173 | 79.50% | 744154 | CP040096.1 |
| Pantoea sp. X85 plasmid unnamed | Pantoea sp. X85 | 535 | 535 | 100% | 4e-173 | 79.26% | 771939 | CP121109.1 |
| Pantoea sp. SS70 plasmid unnamed1 | Pantoea sp. SS70 | 535 | 535 | 100% | 4e-173 | 79.26% | 779368 | CP117200.1 |
| Pantoea agglomerans strain 33.1 plasmid p33.1_1 | Pantoea agglomerans | 535 | 535 | 99% | 5e-173 | 78.57% | 527897 | CP083808.1 |
| Pantoea piersonii strain URMC-2103A041 plasmid p527820 | Pantoea piersonii | 533 | 533 | 99% | 3e-172 | 77.95% | 527820 | CP115896.1 |
| Pantoea piersonii strain GABEKP28 plasmid pGABEKP28_1 | Pantoea piersonii | 531 | 531 | 99% | 1e-171 | 77.64% | 513647 | CP104759.1 |
| Pantoea dispersa strain ESL4 plasmid pESL4.1 | Pantoea dispersa | 529 | 529 | 100% | 9e-171 | 76.78% | 690879 | CP109854.1 |
| Pantoea dispersa strain JL.02bL plasmid pJL.02bL | Pantoea dispersa | 529 | 529 | 100% | 9e-171 | 76.78% | 696693 | CP107574.1 |
| Pantoea dispersa strain Lsch plasmid unnamed | Pantoea dispersa | 529 | 529 | 100% | 1e-170 | 76.47% | 689940 | CP082347.1 |
| Pantoea dispersa strain VWJL.P1 plasmid pVWJL.P1 | Pantoea dispersa | 528 | 528 | 100% | 1e-170 | 76.78% | 708540 | CP118630.1 |
| Pantoea dispersa strain YSD_J2 plasmid unnamed | Pantoea dispersa | 528 | 528 | 100% | 1e-170 | 76.78% | 710238 | CP074351.1 |
| Pantoea dispersa strain ML.8a3 plasmid pML.8a3 | Pantoea dispersa | 526 | 526 | 100% | 6e-170 | 76.16% | 742161 | CP106661.1 |
| Pantoea dispersa strain AHKW2b plasmid unnamed | Pantoea dispersa | 526 | 526 | 100% | 1e-169 | 75.85% | 653898 | CP082342.1 |
| Pantoea sp. PSNIH1 plasmid pPSP-3a9 | Pantoea sp. PSNIH1 | 486 | 486 | 99% | 5e-156 | 72.59% | 329383 | CP010326.1 |
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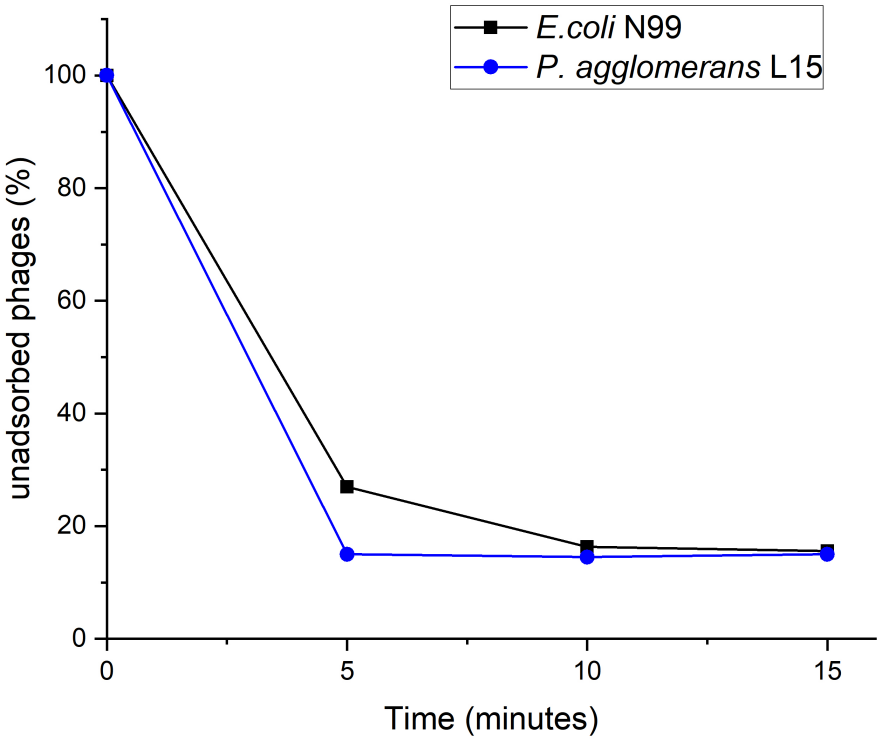
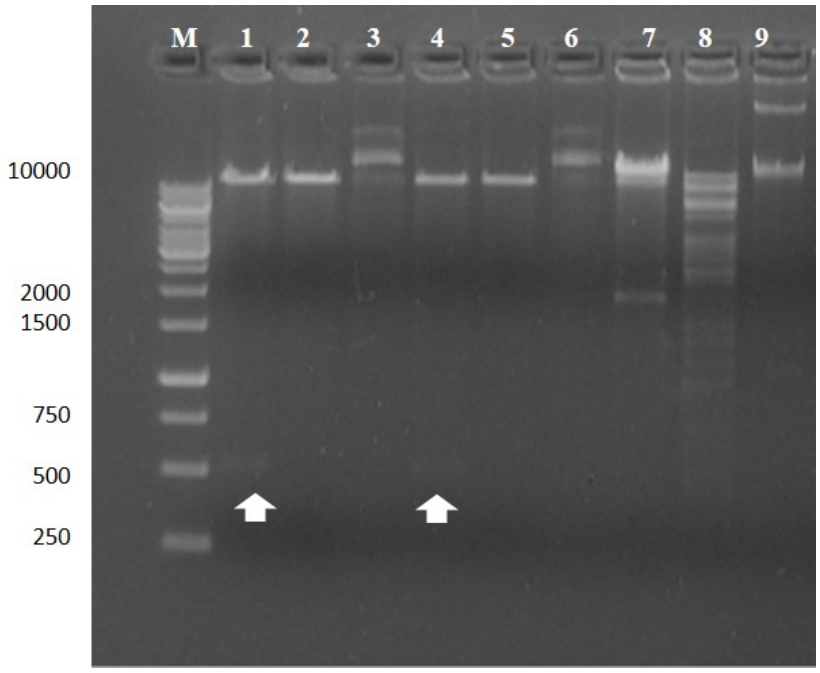
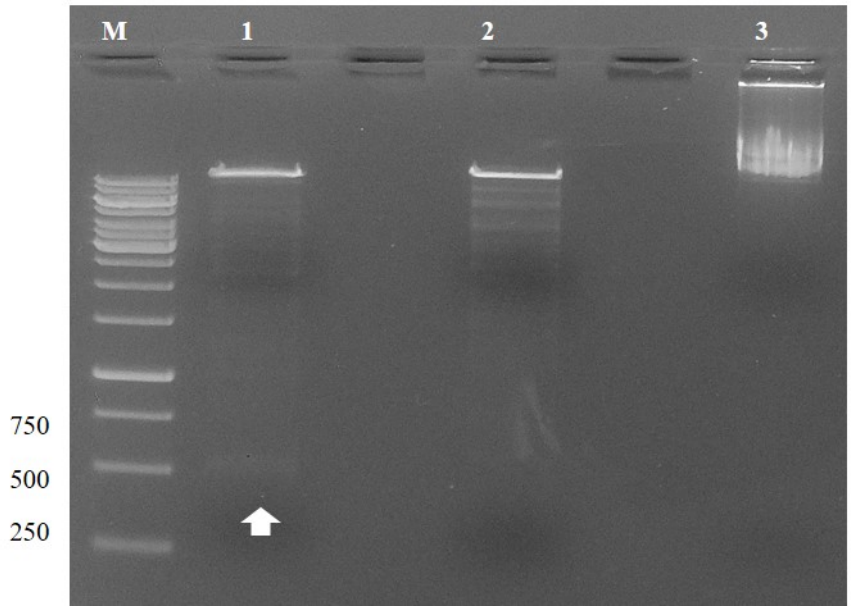
## 2.2. Supplementary Figures



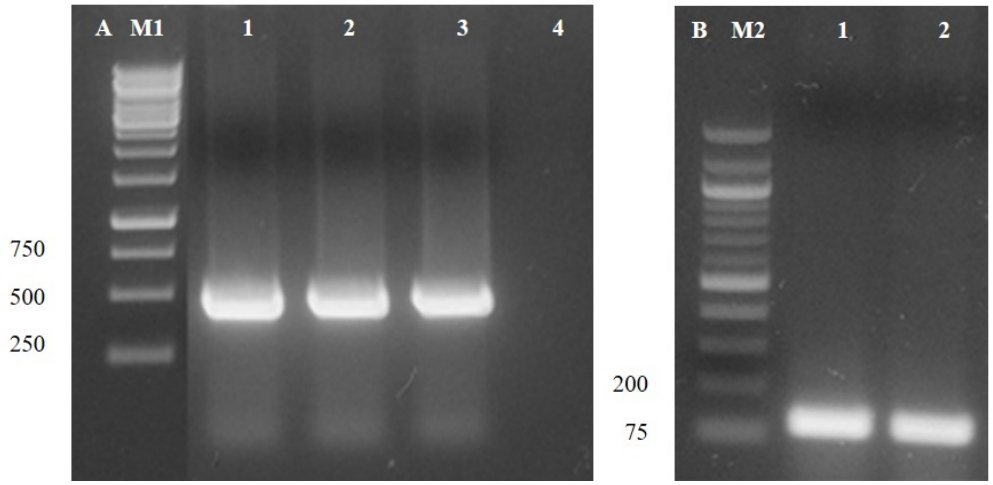

**Supplementary Figure 1.** Adsorption rate of bacteriophage P1 *c1-100* Tn*9* to *E. coli* N99 cells and *P. agglomerans* L15 cells. Cultures for the measurements were grown at 30° C.



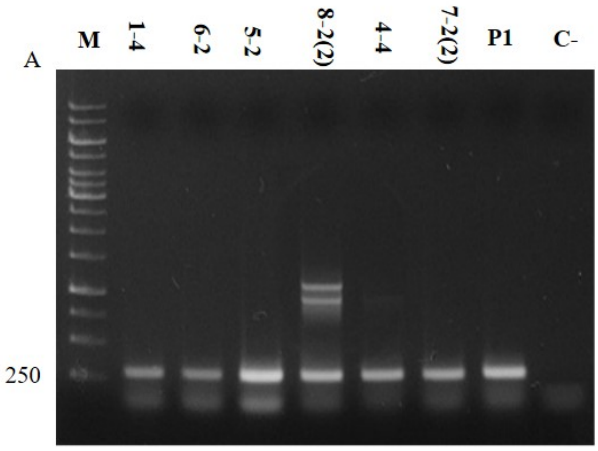

**Supplementary Figure 2**. Verification of the presence of plasmid pKGI5 in the transductants of *E. coli* C600 cells. Plasmid DNA isolated from the transductants obtained as resistant to tetracycline and sensitive to chloramphenicol (lane 1 - 6) or resistant to tetracycline and chloramphenicol (lane 7 - 9) after treatment with P1 *c1-100* Tn*9* induced from tetracycline and chloramphenicol resistant lysogens of the *E. coli* C600/pKGI5 strain was digested with PstI (lanes 1, 4, 7) or EcoRV (lanes 2, 5, 8) and separated in 1% agarose gel. Lanes 3, 6, and 9 represented undigested DNA. GeneRuler$^{TM}$ 1 kb DNA ladder (Thermo Fisher Scientific) was used as a DNA size marker (M). As expected PstI cleaved the plasmids obtained from the $Tc^{R}Cm^{S}$ clones into the ca. 500 bp fragment (indicated by an arrow) representing the cloned fragment of *phddoc* operon that is flanked by the two PstI recognition sites in pKGI5, and over 10 kB fragment representing the rest of pKGI5, while EcoRV which has one recognition site in pKGI5 linearized the plasmid. The pattern of PstI and EcoRV cleavage of plasmid DNA from $Tc^{R}Cm^{R}$ clones was more complex and consistent with the expected cleavage pattern of P1-pKGI5 hybrids, which have three PstI recognition sites (one in the IS*1* sequence of P1 and two in the pKGI5) and several EcoRV sites (31 in the P1 derived DNA and one in pKGI5-derived DNA).

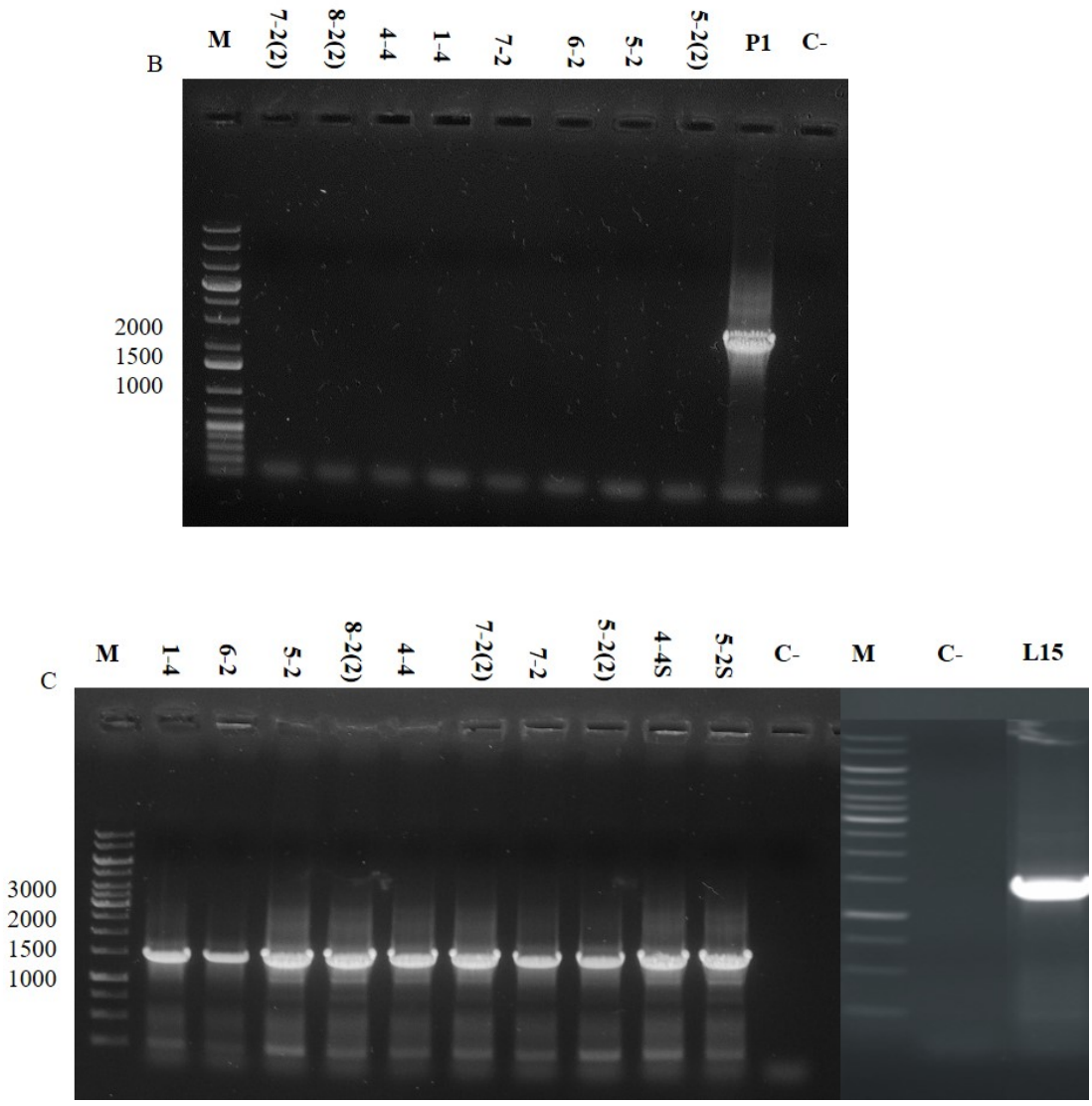



**Supplementary Figure 3.** Verification of the presence of plasmid pKGI5 in the transductants of *P. agglomerans* L15 cells. Plasmid DNA isolated from the transductants obtained as resistant to tetracycline and sensitive to chloramphenicol after infection with hybrid phage P1 *c1-100* Tn*9*-pKGI5 induced from the tetracycline and chloramphenicol resistant lysogen of the *E. coli* C600 strain was digested with PstI (lane 1) or EcoRV (lane 2), and separated in 1% agarose gel. As expected PstI cleaved the plasmid obtained from the $Tc^{R}Cm^{S}$ clones into the ca. 500 bp fragment (indicated by an arrow) representing the cloned fragment of *phddoc* operon, and over 10 kB fragment representing the rest of pKGI5, while EcoRV which has one recognition site in pKGI5 linearized the plasmid. The background of smaller intensity bands in addition to bands representing digestion products of pKGI5 likely represents digested DNA of native *P. agglomerans* L15 plasmids. Lane 3 represents undigested DNA. The presence of native plasmids in the L15 strain is reflected by the smear over the band representing the 10 kb marker fragment. GeneRuler™ 1 kb DNA ladder (Thermo Fisher Scientific, Gdańsk) was used as a DNA size marker (M). The ca. 500 bp Pst-PstI fragment of pKGI5 representing the cloned *phddoc* region is indicated by a arrow.



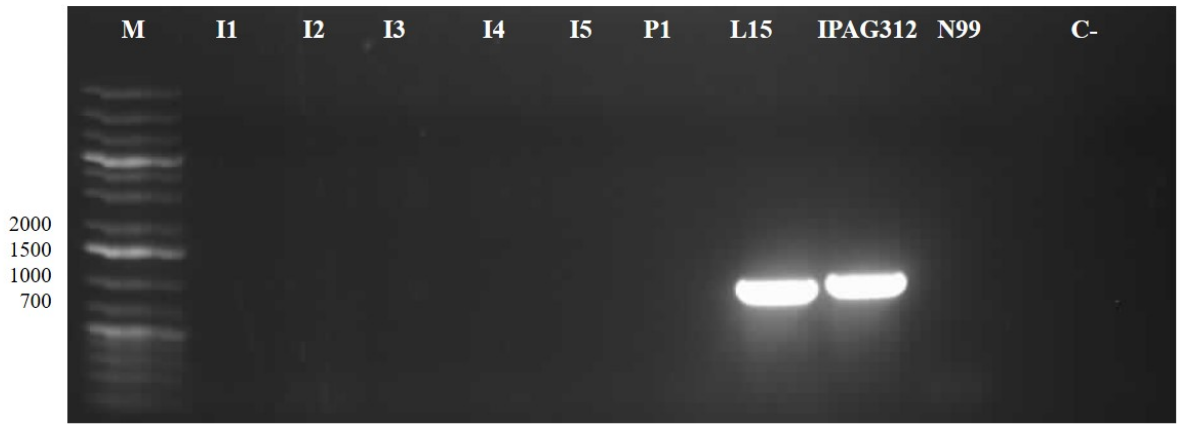

**Supplementary Figure 4**. Verification of the presence of plasmid pKGI5 in the transductants of *P. agglomerans* L15 cells. Plasmid DNA isolated from the transductants obtained as resistant to tetracycline and sensitive to chloramphenicol after infection with P1 *c1-100* Tn*9* induced from tetracycline and chloramphenicol resistant lysogens of *E. coli* C600/pKGI5 strain was used as a template in amplification with primers **(A)** OMLO755 and OMLO756 complementary to the flanking regions of P1 *phddoc* operon fragment cloned in pKGI5, and **(B)** trfAF and trfAR complementary to the region flanking the *trfA trfB* operon of RK2 in the pRK415 plasmid. The amplicons were separated in 1% agarose gel. Lanes 1 and 2 in each gel represent amplicons of plasmid fragments from the transductants. Lane A3 represents the control amplicon with P1 c1-100 Tn9 DNA as a template. Lane A4 represents no DNA control. GeneRuler™ 1 kb DNA ladder (Thermo Fisher Scientific) was used as a DNA size marker (M1); GeneRuler™ 1 kb Plus DNA ladder (Thermo Fisher Scientific) was used as a DNA size marker (M2).



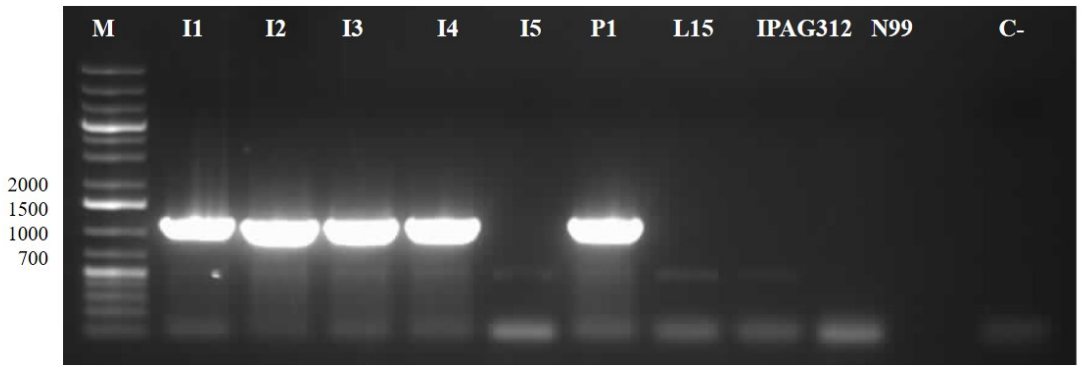



**Supplementary Figure 5**. Detection of P1 *c1-100* Tn*9* genome components in certain clones of P1 *c1-100* Tn*9*-treated *P. agglomerans* L15 cells of stable chloramphenicol resistance phenotype. Cells that were used as a source of templates for colony PCR were taken from the tops of freshly passaged colonies grown on LA medium with chloramphenicol. **(A)** Amplicons obtained with the OMLO533 and OMLO534 primers for the detection of the Tn*9* *cat* gene. **(B)** Amplicons obtained with the OMLO554 and OMLO555 primers for the detection of P1 *par* operon. **(C)** Amplicons obtained with the OMLO531 and OMLO532 primers for the detection of *P. agglomerans gyrB* gene. Gel lanes representing amplicons obtained with P1 *c1-100* Tn*9* and *P. agglomerans* L15 DNA as a template are marked with P1 and L15, respectively. Lanes marked with C indicate control samples without template DNA. Gel lanes marked with M in (A) and (B) represent DNA size marker - GeneRuler™ 1 kb DNA ladder (Thermo Fisher Scientific); the one in (C) represents DNA size marker - GeneRuler™ 1 kb Plus DNA ladder (Thermo Fisher Scientific). Other gel lanes are marked with the numbers representing the designations of clones that served as sources of template DNA in amplification reactions.

**A**

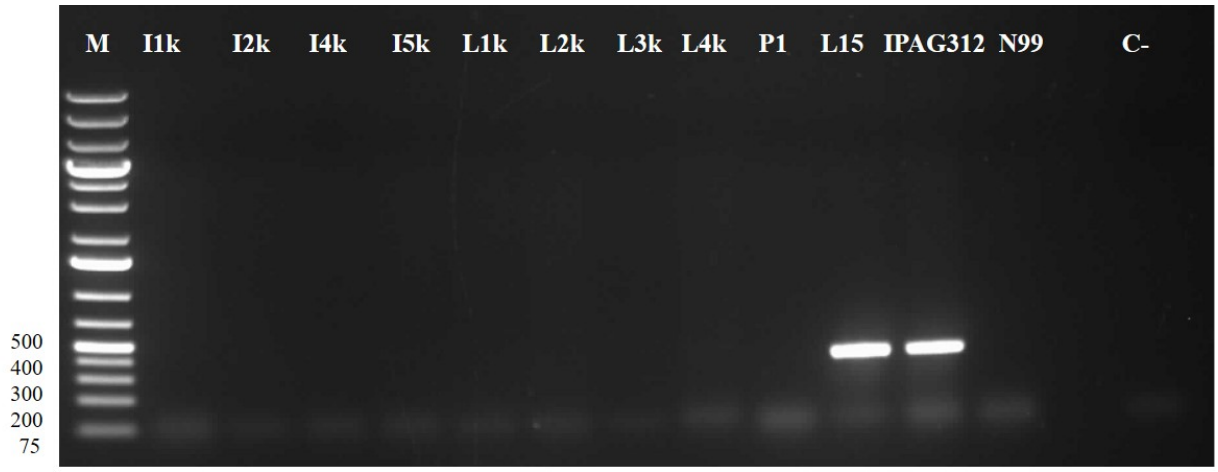



**B**

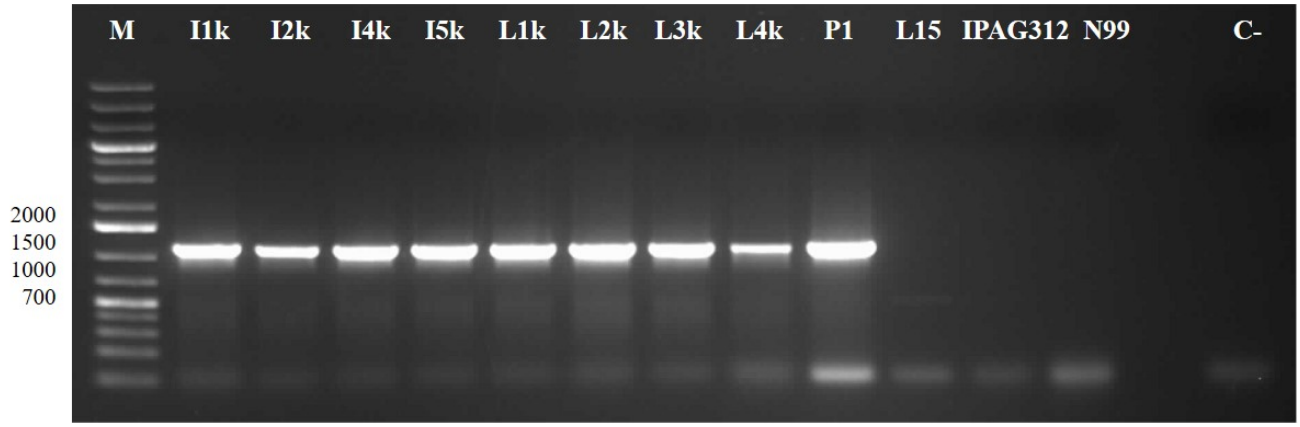



**Supplementary Figure 6.** Detection of plasmid pPagL15_3 DNA (A) and prophage P1 *c1-100* Tn*9* IS*1*::*ccdA*$_{pPagL15\_3}$ DNA (B) in the *P. agglomerans* IPAG312 cells of certain clones lysogenized with P1 *c1-100* Tn*9* IS*1*::*ccdA*$_{pPagL15\_3}$. and restreaked several times on M9 minimal solid medium with glucose, thiamine and chloramphenicol and LA medium with chloramphenicol. A and B show, respectively, amplicons obtained after colony PCR amplification with OMLO921 and OMLO922 specific for the *parB* gene of pPagL15_3 plasmid, and with OMLO919 and OMLO920 primers specific for the bacteriophage P1 *pdcB* gene. Gel lanes representing amplicons obtained with P1, and *P. agglomerans* L15 and IPAG312 DNA as a template are marked with P1, L15, and IPAG312, respectively. Lanes marked with N99 and C indicate control samples with nonspecific DNA and without template DNA, respectively. Gel lanes marked with M represent DNA size marker - GeneRuler$^{TM}$ 1 kb Plus DNA ladder (Thermo Fisher Scientific). Other gel lanes (I1-I5) are marked with the numbers representing the designations of clones that served as sources of template DNA in amplification reactions.

**A**




**B**




**Supplementary Figure 7.** Detection of plasmid pPagL15_3 DNA (A) and prophage P1 *c1-100* Tn*9* IS*1*::km$^R$ DNA (B) in the *P. agglomerans* L15 and IPAG312 cells of certain clones lysogenized with P1 *c1-100* Tn*9* IS*1*::km$^R$, and restreaked several times on M9 minimal solid medium with glucose, thiamine and chloramphenicol and LA medium with chloramphenicol. A and B show, respectively, amplicons obtained after colony PCR amplification with OMLO934 and OMLO952 primers specific for the *ccdA* gene of pPagL15_3 plasmid, and with OMLO919 and OMLO920 primers specific for the bacteriophage P1 *pdcB* gene. Gel lanes representing amplicons obtained with P1, and *P. agglomerans* L15 and IPAG312 DNA as a template are marked with P1, L15, and IPAG312, respectively. Lanes marked with N99 and C indicate control samples with nonspecific DNA and without template DNA, respectively. Gel lanes marked with M represent DNA size marker - GeneRuler$^{TM}$ 1 kb Plus DNA ladder (Thermo Fisher Scientific). Other gel lanes, I1k-I5k, and L1k-l4k, are marked with the numbers representing the designations of clones that served as sources of template DNA in amplification reactions: the IPAG312 lysogens, and the L15 lysogens, respectively.

## 3 Supplementary References

Keen, N. T., Tamaki, S., Kobayashi, D., and Trollinger, D. (1988). Improved broad host- range plasmids for DNA cloning in gram-negative bacteria. *Gene* 70, 191–197. doi: 10.1016/0378-1119(88)90117-5.

Taylor, L. A., and Rose, R. E. (1988). A correction in the nucleotide sequence of the Tn*903* kanamycin resistance determinant in PUC4K. *Nucl. Acids Res.* 16, 358–358. doi: 10.1093/nar/16.1.358.

Vieira, J., and Messing, J. (1982). The pUC plasmids, an M13mp7-derived system for insertion mutagenesis and sequencing with synthetic universal primers. *Gene* 19, 259–268. doi: 10.1016/0378-1119(82)90015-4.