Brevundimonas aurifodinae, sp. nov., an Aerobic Anoxygenic Phototroph Resistant to Metalloid Oxyanions Isolated from Gold Mine Tailings

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Article

Brevundimonas aurifodinae, sp. nov., an Aerobic Anoxygenic Phototroph Resistant to Metalloid Oxyanions Isolated from Gold Mine Tailings

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Abstract: A polyphasic taxonomic study was carried out on the rod-shaped, orange pigmented strain C11^T, isolated from gold mine tailings. Sequencing of the 16S rRNA gene showed relatedness to *Brevundimonas*, with 98.4 % and 98.2 % similarity to *Brevundimonas bacteroides* and *Brevundimonas variabilis*, respectively. Average nucleotide identity and digital DNA–DNA hybridization with the closest phylogenetic neighbor of C11^T indicates distinction at the species level, further confirmed by differences in physiology. $C_{18:1}$ ω7c is the dominant cellular fatty acid. DNA G + C content is 68.3 mol %. The predominant ubiquinone is Q-10; 1,2-Di-O-acyl-3-O-α-D-glucopyranuronosyl glycerol, phosphatidylglycerol, 1,2-di-O-acyl-3-O-α-D-glucopyranosyl glycerol and 1,2-di-O-acyl-3-O-[D-glucopyranosyl-(1→4)-α-D-glucopyranuronosyl] glycerol are the major polar lipid constituents. This bacterium produces bacteriochlorophyll *a* and tolerates high concentrations of (μg/mL): tellurium (>1500), selenium (1000 to >5000), and vanadium (>5000) oxyanions. Data supports the inclusion of C11^T into the genus *Brevundimonas* as a new species with the proposed name *Brevundimonas aurifodinae* sp. nov., (C11^T = NRRL B-61758^T; = DSM 118059^T).

Keywords: Aerobic anoxygenic phototroph; *Brevundimonas*; *Brevundimonas aurifodinae*; Bacteriochlorophyll *a*; Mine tailings; Metalloid oxide resistance; Tellurium; Selenium; Vanadium

1. Introduction

Brevundimonas is a genus, belonging to the family *Caulobacteraceae*, that was proposed in 1994 to re-classify two species, which had a distinct taxonomic position among the *Pseudomonas* [1]. It is also closely related to *Caulobacter*, with several current *Brevundimonas* members formerly residing in the genus [2]. Currently, there are 37 validly recognized members with *B. diminuta* as the type species [3]. Members are gram-negative, rod shaped, aerobic, oligotrophic, contain Q-10 as the major isoprenoid quinone and have relatively high DNA G+C content [4]. However, they vary in traits such as motility, pigmentation, and prosthecae formation [4]. Species have been isolated from a wide range of habitats: soils, marine/freshwater environments, sand, and activated sludge [5,6]. *Brevundimonas* spp. are becoming of greater interest as human pathogens, with *B. diminuta* and *B. vesicularis* being found in clinical specimens of patients with underlying conditions [6]. One interesting feature is some members produce bacteriochlorophyll *a* (Bchl *a*), indicating they can be classified as aerobic anoxygenic phototrophs (AAP) [7]. Currently, three species are known to have this ability: *B. bacteroides* [7], *B. subvibrioides* [8], and *B. variabilis* [9]. AAP are a diverse group found in many different environments and various genera of the *Proteobacteria* [10]. Their core characteristics include requiring oxygen for growth and survival, being incapable of autotrophy and utilizing energy derived from photosynthesis as a supplemental source to cellular respiration [11]. A standout characteristic of AAP is their ability to withstand extremely high levels of metalloid oxyanions [10]. Resistance to toxic metals is a known attribute of many *Brevundimonas* spp. For example, *B.*

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vancanneytii SMA3 mitigates heavy metals cadmium, lead, and mercury from soils [12], *B. diminuta* can survive increased levels of arsenic, cadmium, and zinc [13,14], while *B. vesicularis* remediates copper, lead, and nickel [15,16]. Previously, the tailings of Central Gold Mine in Nopiming Provincial Park, Manitoba, Canada were investigated to explore the diversity of AAP in this extreme environment and their resistance to metalloid oxides [17]. From here, strain C11^T, was isolated and found to produce Bchl *a*, resist high levels of Te, Se, and V oxyanions as well as have close relations to *Brevundimonas* [17]. Since the genus has potential for bioremediation, the discovery of more species which tolerate and remove toxic metals could lead to future applications. As such, we set forth to taxonomically classify C11^T as a new species with the proposed name *Brevundimonas aurifodinae*.

2. Materials and Methods

2.1. Strains and Cultivation

Strain C11^T was isolated from gold mine tailings at Nopiming Provincial Park, Manitoba, Canada using Rich Organic (RO) solid medium [17]. Cells in all experiments were grown aerobically on Caulobacter medium [18] at 30 °C and pH 7.0 in the dark unless otherwise noted. Long term storage was at -80 °C in 30 % glycerol and modified RO with 10% (w/v) organics. The following strains were obtained for comparison: From the Korean Agricultural Culture Collection: *Brevundimonas alba* KACC 12015^T [2], *Brevundimonas bacteroides* KACC 12013^T [2], *Brevundimonas basaltis* KACC 17487^T [19], *Brevundimonas subvibrioides* KACC 12014^T [2], and *Brevundimonas variabilis* KACC 12016^T [2]; From the USDA-ARS Culture Collection (NRRL): *Brevundimonas diminuta* NRRL B-1496^T [1].

2.2. Physiological and Biochemical Experiments

Taxonomical markers such as the production of specific enzymes and utilization of carbon sources was investigated using API ZYM and API 20NE test strips (Biomeriux) and Biolog GEN III Microplate (Biolog Inc.). Motility was determined by the hanging drop method [20]. In addition to the antibiotic susceptibility tested with the Biolog GEN III Microplate, disk diffusion assays were carried out using BD BBL™ Sensi-Disc™ [21] with the following: penicillin G (10 IU), ampicillin (10 µg), polymyxin B (300 IU), tetracycline (30 µg), erythromycin (15 µg), imipenem (10 µg), streptomycin (10 µg), chloramphenicol (30 µg), bacitracin (2 IU), kanamycin (30 µg), and rifampin (5 µg). Temperature range for growth was evaluated from 0 to 50 °C at 5 °C intervals while pH tolerance was assessed from 4.0 to 11.0 with 0.5 increments and NaCl from 0.0 % to 6.0 % at 0.5 % intervals. Gram stain, spore formation, anaerobic growth, catalase, oxidase, methyl red, Voges-Proskauer, indole and other carbon source utilization were completed as described [22].

Anoxygenic photosynthetic complex formation and Bchl *a* synthesis was assessed in absorption spectra taken of whole cells and pigment extracts using standard methods [11]. Resistance and reduction of metal(loid) oxides was evaluated previously [17].

For fatty acid profiling, C11^T was grown in Caulobacter medium at 30 °C for 72 h. Biomass was collected, lipids were extracted with the Folch method [23] and analyzed via gas chromatography [24]. Polar lipids were discerned using two-dimensional TLC with the appropriate detection reagents [25]. Cellular quinones obtained from 100 mg of freeze-dried cells were separated by TLC and identified [25].

2.3. Microscopy

The cell size and shape of a 48 h culture was observed with a phase contrast light microscope (Zeiss Axioskop 2).

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2.4. Phylogenetic Analysis

DNA was extracted as in protocol [26] and sent to Azenta (South Plainfield, NJ, USA) for 16S rRNA gene Sanger sequencing using universal primers 27F (5′-AGAGTTTGATCCTGGCTCAG-3′) and 1492R (5′-GGTTACCTTGTTACGACTT-3′). A 1404 bp fragment (GenBank accession number: PP885399) was produced. Closest relatives were identified with a NCBI standard nucleotide BLAST search. A Maximum Likelihood phylogenetic tree was created in MEGA 11 and pairwise aligned 16S rRNA fragments of other *Brevundimomas* spp. collected from NCBI GenBank [27]. Genome sequence of C11^T was obtained as done previously [28]. Briefly, the sequencing library of the genomic DNA was prepared using the Illumina DNA Library Prep kit. The genome was sequenced with the Illumina MiniSeq platform using 500 µl of a 1.8pM library. Paired-end (2x150 bp) sequencing generated 2,690,380 reads and 406.3 Mbps. Quality control of the reads was performed using FASTQC (v1.0.0), using a k-mer size of 5 and contamination filtering for overrepresented sequences against the default contamination list. Genome assembly with the Illumina sequencing was performed using Unicycler (v0.5.0) [29] within BV-BRC [30]. This resulted in a 3.3 Mbp genome consisting of 26 contigs (116x coverage). It was then annotated using the NCBI prokaryotic genome annotation pipeline [31]. The Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession JBEGDD000000000. The version described in this paper is version JBEGDD010000000. Average nucleotide identity (ANI) was assessed with the OrthoANI algorithm through ChunLab's online ANI calculator [32]. Formula d_4 of the Genome-Genome Distance Calculator from DSMZ [33] was used to define digital DNA:DNA hybridization (dDDH) values. A Genome Blast Distance Phylogeny tree was created with the Type Strain Genome Server (TYGS) from DSMZ [34]. Intergenomic distances were applied to generate a balanced minimum evolution tree via FASTME 2.1.6.1 including SPR post-processing [35]. Branch support was inferred from 100 pseudo-bootstrap replicates each. The genome-based tree was rooted at the midpoint [36] and visualized with PhyD3 [37].

3. Results and Discussion

3.1. Physiology and Morphology of Cells

API ZYM, API 20NE test strips and Biolog Gen III Microplate revealed C11^T used the following carbon sources for growth: gluconate, dextrin, D-cellobiose, gentibiose, sucrose, D-turanose, stachyose, α-D-lactose, D-melibiose, N-acetyl-D-glucosanmine, N-acetyl-beta-D-mannosamine, N-acetyl-D-galactosamine, N-acetyl-nuraminic acid, α-D-glucose, D-mannose, D-galactose, 3-methyl-glucose, D-fucose, L-fucose, L-rhamnose, D-mannitol, D-arabitol, myo-inositol, D-glucose-6-PO_4, D-fructose-6-PO_4, D-aspartic acid, Glycyl-L-proline, L-alanine, L- aspartic acid, L-glutamic acid, L-serine, D-galacuronic acid, L-galacturonic acid, D-gluconic acid, D-glucuronic acid, glucuronamide, quinic acid, D-saccharic acid, D-lactic acid methyl ester, citric acid, α-keto-glutaric acid, D-malic acid, L-malic acid, Bromo-succinate acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, acetoacetic acid, acetic acid, casamino acids, yeast extract, and bactopeptone. Alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, naphthol-AS-Bi-phosphohydrolase, and α-glucosidase activity is present. Esculin and gelatin are hydrolyzed. Carbon sources and enzyme activities not cited here which are included in these test kits, produced negative results. C11^T is susceptible to chloramphenicol, kanamycin, polymyxin B, streptomycin, imipenem, vancomycin, tetrazolium violet, tetrazolium blue, aztreonam, macrolide, rifamycin, minocycline, lincomycin, guanidine HCL, niaproof 4, fusidic acid, D-serine, and sodium bromate, but resistant to nalidixic acid, lithium chloride, penicillin, and ampicillin. C11^T does not require vitamin supplements. Growth occurs between 5 and 40 °C, from pH 6.0 to 10.5 and up to 2.0 % NaCl with optimums at 30 °C, pH 8.0 and 0 %, respectively (Table 1).

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Table 1. Physiological and biochemical features of C11^T compared to related members and the type species of the genus Brevundimonas.[1,2]

Species	*B. aurifodinae*	*B. bacteroides*	*B. variabilis*	*B. basaltis*	*B. alba*	*B. subvibrioides*	*B. diminuta*
Strain	C11^T	KACC 12013^T	KACC 12016^T	KACC 17487^T	KACC 12015^T	KACC 12014^T	NRRL B-1496^T
Temperature	5-40	25-40	10-40	10-40	10-40	25-40	10-40
Optimum	30	30	30	30	30	20	30
pH	6.0-10.5	6.0-8.0	6.0-8.0	5.5-10.0	6.0-8.0	6.0-8.0	6.0-8.0
Optimum	8.0	7.0	7.0	7.5	7.0	7.0	7.0
NaCl Tolerance	2	4	4	4	2	2	6
Utilization of:							
D-maltose	-	-	+	-	-	-	+
D-cellobiose	+	-	+	-	-	+	+
Gentibiose	+	+	+	+	-	-	+
Sucrose	+	-	+	-	-	-	+
Stachyose	+	+	+	-	-	-	+
D-raffinose	-	-	+	-	-	+	+
β-methyl-D-glucoside	-	+	-	+	-	+	+
D-salicin	-	+	+	-	-	+	+
α-D-glucose	+	-	+	+	+	+	+
D-mannose	+	+	-	-	+	+	+
D-fructose	-	-	-	+	-	-	+
Gelatin	+	+	+	-	+	-	+
L-arginine	-	+	+	+	-	-	+
Pectin	-	-	+	+	-	+	+
Mucic acid	-	+	+	+	-	+	+
D-malic acid	+	+	-	+	-	+	+
α-hydroxy-butyric acid	+	+	-	-	-	-	+
α-keto-butyric acid	+	-	-	-	-	-	+
Propionic acid	-	+	-	+	-	-	-
Enzyme							
Amylase	+	+	+	-	-	+	-
Gelatinase	+	+	+	-	+	-	-
Leucine	+	-	+	+	+	+	+
Valine	+	-	+	+	+	+	+
Cysteine	-	-	-	+	-	+	-
α-chymotrypsin	+	-	+	+	+	+	+
α-glucosidase	+	+	+	+	+	+	-
Oxidase	+	+	-	-	+	+	+
Esculin	+	+	+	+	+	+	-

[1] +, Growth occurs, enzyme activity detected; -, No growth, no enzyme activity [2] Physiological results not included here produced identical results among C11^T and *Brevundimonas* spp. tested.

C11^T was assessed for its ability to resist and potentially reduce metal(loid) oxyanions [17]. It had the broadest and greatest tolerance among other isolates from the gold mine tailings in Nopiming Provincial Park. This included surviving high levels of (μg/ml): tellurite (>1500), tellurate (>1500), selenite (1000), selenate (>5000), metavanadate (>5000), and orthovanadate (>5000). Furthermore,

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C11^T has potential bioremediation and biometallurgy applications as it reduced tellurite to elemental tellurium [17].

In vivo, C11^T has an anoxygenic photosynthesis complex containing a light-harvesting I complex (870 nm) and reaction center (802 nm) (Figure 1A, light orange line). Bchl a is detected in the pigment extract absorbance spectrum (770 nm, Figure 1A, dashed dark orange line). As such, C11^T is classified as an aerobic anoxygenic phototroph. Carotenoids are also synthesized (Figure 1A orange line: 458, 515 nm; Figure 1A, dashed dark orange line: 423, 453, 481, 531 nm).

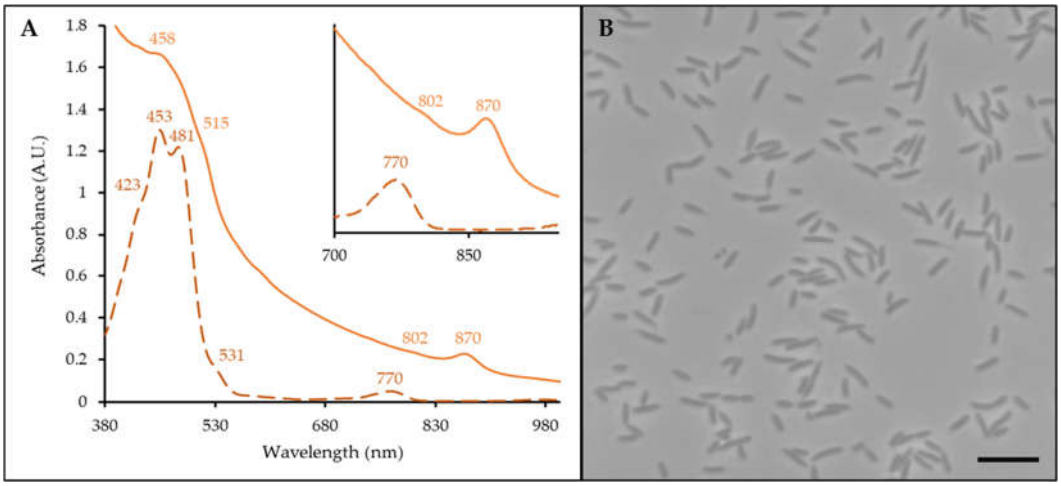

Figure 1. Photosynthetic complex and cell morphology of C11^T. (A) Whole cell (light orange line) and pigment extract (dark orange, dashed line) absorbance spectra. Peaks and shoulders of importance are indicated. (B) Phase contrast micrograph of cells. Bar is 5 μm.

Strain C11^T is gram-negative, oxidase- and catalase-positive, non-spore forming and obligately aerobic. It produces circular (1-2 mm), raised, orange colonies with entire margins and a mucoid consistency on Caulobacter media plates after 72 h. Morphologically, cells are rod shaped, 1.5-2.0 μm in length and 0.75-1.0 μm in width and do not form prosthecae after 48 h of growth (Figure 1B).

3.2. Chemotaxonomic Characterization

Whole cell fatty acid analysis revealed C11^T contains predominately $C_{18:1}$ ω7c. The major polar lipids are 1,2-Di-O-acyl-3-O-α-D-glucopyranuronosyl glycerol (MGDOx), phosphatidylglycerol (PG), 1,2-di-O-acyl-3-O-α-D-glucopyranosyl glycerol (MGD) and 1,2-di-O-acyl-3-O-[D-glucopyranosyl-(1→4)-α-D-glucopyranuronosyl]glycerol (DGL). MGDOx production differentiates Brevundimonas from Caulobacter and as such, its presence in C11^T supports the conclusions [4]. The predominant ubiquinone in the cells is Q-10. Fatty acid, polar lipid and quinone profiles are representative of Brevundimonas spp. [4], solidifying its genus placement.

3.3. Phylogenetic and Genomic Analysis

A nearly complete 16S rRNA fragment (1404 bp) of C11^T was produced via Sanger sequencing with the full gene (1461 bp) identified in the genome on contig 7. Pairwise comparisons to type species revealed 16S rRNA relatedness of strain C11^T was 98.4% to *B. bacteroides* KACC 12013^T [2] and 98.2% to *B. variabilis* KACC 12016^T [2]. Using these sequences and those from validated *Brevundimonas* members, a Maximum-Likelihood 16S rRNA gene phylogenetic tree was created (Figure 2).

The final product positions C11^T within the genus (Figure 2).

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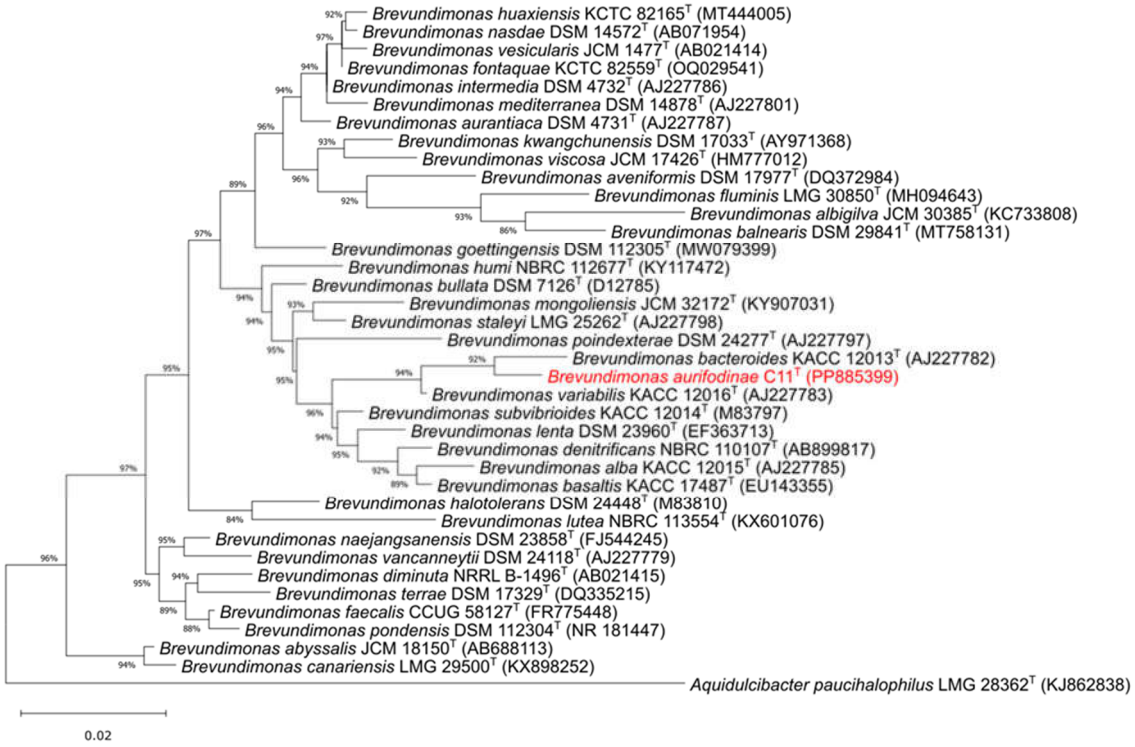

Figure 2. Maximum Likelihood 16S rRNA phylogenetic tree of strain C11^T and validated species in *Brevundimonas*. The scale bar represents the amount of substitutions per nucleotide. Accession numbers are in parenthesis. Value at nodes indicate the bootstrap support calculated with neighbor joining analysis of 1000 resampled datasets; only values >50 % are shown. *Aquidulcibacter paucihalophilus* LMG 28362^T was used as the outgroup.

Table 2. General genome features of C11^T compared to related species, and the type strain, of the genus *Brevundimonas*.

Species	*B. aurifodinae*	*B. bacteroides*	*B. variabilis*	*B. basaltis*	*B. alba*	*B. subvibrioides*	*B. diminuta*
Strain[1]	C11^T	KACC 12013^T	KACC 12016^T	KACC 17487^T	KACC 12015^T	KACC 12014^T	NRRL B-1496^T
16s rRNA Gene Similarity (%)[2]	100	98.4	98.2	97.5	97.4	97.2	94.8
Genome Size (Mb)	3.3	3.2	3.4	2.6	3.1	3.4	3.4
G+C Content	68.3	68.2	65.3	68.5	68.6	68.4	67.3
Genes	3258	3225	3320	2715	3056	3385	3438
Protein-coding genes	3186	3169	3246	2649	3000	3325	3358
No. of contigs	26	17	8	8	3	1	2
No. of tRNA operons	43	44	46	43	46	47	53
L50	5	4	2	2	1	1	1
OrthoANI (%)[2]	100	83.5	77.7	77.7	77.4	80.9	77.3
dDDH (%)[2]	100	26.6	21.8	21.4	21.3	23.5	20.8

[1]GenBank Assembly Accession numbers of strains from left to right: GCA_040195595.1, GCA_000701445.1, GCA_014199945.1, GCA_014202075.1, GCA_011927945.1, GCA_000144605.1, GCA_900445995.1. [2] Compared to C11^T.

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The genome of C11^T is 3.3 Mb and has a G + C content of 68.3 mol %, falling within range of other genus members (Table 2) [4]. It contains 26 contigs an L50 of 5, and 3186 protein-coding genes. OrthoANI between C11^T and *B. bacteroides* is 83.5 % and dDDH is 26.6 %. For *B. variabilis* it is 77.7 % and 21.8 %, respectively. All fall below the accepted cutoffs for species differentiation [38]. The Genome Blast Distance Phylogeny tree created shows a distinct lineage for C11^T among other *Brevundimonas* spp. that supports its classification as a new species (Figure 3).

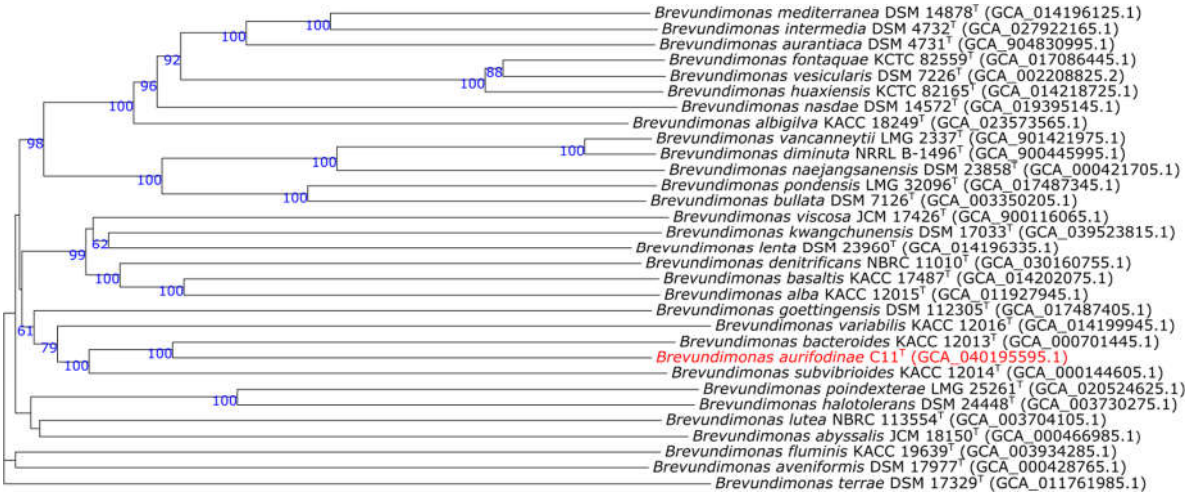

Figure 3. Genome Blast Distance Phylogeny tree of C11^T among species of the genus *Brevundimonas*. The numbers above branches are pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 80.1 %. The tree was rooted at the midpoint.

While cells were non-motile under test conditions, C11^T possesses the genes for flagellar production. As shown via spectrophotometry, C11^T synthesizes Bchl *a* and as such, has *bhcB, bchC, bchF, bchL, bchM, bchY,* and *bchZ* sequences within its genome. Besides being resistant to very high levels of tellurite, tellurate, selenite, selenate, metavanadate, and orthovanadate [17], copper and silver resistance via a resistance-nodulation-division efflux transporter is also encoded, suggesting C11^T may be able to tolerate high levels of Cu and Ag. These genes alongside those encoding for conjugative transfer, polygalacturonase as well as additional hypothetical proteins, comprise the 404 PATRIC cross-genus families found in C11^T but not in closest relatives *B. bacteroides*, *B. subvibrioides* and *B. variabilis*.

4. Conclusion

Strain C11^T, isolated from gold mine tailings in Nopiming Provincial Park, possesses significant differences in both phenotype (carbon metabolism and enzyme activities) and genotype (ANI and dDDH), which sufficiently differentiate it from the closest relatives. As such, this bacterium represents a new species in the genus and the name *Brevundimonas aurifodinae* is proposed.

4.1. Description of Brevundimonas aurifodinae sp. nov.

Brevundimonas aurifodinae (au.ri.fo.di'nae. L. neut. n. aurum, gold; L. fem. n. fodina, mine; N.L. gen. n. aurifodinae, indicates discovery at a gold mine).

Gram-negative, non-motile, non-spore forming and obligately aerobic. Circular (1-2 mm), raised, orange colonies with entire margins and a mucoid consistency form on Caulobacter medium plates after 72 h. Cells are rod-shaped, 1.5-2.0 µm in length and 0.8-1.0 µm in width, non-prosthecate. Catalase- and oxidase-positive. Growth occurs in the following conditions (optimum): between 5 and 40 °C (30 °C), from pH 6.0 to 10.5 (8.0) and up to 2.0 % NaCl (0 %). Carbon sources utilized include: Gluconate, dextrin, D-cellobiose, gentibiose, sucrose, D-turanose, stachyose, α-D-lactose, D-melibiose, N-acetyl-D-glucosanmine, N-acetyl-beta-D-mannosamine, N-acetyl-D-galactosamine, N-acetyl-nuraminic acid, α-D-glucose, D-mannose, D-galactose, 3-methyl-glucose, D-fucose, L-fucose,

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L-rhamnose, D-mannitol, D-arabitol, myo-inositol, D-glucose-6-PO_4, D-fructose-6-PO_4, D-aspartic acid, Glycyl-L-proline, L-alanine, L- aspartic acid, L-glutamic acid, L-serine, D-galacuronic acid, L-galacturonic acid, D-gluconic acid, D-glucuronic acid, glucuronamide, quinic acid, D-saccharic acid, D-lactic acid methyl ester, citric acid, α-keto-glutaric acid, D-malic acid, L-malic acid, Bromo-succinate acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, acetoacetic acid, acetic acid, casamino acids, yeast extract, and bactopeptone. Alternatively, capric acid, adipic acid, phenylacetic acid, D-maltose, D-trehalose, D-raffinose, β-methyl-D-glucoside, D-salicin, D-fructose, inosine, D-sorbitol, glycerol, D-serine, L-arginine, L-histidine, L-pyroglutamic acid, pectin, mucic acid, p-hydroxy-phenylacetic acid, methyl pyruvate, L-lactic acid, ɣ-amino-butyric acid, propionic acid, ethanol, methanol, and formic acid were not. Can grow without vitamins supplemented. Alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, naphthol-AS-Bi-phosphohydrolase, α-glucosidase, and amylase activity were present, while arginine dihydrolase, lipase, cystine arylamidase, α-galactosidase, β-galactosidase, β-glucuronidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase, α-fucosidase, urease, and nitrate reductase were not. Esculin and gelatin were hydrolyzed. Indole, methyl red, and Voges-Proskauer were negative. The primary fatty acid was $C_{18:1}$ ω7c. Ubiquinone Q-10 was the dominant isoprenoid quinone. MGDOx, PG, MGD, and DGL were the major polar lipids. Produces bacteriochlorophyll *a* and is resistant to high levels of (μg/ml): tellurite (>1500), tellurate (>1500), selenite (1000), selenate (>5000), metavanadate (>5000), and orthovanadate (>5000). Can reduce tellurite to elemental tellurium. The DNA G + C content is 68.3 mol %.

The type strain C11^T (= NRRL B-61758^T = DSM 118059^T) was isolated from gold mine tailings at Nopiming Provincial Park, Manitoba, Canada. Strain C11^T ribosomal 16S rRNA gene sequence under GenBank accession number: PP885399. This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession JBEGDD000000000, which is used in this work

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