

Table S2: Table showing presence and comparison of response regulator proteins of Two-component system (TCS) in HCH-tolerant strains: RL, *P. aeruginosa* MTB1 and strain TKP.

S.No.	Gene Name	Physiological Function	<i>Pseudomonas</i> sp. RL (%Identity, E-value)	<i>P. aeruginosa</i> MTB1 (%Identity, E-value)	<i>Pseudomonas</i> sp. TKP (%Identity, E-value)
1.	<i>cheR1</i>	Chemotaxis	79.60, 7.79e-078	99.29, 0.0	81.43, 4.70e-099
2.	<i>pilG</i>	Pilus production	88.77, 1.32e-117	99.76, 0.0	86.14, 2.71e-089
3.	<i>pilH</i>	Twitching Mobility	87.77, 6.30e-104	99.73, 0.0	85.48, 2.91e-067
4.	<i>pilI</i>	Pilus biosynthesis	84.04, 4.63e-084	100, 0.0	Absent
5.	<i>pilJ</i>	Pilus biosynthesis	88.74, 0.0	99.51, 0.0	81.23, 6.64e-177
6.	<i>algR</i>	Alginate biosynthesis	83.54, 5.06e-103	99.33, 0.0	Absent
7.	<i>cheB</i>	Chemotaxis	85.79, 4.68e-138	98.55, 0.0	84.42, 5.70e-105
8.	<i>cheY</i>	Chemotaxis	84.53, 4.51e-077	84.80, 3.18e-079	79.62, 1.19e-032
9.	<i>fleR</i>	Motility and adhesion	82.40, 1.44e-135	83.01, 1.057e-140	83.62, 0.0
10.	<i>gacA</i>	Quorum sensing and virulence factors	84.63, 1.84e-108	98.91, 0.0	79.14, 6.35e-048
11.	<i>narL</i>	Nitrate/nitrite respiration	79.62, 1.53e-019	Absent	81.56, 1.62e-085
12.	<i>phoB</i>	Phosphate regulation	87.41, 0.0	99.57, 0.0	86.81, 0.0

Table S3: A table showing annotated potential HGT candidates in strain RL and its reference genotypes as predicted using SIGI-HMM.

S.No	<i>Pseudomonas</i> Genomes	HGT candidates with assigned K0- Number using KAAS	Probable pathways mapped using MinPath
1	<i>P. sp. RL</i>	Uncharacterized protein/K06959	RNA binding domain (ACLAME)
2	<i>P. stutzeri</i> A1501	Uncharacterized protein/K06959	RNA binding domain (ACLAME)
3	<i>P. mendocina</i> ymp	5-methyl tetrahydrofolate- homocysteine methyltransferase/K00548	1. Biosynthesis of amino acids 2. One carbon pool by folate 3. Biosynthesis of secondary metabolites 4. Selenocompound metabolism 5. Cysteine and methionine metabolism
4	<i>P. stutzeri</i> ATCC 14405	nitrate reductase alpha subunit/K00370	1. Nitrogen metabolism 2. Two component system
5	<i>P. stutzeri</i> CCUG 29243	5-methyl tetrahydrofolate- homocysteine methyltransferase/K00548	1. Biosynthesis of amino acids 2. One carbon pool by folate 3. Selenocompound metabolism 4. Cysteine and methionine metabolism
6	<i>P. stutzeri</i> XLDN-R	nitrate reductase alpha subunit/K00370	1. Nitrogen metabolism 2. Two component system
7	<i>P. stutzeri</i> T13	nitrate reductase alpha subunit/K00370	1. Nitrogen metabolism 2. Two component system
8	<i>P. sp. TKP</i>	alcohol dehydrogenase (cytochrome c)/K00114	1. Glycolysis/Gluconeogenesis 2. Propanoate metabolism 3. Chloroalkane and chloroalkene degradation
9	<i>P. denitrificans</i> ATCC 13867	type I restriction enzyme, R subunit/KO 1153	NA

Table S4: Annotated MGIs in *Pseudomonas* sp. RL after the metagenomic recruitment of RL genome on pond metagenome reads.

S.No.	Coordinates (Begin)	Coordinates (End)	ORFs annotated	Function assigned
1	743459	753606	10	Ribonucleotide reductase, alpha subunit Divalent heavy metal cations transporter Homoserine kinase Hypothetical protein PIN domain of 5'-3' exonuclease GTP binding protein-EngB Cytochrome Thiol-disulphide interchange protein Exonuclease
2	757852	766941	1	Spermidine/putrescine ABC transporter
3	854524	856180	1	Molybdopterin converting factor, large and small subunits
4	862162	864142	1	ATP-dependent protease
5	879708	881968	1	ATP-dependent helicase HepA
6	897349	910283	2	Electron transport complex protein Rnfc Electron transport complex protein Rnfb
7	962380	964081	1	PhnA protein: part of a large operon associated with alkylphosphonate uptake and carbon-phosphorus bond cleavage
8	1422893	1406724	5	Unknown function protein DUF334 Unknown function protein DUF752 FAD dependent oxido reductase Polyphosphate kinase Nicotine nucleotide pyrophosphorylase
9	1422982	1434847	6	ABC type Fe3+ transport system Periplasmic component Peptidylprolyl isomerase FK3P type Zn binding domain protein C-terminal processing peptidase Serine peptidase
10	1450029	1436815	4	Putative M18 family aminopeptidase 2 Adenyl cyclase toxin CyaB Hypothetical protein Cation/acetamide symporter

11	2196580	2189660	4	Hypothetical protein Putative outer membrane transporter protein Conserved hypothetical protein Outer membrane heavy metal efflux protein-permease
12	2516904	2508048	2	Arabinose efflux permease family protein Peptidylprolyl isomerase FK3P type
13	2521831	2536824		Glycogen synthase
14	2598875	2590005	2	N-actely neuramic acid synthetase NcuB Thiamine pyrophosphate binding domain containing protein
15	2607521	2614867	3	Flagellar basal body L-ring protein Flagellar basal body rod protein FlgG, FlgF Flagellar basal body P-ring protein
16	2729503	2705723	4	Putrescine ABC transporter Putative glutamine synthetase Glutamate-ammonia ligase Putative aminotransferase
17	3124352	3131784	5	Glutathione peroxidase Acyl transferase Peptidyl-prolyl cis-trans isomerase Acetate kinase Catalytic LigB subunit of aromatic ring opening-dioxygenase