

***Craterilacuimicrobium aquaticum* gen. nov. sp. nov., a novel member of the order *Neisseriales* isolated from crater lake**

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Author Notes: The GenBank/EMBL/DDBJ accession number for 16S rRNA gene of strain TC5R-5^T is OK487579. The Whole Genome Shotgun project of strain TC5R-5^T has been deposited at DDBJ/ENA/GenBank under the accession number JACCFC000000000.

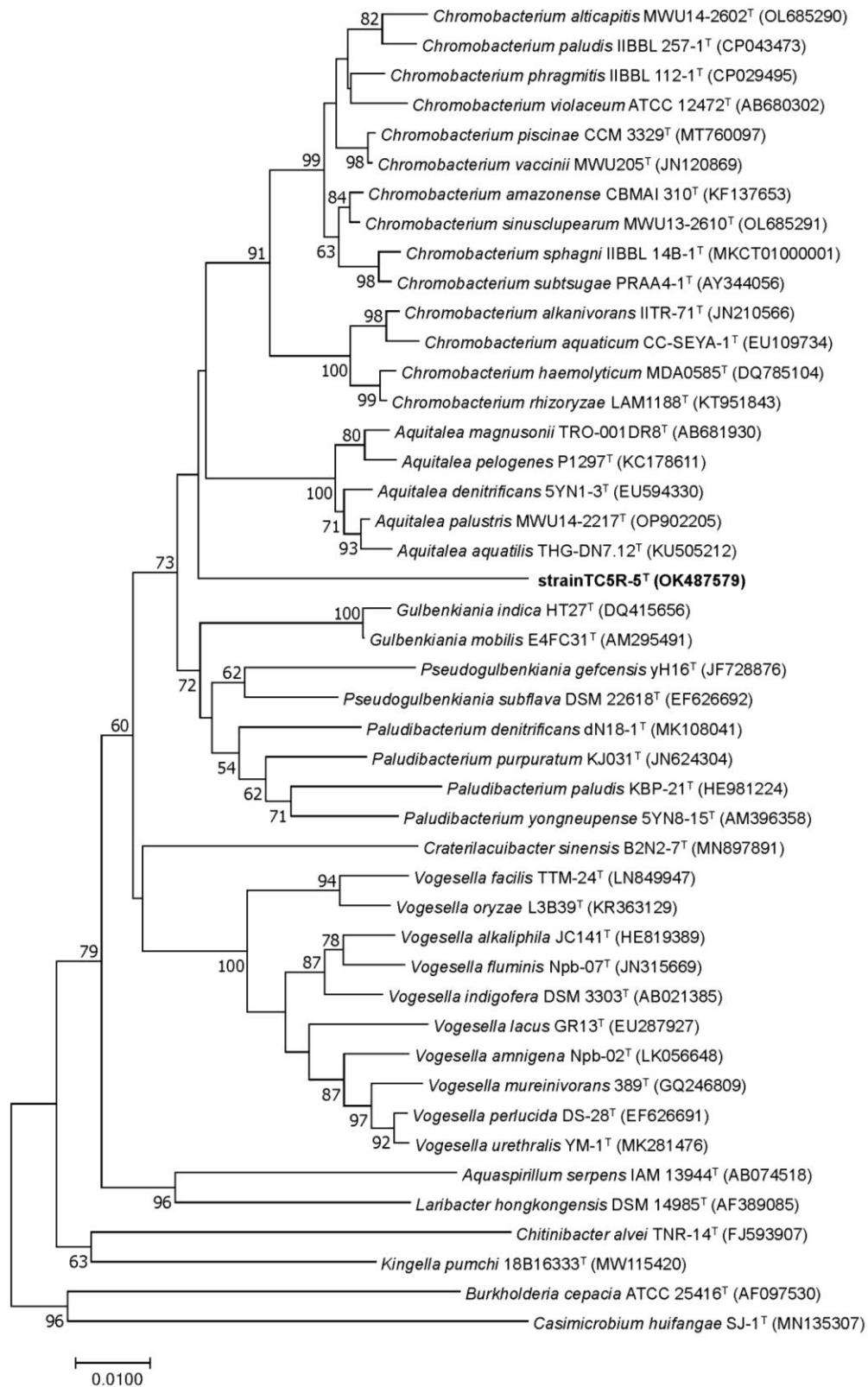
Abbreviations

ANI, average nucleotide identity; APL, unidentified aminophospholipid; CDS, coding

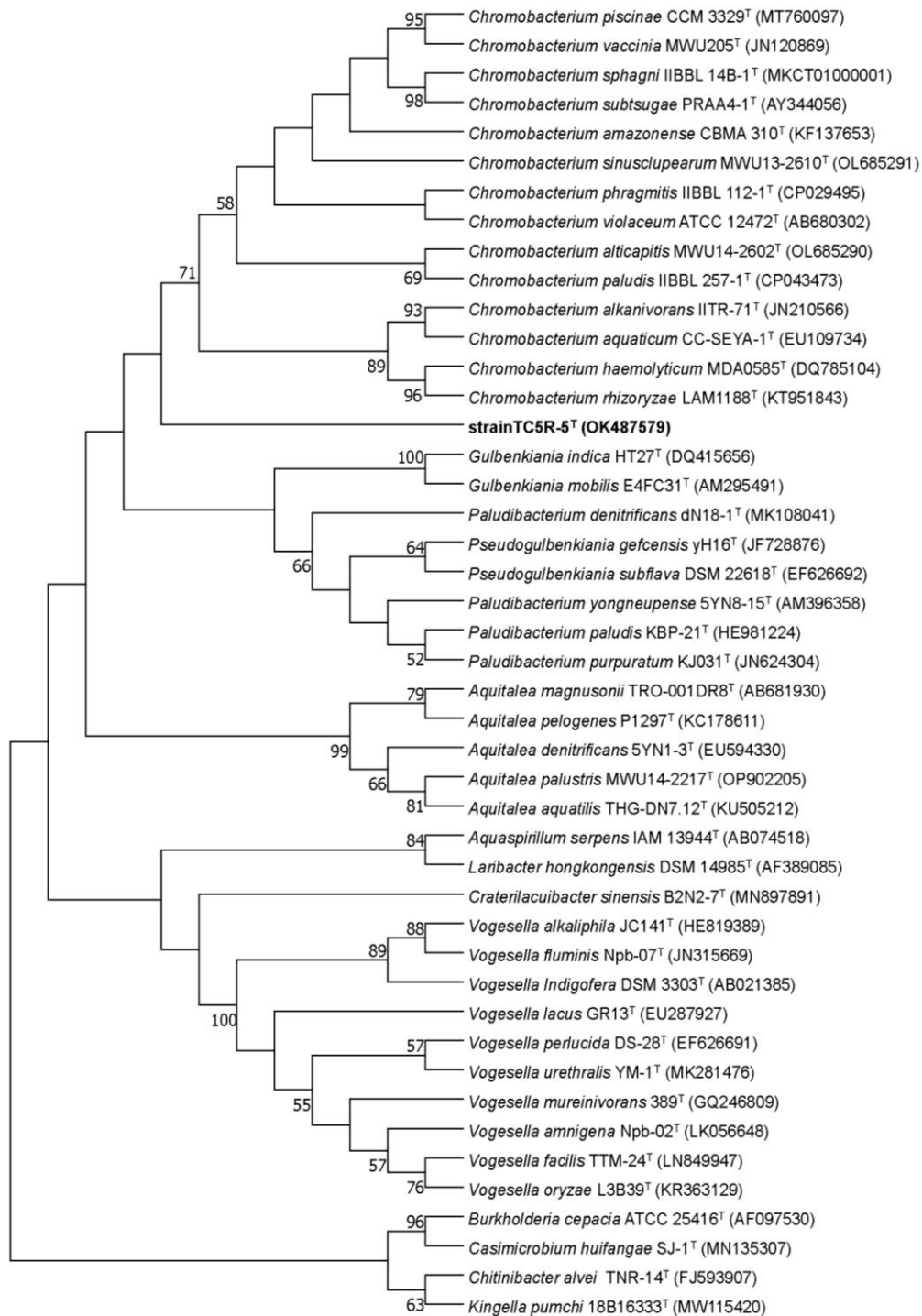
sequences; DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PL, unidentified phospholipid; AGP, aminoglycophospholipid; L, unidentified polar lipid; NRPS, nonribosomal peptide synthetase.

Table S1. ANI values calculated with the OrthoANI algorithm comparing strain TC5R-5^T with *Chromobacterium alkanivorans* IITR-71^T, *Aquitalea palustris* CCM7557^T, *Andreprevotia chitinilytica* DSM 18519, *Halomonas humidisoli* WN018^T and *Vreelandella glaciei* DD39^T.

	<i>Chromobacterium alkanivorans</i> IITR-71 ^T	<i>Aquitalea palustris</i> CCM7557 ^T	<i>Andreprevotia chitinilytica</i> DSM 18519 ^T	<i>Halomonas humidisoli</i> WN018 ^T	<i>Vreelandella glaciei</i> DD39 ^T
ANI (%)	73.48	72.49	68.49	64.26	64.73
Genome A length (bp)	3,455,760	3,455,760	3,455,760	3,455,760	3,455,760
Genome B length (bp)	5,215,260	4,198,320	5,118,360	4,039,200	4,914,360
Average aligned length (bp)	925,479	865,053	342,924	172,982	169,684
Genome A coverage (%)	26.78	25.03	9.92	5.01	4.91
Genome B coverage (%)	17.75	20.60	6.70	4.28	3.45



(a)



(b)

Figure S1. The Phylogenetic tree of strain TC5R-5T and the related strains based on 16SrRNA gene sequences using Neighbor-joining method (a) and Maximum-parsimony (b). Bootstrap values (>50 %) based on 1,000 replicates are shown at the branch nodes. Bar, 0.01 substitutions per nucleotide positions.

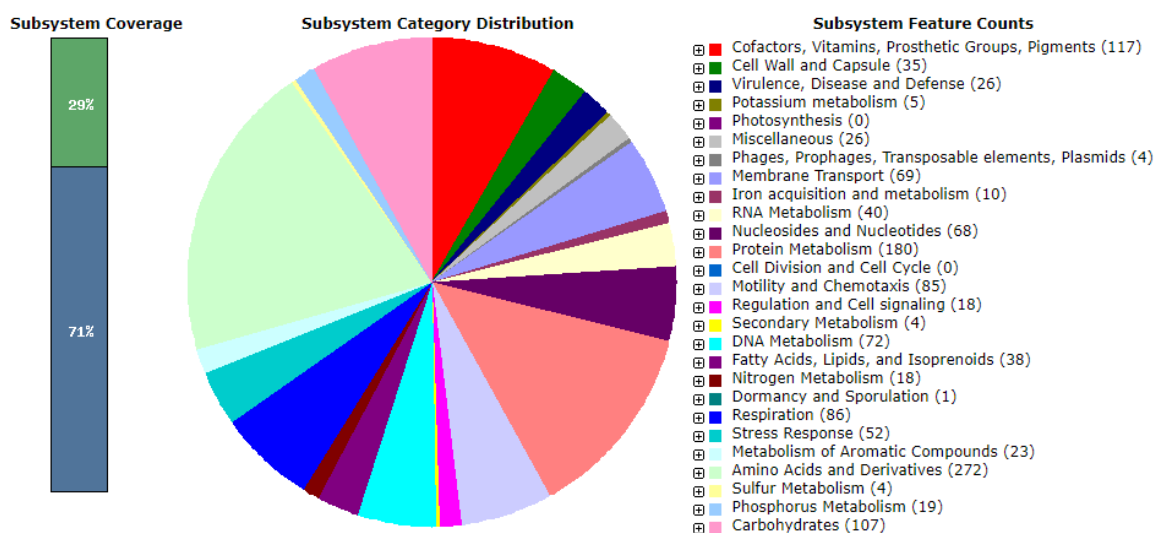


Figure S2. Genome annotation of strain TC5R-5^T using the RAST server. Green part in bar chart corresponds to percentage of proteins included. Pie chart and count of subsystem features in right panel show percentage distribution and category of subsystems in strain TC5R-5^T.

Paraburkholderia rhizoxinica HKI 454

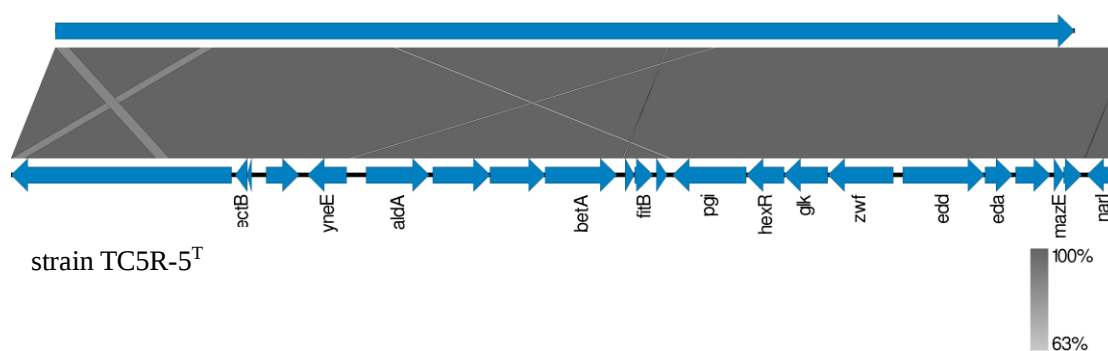


Figure S3. Comparison of NRPS Gene cluster of strain TC5R-5^T with rhizomide A biosynthetic gene cluster from *Paraburkholderia rhizoxinica* HKI 454.

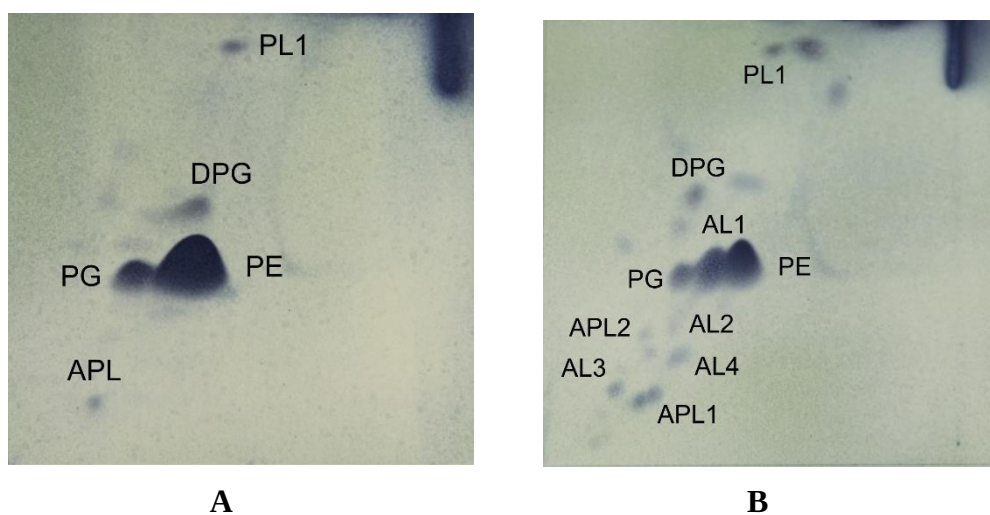


Figure S4. Two-dimensional TLC of the total polar lipids of new isolate TC5R-5^T (A) and reference strain *Chromobacterium alkanivorans* IITR-71^T (B) stained with ethanolic phosphomolybdic acid. (PG, phosphatidylglycerol; DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; APL, unidentified aminophospholipid; PL, unidentified phospholipid; AL, unidentified aminolipid).