

Supplementary data on *P. rettgeri* PR002 strain

Supplementary Table S1. Metadata (biosample data) of all sequenced *Providencia rettgeri* isolates from NCBI GenBank database

No.	Strain name	Assembly accession	Accession number	Isolation source	Host	Continent (Country:city)	Collection date	Beta-lactamase
1	RB151	GCA_001874625.1	CP017671-2	Urine	Human	South-America (Colombia:Bucaramanga)	Jan 2013	NDM-1, OXA-2
2	FDAARGOS_330	GCA_002984195.1	CP027418.1	Urine	Human	USA:DC	Jan 2015	
3	AR_0082	GCA_003204135.1	CP029736		Human	USA:DC	2015	
4	Dmel1	GCA_000314835.2	AJSB00000000	Haemolymph	Animal (Fruit fly) <i>Drosophila melanogaster</i>	North-America (USA:Pennsylvania)	1999	-
5	DSM 1131	GCA_000158055.1	ACCI00000000	Faeces	Human	North-America (USA)	2009	-
6	PR1	GCA_002265395.1	NOWC00000000	Foot infection	Human	North-America (USA:Missouri)	April 2016	IMP-27
7	CCBH11880	GCA_000805715.1	JSEQ00000000	Surgical wound	Human	South-America (Brazil)	Feb 2014	NDM-1, OXA-1
8	H1736	GCA_001049815.1	CVLT00000000	Rectal swab	Human	Israel/France	May 2015	NDM-1, OXA-1
9	PR002	GCA_002417505.1	NXKD00000000	Urine	Human	Africa (South Africa:Pretoria)	2013	DHA-1, OXA-1,2,10, PER-7,
10	TUM9994	GCA_003176635.1	BGMI01		Human	Japan	Jul 2010	

11	Pret_2032	GCA_003226135.1	QKNQ01	Rectal smear	Human	Spain:Barcelona	Oct 2015	
12	NVIT03	GCA_003426175.1	QUAF01	Gut	<i>Nosonia vitripennis</i>	USA	Jan 2017	
13	NCTC11801	GCA_900455085.1	UGTZ01					-
14	NCTC7476	GCA_900455265.1	UAUG01				1947	-
15	PR_162	GCA_003936755.1	RHRR01	ICU washroom sink	Hospital environment	Pakistan	Feb 2016	
16	MR4	GCA_001027325.1	LCVM00000000	Stem	Plant (Abutilon indicum)	Asia (India:Gujarat)	2013	-
17	729/12	GCA_001680125.1	LYBX00000000	Sewage	Water	South-America (Brazil)	Nov 2011	-
18	UBA5024	GCA_002416295.1	DICO00000000	Metagenome	Fomite (Metal)	North-America (USA:New York City)	2017	-

Supplementary Table S2. Genes associated with general COG functional categories in the genome of *Providencia rettgeri* PR002.

No.	Functional category of in silico predicted proteins	Number of genes
1	Cofactors, Vitamins, Prosthetic Groups, Pigments	205
2	Cell Wall and Capsule	104
3	Virulence, Disease and Defense	100
4	Potassium metabolism	27
5	Miscellaneous	17
6	Phages, Prophages, Transposable elements, Plasmids	50
7	Membrane Transport	180
8	Iron acquisition and metabolism	41
9	RNA Metabolism	133
10	Nucleosides and Nucleotides	109
11	Protein Metabolism	252
12	Cell Division and Cell Cycle	31
13	Motility and Chemotaxis	15
14	Regulation and Cell signalling	89
15	Secondary Metabolism	5
16	DNA Metabolism	162
17	Fatty Acids, Lipids, and Isoprenoids	69
18	Nitrogen Metabolism	36
19	Dormancy and Sporulation	6
20	Respiration	146
21	Stress Response	117
22	Metabolism of Aromatic Compounds	33
23	Amino Acids and Derivatives	429
24	Sulfur Metabolism	41
25	Phosphorus Metabolism	38
26	Carbohydrate Metabolism	342

Supplementary Table S3: Pathogenicity Islands (PAIs) predicted for PR002 from VFBD (http://www.paidb.re.kr/about_paidb.php).

Name	PAI accession	PAI	Host strain	Product	Function
1 pspA	NP_344663	Virulence gene	<i>Streptococcus pneumoniae</i>	surface protein A	Virulence gene
2 lepB	YP_096497	Virulence gene	<i>Legionella pneumophila</i>	hypothetical protein lpg2490	Virulence gene
3 unnamed	AF447814	PAI II CFT073	<i>Escherichia coli</i>	unknown	-
4 tcdA4	AF346500	tcd island	<i>Photorhabdus luminescens</i>	TcdA4	-
5 unnamed	CCQ20483	Resistance gene	<i>Listeria monocytogenes</i>	Sensor protein VanSB	Resistance gene
6 folP	CAJ68315	Resistance gene	<i>Peptoclostridium difficile</i>	Dihydropteroate synthase	Resistance gene
7 fliD	NP_249785	Virulence gene	<i>Pseudomonas aeruginosa</i>	flagellar capping protein FliD	Virulence gene

Supplementary Table S4. Orthologous biofilm-forming and virulence genes identified in the PR002 genome.

<i>Function</i>	<i>Biofilm gene</i>	Reference sequence [Accession number]	Corresponding orthologues [Protein ID]	Description of product
<i>Motility</i>	<i>flgA</i>	WP_004255676.1	PCQ37092.1	flagellar biosynthesis protein FlgA
	<i>flgB</i>	WP_004255669.1	PCQ37043.1	flagellar basal body rod protein FlgB
	<i>flgC</i>	WP_004236840.1	PCQ37044.1	flagellar basal body rod protein FlgC
	<i>flgD</i>	CQA26_15915	PGF_01602421	flagellar basal-body rod modification protein FlgD
	<i>flgE</i>	WP_008911687.1	PCQ37046.1	flagellar hook protein FlgE
	<i>flgF</i>	WP_014658059.1	PCQ37047.1	flagellar basal body rod protein FlgF
	<i>flgG</i>	WP_006813422.1	PCQ37048.1	flagellar basal-body rod protein FlgG
	<i>flgH</i>	WP_004236833.1	PCQ37049.1	flagellar basal body L-ring protein FlgH
	<i>flgI</i>	CQA26_15940	PGF_00005288	flagellar P-ring protein FlgI
	<i>flgJ</i>	WP_004918619.1	PCQ37051.1	flagellar assembly peptidoglycan hydrolase FlgJ
	<i>flgK</i>	WP_014658062.1	PCQ37052.1	flagellar hook-associated protein FlgK
	<i>flgL</i>	WP_006662048.1	PCQ37053.1	flagellar hook-filament junction protein FlgL
	<i>flgM</i>	WP_006657506.1	PCQ37042.1	flagellar biosynthesis anti-sigma factor FlgM
	<i>flgN</i>	WP_006813432.1	PCQ37041.1	flagellar biosynthesis protein FlgN
	<i>flhA</i>	WP_014658057.1	PCQ37039.1	flagellar biosynthesis protein FlhA
<i>flhB</i>	WP_004934847.1	PCQ37038.1	flagellar type III secretion system protein FlhB	

<i>flhC</i>	WP_008911706.1	PCQ37025.1	flagellar transcriptional regulator FlhC
<i>flhD</i>	WP_006813451.1	PCQ37024.1	flagellar transcriptional regulator FlhD
<i>fliA</i>	WP_006662027.1	PCQ37095.1	RNA polymerase sigma factor FliA
<i>fliC</i>	WP_004240059.1	PCQ37085.1	flagellin FliC
<i>fliD</i>	WP_014658079.1	PCQ37084.1	flagellar filament capping protein FliD
<i>fliE</i>	WP_006657532.1	PCQ37074.1	flagellar hook-basal body complex protein FliE
<i>fliF</i>	WP_014658076.1	PCQ37073.1	flagellar M-ring protein FliF
<i>fliG</i>	YP_001006742.1	PCQ37072.1	flagellar motor switch protein FliG
<i>fliH</i>	WP_004918683.1	PCQ37071.1	flagellar assembly protein FliH
<i>fliI</i>	WP_004918680.1	PCQ37070.1	flagellum-specific ATP synthase FliL
<i>fliJ</i>	WP_004918676.1	PCQ37069.1	flagella biosynthesis chaperone FliJ
<i>fliK</i>	WP_004255613.1	PCQ37068.1	flagellar hook-length control protein FliK
<i>fliM</i>	WP_004918669.1	PCQ37066.1	flagellar motor switch protein FliM
<i>fliN</i>	WP_004918665.1	PCQ37065.1	flagellar motor switch protein FliN
<i>fliO</i>	WP_004918662.1	PCQ37093.1	flagellar biosynthetic protein FliO
<i>fliP</i>	WP_006813412.1	PCQ37064.1	flagellar biosynthetic protein FliP
<i>fliQ</i>	WP_006657520.1	PCQ37062.1	flagellar biosynthetic protein FliQ
<i>fliR</i>	WP_006657519.1	PCQ37062.1	flagellar biosynthetic protein FliR
<i>fliS</i>	WP_006813390.1	PCQ37083.1	flagella export chaperone FliS

	<i>fliT</i>	WP_006657542.1	PCQ37082.1	flagellar protein FliT
	<i>fliZ</i>	WP_004255757.1	PCQ36983.1	flagellar regulatory protein FliZ
	<i>motA</i>	WP_004918567.1	PCQ37026.1	flagellar motor stator protein MotA
	<i>motB</i>	CQA26_15810	PGF_01899924	flagellar motor rotation protein MotB
<i>Type 1 secretion system</i>	<i>fimA</i>	CQA26_17535	PGF_07739729	type 1 fimbriae major subunit FimA
	<i>fimB</i>	CQA26_20435	PGF_00006378	type 1 fimbriae regulatory protein, FimB family
	<i>fimD</i>	CQA26_17545	PGF_06517630	type 1 fimbriae anchoring protein FimD
	<i>fimE</i>	CQA26_20435	PGF_00006378	type 1 fimbriae regulatory protein, FimE family
	<i>fimG</i>	CQA26_03980	PGF_02912435	
	<i>csgD</i>	CQA26_16535	PGF_00419816	Curlin genes transcriptional activator
	<i>gmhB</i>	CQA26_16450	PGF_00447438	D-sedoheptulose 7-phosphate isomerase (EC 5.3.1.28)
	<i>rfaH</i>	CQA26_20875	PGF_00057520	Transcriptional activator RfaH
	<i>rfaP</i>	CQA26_04955	PGF_00017275	Lipopolysaccharide core heptose(I) kinase RfaP
<i>Other</i>	<i>btuB</i>	CQA26_04460	PGF_00580417	Outer membrane vitamin B12 receptor BtuB
	<i>cheZ</i>	WP_008911696.1	PCQ37034.1	protein phosphatase CheZ
	<i>dgkA</i>	CQA26_19955	PGF_02010018	Diacylglycerol kinase (EC 2.7.1.107) dgkA
	<i>dnaK</i>	CQA26_14485	PGF_0041733	Chaperone protein DnaK
	<i>dsbA</i>	CQA26_04295	PGF_0031127	Periplasmic thiol:disulfide interchange protein DsbA
	<i>dsbB</i>	CQA26_06505	PGF_06706859	Periplasmic thiol:disulfide oxidoreductase DsbB, required for DsbA reoxidation

<i>fruR</i>	CQA26_00370	PGF_00006376	Fructose repressor FruR, LacI family
<i>galU</i>	CQA26_06395	PGF_00064393	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)
<i>gcuA</i>	CQA26_00610	PGF_03932611	DNA-binding transcriptional dual regulator Rob
<i>greA</i>	CQA26_12075	PGF_01423501	Transcription elongation factor GreA
<i>hfq</i>	CQA26_12305	PGF_00046622	RNA-binding protein Hfq
<i>hscB</i>	CQA26_02940	PGF_03063012	Chaperone protein HscB
<i>hsrA</i>	CQA26_05535	PGF_02893007	Probable transport protein HsrA
<i>ihfB</i>	CQA26_11275	PGF_05693577	Integration host factor beta subunit
<i>nagA</i>	CQA26_19720	PGF_02908669	N-acetylgalactosamine-6-phosphate deacetylase nagA
<i>YjhA/nanC</i>	CQA26_12585	PGF_00406917	N-acetylneuraminic acid outer membrane channel protein NanC
<i>nlpD</i>	CQA26_21150	PGF_00017400	Murein hydrolase activator NlpD
<i>nlpI</i>	CQA26_11995	PGF_00017407	Lipoprotein NlpI
<i>ompR</i>	CQA26_03880	PGF_00414228	Two-component system response regulator OmpR
<i>proQ</i>	CQA26_06560	PGF_00036688	RNA chaperone ProQ
<i>ptsI</i>	CQA26_03100	PGF_00033423	Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) ptsI
<i>rcsC</i>	CQA26_17790	PGF_00050577	Sensor histidine kinase RcsC (EC 2.7.13.3)
<i>rpoS</i>	CQA26_21155	PGF_00046348	RNA polymerase sigma factor RpoS
<i>sdhC</i>	CQA26_21430	PGF_02069837	Succinate dehydrogenase cytochrome b-556 subunit

	<i>surA</i>	CQA26_09410	PGF_00055354	Periplasmic chaperone and peptidyl-prolyl cis-trans isomerase of outer membrane proteins SurA (EC 5.2.1.8)
	<i>tolA</i>	CQA26_21505	PGF_02913387	TolA protein
	<i>tolB</i>	CQA26_21510	PGF_05769513	Tol-Pal system beta propeller repeat protein TolB
	<i>tolR</i>	CQA26_21500	PGF_0057016	Tol biopolymer transport system, TolR protein
<i>Uncharacterized</i>	<i>ycfM</i>	CQA26_07080	PGF_00017409	Lipoprotein YcfM, part of a salvage pathway of unknown substrate

Supplementary Table S5: Diversity of metal resistance genetic determinant from PR002 genome

Metal Resistance	Resistance Determinants	Reference sequence [Accession number]	Corresponding orthologues [Protein ID]	Description of product
Copper homeostasis: copper tolerance	ScsA	CQA26_18525	PGF_00055288	Suppression of copper sensitivity: putative copper binding protein ScsA
	ScsB	CQA26_18520	PGF_00020062	Membrane protein, suppressor for copper-sensitivity ScsB
	ScsB	CQA26_18515	PGF_00050223	Secreted protein, suppressor for copper-sensitivity ScsC
	ScsD	CQA26_18510	PGF_02913457	Membrane protein, suppressor for copper-sensitivity ScsD
	CueR	CQA26_01145	PGF_00419572	Copper resistance transcriptional regulator CueR (MerR family)
	CorC efflux	CQA26_18480	PGF_00018560	Magnesium and cobalt efflux protein CorC
	CutC	CQA26_17430	PGF_00420612	Cytoplasmic copper homeostasis protein CutC
	CutE	CQA26_18485	PGF_02325838	Apolipoprotein N-acyltransferase / Copper homeostasis protein CutE
	CutF	CQA26_09730	PGF_00419533	Copper homeostasis protein CutF precursor / Lipoprotein NlpE involved in surface adhesion
	CcmH	CQA26_00645	PGF_00420346	Cytochrome c heme lyase subunit CcmL / Cytochrome c heme lyase subunit CcmH
	CopC	CQA26_06600	PGF_00572136	Copper resistance protein CopC
	CopD	CQA26_06595	PGF_00419560	Copper resistance protein CopD
	CopG	CQA26_14515	PGF_02216306	CopG protein
CueO	CQA26_01480	PGF_02983541	Blue copper oxidase CueO precursor	
Cobalt-zinc-cadmium resistance	CzcB efflux	CQA26_14525	PGF_03778521	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family
	CusS	CQA26_14545	PGF_00419578	Copper sensory histidine kinase CusS
	CusA efflux	CQA26_14520	PGF_05430047	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
	CusC efflux	CQA26_14535	PGF_00416745	Cation efflux system protein CusC precursor
	CzcA	CQA26_14520	PGF_05430047	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA
	CusF	CQA26_14530	PGF_00758959	Cation efflux system protein CusF precursor
Mercury resistance	MerC	CQA26_01775	PGF_00020297	Mercuric transport protein, MerC
	MerT	CQA26_01765	PGF_00020300	Mercuric transport protein, MerT
	MerE	CQA26_22390	PGF_00020298	Mercuric transport protein, MerE
	MerD	CQA26_22385	PGF_00020282	Mercuric resistance operon coregulator
Arsenic resistance	ArsD	CQA26_19160	PGF_02772315	Arsenical resistance operon trans-acting repressor ArsD

PlasmidFinder-2.0 Server - Results

Organism(s): *Enterobacteriaceae, Gram Positive*

Enterobacteriaceae						
Plasmid	Identity	Query / Template length	Contig	Position in contig	Note	Accession number
IncA/C2	100	417 / 417	NXKD01000024.1 <i>Providencia rettgeri</i> strain PR002 NODE_24_length_68021_cov_42.6535, whole genome shotgun sequence	28081..28497		JN157804

Gram Positive						
Plasmid	Identity	Query / Template length	Contig	Position in contig	Note	Accession number
No hit found						

IncA/C2_JN157804

template GAGAACCAAAGACAAAGACCTGGAGAAACTCGACGTAATCAAAGACTCACCGCAAATGAG
query GAGAACCAAAGACAAAGACCTGGAGAAACTCGACGTAATCAAAGACTCACCGCAAATGAG

template CCTGTTTGAGATCATTGAATCTCCGGCCAAGAAAGACGACTACTCCAACACCATCGAGAT
query CCTGTTTGAGATCATTGAATCTCCGGCCAAGAAAGACGACTACTCCAACACCATCGAGAT

template CTACGATGCGCTGCCGAAGTACATTTGGGACCAAAGCGTGAGCATGAAGATTTATCCAA
query CTACGATGCGCTGCCGAAGTACATTTGGGACCAAAGCGTGAGCATGAAGATTTATCCAA

template CGCTGTAGTGACACGACAATGCACCATCAGAGGCCAGCATTTCACGGTGAAGGTGAAGCC
query CGCTGTAGTGACACGACAATGCACCATCAGAGGCCAGCATTTCACGGTGAAGGTGAAGCC

template AGCCATCATCGAGAAGGATGACGGAAGAACCGTGCTGATCTACGCGGGACAGCGAGAGGA
query AGCCATCATCGAGAAGGATGACGGAAGAACCGTGCTGATCTACGCGGGACAGCGAGAGGA

template AATCCTTGAGGATGCTCTACGCAAGCTCGCAGTGAACGGGAAAGGCCATATCATCGAGGG
query AATCCTTGAGGATGCTCTACGCAAGCTCGCAGTGAACGGGAAAGGCCATATCATCGAGGG

template CAAGGCTGGAGTCATGTTCACTCTGTACGAACTCCAGAAAGAGCTCTCGAAGATGGG
query CAAGGCTGGAGTCATGTTCACTCTGTACGAACTCCAGAAAGAGCTCTCGAAGATGGG