

Table S13. Mobile genetic elements in the genomes of the *Pseudomonas fluorescens* group^a

| MGE type | Integrase | Insertion site | Size (kb) | Start locus tag | Stop locus tag | Cargo genes and predicted functions |
|-------------------------|------------|--------------------------------|-----------|-----------------|----------------|---|
| Strain 30-84 | | | | | | |
| prophage 1 | none | <i>mutS-cinA</i> | 33.8 | Pchl3084_1193 | Pchl3084_1232 | Bacteriocin, LlpA family; gene blocks I, II, and IV |
| prophage 2 ^b | not intact | tRNA-Gly | 3.4 | Pchl3084_1391 | Pchl3084_1393 | Pilus assembly chaperone CupC2; flanked by <i>attL</i> and <i>attR</i> |
| prophage 3 ^b | not intact | tRNA-Val | 5.2 | Pchl3084_2012 | Pchl3084_2016 | Acytransferase; flanked by <i>attL</i> and <i>attR</i> |
| island 1 | intact | tmRNA <i>ssrA</i> | 14.6 | Pchl3084_0791 | Pchl3084_0800 | Type I restriction modification system |
| island 2 | intact | | 74.1 | Pchl3084_2928 | Pchl3084_2967 | Toxin complex (Tc) proteins; Mu-like transposase; ISPpu8-like transposase |
| island 3 | intact | tRNA-Leu | 23.0 | Pchl3084_4769 | Pchl3084_4791 | Polyphosphate kinase; two-component signal-transduction system |
| Strain O6 | | | | | | |
| prophage 1 | intact | <i>mutS-cinA</i> | 72.3 | PchlO6_1205 | PchlO6_1304 | DNA helicase, phosphatase family protein; transcriptional regulators; gene blocks I and II |
| prophage 2 | intact | tRNA-Ser | 36.5 | PchlO6_1500 | PchlO6_1543 | N6 adenine-specific DNA methyltransferase; bifunctional DNA primase/polymerase |
| prophage 3 | intact | tRNA dihydrouridine synthase A | 56.9 | PchlO6_2092 | PchlO6_2179 | C-5 cytosine-specific DNA methylase family protein |
| island 1 ^b | intact | tRNA-Leu | 41.6 | PchlO6_3551 | PchlO6_3585 | Glutathione S-transferase 2; TonB-dependent siderophore receptor; molybdopterin-binding oxidoreductase; heavy metal two-component signal-transduction system; MFS transporter |
| island 2 | intact | tRNA-Leu | 23.6 | PchlO6_5017 | PchlO6_5042 | Transcriptional regulators; nucleoid-associated protein; polyphosphate kinase; two-component signal-transduction system |
| island 3 | intact | putative Mg chelatase | 125.1 | PchlO6_6034 | PchlO6_6114 | Mevalonate-independent pathway for isoprenoid production; biofilm associated proteins |

| Strain Q8r1-96 | | | | | | |
|-----------------------|------------|--------------------------------|------|--------------|--------------|---|
| prophage 1 | none | <i>mutS-cinA</i> | 22.0 | PflQ8_1124 | PflQ8_1150 | Bacteriocin, colicin M family; gene block II |
| prophage 2 | intact | tRNA dihydrouridine synthase A | 37.7 | PflQ8_1855 | PflQ8_1897 | Ultraviolet light resistance proteins RulAB; C-5 cytosine-specific DNA methylase |
| island 1 | intact | tmRNA ssrA | 16.5 | PflQ8_0767 | PflQ8_0776 | Type II restriction enzyme; putative nuclease |
| island 2 | not intact | tRNA-Gly | 62.2 | PflQ8_2129 | PflQ8_2160 | Catalase; UvrD/REP helicase family protein |
| island 3b | intact | tRNA-Pro | 7.1 | PflQ8_3770 | PflQ8_3779 | C-5 cytosine-specific DNA methylase; N-4 cytosine methyltransferase |
| island 4 | intact | tRNA-Met | 16.9 | PflQ8_4877 | PflQ8_4889 | Reverse transcriptase-like protein; transcriptional regulator |
| transposon | none | oxidoreductase | 5.2 | PflQ8_3538 | PflQ8_3542 | Catabolism of herbicide bromoxynil flanked by IS5 elements; transcriptional regulator; cation:acetate symporter, ActP family; hydrolase, carbon-nitrogen family |
| Strain Q2-87 | | | | | | |
| prophage 1 | none | <i>mutS-cinA</i> | 17.0 | PflQ2_4322 | PflQ2_4342 | Conserved hypothetical proteins; gene block I |
| prophage 2 | intact | tRNA dihydrouridine synthase A | 48.2 | PflQ2_3538 | PflQ2_3584 | N6 adenine-specific DNA methyltransferases; ultraviolet light resistance proteins RulAB |
| island 1 | intact | tRNA-Thr | 11.8 | PflQ2_5389 | PflQ2_5396 | DEAD/DEAH box helicase-like protein; ISPpu14-like transposon |
| island 2 | intact | tRNA-Met | 20.5 | PflQ2_4617 | PflQ2_4632 | ISPpu14-like transposon; transcriptional regulator |
| island 3 ^b | intact | tRNA-Gly | 15.5 | PflQ2_3275 | PflQ2_3289 | ISPsy24-like transposon (inactive) |
| island 4 | not intact | tRNA-Val | 9.4 | PflQ2_1752 | PflQ2_1766 | Transcriptional regulator; integral membrane protein |
| island 5 ^b | intact | tRNA-Met | 9.4 | PflQ2_0575 | PflQ2_0586 | Plasmid conjugation machinery |
| Strain BG33R | | | | | | |
| prophage 1 | intact | <i>mutS-cinA</i> | 64.0 | PseBG33_1169 | PseBG33_1255 | Phosphatase family protein; transcriptional regulators; endonuclease; gene blocks I, III, and V |

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|-----------------------|------------|----------------------------------|-------|--------------|--------------|--|
| prophage 2 | intact | | 50.7 | PseBG33_1320 | PseBG33_1392 | C-5 cytosine-specific DNA methylase; flanked by <i>attL</i> and <i>attR</i> |
| prophage 3 | Intact | tRNA dihydrouridine synthase A | 12.7 | PseBG33_1691 | PseBG33_1701 | Conserved hypothetical proteins |
| prophage 4 | intact | | 37.2 | PseBG33_3468 | PseBG33_3517 | D12 class N6 adenine-specific DNA methyltransferase; transcriptional regulators; integrase domain protein |
| island 1 | intact | | 20.5 | PseBG33_0005 | PseBG33_0024 | Reverse transcriptase-like protein; N-6 DNA methylase family protein; plasmid partitioning |
| island 2 | intact | tRNA-Arg | 16.6 | PseBG33_0201 | PseBG33_0214 | Conserved hypothetical proteins |
| island 3 ^c | intact | tRNA-Gly | 154.3 | PseBG33_2111 | PseBG33_2266 | IAA uptake and catabolism; MexCD-like MDR transporter; pertussis toxin subunit-like protein; haloaromatics catabolism; plasmid replication, partitioning and conjugation; transposons; TonB-dependent receptors; <i>attL</i> |
| island 4 | intact | | 2.3 | PseBG33_2835 | PseBG33_2837 | Transporter, Bcr/CfIA subfamily |
| island 5 | not intact | tRNA-Pro | 6.5 | PseBG33_3641 | PseBG33_3651 | Phage repressor; kinase domain protein (zeta toxin) |
| island 6 | intact | SRP RNA ^d | 11.3 | PseBG33_4068 | PseBG33_4075 | Resolvase domain protein; reverse transcriptase |
| island 7 ^e | intact | tmRNA | 3.1 | PseBG33_4754 | PseBG33_4757 | Transcriptional regulator |
| Strain A506 | | | | | | |
| prophage 1 | none | <i>mutS-cinA</i> | 19.5 | PfIA506_1133 | PfIA506_1160 | D-isomer specific 2-hydroxyacid dehydrogenase; dimethylmenaquinone methyltransferase; ultraviolet light resistance protein; gene block I |
| prophage 2 | intact | tRNA dihydrouridine synthase A | 35.0 | PfIA506_1613 | PfIA506_1663 | D12 class N6 adenine-specific DNA methyltransferase; DNA-cytosine methyltransferase |
| prophage 3 | intact | alpha/beta superfamily hydrolase | 52.5 | PfIA506_2008 | PfIA506_2084 | Bacteriocin, LlpA family; reverse transcriptase domain protein |

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|----------|--------|------------|------|---------------|---------------|--|
| island 1 | intact | tRNA-Ser | 75.3 | PfIA506_1413 | PfIA506_1490 | Bacteriocin, Pyocin S5 family; adenine-specific modification methylase; DNA ligase; flanked by <i>attL</i> and <i>attR</i> |
| island 2 | intact | | 20.9 | PfIA506_2668 | PfIA506_2677 | Hypothetical proteins; flanked by direct repeats |
| island 3 | intact | tmRNA ssrA | 20.3 | PfIA506_4578 | PfIA506_4587 | Helicase domain protein; DNA methylase N-4/N-6 domain protein; flanked by direct repeats |
| plasmid | intact | | 57.0 | PfIA506_p0001 | PfIA506_p0066 | Conserved hypothetical proteins, lesion bypass DNA polymerase |

Strain SS101

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|-----------------------|--------|----------------------|------|---------------|---------------|---|
| prophage 1 | none | <i>mutS-cinA</i> | 19.8 | PfISS101_1171 | PfISS101_1199 | N-acetylmuramoyl-L-alanine amidase domain protein; gene block I |
| island 1 | intact | tRNA-Arg | 16.6 | PfISS101_0186 | PfISS101_0197 | Conserved hypothetical proteins |
| island 2 ^c | intact | tRNA-Ser | 20.5 | PfISS101_1457 | PfISS101_1490 | Thiol:disulfide interchange protein; cyclic diguanylate phosphodiesterase domain proteins; sensory box His kinases/response regulators; DNA-binding response regulators; cluster of fimbrial proteins; ISPpu14-like transposon; flanked by <i>attL</i> and <i>attR</i> |
| island 3 | intact | | 8.5 | PfISS101_2599 | PfISS101_2606 | Methyl-accepting chemotaxis protein; transporter, Bcr/CflA subfamily; conserved hypothetical proteins |
| island 4 | intact | tRNA-Leu | 86.1 | PfISS101_2702 | PfISS101_2799 | Relaxase; nucleases; ultraviolet light resistance proteins RulAB; beta-lactamase; transcriptional regulators; restriction endonuclease; Ser/Thr phosphatase family protein |
| island 5 | intact | SRP RNA ^c | 12.9 | PfISS101_3912 | PfISS101_3925 | Resolvase domain protein |
| island 6 | intact | tRNA-Ser | 61.0 | PfISS101_4000 | PfISS101_4040 | Fimbrial biogenesis; two-component signal-transduction system; transcriptional regulators; type I secretion transporter system; surface adhesins/hemagglutinins; topoisomerase DNA-binding C4 zinc finger domain protein; transposons; flanked by <i>attL</i> and <i>attR</i> |

island 7 intact tmRNA 14.5 PflSS101_4646 PflSS101_4655 DEAD/DEAH box helicase-like protein

^a Strains Pf-5, Pf0-1, and SBW25 were not considered in this analysis; ^b Prophage remnant; for islands, part of the island is a prophage remnant; ^c Integrative conjugative element; ^d Signal recognition particle RNA (SRP RNA); ^e Island remnant