

# A report of 37 unrecorded anaerobic bacterial species isolated from the Geum River in South Korea

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A total of 37 anaerobic bacteria strains within the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Bacteroidia*, *Flavobacteriia*, *Bacilli*, *Clostridia*, and *Fusobacteriia* were isolated from freshwater and sediment of the Geum River in Korea. The unreported species were related with *Rhizobium* and *Oleomonas* of the class *Alphaproteobacteria*; *Acidovorax*, *Pseudogulbenkiania*, and *Aromatoleum* of the class *Betaproteobacteria*; *Tolomonas*, *Aeromonas*, *Cronobacter*, *Lonsdalea*, and *Phytobacter* of the class *Gammaproteobacteria*; *Bacteroides*, *Dysgonomonas*, *Macellibacteroides*, and *Parabacteroides* of the class *Bacteroidia*; *Flavobacterium* of the class *Flavobacteriia*; *Bacillus* and *Paenibacillus* of the class *Bacilli*; *Clostridium*, *Clostridioides*, *Paraclostridium*, *Romboutsia*, *Sporacetigenium*, and *Terrisporobacter* of the class *Clostridia*; and *Cetobacterium* and *Ilyobacter* of the class *Fusobacteriia*. A total of 37 strains, with >98.7% 16S rRNA gene sequence similarity with validly published bacterial species, but not reported in Korea, were determined to be unrecorded anaerobic bacterial species in Korea.

Keywords: 16S rRNA, anaerobic bacteria, bacterial diversity, taxonomy, unrecorded species

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## INTRODUCTION

Since the Nagoya Protocol and the Convention on Biological Diversity, securing and managing of biological resources have become more important (Buck & Hamilton, 2011). In order to be competitive with national biological resources, various biological resources should be secured. However, to date, systematic research on domestic freshwater biological resources is insufficient. Freshwater basins are expected to have high diversity due to their diverse environmental conditions. According to the Korean Society of Ecology, reported in 1994, it is estimated that 100,000 native species inhabit Korea, while 52,628 species have been reported (National species list of Korea, 2019); so there is an urgent need to study unreported species. In particular, prokaryotes are a resource of biological industry and have the highest industrial value, but reported species are less than 1% of the estimated species. Most aerobic prokaryotes are being investigated among reported species. Although anaerobic prokaryotic microorganisms derived from freshwater environment are actively being studied globally due to their high novelty as biological resources, there are few cases of purely iso-

lated culture in Korea.

In the present study, we attempted to isolate anaerobic microorganisms from freshwater and sediment in the Geum River of Korea. Here, 37 unreported species belonging to the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Bacteroidia*, *Flavobacteriia*, *Bacilli*, *Clostridia*, and *Fusobacteriia* are reported and described.

## MATERIALS AND METHODS

Freshwater and sediment samples were collected from urban streams and wetland of the Geum River watershed in 2019. A total of 37 anaerobic bacteria were isolated using various agar plates made of Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) medium No. 311c, DSMZ medium No. 320, DSMZ medium No. 1451, and reinforced clostridial medium. These agar plates were incubated at 15–25°C under anaerobic condition (BD GasPak EZ Anaerobe Pouch System) for 3–7 days. Isolated bacterial strains were purified by serial dilution spreading and the pure cells were preserved in 20%

(v/v) glycerol suspension containing 10% skimmed milk at  $-80^{\circ}\text{C}$  and as lyophilized ampoules.

Colony morphology of the strains was observed by eye or a magnifying glass after the cells were cultivated to their stationary phase on agar plates. Cellular morphology and cell size were examined by field emission transmission electron microscopy (JEM 2100F; Jeol). Growth in the presence of oxygen was tested by aerobic incubation for seven days. Gram staining was performed using a Gram-staining kit (BD). Biochemical characteristics were evaluated by using API 20NE (bioMérieux) according to the manufacturer's instructions.

Chromosomal DNA extraction, PCR amplification, and 16S rRNA gene sequencing were performed using standard procedures as described elsewhere (Kim *et al.*, 2019). For the determination of 16S rRNA gene sequences, primers 27F, 337F, 518R, 785F, and 1492R were used. Based on full 16S rRNA gene sequences, the closely related type species were obtained using the EzBioCloud server (Yoon *et al.*, 2017). 16S rRNA gene sequences were aligned with the most closely related strains using Clustal W (Thompson *et al.*, 1994). The phylogenetic trees were constructed using neighbor-joining (Saitou & Nei, 1987), maximum likelihood (Felsenstein, 1981), and maximum parsimony methods (Fitch, 1971) in MEGA7 (Kumar *et al.*, 2016) with bootstrap values based on 1,000 randomly generated trees.

## RESULTS AND DISCUSSION

The designation of strains, ID, similarity, and source of isolation are described at Table 1. Thirty-seven strains were distributed into eight classes: two strains in *Alphaproteobacteria*, four strains in *Bacilli*, four strains in *Bacteroidia*, three strains in *Betaproteobacteria*, 16 strains in *Clostridia*, one strain in the *Flavobacteriia*, two strains in *Fusobacteriia*, and five strains in *Gammaproteobacteria*. Unrecorded anaerobic bacterial strains in the eight classes were identified as following species in the order of strain ID (Fig. 1): *Clostridioides manganotii*, *Clostridium botulinum*, *Clostridium lundense* (Cirne *et al.*, 2006), *Pseudogulbenkiania subflava*, *Rhizobium alvei* (Sheu *et al.*, 2015), *Sporacetigenium mesophilum* (Chen *et al.*, 2006), *Terrisporobacter glycolicus* (Collins *et al.*, 1994), *Clostridium huakuii* (Ruan *et al.*, 2014), *Oleomonas sagaranensis*, *Clostridium algidicarnis*, *Clostridium intestinale* (Collins *et al.*, 1994), *Paenibacillus sonchi* (Hong *et al.*, 2009), *Paenibacillus riograndensis*, *Clostridium sartagoforme* (Stackebrandt *et al.*, 1999), *Clostridium gasigenes* (Broda *et al.*, 2000), *Romboutsia sedimentorum* (Wang *et al.*, 2015), *Bacillus benzoovorans*, *Clostridium senegalense* (Mishra *et al.*, 2012), *Clostridi-*

*um aurantibutyricum*, *Acidovorax wautersii*, *Bacteroides luti*, *Flavobacterium tyrosinilyticum* (Du & Yi, 2016), *Lonsdalea britannica* (Brady *et al.*, 2012), *Macellibacteroides fermentans* (Jabari *et al.*, 2012), *Paraclostridium benzoelyticum* (Tushar *et al.*, 2015), *Tolomonas auensis* (Chertkov *et al.*, 2011), *Aeromonas rivipollensis* (Marti & Balcázar, 2015), *Cronobacter dublinensis* subsp. *lausannensis* (Grim *et al.*, 2013), *Cetobacterium somerae* (Finegold *et al.*, 2003), *Aromatoleum toluolicum* (Krieger *et al.*, 1999), *Parabacteroides chartae* (Tan *et al.*, 2012), *Dysgonomonas oryzae* (Kodama *et al.*, 2012), *Clostridium amazonense* (O'Neal *et al.*, 2015), *Clostridium chromiireducens* (Inglett *et al.*, 2011), *Ilyobacter delafieldii*, *Phytobacter diazotrophicus* (Zhang *et al.*, 2008), and *Bacillus endoradicis* (Zhang *et al.*, 2012).

Fourteen strains were isolated from freshwater and the others were isolated from sediment. Based on 16S rRNA gene sequences, phylogenetic position of 37 unrecorded strains is shown in Fig. 2. Detailed physiological and morphological characteristics of the 37 unrecorded bacterial strains determined in present study are given in the following strain descriptions.

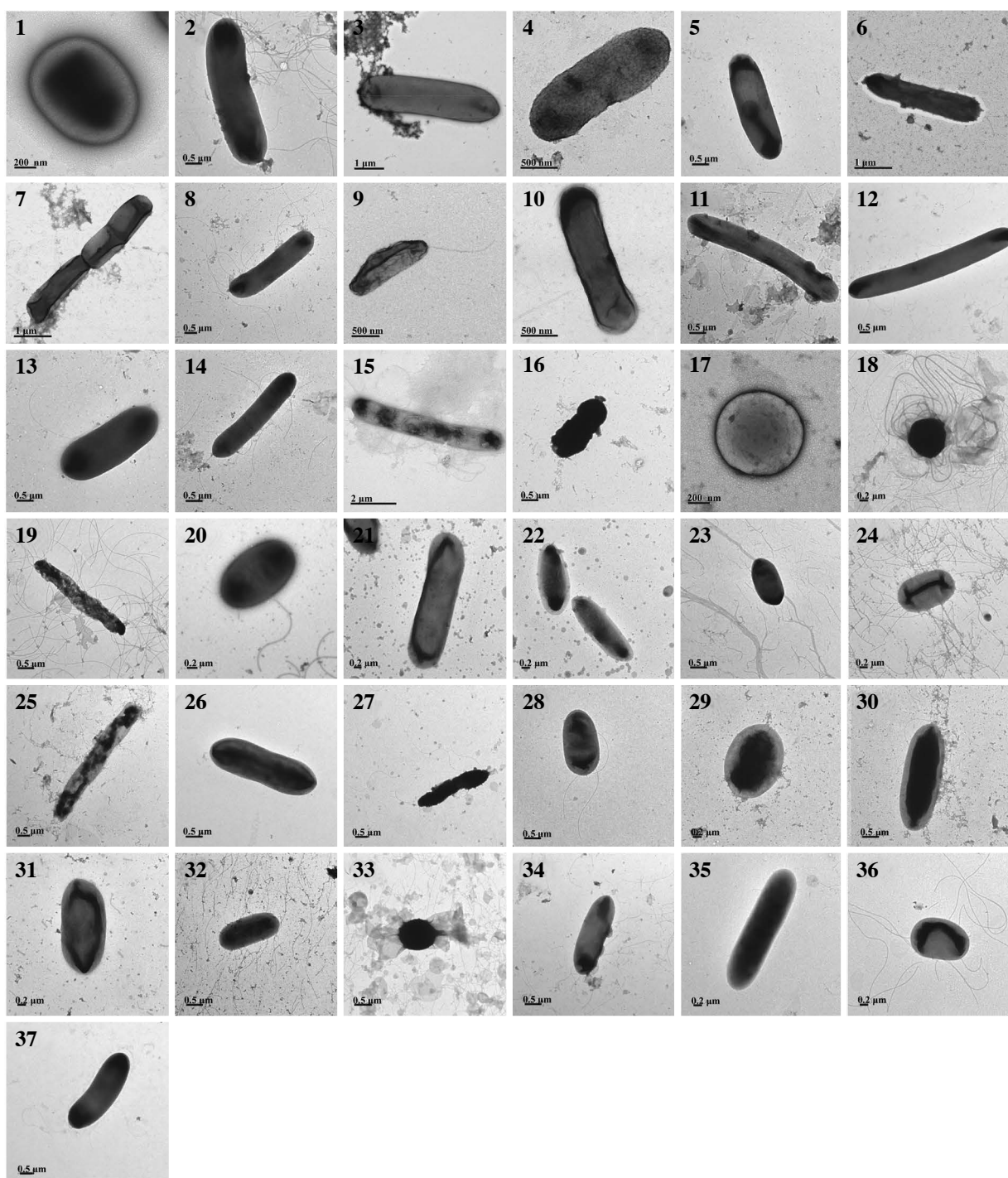
### Description of *Clostridioides manganotii* CBA7501

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and cocci-shaped. Colonies are circular, convex, and entire after incubation for four days on DSMZ medium No. 311c at  $25^{\circ}\text{C}$ . Positive for esculin hydrolysis and gelatinase. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7501 (= NNIBR2019644BA4) was isolated from a sediment sample, Jinan-gun, Jeollabuk-do, Korea.

### Description of *Clostridium botulinum* CBA7502

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are irregular, raised, and entire after incubation for four days on DSMZ medium No. 311c at  $25^{\circ}\text{C}$ . Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7502 (= NNIBR2019644BA41) was isolated from a sediment sample, Jangsu-gun, Jeollabuk-do, Korea.



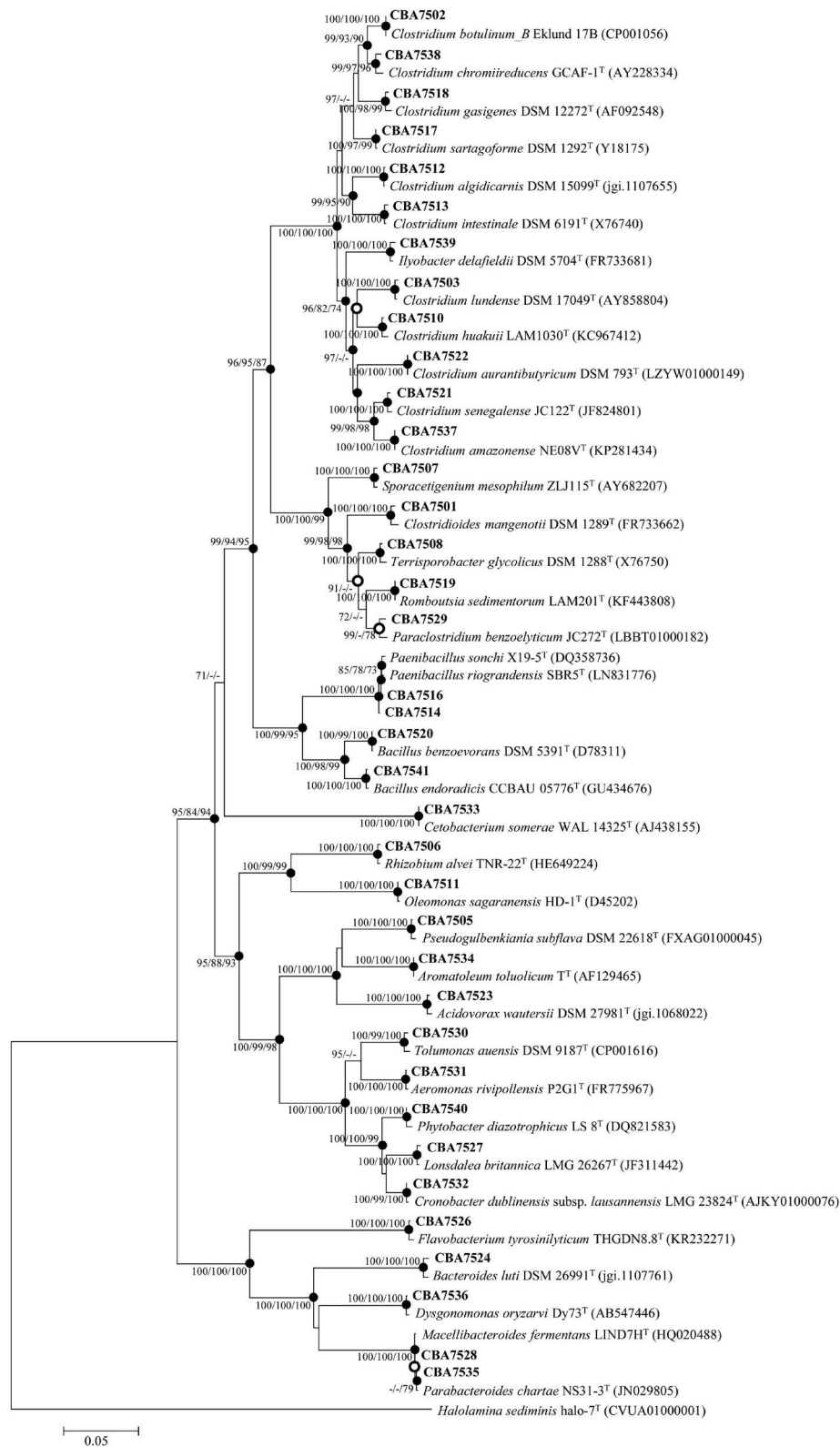


**Fig. 1.** Transmission electron micrographs of cells. Strains: 1, CBA7501; 2, CBA7502; 3, CBA7503; 4, CBA7505; 5, CBA7506; 6, CBA7507; 7, CBA7508; 8, CBA7510; 9, CBA7511; 10, CBA7512; 11, CBA7513; 12, CBA7514; 13, CBA7516; 14, CBA7517; 15, CBA7518; 16, CBA7519; 17, CBA7520; 18, CBA7521; 19, CBA7522; 20, CBA7523; 21, CBA7524; 22, CBA7526; 23, CBA7527; 24, CBA7528; 25, CBA7529; 26, CBA7530; 27, CBA7531; 28, CBA7532; 29, CBA7533; 30, CBA7534; 31, CBA7535; 32, CBA7536; 33, CBA7537; 34, CBA7538; 35, CBA7539; 36, CBA7540; 37, CBA7541.

#### Description of *Clostridium lundense* CBA7503

Cells are obligate anaerobic, Gram-stain-positive, non-

pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for four days on DSMZ medium No. 311c at 25°C. Positive for glucose fermentation



**Fig. 2.** Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study. Bootstrap values (expressed as percentages of 1000 replications) of above 70% are shown at branch points. Filled circles and empty circles indicate nodes recovered by all three or two algorithms (neighbor-joining, maximum likelihood, and maximum parsimony), respectively. *Halolamina sediminis* halo-7<sup>T</sup> (CVUA01000001) was used as an outgroup. Bar, 0.05 substitutions per nucleotide position.

and esculin hydrolysis. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7503 (= NNIBR2019644BA5) was isolated from a sediment sample, Jinan-gun, Jeollabuk-do, Korea.

#### **Description of *Pseudogulbenkiania subflava* CBA7505**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 311c at 25°C. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Utilizes D-glucose, D-maltose, and potassium gluconate. Does not utilize L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7505 (= NNIBR2019644BA6) was isolated from a sediment sample, Dong-gu, Daejeon, Korea.

#### **Description of *Rhizobium alvei* CBA7506**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and curled after incubation for three days on DSMZ medium No. 311c at 25°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7506 (= NNIBR2019644BA7) was isolated from a freshwater sample, Buyeo-gun, Chungcheongnam-do, Korea.

#### **Description of *Sporacetigenium mesophilum* CBA7507**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 311c at 25°C. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7507 (= NNIBR2019644BA8) was iso-

lated from a sediment sample, Buyeo-gun, Chungcheongnam-do, Korea.

#### **Description of *Terrisporobacter glycolicus* CBA7508**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 311c at 25°C. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Utilize D-glucose. Does not utilize L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7508 (= NNIBR2019644BA9) was isolated from a freshwater sample, Jinan-gun, Jeollabuk-do, Korea.

#### **Description of *Clostridium huakuii* CBA7510**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for four days on DSMZ medium No. 311c at 25°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7510 (= NNIBR2019644BA11) was isolated from a freshwater sample, Dong-gu, Daejeon, Korea.

#### **Description of *Oleomonas saganensis* CBA7511**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 320 at 25°C. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7511 (= NNIBR2019644BA12) was isolated from a freshwater sample, Gunsan-si, Jeollabuk-do, Korea.

#### **Description of *Clostridium algidicarnis* CBA7512**

Cells are facultative anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are punctiform, convex, and lobate after incubation for four days

on DSMZ medium No. 311c at 25°C. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7512 (= NNIBR2019644BA13) was isolated from a sediment sample, Dong-gu, Daejeon, Korea.

#### **Description of *Clostridium intestinale* CBA7513**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for four days on DSMZ medium No. 1451 at 15°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Utilizes D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, and malic acid. Does not utilize L-arabinose, potassium gluconate, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain CBA7513 (= NNIBR2019644BA14) was isolated from a sediment sample, Jangsu-gun, Jeollabuk-do, Korea.

#### **Description of *Paenibacillus sonchi* CBA7514**

Cells are facultative anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, umbonate, and entire after incubation for three days on DSMZ medium No. 1451 at 15°C. Positive for glucose fermentation and esculin hydrolysis. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Utilizes D-mannitol, potassium gluconate, D-maltose, and adipic acid. Does not utilize D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, capric acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7514 (= NNIBR2019644BA15) was isolated from a sediment sample, Dong-gu, Daejeon, Korea.

#### **Description of *Paenibacillus riograndensis* CBA7516**

Cells are facultative anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 1451 at 15°C. Positive for glucose fermentation, esculin hydrolysis, and  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, and gelatinase. Utilizes L-arabinose, *N*-acetyl-glucosamine, potassium gluconate, and D-maltose. Does not utilize D-glucose, D-mannose, D-mannitol, capric acid, adipic acid, malic acid, trisodium

citrate, and phenylacetic acid. Strain CBA7516 (= NNIBR2019644BA16) was isolated from a sediment sample, Dong-gu, Daejeon, Korea.

#### **Description of *Clostridium sartagoforme* CBA7517**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for four days on DSMZ medium No. 1451 at 15°C. Positive for glucose fermentation and esculin hydrolysis. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Utilizes D-glucose, D-mannitol, *N*-acetyl-glucosamine, and D-maltose. Does not utilize L-arabinose, D-mannose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7517 (= NNIBR2019644BA17) was isolated from a sediment sample, Buyeo-gun, Chungcheongnam-do, Korea.

#### **Description of *Clostridium gasigenes* CBA7518**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for four days on DSMZ medium No. 320 at 15°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Utilize D-mannitol. Does not utilize D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7518 (= NNIBR2019644BA18) was isolated from a freshwater sample, Buyeo-gun, Chungcheongnam-do, Korea.

#### **Description of *Romboutsia sedimentorum* CBA7519**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are irregular, convex, and undulate after incubation for three days on DSMZ medium No. 1451 at 25°C. Positive for glucose fermentation. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7519 (= NNIBR2019644BA19) was isolated from a sediment sample, Jangsu-gun, Jeollabuk-do, Korea.

#### **Description of *Bacillus benzeovorans* CBA7520**

Cells are facultative anaerobic, Gram-stain-positive, non-pigmented, and cocci-shaped. Colonies are circular,

umbonate, and entire after incubation for three days on DSMZ medium No. 1451 at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Utilizes L-arabinose, D-mannitol, and adipic acid. Does not utilize D-glucose, D-mannose, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7520 (= NNIBR2019644BA20) was isolated from a sediment sample, Buyeo-gun, Chungcheongnam-do, Korea.

#### **Description of *Clostridium senegalense* CBA7521**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and cocci-shaped. Colonies are irregular, convex, and undulate after incubation for four days on reinforced clostridial medium at 25°C. Positive for glucose fermentation and gelatinase. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7521 (= NNIBR2019644BA21) was isolated from a sediment sample, Buyeo-gun, Chungcheongnam-do, Korea.

#### **Description of *Clostridium aurantibutyricum* CBA7522**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for four days on DSMZ medium No. 311c at 25°C. Positive for glucose fermentation, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, arginine dihydrolase, and urease. Utilizes D-glucose and D-mannose. Does not utilize L-arabinose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7522 (= NNIBR2019644BA22) was isolated from a sediment sample, Jinan-gun, Jeollabuk-do, Korea.

#### **Description of *Acidovorax wautersii* CBA7523**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and short rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 320 at 25°C. Positive for nitrate reduction and glucose fermentation. Negative for indole production, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Utilizes D-mannitol, malic acid, and trisodium citrate. Does not

utilize D-glucose, L-arabinose, D-mannose, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, and phenylacetic acid. Strain CBA7523 (= NNIBR2019644BA23) was isolated from a freshwater sample, Dong-gu, Daejeon, Korea.

#### **Description of *Bacteroides luti* CBA7524**

Cells are obligate anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for seven days on DSMZ medium No. 311c at 25°C. Positive for  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7524 (= NNIBR2019644BA24) was isolated from a freshwater sample, Jangsu-gun, Jeollabuk-do, Korea.

#### **Description of *Flavobacterium tyrosinilyticum* CBA7526**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 320 at 25°C. Positive for glucose fermentation, esculin hydrolysis, and  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, and gelatinase. Utilize capric acid. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7526 (= NNIBR2019644BA26) was isolated from a freshwater sample, Jangsu-gun, Jeollabuk-do, Korea.

#### **Description of *Lonsdalea britannica* CBA7527**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 311c at 25°C. Positive for glucose fermentation and esculin hydrolysis. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Utilize capric acid. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7527 (= NNIBR2019644BA27) was isolated from a freshwater sample, Dong-gu, Daejeon, Korea.



**Description of *Macellibacteroides fermentans* CBA7528**

Cells are facultative anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, umbonate, and entire after incubation for three days on DSMZ medium No. 1451 at 25°C. Positive for nitrate reduction, glucose fermentation, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Negative for indole production, arginine dihydrolase, and urease. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7528 (=NNIBR2019644BA28) was isolated from a sediment sample, Jangsu-gun, Jeollabuk-do, Korea.

**Description of *Paraclostridium benzoelyticum* CBA7529**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are irregular, flat, and curled after incubation for three days on reinforced clostridial medium at 25°C. Positive for glucose fermentation. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7529 (=NNIBR2019644BA29) was isolated from a sediment sample, Jangsu-gun, Jeollabuk-do, Korea.

**Description of *Tolumonas auensis* CBA7530**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 1451 at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7530 (=NNIBR2019644BA30) was isolated from a sediment sample, Dong-gu, Daejeon, Korea.

**Description of *Aeromonas rivipollensis* CBA7531**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 311c at 25°C. Positive for glucose

fermentation. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7531 (=NNIBR2019644BA31) was isolated from a freshwater sample, Dong-gu, Daejeon, Korea.

**Description of *Cronobacter dublinensis* subsp. *lausannensis* CBA7532**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, pulvinate, and entire after incubation for three days on DSMZ medium No. 311c at 25°C. Positive for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Negative for urease. Utilizes potassium gluconate, malic acid, and trisodium citrate. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, capric acid, adipic acid, and phenylacetic acid. Strain CBA7532 (=NNIBR2019644BA32) was isolated from a freshwater sample, Dong-gu, Daejeon, Korea.

**Description of *Cetobacterium somerae* CBA7533**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and cocci-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 320 at 25°C. Positive for glucose fermentation, esculin hydrolysis, and  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, and gelatinase. Utilize capric acid. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7533 (=NNIBR2019644BA33) was isolated from a freshwater sample, Dong-gu, Daejeon, Korea.

**Description of *Aromatoleum toluolicum* CBA7534**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 320 at 25°C. Positive for nitrate reduction and glucose fermentation. Negative for indole production, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate,

and phenylacetic acid. Strain CBA7534 (= NNIBR2019644BA34) was isolated from a sediment sample, Dong-gu, Daejeon, Korea.

#### **Description of *Parabacteroides chartae* CBA7535**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on reinforced clostridial medium at 25°C. Positive for glucose fermentation, esculin hydrolysis, and  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7535 (= NNIBR2019644BA35) was isolated from a sediment sample, Jangsu-gun, Jeollabuk-do, Korea.

#### **Description of *Dysgonomonas oryzae* CBA7536**

Cells are obligate anaerobic, Gram-stain-negative, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 311c at 25°C. Positive for glucose fermentation, esculin hydrolysis, and  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7536 (= NNIBR2019644BA36) was isolated from a sediment sample, Jangsu-gun, Jeollabuk-do, Korea.

#### **Description of *Clostridium amazonense* CBA7537**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and cocci-shaped. Colonies are irregular, convex, and lobate after incubation for four days on reinforced clostridial medium at 25°C. Positive for  $\beta$ -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatinase. Utilize capric acid. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7537 (= NNIBR2019644BA37) was isolated from a freshwater sample, Dong-gu, Daejeon, Korea.

#### **Description of *Clostridium chromireducens* CBA7538**

Cells are obligate anaerobic, Gram-stain-positive, non-

pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for four days on DSMZ medium No. 311c at 25°C. Positive for glucose fermentation. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7538 (= NNIBR2019644BA38) was isolated from a sediment sample, Jangsu-gun, Jeollabuk-do, Korea.

#### **Description of *Ilyobacter delafieldii* CBA7539**

Cells are obligate anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 1451 at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7539 (= NNIBR2019644BA39) was isolated from a sediment sample, Dong-gu, Daejeon, Korea.

#### **Description of *Phytobacter diazotrophicus* CBA7540**

Cells are facultative anaerobic, Gram-stain-negative, non-pigmented, and short rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 1451 at 25°C. Positive for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, gelatinase, and  $\beta$ -galactosidase activity. Negative for arginine dihydrolase and urease. Utilizes D-mannitol, potassium gluconate, malic acid, and trisodium citrate. Does not utilize D-glucose, L-arabinose, D-mannose, N-acetyl-glucosamine, D-maltose, capric acid, adipic acid, and phenylacetic acid. Strain CBA7540 (= NNIBR2019644BA40) was isolated from a freshwater sample, Dong-gu, Daejeon, Korea.

#### **Description of *Bacillus endoradicis* CBA7541**

Cells are facultative anaerobic, Gram-stain-positive, non-pigmented, and rod-shaped. Colonies are circular, convex, and entire after incubation for three days on DSMZ medium No. 320 at 25°C. Positive for glucose fermentation and esculin hydrolysis. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatinase, and  $\beta$ -galactosidase activity. Utilizes D-glucose, L-arabinose, D-mannose, N-acetyl-glucosamine, and D-maltose. Does not utilize D-mannitol, potassium

gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CBA7541 (=NNIBR2019644BA42) was isolated from a sediment sample, Jangsu-gun, Jeollabuk-do, Korea.

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## REFERENCES

- Brady, C.L., I. Cleenwerck, S. Denman, S.N. Venter, P. Rodríguez-Palenzuela, T.A. Coutinho and P. De Vos. 2012. Proposal to reclassify *Brenneria quercina* (Hildebrand and Schroth 1967) Hauben *et al.* 1999 into a new genus, *Lonsdalea* gen. nov., as *Lonsdalea quercina* comb. nov., descriptions of *Lonsdalea quercina* subsp. *quercina* comb. nov., *Lonsdalea quercina* subsp. *iberica* subsp. nov. and *Lonsdalea quercina* subsp. *britannica* subsp. nov., emendation of the description of the genus *Brenneria*, reclassification of *Dickeya dieffenbachiae* as *Dickeya dadantii* subsp. *dieffenbachiae* comb. nov., and emendation of the description of *Dickeya dadantii*. *International Journal of Systematic and Evolutionary Microbiology* 62(7):1592-1602.
- Broda, D., D. Saul, P. Lawson, R. Bell and D. Musgrave. 2000. *Clostridium gasigenes* sp. nov., a psychrophile causing spoilage of vacuum-packed meat. *International Journal of Systematic and Evolutionary Microbiology* 50(1):107-118.
- Buck, M. and C. Hamilton. 2011. The Nagoya Protocol on access to genetic resources and the fair and equitable sharing of benefits arising from their utilization to the Convention on Biological Diversity. *Review of European Community & International Environmental Law* 20(1):47-61.
- Chen, S., L. Song and X. Dong. 2006. *Sporacetigenium mesophilum* gen. nov., sp. nov., isolated from an anaerobic digester treating municipal solid waste and sewage. *International Journal of Systematic and Evolutionary Microbiology* 56(4):721-725.
- Chertkov, O., A. Copeland, S. Lucas, A. Lapidus, K.W. Berry, J.C. Detter, T.G. Del Rio, N. Hammon, E. Dalin and H. Tice. 2011. Complete genome sequence of *Tolomonas auensis* type strain (TA 4<sup>T</sup>). *Standards in Genomic Sciences* 5(1):112.
- Cirne, D.G., O.D. Delgado, S. Marichamy and B. Mattiasson. 2006. *Clostridium lundense* sp. nov., a novel anaerobic lipolytic bacterium isolated from bovine rumen. *International Journal of Systematic and Evolutionary Microbiology* 56(3):625-628.
- Collins, M., P. Lawson, A. Willems, J. Cordoba, J. Fernandez-Garayzabal, P. Garcia, J. Cai, H. Hippe and J. Farrow. 1994. The phylogeny of the genus *Clostridium*: proposal of five new genera and eleven new species combinations. *International Journal of Systematic and Evolutionary Microbiology* 44(4):812-826.
- Du, J. and T.-H. Yi. 2016. *Flavobacterium tyrosinilyticum* sp. nov., isolated from the rhizosphere of wild strawberry. *International Journal of Systematic and Evolutionary Microbiology* 66(7):2629-2634.
- Felsenstein, J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. *Journal of Molecular Evolution* 17(6):368-376.
- Finegold, S.M., M.-L. Vaisanen, D.R. Molitoris, T.J. Tomzynski, Y. Song, C. Liu, M.D. Collins and P.A. Lawson. 2003. *Cetobacterium somerae* sp. nov. from human feces and emended description of the genus *Cetobacterium*. *Systematic and Applied Microbiology* 26(2):177-181.
- Fitch, W.M. 1971. Toward defining the course of evolution: minimum change for a specific tree topology. *Systematic Biology* 20(4):406-416.
- Grim, C.J., M.L. Kotewicz, K.A. Power, G. Gopinath, A.A. Franco, K.G. Jarvis, Q.Q. Yan, S.A. Jackson, V. Sathyamoorthy and L. Hu. 2013. Pan-genome analysis of the emerging foodborne pathogen *Cronobacter* spp. suggests a species-level bidirectional divergence driven by niche adaptation. *BMC Genomics* 14(1):366.
- Hong, Y.-Y., Y.-C. Ma, Y.-G. Zhou, F. Gao, H.-C. Liu and S.-F. Chen. 2009. *Paenibacillus sonchi* sp. nov., a nitrogen-fixing species isolated from the rhizosphere of *Sonchus oleraceus*. *International Journal of Systematic and Evolutionary Microbiology* 59(11):2656-2661.
- Inglett, K., H. Bae, H. Aldrich, K. Hatfield and A. Ogram. 2011. *Clostridium chromiireducens* sp. nov., isolated from Cr(VI)-contaminated soil. *International Journal of Systematic and Evolutionary Microbiology* 61(11):2626-2631.
- Jabari, L., H. Gannoun, J.-L. Cayol, A. Hedi, M. Sakamoto, E. Falsen, M. Ohkuma, M. Hamdi, G. Fauque and B. Ollivier. 2012. *Macellibacteroides fermentans* gen. nov., sp. nov., a member of the family *Porphyromonadaceae* isolated from an upflow anaerobic filter treating abattoir wastewaters. *International Journal of Systematic and Evolutionary Microbiology* 62(10):2522-2527.
- Kim, J., J.Y. Kim, H.S. Song, I.-T. Cha, S.W. Roh and S.H. Lee. 2019. *Paracoccus jeotgali* sp. nov., isolated from Korean salted and fermented shrimp. *Journal of Microbiology* 57(6):444-449.
- Kodama, Y., T. Shimoyama and K. Watanabe. 2012. *Dysgonomonas oryzae* sp. nov., isolated from a microbial fuel cell. *International Journal of Systematic and Evolutionary Microbiology* 62(12):3055-3059.
- Krieger, C.J., H.R. Beller, M. Reinhard and A.M. Spormann. 1999. Initial reactions in anaerobic oxidation of m-xylene by the denitrifying bacterium *Azoarcus* sp. strain T.

- Journal of Bacteriology 181(20):6403-6410.
- Kumar, S., G. Stecher and K. Tamura. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution* 33(7):1870-1874.
- Marti, E. and J.L. Balcázar. 2015. *Aeromonas rivipollensis* sp. nov., a novel species isolated from aquatic samples. *Journal of Basic Microbiology* 55(12):1435-1439.
- Mishra, A.K., J.-C. Lagier, C. Robert, D. Raoult and P.-E. Fournier. 2012. Non-contiguous finished genome sequence and description of *Clostridium senegalense* sp. nov. *Standards in Genomic Sciences* 6(3):386.
- National species list of Korea. 2019. National Institute of Biological Resources, online at <http://www.kbr.go.kr>, accessed on 1 April 2020.
- O'Neal, L., A.J. Obregón-Tito, R.Y. Tito, A.T. Ozga, S.I. Polo, C.M. Lewis Jr and P.A. Lawson. 2015. *Clostridium amazonense* sp. nov. an obligately anaerobic bacterium isolated from a remote Amazonian community in Peru. *Anaerobe* 35:33-37.
- Ruan, Z., Y. Wang, C. Zhang, J. Song, Y. Zhai, Y. Zhuang, H. Wang, X. Chen, Y. Li and B. Zhao. 2014. *Clostridium huakuii* sp. nov., an anaerobic, acetogenic bacterium isolated from methanogenic consortia. *International Journal of Systematic and Evolutionary Microbiology* 64(12):4027-4032.
- Saitou, N. and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4(4):406-425.
- Sheu, S.-Y., H.-W. Huang, C.-C. Young and W.-M. Chen. 2015. *Rhizobium alvei* sp. nov., isolated from a freshwater river. *International Journal of Systematic and Evolutionary Microbiology* 65(2):472-478.
- Stackebrandt, E., I. Kramer, J. Swiderski and H. Hippe. 1999. Phylogenetic basis for a taxonomic dissection of the genus *Clostridium*. *FEMS Immunology & Medical Microbiology* 24(3):253-258.
- Tan, H.-Q., T.-T. Li, C. Zhu, X.-Q. Zhang, M. Wu and X.-F. Zhu. 2012. *Parabacteroides chartae* sp. nov., an obligately anaerobic species from wastewater of a paper mill. *International Journal of Systematic and Evolutionary Microbiology* 62(11):2613-2617.
- Thompson, J.D., D.G. Higgins and T.J. Gibson. 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Research* 22(22):4673-4680.
- Tushar, L., T.S. Jyothsna, C. Sasikala and C. Ramana. 2015. Draft genome sequence of antimicrobial-producing *Clostridium* sp. JC272, isolated from marine sediment. *Genome Announc.* 3(3):e00650-15.
- Wang, Y., J. Song, Y. Zhai, C. Zhang, J. Gerritsen, H. Wang, X. Chen, Y. Li, B. Zhao and B. Zhao. 2015. *Romboutsia sedimentorum* sp. nov., isolated from an alkaline-saline lake sediment and emended description of the genus *Romboutsia*. *International Journal of Systematic and Evolutionary Microbiology* 65(4):1193-1198.
- Yoon, S.-H., S.-M. Ha, S. Kwon, J. Lim, Y. Kim, H. Seo and J. Chun. 2017. Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. *International Journal of Systematic and Evolutionary Microbiology* 67(5):1613.
- Zhang, G.X., G.X. Peng, E.T. Wang, H. Yan, Q.H. Yuan, W. Zhang, X. Lou, H. Wu and Z.Y. Tan. 2008. Diverse endophytic nitrogen-fixing bacteria isolated from wild rice *Oryza rufipogon* and description of *Phytobacter diazotrophicus* gen. nov. sp. nov. *Archives of Microbiology* 189(5):431-439.
- Zhang, Y.Z., W.F. Chen, M. Li, X.H. Sui, H.-C. Liu, X.X. Zhang and W.X. Chen. 2012. *Bacillus endoradicis* sp. nov., an endophytic bacterium isolated from soybean root. *International Journal of Systematic and Evolutionary Microbiology* 62(2):359-363.

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