



Description of *Albimonas marina* sp. nov., isolated from sea sand on the Yellow Sea Coast

Hyunwoo Jung¹ · Young Rok Kim¹ · Eunseo Cho¹ · Jung-Sook Lee² · Jung-Hoon Yoon³ · Ampaitip Sukhoom⁴ · Wonyong Kim^{1,5} 

Received: 16 August 2025 / Accepted: 23 October 2025
© The Author(s) 2025

Abstract

A Gram-stain-negative, anaerobic, short rod-shaped bacterium, designated as CAU 1670^T, was isolated from a sea sand sample collected from Masiran Beach, Republic of Korea. Optimal growth conditions for the bacterium were identified as growth media containing 0–3% (w/v) NaCl at 30 °C and pH 5.5. Strain CAU 1670^T exhibited high 16S rRNA gene sequence similarity with *Albimonas pacifica* CGMCC 1.11030^T (97.8% similarity) and *Albimonas donghaensis* DSM 17,890^T (94.8% similarity). The phylogeny tree based on the 16 S rRNA gene and core housekeeping gene sequences showed that strain CAU 1670^T belonged to the genus *Albimonas*. The major fatty acids included summed feature 8 (C_{18:1} ω7c and/or C_{18:1} ω6c), and the predominant respiratory quinone was Q-10. The G+C content of the type strain genome was 72.6%. The average nucleotide identity and digital DNA–DNA hybridization values between strain CAU 1670^T and reference strains were 78.5–86.4% and 22.1–31.0%, respectively. Pan-genome analysis demonstrated that strain CAU 1670^T and reference strains shared 2,010 core genes. Based on phenotypic, phylogenetic, and chemotaxonomic characteristics, strain CAU 1670^T represents a novel species within the genus *Albimonas*, for which the name *Albimonas marina* sp. nov. is proposed. The type strain is CAU 1670^T (=KCTC 92734^T; =MCCC 1K08481^T).

Introduction

The genus *Albimonas*, classified to the family *Rhodobacteraceae* in the class *Alphaproteobacteria*, was first proposed by Lim et al. [1]. To date, the genus *Albimonas* comprises two species, *Albimonas donghaensis* and *Albimonas pacifica* [2], validly published under the International Code

of Nomenclature of Prokaryotes (ICNP), and listed in the List of Prokaryotic names with Standing in Nomenclature (LPSN; <https://lpsn.dsmz.de/>, accessed on 11 August 2025). The species of the genus *Albimonas* are Gram-stain-negative, aerobic, and rod-shaped, with Q-10 as the major respiratory quinone and C_{18:1} ω7c as the major fatty acid. Members of the genus *Albimonas* have been isolated from marine environments, especially seawater. This study was driven by the ecological importance of coastal sediments, which serve as reservoirs for phylogenetically diverse and metabolically versatile bacterial communities. Despite their potential, marine sandy environments—such as those found at Masiran Beach—remain largely underexplored. These habitats may harbor previously uncharacterized microbial taxa with promising biotechnological applications, particularly in the areas of nutrient cycling and the production of bioactive secondary metabolites. During the screening of novel bacteria with biotechnology potential, strain CAU 1670^T was isolated from a sea sand sample. In this study, a novel *Albimonas* strain, designated as CAU 1670^T, was characterized using a polyphasic approach including genomic, chemotaxonomic, and physiological analyses to determine its taxonomic properties.

Hyunwoo Jung, Young Rok Kim and Eunseo Cho contributed equally to this work.

✉ Wonyong Kim
kimwy@cau.ac.kr

¹ Department of Microbiology, Chung-Ang University College of Medicine, Seoul 06974, Republic of Korea

² Korean Collection for Type Cultures, Korea Research Institute of Bioscience and Biotechnology, Jeongeup, Republic of Korea

³ Department of Food Science and Biotechnology, Sungkyunkwan University, Suwon, Republic of Korea

⁴ Division of Biological Science, Faculty of Science, Prince of Songkla University, Songkhla, Thailand

⁵ LuxBiome Co., Ltd, Seoul, Republic of Korea

Materials and Methods

Isolation and Culture Conditions

For bacterial isolation from a sea sand sample collected from Masiran Beach in Incheon, Republic of Korea (37°26′00.7″N 126°24′53.3″E), 1 g of the sea sand sample was placed in autoclaved 0.85% (w/v) NaCl solution and serially diluted. Each of the diluted samples was spread on Marine Agar 2216 (MA). After the MA plates were placed in an incubator at 30 °C for 5 days, colonies with a cream color were separated and purified by re-streaking on fresh MA plates. Among the colonies exhibiting different morphologies, strain CAU 1670^T was selected for further characterization. It represented a distinct colony phenotype and showed relatively low 16 S rRNA gene sequence similarity to recognized species of *Albimonas*. Although the relative abundance of the novel taxon in the sand sample could not be quantified, CAU 1670^T was recovered as a minority colony type, whereas most isolates were affiliated with previously described members of the family *Rhodobacteraceae*. The purified strain CAU 1670^T, which was dissolved in 25% (v/v) glycerol with Marine Broth 2216 (MB; Difco, Detroit, MI, USA), was stored at −80 °C. Strain CAU 1670^T was deposited at the Korean Collection for Type Cultures (KCTC; Jeongseup, Korea) and the Marine Culture Collection of China (MCCC; Fujian, China) under the accession numbers KCTC 92,734^T and MCCC 1K08481^T, respectively. *Albimonas pacifica* KACC 16,527^T and *Albimonas donghaensis* KCTC 12,586^T were selected as reference strains based on 16 S rRNA sequence similarity and acquired from the Korean Agricultural Culture Collection (KACC; Wanju, Korea) and the KCTC, respectively.

16 S rRNA Gene Sequence and Phylogenetic Tree

The full-length 16 S rRNA gene sequence of strain CAU 1670^T was extracted from the whole-genome sequence and compared with sequences available in the EzBioCloud database (<http://www.ezbiocloud.net/identify>) using Basic Local Alignment Search Tool (BLAST; <https://blast.ncbi.nlm.nih.gov/Blast.cgi>). Multiple sequence alignment was performed using ClustalW [3] with MEGA 7 software [4]. Phylogenetic analysis based on the 16 S rRNA sequence of strain CAU 1670^T was also conducted using MEGA 7 software. The neighbor-joining (NJ) [5], maximum-likelihood (ML) [6], and maximum parsimony (MP) [7] methods were applied to generate phylogenetic trees. Genetic distances were assessed using the Kimura two-parameter model [8], and the tree topology was evaluated by bootstrap analysis with 1,000 random replications for each method [9]. To ensure the authenticity of the genome, the 16 S rRNA gene

sequence obtained from PCR was compared with the 16 S rRNA gene sequence extracted from the whole genome (https://www.ncbi.nlm.nih.gov/nucore/NZ_JARHUC000000.1) by aligning sequences with BLAST.

Whole-genome Sequencing and Genome Analysis

Whole-genome sequencing of strain CAU 1670^T was performed by Macrogen (Seoul, Korea) using the Illumina HiSeq Sequencer, and de novo assembly was conducted with SPAdes version 3.15.0. The G + C content of the genomic DNA was measured. For genome analysis, the genomic data were obtained from the National Center for Biotechnology Information (NCBI) database. Rapid Annotation using Subsystem Technology (RAST) [10] and PATRIC (ver 3.35.5) [11] were utilized to annotate the whole-genome sequence. In addition, eggNOG-mapper (ver 5.0) was used to obtain and compare information on the protein function of strain CAU 1670^T and reference strains according to the Clusters of Orthologous Groups (COG) [12]. The contamination and completeness of the genome were predicted with CheckM (ver 1.0.18) from the KBase online platform [13] and BUSCO (ver 3.0.2). A total of 15 reference strains exhibiting high similarity to the 16 S rRNA sequence from strain CAU 1670^T and available genomic data were obtained from EzBioCloud. The phylogenetic tree was reconstructed using an up-to-date bacterial core gene (UBCG) program [14], which relies on 92 core housekeeping genes from whole bacterial genomes. Analysis of secondary metabolite biosynthesis gene clusters was carried out by antiSMASH (ver 7.1.0) [15]. The dbCAN3 annotation tool comprising HMMER, DIAMOND, Hotpep, and CGC-Finder [16] was used to predict the carbohydrate-active enzymes (CAZymes) of strain CAU 1670^T.

Comparative Genome Analysis

For pan-genome analysis, the genome sequence data of strain CAU 1670^T and two reference strains acquired from the NCBI database were annotated by Prokka (ver 1.14.6) [17]. Pan-genome calculation was performed using Roary (ver 3.13.0) with a minimum sequence identity of 70% [18]. The results were visualized with the R program and Phandango server (<https://jameshadfield.github.io/phandango>) [19]. Between strain CAU 1670^T and reference strains affiliated to the genus *Albimonas*, the values of average nucleotide identity (ANI) and digital DNA–DNA hybridization (dDDH) were calculated using the OrthoANI algorithm [20] and Genome-to-Genome Distance Calculator (GGDC 3.0; <http://ggdc.dsmz.de/ggdc.php>) [21], respectively. Average Amino Acid Identity (AAI) values were obtained with the EzAAI pipeline (v1.2.4) implemented

in a Conda environment. Gene prediction was performed using Prodigal, and pairwise protein similarity was assessed with MMseqs2, following the approach outlined by Kim et al. [22]. Furthermore, comparative gene cluster analysis between strains in a Venn diagram was performed by the OrthoVenn3 online server (<https://orthovenn3.bioinfotoolkits.net/home>) [23].

Morphological, physiological, and Biochemical Analysis

The growth of strain CAU 1670^T was tested on several media including MA, tryptic soy agar (TSA), brain heart infusion (BHI) agar, nutrient agar (NA), Luria-Bertani (LB) agar, and glucose yeast extract (GYE) agar under identical conditions (30 °C, aerobic, and 7 days). Growth was examined at 4 °C, 10 °C, 20 °C, 30 °C, 37 °C, and 45 °C, and the pH optimal for growth was evaluated from pH 4.5 to 12.0 (intervals of 0.5 pH units) separately. The pH level was adjusted with sterile biological buffers (1 N H₂SO₄; pH 4.5–6.5, 2 N NaOH; pH 7.0–12.0). Anaerobic growth was investigated using a Bactron anaerobic chamber (Sheldon Manufacturing Inc., Cornelius, OR, USA). The effect of NaCl on growth was measured by culturing the strains in LB with various NaCl concentrations (0–15%; intervals of 1%, w/v) at 30 °C [24]. After strain CAU 1670^T was cultured on MA for 3 days at 30 °C, cellular morphology was observed by light microscopy (Model DM1000; Leica Microsystems, Danaher Corp., Wetzlar, Germany). In addition, the presence of flagella was determined by transmission electron microscopy (TEM; Model JEM 1010; JEOL Ltd., Tokyo, Japan). Motility was assessed by the hanging drop method [25], and Gram staining was performed with a Gram staining kit (bioMérieux, Marcy-l'Étoile, France) according to the manufacturer's manual. The activities of catalase and oxidase were determined by adding H₂O₂ solution (3%, v/v) and tetramethyl-*p*-phenylenediamine (1% w/v) [26]. The method of Smibert and Krieg [27] was applied to investigate the hydrolysis of starch and casein. Following the manufacturer's instructions, enzyme activities and other biochemical features were characterized using the API 20E, API 20NE, API 50CH, and API ZYM kits (bioMérieux, Marcy-l'Étoile, France).

Chemotaxonomic Analysis

Strain CAU 1670^T and reference strains were lyophilized with methanol/isopropyl ether (3:1, v/v) [28] to extract respiratory quinones, which were identified by high-performance liquid chromatography (HPLC). For fatty acid analysis, CAU 1670^T and reference strains were grown on MB at 30 °C for 4 days. After the harvesting of strains in

the late-exponential phase, cellular fatty acids were saponified, extracted, and methylated [29]. Profiles were analyzed using the Sherlock™ Microbial Identification System (Version 6.2; MIDI Inc., Newark, DE, USA; http://midi-inc.com/pages/microbial_id.html) with gas chromatography (Agilent Model 6890 N; Agilent Technologies Inc., Santa Clara, CA, USA) [30].

Results and Discussion

Phylogenetic Analysis Based on the 16 S rRNA Gene Sequence

In sequence comparison, the nearly complete 16 S rRNA gene sequence of strain CAU 1670^T (1,432 bp; GenBank accession number: OP388933) and the 16 S rRNA sequence extracted from the whole genome shared 99.7% (1432/1466) similarity. The 16 S rRNA gene sequence of strain CAU 1670^T was compared with that of closely related strains based on the EzBioCloud database. Strain CAU 1670 was the most closely related to *Albimonas pacifica* CGMCC 1.11030^T (97.8%), followed by *Albimonas donghaensis* DSM 17,890^T (94.8%). A value below 98.7% similarity was used as the threshold to identify different bacterial species [31]. All phylogenetic trees based on the 16 S rRNA gene sequence were constructed using 25 type strains, and *Escherichia coli* ATCC 11,775^T (AB681728) was selected as an outgroup. The phylogenetic tree constructed with the NJ algorithm showed that strain CAU 1670^T was part of the genus *Albimonas* and clustered tightly with *Albimonas pacifica* CGMCC 1.11030^T; this was supported by a bootstrap value of 99% (Fig. 1). Similarly, the trees generated with the ML and MP methods demonstrated a robust phylogenetic relationship (Fig. S1, S2).

Genomic Features

The de novo assembled sequence of strain CAU 1670^T was 5.79 Mbp in genome size, containing 22 contigs, with 732,160 bp of N50 values and 371.2× *k*-mer coverage. A total of 5,268 protein-coding sequences (CDSs) were identified, including 49 tRNAs and 2 rRNAs. The genomic DNA G + C content was 72.6%, which was close to the values of *Albimonas pacifica* CGMCC 1.11030^T (69.0%) and *Albimonas donghaensis* DSM 17,890^T (72.0%) [1, 2]. The genome's completeness was 100% according to the results of BUSCO, and the contamination level was 0.13% according to the results of CheckM. Differences in the genomic features between strain CAU 1670^T and two reference strains are summarized in Table S1. Moreover, the circular genome map of strain CAU 1670^T was generated, as shown

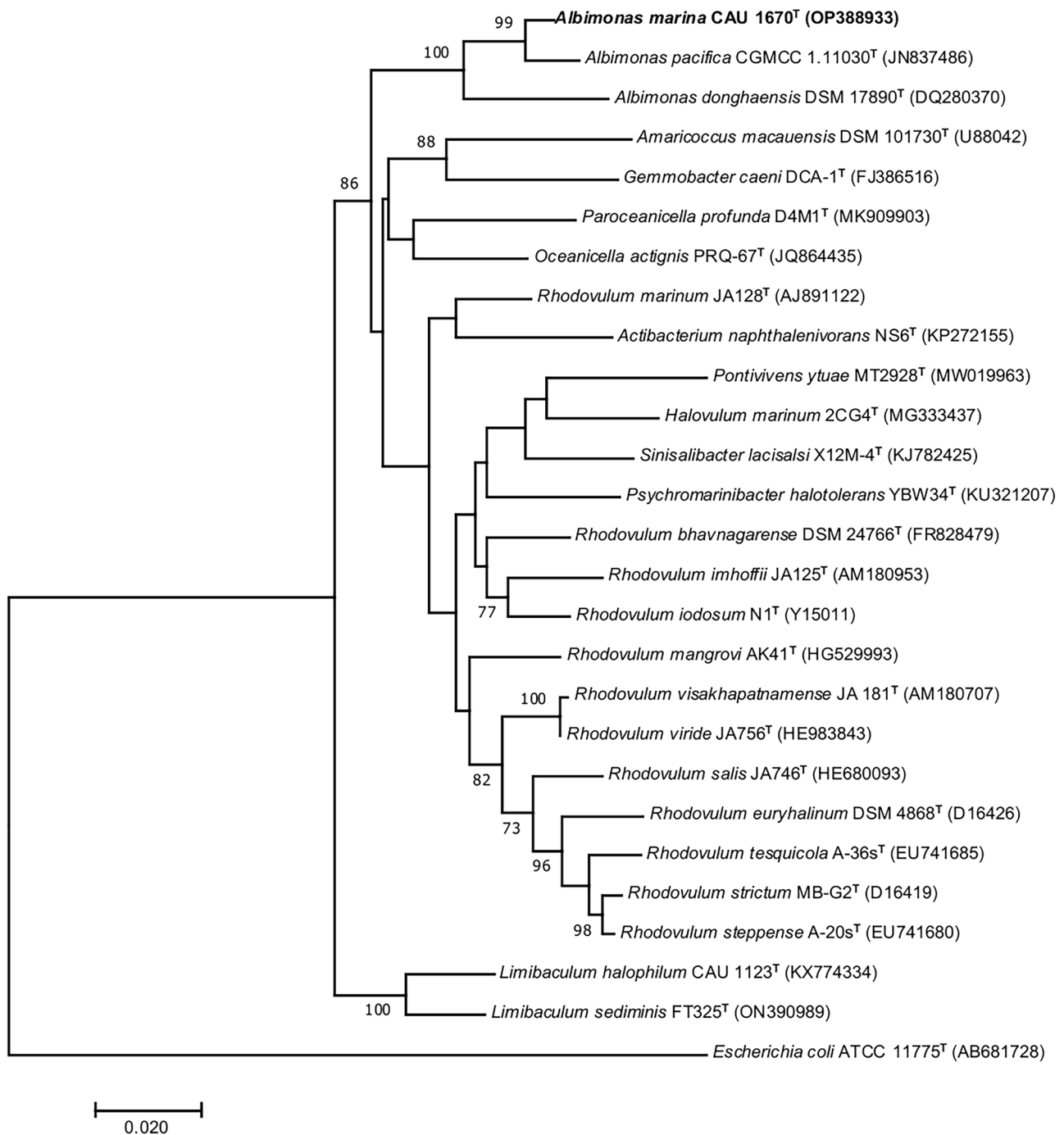


Fig. 1 Neighbor-joining (NJ) phylogenetic tree based on the 16S rRNA gene sequence. The phylogenetic tree demonstrated the relationship of strain CAU 1670^T with closely related species in the genus *Albimonas*. Bootstrap values (>70%) are indicated as percentages of 1,000 resampled datasets.

Escherichia coli ATCC 11,775^T (AB681728) was used as an outgroup. The scale bar represents a 0.02 nucleotide sequence divergence

in Fig. 2. In the phylogenetic tree based on 92 core house-keeping genes, strain CAU 1670^T formed a phylogenetic lineage within the genus *Albimonas* (Fig. 3).

The genes of strain CAU 1670^T were annotated by the RAST program and classified into 308 subsystems and 27

categories; the predominant subsystems (>100 genes) of CAU 1670^T were carbohydrates (317 genes), amino acids and derivatives (309 genes), protein metabolism (191 genes), nucleosides and nucleotides (140 genes), cofactors, vitamins, prosthetic groups, pigments (123 genes),

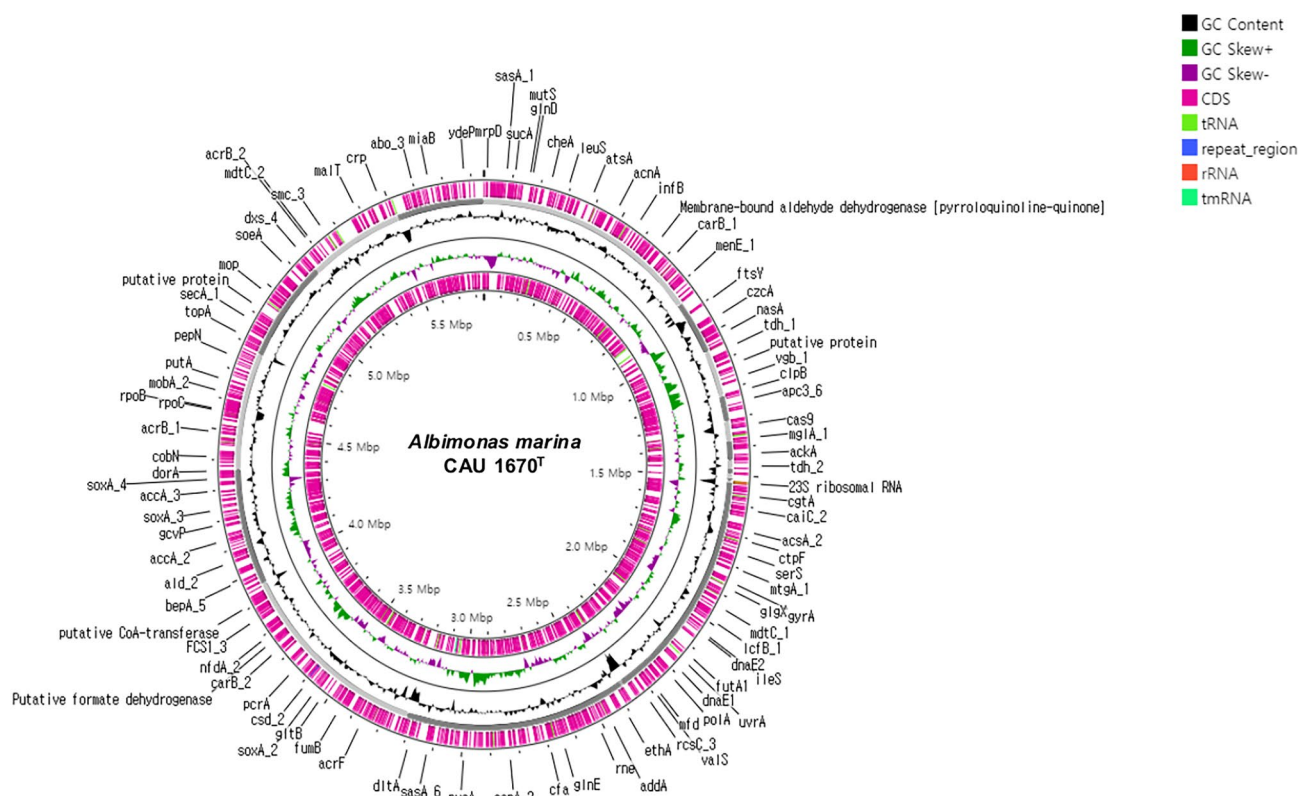


Fig. 2 Graphical genomic map of strain CAU 1670^T

and respiration (112 genes). The distribution of genes in subsystem categories among CAU 1670^T and phylogenetically related members of the genus *Albimonas* based on the results of RAST is presented in Table S2. The results of genome analyses between CAU 1670^T and reference strains are presented in Table S3. Members of the genus *Albimonas* harbored genes encoding for 5-FCL-like protein (FTHFL, MTHFR). In addition, genes related to oxidative stress (NSTR, SoxR, NnrS, AhpC, Irr) were found in the genome of strain CAU 1670^T. In comparison with the reference strains, formate-tetrahydrofolate ligase, redox-sensitive transcriptional activator, and NnrS (protein involved in the response to NO) were exclusively present in CAU 1670^T (Table S2). Strain CAU 1670^T had secondary metabolite clusters encoding for terpene, homoserine lactone (hserlactone), and other unspecified ribosomally synthesized and post-translationally modified peptide (RiPP)-like products (Fig. S4, Table S4). A comparison of CAU 1670^T and phylogenetically related species using antiSMASH is presented in Table S5. In addition, the distribution of COG categories for strain CAU 1670^T is presented in Fig. S4. Based on the COG database, 4,237 CDS genes were divided into functional categories, the three most abundant COG categories, excluding [S] function unknown (782 CDS; 18.5%), were [E] amino acid transport and metabolism (560 CDS;

13.2%), [C] energy production and conversion (343 CDS; 8.1%), and [P] inorganic ion transport and metabolism (334 CDS; 7.9%), which are associated with cellular metabolism. In this analysis, no genes were found in four categories: [A] RNA processing and modification, [R] general function prediction only, [W] extracellular structures, and [Y] nuclear structure. A comparison of COG categories with those of reference strains is shown in Table S6. The results of CAZyme analysis using all three annotation programs (high accuracy) revealed that the genome of CAU 1670^T included 66 genes encoding CAZymes. The most abundant CAZymes were glycosyltransferases (GTs, 27), followed by glycoside hydrolases (GHs, 16), auxiliary activities (AAs, 15), carbohydrate esterases (CEs, 5), and carbohydrate-binding modules (CBMs, 3). Notably, a high number of the predicted CAZymes were correlated with the relevant COG functional category ([G] carbohydrate transport and metabolism, 260 CDSs). The predicted CAZymes of phylogenetically closely related strains are listed in Table S7.

Comparative Genome Analysis

The ANI values for the most closely related strains, *Albimonas donghaensis* and *Albimonas pacifica*, were 78.5% and 86.4%, respectively, whereas dDDH values were 22.1% and

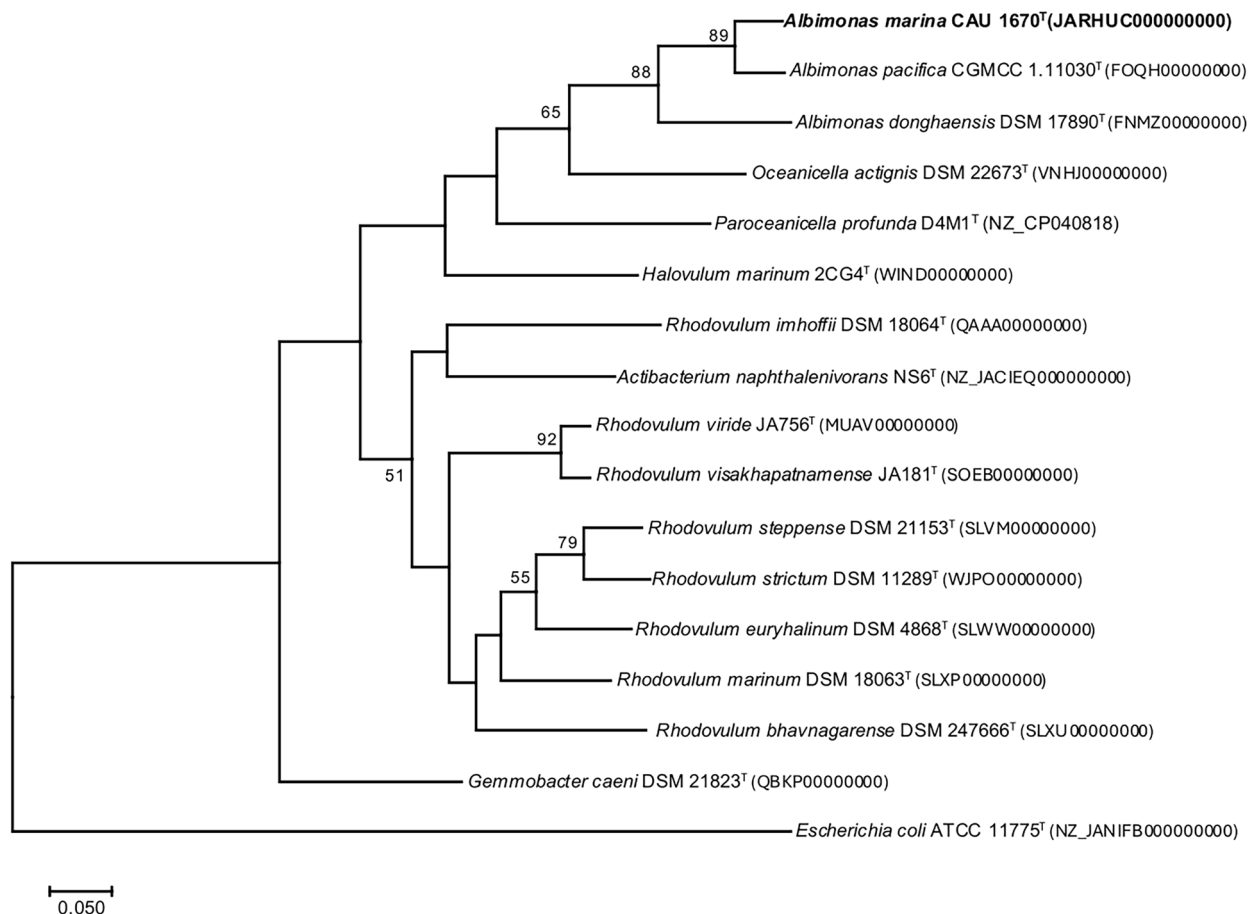


Fig. 3 UBCG phylogenetic tree generated based on the core genome of strain CAU 1670^T and closely related species. *Escherichia coli* ATCC 11,775^T (AB681728) was used as an outgroup. The gene sup-

port index values of 92 UBCGs are indicated at branching points. Only values > 50% are shown. The bar refers to 0.05 substitutions per nucleotide position

31.0%, respectively. In addition, the average amino acid identity (AAI) values between strain CAU 1670^T and the 2 reference strains were 86.8% with *Albimonas pacifica* CGMCC 1.11030^T and 72.9% with *Albimonas donghaensis* DSM 17,890^T (Table S8). These values were markedly lower than the cut-off thresholds for prokaryotic species (ANI, 95%; dDDH, 70%, AAI, 95–96%) [32–34], further supporting the delineation of CAU 1670^T as a distinct species. The genome size of strain CAU 1670^T (5.79 Mbp) and its G + C content (72.6%) are consistent with the genus *Albimonas*, in which reported members show genome sizes of 5.0–6.0 Mbp and G + C contents ranging from 69.0 to 72.0%. Pan-genome analysis was performed to determine the total number of different genes present in strain CAU 1670^T compared with 2 representative strains of *Albimonas* with whole-genome sequence data in the EzBioCloud database. The program generated a pan-genome of 8,514 genes, of which 2,010 genes were shared by all strains (core genes; 99% ≤ strains), and 6,504 genes were classified as accessory and unique genes. With the addition of genome sequences,

the number of pan-genome genes was steadily increased (Fig. 4A); however, the number of core genes was sharply decreased initially (Fig. 4B). Significant genomic differences between the genomes of strain CAU 1670^T and two reference strains were identified using a presence/absence gene matrix (Fig. 4C). Functionally annotated clusters were compared between strain CAU 1670^T and closely related members of the genus *Albimonas* through a Venn diagram (Fig. S5).

Morphological, physiological, and Biochemical Features

Strain CAU 1670^T was aerobic, Gram-stain-negative, non-spore-forming, short rod-shaped, and non-motile, with a cell size of 1.3–1.8 μm in width and 3.5–4.0 μm in length (Fig. S6). After incubation at 30 °C for 3 days under aerobic conditions, colonies on MA agar plates had a cream color and were punctiform with an entire margin, convex, smooth, and translucent. CAU 1670^T grew well on

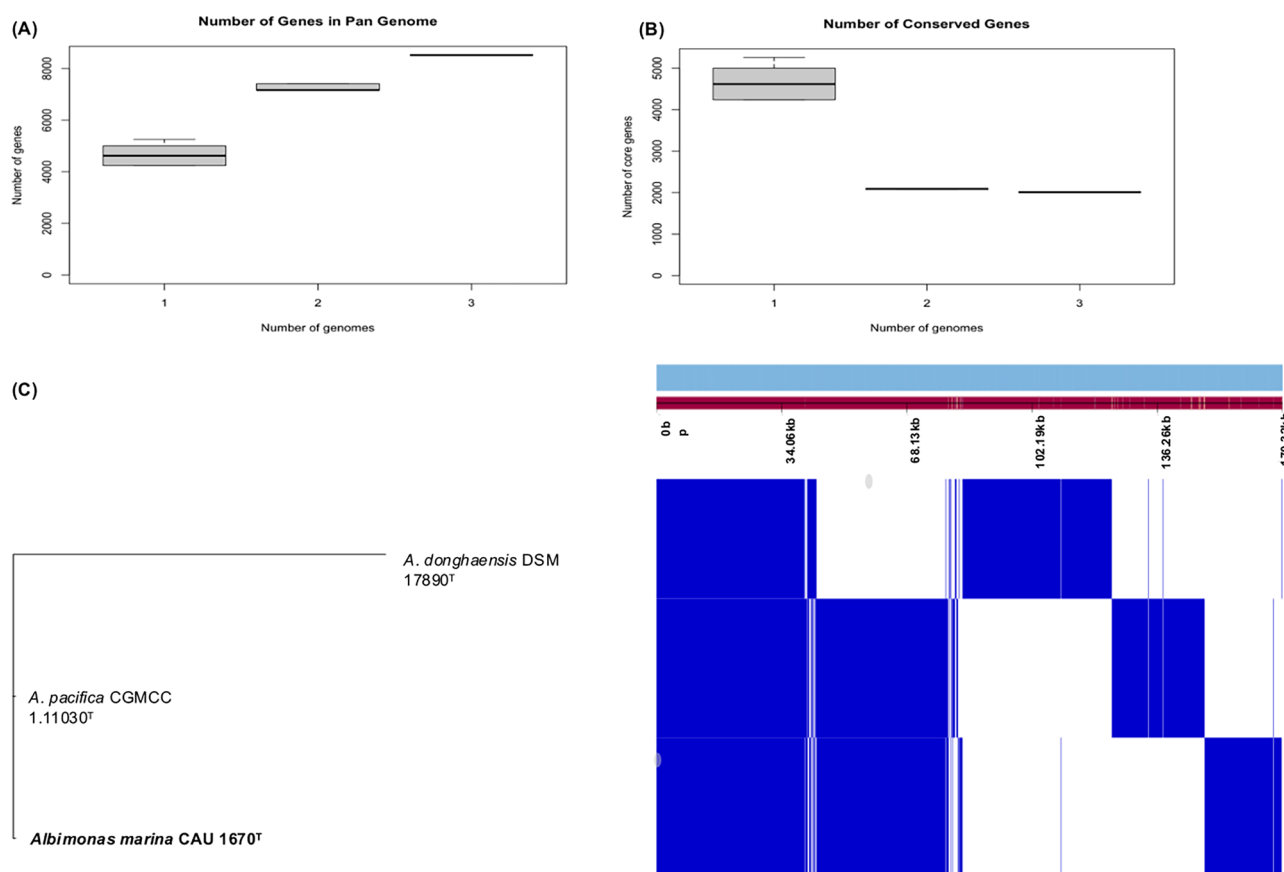


Fig. 4 Pan-genome analysis of strain CAU 1670^T and two reference strains. (A) Box plot of the pan-genome as a function of the number of genomes. (B) Box plot of the core genome as a function of the number

of genomes. (C) Phylogenetic tree and gene presence/absence matrix plot generated by the Phandango server. The blue bar in the matrix represents gene presence

MA agar, showed reduced growth on LB agar, and did not grow on GYE, NA, BHI, and TSA agar. The temperature and pH ranges in which the isolated strain was grown were 20–37 °C (optimum 30 °C) and pH 5.0–10.5 (optimum pH 5.5), respectively. The NaCl concentration range for growth was observed to be 0–9% (w/v), with optimal growth occurring at 0–3% (w/v). CAU 1670^T was found to be catalase-positive and oxidase-positive. However, the hydrolysis of casein and starch was not observed. A comparison of the morphological, physiological, and biochemical characteristics between strain CAU 1670^T and reference strains is presented in Table 1.

Chemotaxonomic Characteristics

The major respiratory quinone of CAU 1670^T was Q-10, which is the predominant respiratory quinone found in *Albimonas* species. The predominant fatty acids (>10%) of strain CAU 1670^T were summed feature 8 (C_{18:1} ω7c and/or C_{18:1} ω6c; 25.5%), C_{19:0} cyclo ω8c (25.3%), C_{18:1} ω7c 11-methyl (13.5%), and C_{16:0}, which are similar to those of

phylogenetically closely related strains. A comparison of the fatty acid compositions of strain CAU 1670^T, *A. pacifica* CGMCC 1.11030^T, and *A. donghaensis* DSM 17,890^T is presented in Table 2.

Taxonomic Conclusion

According to phylogenetic research using the 16 S rRNA gene and genome, CAU 1670^T was identified as belonging to the genus *Albimonas*. Phenotypic and chemotaxonomic features indicated that CAU 1670^T represents a novel species of the genus *Albimonas*; thus, the name *Albimonas marina* sp. nov. is proposed.

Description of *Albimonas marina* sp. nov

Albimonas marina (ma.ri'na. L. fem. adj. *marina*, of the sea, marine).

Albimonas marina is Gram-stain-negative, aerobic, non-spore-forming, non-motile, and short rod-shaped, measuring approximately 3.5–4.0 μm in length and 1.3–1.8 μm in

Table 1 Differential characteristics of CAU 1670^T and other species that are closely related.

Characteristics	1	2	3
Cell size (μm)	1.3–1.8 × 3.5–4.0	0.8–1.2 × 2.0–4.0	1.0– 1.4 × 1.6–2.6
Temperature range (°C)	25–37	10–40	10–38
pH range	5.0–10.5	6.0–9.5	6.0–9.5
NaCl range (% w/v)	0–9	0–12	0–14
Nitrate reduction	–	+	–
Hydrolysis of			
Urease	–	–	+
Gelatin	–	–	+
Acid production from			
L-arabinose	–	–	+
Enzymatic activity of			
Valine arylamidase	+	+	–
Crystine arylamidase	–	+	–
DNA G + C content (%)	72.6	69.0	72.0

Strains: 1, CAU 1670^T; 2, *A. pacifica* CGMCC 1.11030^T [1]; 3, *A. donghaensis* DSM 17,890^T [2]. +, positive; –, negative. All strains are negative for Indole production, ONPG reaction, lipase (C14), trypsin, α-chymotrypsin, α-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase but positive for alkaline, esterase (C4), esterase lipase (C8), leucine arylamidase, acid phosphatase, and naphthol-AS-BI-phosphohydrolase

width. Colonies are punctiform, 0.5–1.0 mm in diameter, convex, smooth, translucent, and cream-colored after 3 days of incubation at 30 °C under aerobic conditions on marine agar. Optimal growth occurs at 30 °C (range 20–37 °C), pH 5.5 (range pH 5.0–10.5), and 1–3% NaCl (range 1–9%). *Albimonas marina* produces catalase and oxidase but does not hydrolyze casein or starch. Carbohydrate utilization tests indicate no acid production from tested carbohydrates. The species produces alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, acid phosphatase, and naphthol-AS-BI-phosphohydrolase but not lipase (C14), trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase, or α-fucosidase. In biochemical assays, it produces L-tryptophan deaminase but does not produce β-galactosidase, hydrogen sulfide, urease, L-ornithine decarboxylase, indole, gelatinase, acetoin (Voges-Proskauer), or L-arginine dihydrolase, and does not ferment citrate, D-glucose, D-mannitol, inositol, D-sorbitol, L-rhamnose, D-sucrose, D-melibiose, amygdalin, or L-arabinose. Further biochemical characterization shows that it produces β-glucosidase but does not reduce nitrate, produce indole, ferment glucose, produce L-arginine dihydrolase, urease, gelatinase, or β-galactosidase, and does not assimilate D-glucose, D-arabinose, D-mannose, D-mannitol, maltose, adipic acid, malate, potassium gluconate, trisodium citrate, N-acetyl-glucosamine, capric acid, or phenylacetic

Table 2 Cellular fatty acid contents (% of total) of strain CAU 1670^T and reference strains.

Fatty acids	1	2	3
<i>Saturated</i>			
C _{14:0}	TR	TR	–
C _{16:0}	11.0	10.7	4.74
C _{17:0}	1.9	1.9	TR
C _{18:0}	3.7	5.8	1.71
<i>Branched</i>			
anteiso-C _{15:0}	TR	TR	TR
iso-C _{16:0}	TR	TR	TR
anteiso-C _{16:0}	TR	TR	TR
C _{16:0} N alcohol	TR	TR	–
<i>Unsaturated</i>			
C _{13:1} at 12–13	TR	TR	TR
C _{17:0} cyclo	TR	–	–
C _{18:1} ω5c	TR	–	–
C _{18:1} ω7c 11-methyl	13.5	15.8	26.6
C _{19:0} cyclo ω8c	25.2	20.8	–
C _{20:2} ω6,9c	2.7	1.9	–
C _{20:1} ω9c	–	TR	–
<i>Hydroxy</i>			
C _{16:1} 2-OH	–	TR	–
C _{16:0} 3-OH	TR	TR	TR
C _{17:0} 2-OH	–	TR	–
C _{17:0} 3-OH	TR	–	–
C _{18:0} 3-OH	3.6	–	6.9
<i>Summed features*</i>			
2	6.0	5.8	6.4
3	2.4	1.3	1.6
7	–	1.1	–
8	25.23	25.80	48.40

*Summed features represent two or three fatty acids that could not be separated by gas chromatography with the MIDI system. Summed feature 2 consists of C_{12:0} aldehyde and/or unknown fatty acids. Summed feature 3 consists of C_{16:1} ω7c/C_{16:1} ω6c. Summed feature 7 consists of C_{19:1} ω7c/C_{19:1} ω6c and/or C_{19:1} ω7c/C_{19:1} ω6c/C_{19:0} cyclo. Summed feature.

8 consists of C_{18:1} ω7c and/or C_{18:1} ω6c.

Strains: 1, CAU 1670^T; 2, *A. pacifica* CGMCC 1.11030^T; 3, *A. donghaensis* DSM 17,890^T. –, not detected; TR, trace amount (<1%). Only fatty acids accounting for >1% of the total are shown; major fatty acids (>10%) are shown in bold.

acid. The major respiratory quinone is Q-10, and the predominant fatty acids are Summed feature 8, C_{19:0} cyclo ω8c, and C_{18:1} ω7c 11-methyl.

The type strain CAU 1670^T (=KCTC 92734^T; =MCCC 1K08481^T) was isolated from a sea sand sample collected from Masiran beach in Incheon, Republic of Korea. The G+C content of the genomic DNA is 72.6%. The 16 S rRNA gene sequence and the genomic sequence of strain CAU 1670^T have been deposited under the GenBank/EMBL/DBJ accession numbers OP388933 and JAR-HUC000000000, respectively.

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1007/s00284-025-04587-2>.

Acknowledgements We thank Prof. Bernhard Schink (University of Konstanz, Germany) for reviewing the nomenclature proposed in this study.

Author contributions WK conceived and designed the study. HJ, YRK, and J-SL performed the experiments. EC, J-HY, and AS carried out the statistical analyses, and HJ drafted the manuscript, with major input from WK.

Funding Open Access funding enabled and organized by Chung-Ang University Hospital. This work was supported by a grant from the National Institute of Biological Resources (NIBR) funded by the Ministry of the Environment (MOE) of the Republic of Korea (NIBR202304204) and the Chung-Ang University Research Grants in 2024.

Declarations

Conflict of interest The authors declare that there are no conflicts of interest.

Ethics Approval This article does not contain any studies with human participants and/or animals performed by any of the authors. Informed consent is not required in this study.

Open Access This article is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License, which permits any non-commercial use, sharing, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if you modified the licensed material. You do not have permission under this licence to share adapted material derived from this article or parts of it. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by-nc-nd/4.0/>.

References

- Lim JM, Jeon CO, Jang HH, Park DJ, Shin YK et al (2008) *Albimonas donghaensis* gen. nov., sp. nov., a non-photosynthetic member of the class *Alphaproteobacteria* isolated from seawater. *Int J Syst Evol Microbiol* 58:282–285. <https://doi.org/10.1099/ijs.0.65429-0>
- Li GW, Zhang XY, Wang CS, Zhang YJ, Xu XW et al (2013) *Albimonas Pacifica* sp. nov., isolated from seawater of the Pacific, and emended description of the genus *Albimonas*. *Int J Syst Evol Microbiol* 63:3597–3601. <https://doi.org/10.1099/ijs.0.049742-0>
- Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA et al (2007) Clustal w and clustal x version 2.0. *Bioinformatics* 23:2947–2948. <https://doi.org/10.1093/bioinformatics/btm404>
- Kumar S, Stecher G, Tamura K (2016) MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol* 33:1870–1874. <https://doi.org/10.1093/molbev/msw054>
- Saitou N, Nei M (1987) The neighbor-joining method - a new method for reconstructing phylogenetic trees. *Mol Biol Evol* 4:406–425. <https://doi.org/10.1093/oxfordjournals.molbev.a040454>
- Kishino H, Hasegawa M (1989) Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data, and the branching order in *Homoidea*. *J Mol Evol* 29:170–179. <https://doi.org/10.1007/Bf02100115>
- Czelusniak J, Goodman M, Moncrief ND, Kehoe SM (1990) Maximum parsimony approach to construction of evolutionary trees from aligned homologous sequences. *Methods Enzymol* 183:601–615. [https://doi.org/10.1016/0076-6879\(90\)83039-C](https://doi.org/10.1016/0076-6879(90)83039-C)
- Kimura M (1980) A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J Mol Evol* 16:111–120. <https://doi.org/10.1007/Bf01731581>
- Felsenstein J (1985) Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* 39:783–791. <https://doi.org/10.2307/2408678>
- Aziz RK, Bartels D, Best AA, DeJongh M, Disz T et al (2008) The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:1–15. <https://doi.org/10.1186/1471-2164-9-75>
- Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T et al (2017) Improvements to PATRIC, the all-bacterial bioinformatics database and analysis resource center. *Nucleic Acids Res* 45:D535–D542. <https://doi.org/10.1093/nar/gkw1017>
- Huerta-Cepas J, Szklarczyk D, Heller D, Hernández-Plaza A, Forslund SK et al (2019) EggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. *Nucleic Acids Res* 47(D1):D309–D314. <https://doi.org/10.1093/nar/gky1085>
- Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW (2015) Checkm: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res* 25:1043–1055. <https://doi.org/10.1101/gr.186072.114>
- Na S-I, Kim YO, Yoon S-H, Ha S-m, Baek I et al (2018) UBCG: up-to-date bacterial core gene set and pipeline for phylogenomic tree reconstruction. *J Microbiol* 56:280–285. <https://doi.org/10.1007/s12275-018-8014-6>
- Blin K, Shaw S, Augustijn HE, Reitz ZL, Biermann F et al (2023) Antismash 7.0: new and improved predictions for detection, regulation, chemical structures and visualisation. *Nucleic Acids Res* 51:W46–W50. <https://doi.org/10.1093/nar/gkad344>
- Zheng J, Ge Q, Yan Y, Zhang X, Huang L et al (2023) dbCAN3: automated carbohydrate-active enzyme and substrate annotation. *Nucleic Acids Res* 51:W115–W121. <https://doi.org/10.1093/nar/gkad328>
- Seemann T (2014) Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>
- Page AJ, Cummins CA, Hunt M, Wong VK, Reuter S et al (2015) Roary: rapid large-scale prokaryote pan genome analysis. *Bioinformatics* 31:3691–3693. <https://doi.org/10.1093/bioinformatics/btv421>
- Hadfield J, Croucher NJ, Goater RJ, Abudahab K, Aanensen DM et al (2017) Phandango: an interactive viewer for bacterial population genomics. *Bioinformatics* 34:292–293. <https://doi.org/10.1093/bioinformatics/btx610>
- Yoon S-H, Ha S-m, Lim J, Kwon S, Chun J (2017) A large-scale evaluation of algorithms to calculate average nucleotide identity. *Antonie Van Leeuwenhoek* 110:1281–1286. <https://doi.org/10.1007/s10482-017-0844-4>

21. Meier-Kolthoff JP, Auch AF, Klenk H-P, Göker M (2013) Genome sequence-based species delimitation with confidence intervals and improved distance functions. *BMC Bioinformatics* 14:60. <https://doi.org/10.1186/1471-2105-14-60>
22. Kim D, Park S, Chun J (2021) Introducing ezaai: a pipeline for high throughput calculations of prokaryotic average amino acid identity. *J Microbiol* 59:476–480. <https://doi.org/10.1007/s12275-021-1154-0>
23. Sun J, Lu F, Luo Y, Bie L, Xu L, Wang Y (2023) Orthovenn3: an integrated platform for exploring and visualizing orthologous data across genomes. *Nucleic Acids Res* 51:W397–W403. <https://doi.org/10.1093/nar/gkad313>
24. Rodriguez-Valera F, Ruiz-Berraquero F, Ramos-Cormenzana A (1981) Characteristics of the heterotrophic bacterial populations in hypersaline environments of different salt concentrations. *Microb Ecol* 7:235–243. <https://doi.org/10.1007/BF02010306>
25. Bowman JP (2000) Description of *Cellulophaga algicola* sp. nov., isolated from the surfaces of Antarctic algae, and reclassification of *Cytophaga uliginosa* (ZoBell and Upham 1944) Reichenbach 1989 as *Cellulophaga uliginosa* comb. nov. *Int J Syst Evol Microbiol* 50:1861–1868. <https://doi.org/10.1099/0020-7713-50-5-1861>
26. Kang HS, Yang HL, Lee SD (2009) *Nitratireductor kimnyeongensis* sp. nov., isolated from seaweed. *Int J Syst Evol Microbiol* 59:1036–1039. <https://doi.org/10.1099/ijms.0.65734-0>
27. Smibert RM, Krieg NR (1994) Phenotypic characterization. In: Gerhardt P, Murray RG, Wood WA, Krieg NR (eds) *Methods for general and molecular bacteriology*. American Society of Microbiology, Washington DC, pp 611–654
28. Komagata K, Suzuki K-I (1988) 4 lipid and cell-wall analysis in bacterial systematics. *Methods Microbiol* 19:161–207. [https://doi.org/10.1016/S0580-9517\(08\)70410-0](https://doi.org/10.1016/S0580-9517(08)70410-0)
29. Kiykendall LD, ROY MA, O'Neill JJ, Devine TE (1988) Fatty acids, antibiotic resistance, and deoxyribonucleic acid homology groups of *Bradyrhizobium Japonicum*. *Int J Syst Evol Microbiol* 38:358–361. <https://doi.org/10.1099/00207713-38-4-358>
30. Piñero-Vidal M, Pazos F, Santos Y (2008) Fatty acid analysis as a chemotaxonomic tool for taxonomic and epidemiological characterization of four fish pathogenic *Tenacibaculum* species. *Lett Appl Microbiol* 46:548–554. <https://doi.org/10.1111/j.1472-765X.2008.02348.x>
31. Kim M, Oh H-S, Park S-C, Chun J (2014) Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes. *Int J Syst Evol Microbiol* 64:346–351. <https://doi.org/10.1099/ijms.0.059774-0>
32. Lee I, Ouk Kim Y, Park S-C, Chun J (2016) OrthoANI: an improved algorithm and software for calculating average nucleotide identity. *Int J Syst Evol Microbiol* 66:1100–1103. <https://doi.org/10.1099/ijsem.0.000760>
33. Meier-Kolthoff JP, Göker M, Spröer C, Klenk H-P (2013) When should a DDH experiment be mandatory in microbial taxonomy? *Arch Microbiol* 195:413–418. <https://doi.org/10.1007/s00203-013-0888-4>
34. Konstantinidis KT, Tiedje JM (2005) Genomic insights that advance the species definition for prokaryotes. *Proc Natl Acad Sci USA* 102(7):2567–2572. <https://doi.org/10.1073/pnas.0409727102>

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.