
Supplementary Materials

Table S1. Diffraction peaks location of XRD of strain Ery5 and Ery15

Peaks	Strain Ery5	Strain Ery15
1	24.11804	24.11804
2	31.12594	31.12594
3	37.35518	37.33469
4	41.20748	41.18699
5	44.95732	44.93683
6	49.36287	49.38336
7	50.98166	49.38336
8	51.30951	51.30951
9	58.89116	58.85017
10	59.81325	59.79276
11	63.48112	63.48112
12	64.8745	64.8745
13	67.35391	67.33342

Table S2. Genomic features of Ery5 and Ery15.

	Strain Ery5	Strain Ery15
Size (bp)	3836718	3633189
G+C (%)	62.5	62.2
Coding genes	3646	3570
Protein	3525	3463
rRNA	6	6
tRNA	50	50
Accession	CP087587	CP087588

Table S3. The 16S rRNA gene sequence similarities between strains Ery5, Ery15 and the type strains of the genus *Croceicoccus*.

Strains	Similarity (%)	
	Strain Ery5	Strain Ery15
1. Strain Ery5	100	100
2. Strain Ery15	100	100
3. <i>C. marinus</i> E4A9 ^T	98.1	98.1
4. <i>C. mobilis</i> Ery22 ^T	98.1	98.1
5. <i>C. pelagius</i> Ery9 ^T	96.5	96.5
6. <i>C. bisphenolivorans</i> H4 ^T	96.3	96.3
7. <i>C. ponticola</i> GM-16 ^T	96.0	96.0
8. <i>C. naphthovorans</i> PQ-2 ^T	95.8	95.8
9. <i>C. sediminis</i> S2-4-2 ^T	95.7	95.7

Table S4. The ANI values and the genome-to-genome distance of strains Ery5, Ery15 and the type strains of their closely relatives.

Strains	ANI values (%)		In silico DDH (%)	
	Strain	Strain	Strain	Strain
	Ery5	Ery15	Ery5	Ery15
1. Strain Ery5 (CP087587)	/		/	
2. Strain Ery15 (CP087588)	95.5	/	63.8	/
3. <i>C. marinus</i> E4A9 ^T (LYPP000000000)	82.9	83.0	25.9	25.6
4. <i>C. mobilis</i> Ery22 ^T (LYWZ000000000)	79.2	78.6	21.6	21.3
5. <i>C. pelagius</i> Ery9 ^T (LYWY000000000)	75.2	77.0	20.6	24.0

Table S5. Annotated genes with putative function in resistance to heavy metals between strains Ery5 and Ery15.

Related to	Function annotation	Ery5	Ery15
Transcriptional regulator	Transcriptional regulator, MerR family	3	3
	Nickel responsive regulator NikR	1	1
	Heavy metal resistance transcriptional regulator HmrR	0	1
RND efflux system	RND efflux system (including CzcCBA)	18	20
	Copper/silver efflux RND transporter (CusCBA)	3	6
P-type ATPase	Lead, cadmium, zinc and mercury transporting ATPase	5	6
Cation transporter	Cobalt/zinc/cadmium resistance protein CzcD	6	9
	Magnesium and cobalt efflux protein CorC	2	4
Copper	CopG protein	2	3
	Copper resistance protein B	4	4
	Periplasmic divalent cation tolerance protein CutA	0	1
	Copper homeostasis protein CutE	1	1
Manganese	Multicopper oxidase	7	6
Mercury	Periplasmic mercury (+2) binding protein, MerP	0	1
	Mercuric transport protein MerT	0	1
	Mercuric resistance operon regulatory protein MerR	0	1
Others	HoxN/HupN/NixA family nickel/cobalt transporter	1	0
	Nickel-cobalt-cadmium resistance protein nccX	1	3
	Hypothetical protein involved in heavy metal export	1	4

Figure S1. Locations of the two sampling sites of strains Ery5 and Ery15.

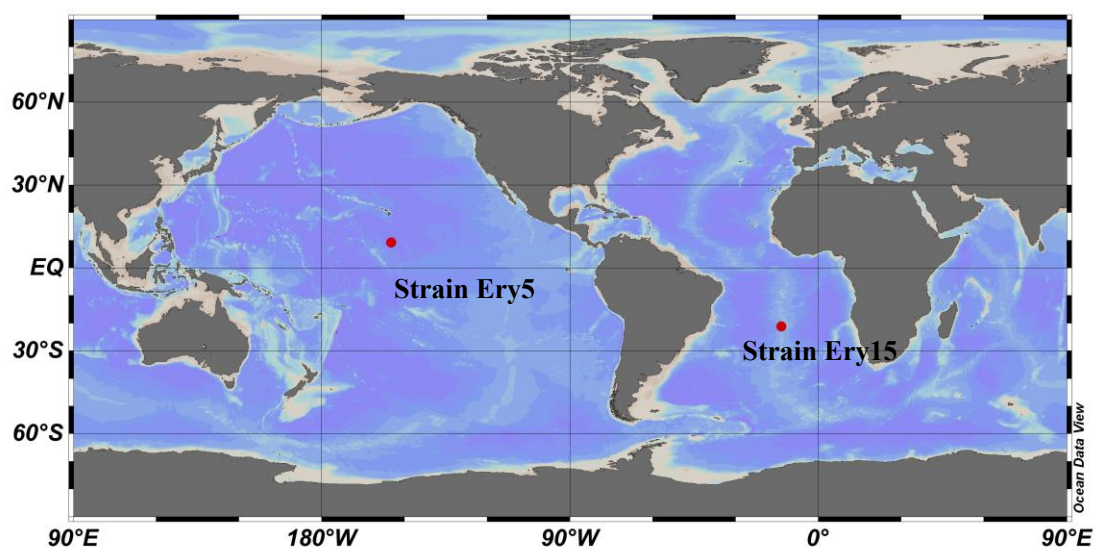


Figure S2. Removal efficiency of Mn^{2+} in strains Ery5 (a) and strain Ery15 (b).

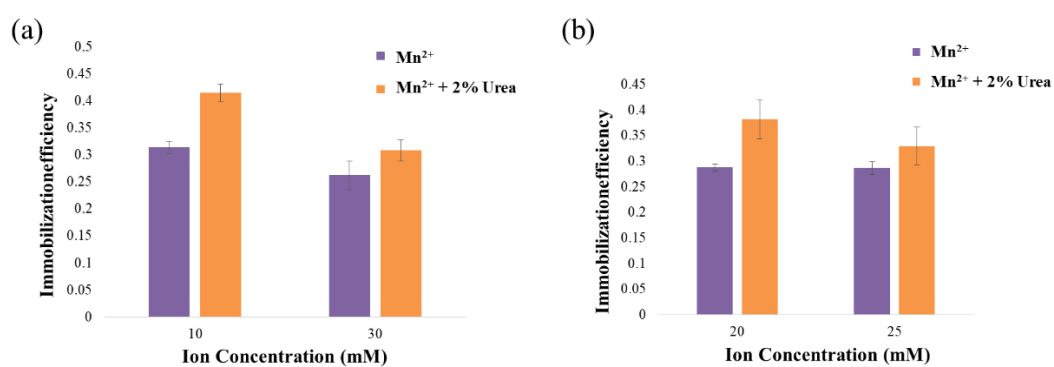


Figure S3. XRD images of strains Ery5 (a) and strain Ery15 (b).

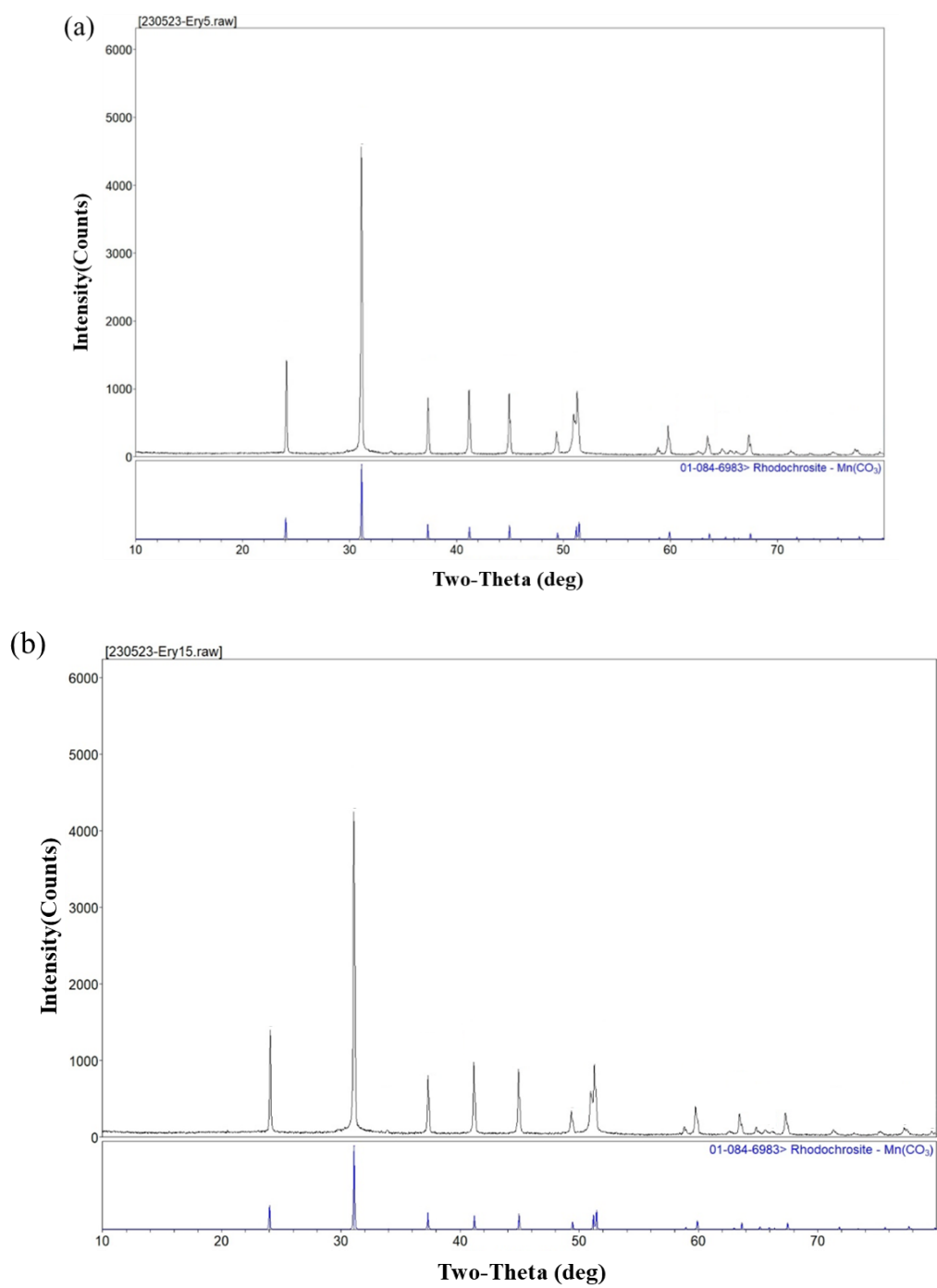


Figure S4. Transmission electron micrographs of strains Ery5 and Ery15. (a) the cell morphology of strain Ery5; (b) the ultrastructure of strains Ery5; (c) the cell morphology of strains Ery15; (d) the ultrastructure of strains Ery15.

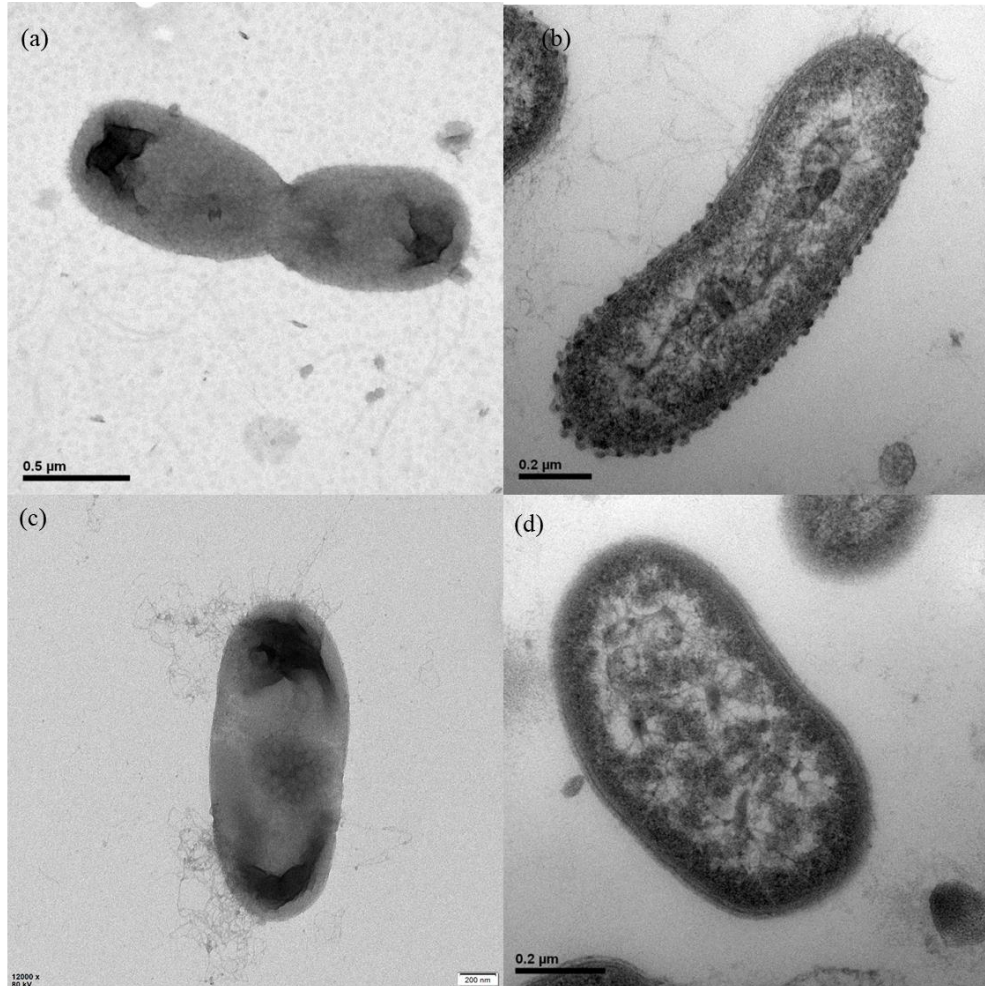


Figure S5. Thin-layer chromatograms after staining with molybdatophosphoric acid showing the total polar lipid profiles of two strains. (a) Strain Ery5; (b) Strain Ery15. PC, Phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; SGL, sphingoglycolipid; PL, phospholipid; GL, glycolipid; AL, aminolipid; L, lipid.

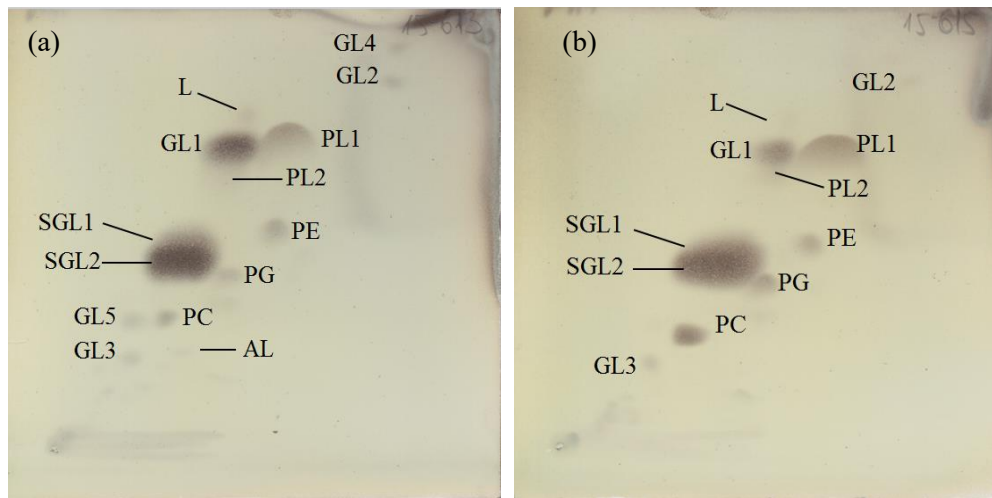


Figure S6. Maximum-likelihood tree based on concatenated 844 protein sequences from genomic sequences showing the phylogenetic relationship of the strains Ery5 and Ery15 with the related taxa. Bootstrap values based on 100 replications. Bar, 0.050 substitutions per amino acid position. *Sphingosinicella microcystinivorans* DSM 19791^T (GenBank accession number is RBWX000000000) was used as outgroup.

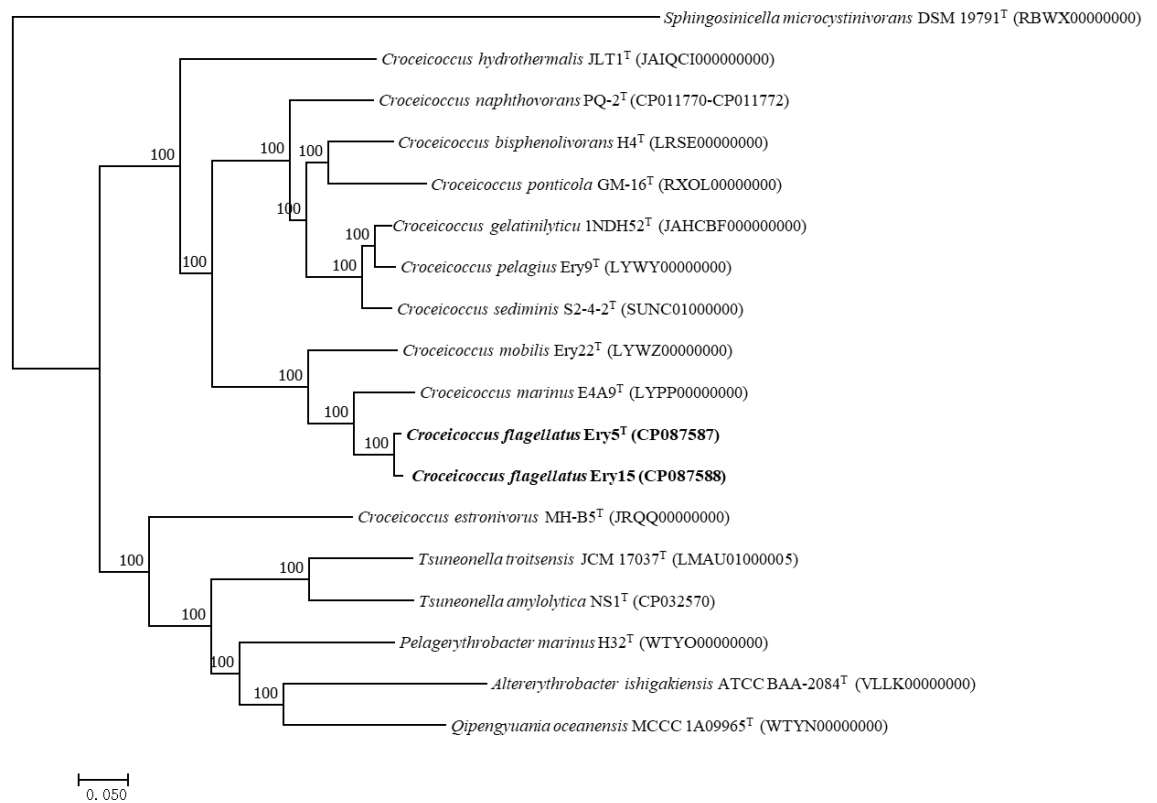


Figure S7. Comparison of COG profile of unique proteins.

