

**Comparative genome analysis of two heterotrophic nitrifying
Pseudomonas putida strains isolated from freshwater shrimp ponds
in Soc Trang province**

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Supplementary

Table S1. The gene sequences involved in nitrogen metabolism in 33 genomes.

[illegible]

[illegible]

8	Denitrifying reductase gene clusters	Nitrous oxide reductase maturation protein NosD	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
		Nitrous oxide reductase maturation protein NosF (ATPase)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
		Nitrous oxide reductase maturation protein NosR	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
		Nitrous oxide reductase maturation protein, outer membrane lipoprotein NosL	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
		Nitrous oxide reductase maturation transmembrane protein NosY	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
		Nitrous oxide reductase (EC 1.7.99.6)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
		Nitric oxide responding transcriptional regulator Dnr (Crp/Fnr family)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
		Copper containing nitrite reductase (EC 1.7.2.1)	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		Nitrate/nitrite transporter NarK	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
		Nitric oxide responding transcriptional regulator NnrA (Crp/Fnr family)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
		Respiratory nitrate reductase alpha chain (EC 1.7.99.4)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
		Respiratory nitrate reductase beta chain (EC 1.7.99.4)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
		Respiratory nitrate reductase delta chain (EC 1.7.99.4)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
		Respiratory nitrate reductase gamma chain (EC 1.7.99.4)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
		Nitric oxide reductase activation protein NorF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0

Table S2. BPGA analysis.

Number	Organism name	Number of core genes	Number of accessory genes	Number of unique genes	Number of absent genes	exclusively
1	<i>P. entomophila</i> L48		1929	2501	441	3
2	<i>P. fluorescens</i> A506		1929	2744	506	12
3	<i>P. fluorescens</i> F113		1929	3050	752	5
4	<i>P. fluorescens</i> NCIMB 11764		1929	3219	799	2
5	<i>P. fluorescens</i> Pf0 1		1929	3029	503	1
6	<i>P. fluorescens</i> SBW25		1929	3254	561	8
7	<i>P. knackmussii</i> B13		1929	1835	1557	245
8	<i>P. protegens</i> Pf 5		1929	3179	907	7
9	<i>P. putida</i> BIRD 1		1929	2838	184	0
10	<i>P. putida</i> DLL E4		1929	2947	229	0
11	<i>P. putida</i> E41		1929	2899	287	2
12	<i>P. putida</i> F1		1929	3015	110	0
13	<i>P. putida</i> GB 1		1929	2971	290	1
14	<i>P. putida</i> H8234		1929	3480	460	0
15	<i>P. putida</i> HB3267 PC9		1929	2931	241	2
16	<i>P. putida</i> KF715		1929	3339	263	1
17	<i>P. putida</i> KT2440		1929	3040	294	0
18	<i>P. putida</i> NBRC 14164		1929	3048	177	1
19	<i>P. putida</i> ND6		1929	3097	149	1
20	<i>P. putida</i> PC2		1929	2597	425	3
21	<i>P. putida</i> S12		1929	2901	61	0
22	<i>P. putida</i> S16		1929	3005	151	0
23	<i>P. putida</i> W619		1929	2720	334	4
24	<i>P. savastanoi</i> pv. <i>savastanoi</i> NCPPB 3335		1929	2739	349	15

25	<i>P. syringae</i> CC1557	1929	2601	297	12
26	<i>P. syringae</i> pv. <i>actinidiae</i> ICMP 9853	1929	2911	203	2
27	<i>P. syringae</i> pv. <i>actinidiae</i> ICMP 18884	1929	2972	296	1
28	<i>P. syringae</i> pv. <i>syringae</i> B728a	1929	2929	144	0
29	<i>P. syringae</i> pv. <i>syringae</i> HS191	1929	2810	193	3
30	<i>P. syringae</i> pv <i>syringae</i> B301D	1929	2897	164	1
31	<i>P. syringae</i> UMAF0158	1929	2749	155	0
32	TT321	1929	2899	1	0
33	TT322	1929	2900	2	0

Table S3. The number of Genome Islands (GIs) in 33 genomes.

Number	Organism	Number of GIs
1	<i>P. putida</i> TT321	28
2	<i>P. putida</i> TT322	27
3	<i>P. fluorescens</i> F113	81
4	<i>P. fluorescens</i> SBW25	132
5	<i>P. putida</i> BIRD 1	80
6	<i>P. putida</i> F1	91
7	<i>P. putida</i> GB 1	68
8	<i>P. putida</i> H8234	151
9	<i>P. putida</i> DLL E4	107
10	<i>P. putida</i> KT2440	114
11	<i>P. putida</i> NBRC 14164	70
12	<i>P. putida</i> PC2	63
13	<i>P. putida</i> S16	93
14	<i>P. putida</i> W619	90
15	<i>P. syringae</i> pv. <i>syringae</i> B301D	72
16	<i>P. syringae</i> pv. <i>syringae</i> B728a	70
17	<i>P. entomophila</i> L48	93
18	<i>P. fluorescens</i> A506	61
19	<i>P. fluorescens</i> NCIMB 11764	147
20	<i>P. fluorescens</i> Pf0 1	64
21	<i>P. knackmussii</i> B13	96
22	<i>P. protegens</i> Pf 5	40
23	<i>P. putida</i> E41	88
24	<i>P. putida</i> HB3267	80
25	<i>P. putida</i> KF715	107
26	<i>P. putida</i> ND6	93
27	<i>P. putida</i> S12	89
28	<i>P. savastanoi</i> pv. <i>savastanoi</i> NCPPB 3335	86
29	<i>P. syringae</i> CC1557	54
30	<i>P. syringae</i> pv. <i>actinidiae</i> ICMP 9853	96
31	<i>P. syringae</i> pv. <i>actinidiae</i> ICMP 18884	113
32	<i>P. syringae</i> pv. <i>syringae</i> HS191	165
33	<i>P. syringae</i> UMAF0158	47

Table S4. The integrated genomic islands on TT321.

Number	Start	End	Size
1	116,946	123,443	6,497
2	116,946	162,645	45,699
3	295,965	308,844	12,879
4	569,558	587,468	17,910
5	580,722	587,468	6,746
6	603,821	609,715	5,894
7	863,516	910,902	47,386
8	866,355	873,222	6,867
9	884,046	893,083	9,037
10	903,733	913,104	9,371
11	1,169,928	1,176,099	6,171
12	1,900,946	1,906,645	5,699
13	1,927,936	1,964,863	36,927
14	1,940,036	1,945,671	5,635
15	1,946,552	1,953,146	6,594
16	2,396,815	2,408,209	11,394
17	2,638,646	2,663,508	24,862
18	3,095,323	3,101,169	5,846
19	3,181,599	3,186,986	5,387
20	3,194,208	3,198,505	4,297
21	3,875,453	3,889,420	13,967
22	3,959,861	3,976,263	16,402
23	3,961,064	3,966,047	4,983
24	4,298,394	4,308,693	10,299
25	4,303,122	4,318,979	15,857
26	4,693,660	4,710,876	17,216
27	4,697,630	4,705,902	8,272
28	5,431,241	5,448,714	17,473
29	5,583,173	5,588,433	5,260

Table S5. The integrated genomic islands on TT322.

Number	Start	End	Size
1	116,946	123,443	6,497
2	116,946	162,645	45,699
3	295,965	308,844	12,879
4	568,666	586,576	17,910
5	579,830	586,576	6,746
6	602,929	608,823	5,894
7	863,505	910,891	47,386
8	866,344	873,211	6,867
9	884,035	893,072	9,037
10	903,722	913,093	9,371
11	1,169,964	1,176,135	6,171
12	1,900,949	1,906,648	5,699
13	1,927,939	1,964,986	37,047
14	1,940,039	1,945,674	5,635
15	1,946,555	1,953,149	6,594
16	2,412,604	2,423,998	11,394
17	2,653,574	2,678,439	24,865
18	3,111,237	3,116,190	4,953
19	3,196,620	3,202,007	5,387
20	3,887,204	3,901,171	13,967
21	3,971,612	3,988,014	16,402
22	3,972,815	3,977,798	4,983
23	4,292,268	4,302,567	10,299
24	4,296,996	4,312,853	15,857
25	4,687,298	4,704,514	17,216
26	4,691,268	4,699,540	8,272
27	5,424,949	5,442,422	17,473
28	5,610,705	5,615,449	4,744

Table S6. The presence of arginase, carbamoyl phosphate synthetase I and carbamate kinase in 33 genomes.

Number	Name	Arginase	Cpsl	Carbamate kinase
1	<i>P. fluorescens</i> F113	-	-	+
2	TT321	-	-	+
3	TT322	-	-	+
4	<i>P. fluorescens</i> SBW25	+		+
5	<i>P. putida</i> BIRD 1	-	-	+
6	<i>P. putida</i> F1	-	-	+
7	<i>P. putida</i> GB 1	-	-	+
8	<i>P. putida</i> H8234	-	-	+
9	<i>P. putida</i> DLL E4	-	-	+
10	<i>P. putida</i> KT2440	-	-	+
11	<i>P. putida</i> NBRC 14164	-	-	+
12	<i>P. putida</i> PC2	-	-	+
13	<i>P. putida</i> S16	-	-	+
14	<i>P. putida</i> W619	-	-	+
15	<i>P. syringae</i> pv. <i>syringae</i> B301D	+	-	-
16	<i>P. syringae</i> pv. <i>syringae</i> B728a	+	-	+
17	<i>P. entomophila</i> L48		-	+
18	<i>P. fluorescens</i> A506	+	-	+
19	<i>P. fluorescens</i> NCIMB 11764	-	-	+
20	<i>P. fluorescens</i> Pf0 1	-	-	+
21	<i>P. knackmussii</i> B13	-	-	+
22	<i>P. protegens</i> Pf 5	+	-	+
23	<i>P. putida</i> E41	-	-	+
24	<i>P. putida</i> HB3267 PC9	-	-	+
25	<i>P. putida</i> KF715	-	-	+
26	<i>P. putida</i> ND6	-	-	+
27	<i>P. putida</i> S12	-	-	+
28	<i>P. savastanoi</i> pv. <i>savastanoi</i> NCPPB 3335	-	-	-
29	<i>P. syringae</i> CC1557	-	-	+
30	<i>P. syringae</i> pv. <i>actinidiae</i> ICMP 9853	-	-	-
31	<i>P. syringae</i> pv. <i>actinidiae</i> ICMP 18884	-	-	-
32	<i>P. syringae</i> pv. <i>syringae</i> HS191	-	-	-
33	<i>P. syringae</i> UMAF0158	+	-	-