

Register list for 16 new names including *Andeanibacterium* gen. nov.

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Genus *Andeanibacterium*

Etymology

[An.de.a.ni.bac.te'ri.um] N.L. masc. adj. *andeanus*, pertaining to the Andes; N.L. neut. n. *bacterium*, small rod; N.L. neut. n. *Andeanibacterium*, Andean rod

Nomenclatural type

Species *Andeanibacterium colombiense*^{Ts}

Description

A genus established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction, and phylogenomic analyses and is classified as a member of the *Sphingomonadaceae* family. Genomic metrics include ANI (79.88), AAI (61.59) and dDDH d4 (20.1). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 54 CAZymes, 15 of them involved in lignocellulose degradation. In addition, putative genes for PET hydrolysis were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Sphingomonadales* » *Sphingomonadaceae* » *Andeanibacterium*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24097>

Species *Andeanibacterium colombiense*^{Ts}

Etymology

[co.lom.bi.en'se.] N.L. neut. adj. *colombiense*, belonging to Colombia

Nomenclatural type

[INSDC Nucleotide: CP119316](#)^{Ts}

Description

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction, and phylogenomic analyses and is classified as a member of the *Sphingomonadaceae* family. The type species of the genus is *Andeanibacterium colombiense*. Genomic metrics include ANI (79.88), AAI (61.59) and dDDH d4 (20.1). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 54 CAZymes, 15 of them involved in lignocellulose degradation. In addition, putative genes for PET hydrolysis were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Sphingomonadales* » *Sphingomonadaceae* » *Andeanibacterium* » *Andeanibacterium colombiense*^{Ts}

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:31306>

Species *Pedobacter colombiensis*

Etymology

[co.lom.bi.en'sis] **N.L. masc. adj.** *colombiensis*, belonging to Colombia

Nomenclatural type

[INSDC Nucleotide: CP119313](#) ^{Ts}

Description

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_3858. Genomic metrics include ANI (81.7), AAI (81.02) and dDDH d4 (29.6). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 254 CAZymes, 63 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolisis were found within the MAG.

Classification

Bacteria » *Bacteroidota* » *Sphingobacteriia* » *Sphingobacteriales* » *Sphingobacteriaceae* » *Pedobacter* » *Pedobacter colombiensis*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24104>

Species *Pseudomonas colombiensis*

Etymology

[co.lom.bi.en'sis] **N.L. fem. adj.** *colombiensis*, belonging to Colombia

Nomenclatural type

[INSDC Nucleotide: CP119322](#) ^{Ts}

Description

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_425. Genomic metrics include ANI (86.68), AAI (86.03) and dDDH d4 (29.3). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 103 CAZymes, 19 of them involved in lignocellulose degradation. In addition, putative genes for PUR hydrolisis were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Gammaproteobacteria* » *Moraxellales* » *Pseudomonadaceae* » *Pseudomonas* » *Pseudomonas colombiensis*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24106>

Species *Sphingomonas colombiensis*

Etymology

[co.lom.bi.en'sis] **N.L. fem. adj.** *colombiensis*, belonging to Colombia

Nomenclatural type[INSDC Nucleotide: CP119315](#)^{Ts}**Description**

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_27. Genomic metrics include ANI (85.46), AAI (66.97) and dDDH d4 (20.8). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 59 CAZymes, 10 of them involved in lignocellulose degradation. In addition, putative genes for PET hydrolysis were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Sphingomonadales* » *Sphingomonadaceae* » *Sphingomonas* » *Sphingomonas colombiensis*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL<https://seqco.de/i:24102>

Species *Kaistia colombiensis*

Etymology

[co.lom.bi.en'sis] N.L. fem. adj. *colombiensis*, belonging to Colombia

Nomenclatural type[INSDC Nucleotide: CP119318](#)^{Ts}**Description**

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_2176. Genomic metrics include ANI (86.41), AAI (77.29) and dDDH d4 (28.1). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 95 CAZymes, 18 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Hyphomicrobiales* » *Kaistiaceae* » *Kaistia* » *Kaistia colombiensis*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL<https://seqco.de/i:24101>

Species *Microbacterium colombiense*

Etymology

[co.lom.bi.en'se.] N.L. neut. adj. *colombiense*, belonging to Colombia

Nomenclatural type[INSDC Nucleotide: CP119308](#)^{Ts}**Description**

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_1911. Genomic metrics include ANI (85.9), AAI (81.1) and dDDH d4 (28.3). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 82 CAZymes, 30 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.

Classification

Bacteria » *Actinomycetota* » *Actinobacteria* » *Micrococcales* » *Microbacteriaceae* » *Microbacterium* » *Microbacterium colombiense*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24100>

Species *Pseudobacter hemicellulosilyticus*

Etymology

[he.mi.cel.lu.lo.si.ly'ti.cus] N.L. neut. n. *hemicellulosum*, hemicellulose; N.L. masc. adj. *lyticus*, able to dissolve; N.L. masc. adj. *hemicellulosilyticus*, hemicellulose dissolving

Nomenclatural type

[INSDC Nucleotide: CP119311](#)^{Ts}

Description

The species is established on the basis of MiGA taxonomic novelty analysis, the taxonomic placement using maximum likelihood trees with 120 bacterial marker genes (bac120) and the type material is the genome MAG_7. Genomic metrics include ANI (69.21), AAI (65.96) and dDDH d4 (22.1). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 237 CAZymes, 99 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.

Classification

Bacteria » *Bacteroidota* » *Chitinophagia* » *Chitinophagales* » *Chitinophagaceae* » *Pseudobacter* » *Pseudobacter hemicellulosilyticus*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24095>

Species *Sphingomonas phytovorans*

Etymology

[phy.to.vo'rans.] Gr. neut. n. *phyton*, plant; L. pres. part. *vorans*, devouring, destroying; N.L. fem. part. adj. *phytvorans*, plant-devouring

Nomenclatural type

[INSDC Nucleotide: CP119314](#)^{Ts}

Description

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_3606. Genomic metrics include ANI (80.99), AAI (80.97) and dDDH d4 (22.2). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 95 CAZymes, 29 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Sphingomonadales* » *Sphingomonadaceae* » *Sphingomonas* » *Sphingomonas phytovorans*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL<https://seqco.de/i:24103>

Species *Devosia phytovorans*

Etymology

[phy.to.vo'rans.] Gr. neut. n. *phyton*, plant; L. pres. part. *vorans*, devouring, destroying; N.L. fem. part. adj. *phytvorans*, plant-devouring

Nomenclatural type[INSDC Nucleotide: CP119312](#) ^{Ts}**Description**

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_4196. Genomic metrics include ANI (84.84), AAI (74.37) and dDDH d4 (23.5). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 90 CAZymes, 17 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolisis were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Hyphomicrobiales* » *Devosiaceae* » *Devosia* » *Devosia phytovorans*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL<https://seqco.de/i:24105>

Species *Microbacterium phytovorans*

Etymology

[phy.to.vo'rans.] Gr. neut. n. *phyton*, plant; L. pres. part. *vorans*, devouring, destroying; N.L. neut. part. adj. *phytvorans*, plant-devouring

Nomenclatural type[INSDC Nucleotide: CP119321](#) ^{Ts}**Description**

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_4610. Genomic metrics include ANI (82.28), AAI (73.07) and dDDH d4 (21.5). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 74 CAZymes, 31 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolisis were found within the MAG.

Classification

Bacteria » *Actinomycetota* » *Actinobacteria* » *Micrococcales* » *Microbacteriaceae* » *Microbacterium* » *Microbacterium phytovorans*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL<https://seqco.de/i:24107>

Species *Cohnella colombiensis*

Etymology

[co.lom.bi.en'sis] N.L. fem. adj. *colombiensis*, belonging to Colombia

Nomenclatural type

[INSDC Nucleotide: CP119317.1](#)^{Ts}

Description

The species is established on the basis of MiGA taxonomic novelty analysis, the taxonomic placement using maximum likelihood trees with 120 bacterial marker genes (bac120) and the type material is the genome MAG_2441. Genomic metrics include ANI (67.06), AAI (67.21) and dDDH d4 (30.4). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 149 CAZymes, 44 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.

Classification

Bacteria » *Bacillota* » *Bacilli* » *Caryophanales* » *Paenibacillaceae* » *Cohnella* » *Cohnella colombiensis*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24096>

Species *Brevundimonas colombiensis*

Etymology

[co.lom.bi.en'sis] N.L. fem. adj. *colombiensis*, belonging to Colombia

Nomenclatural type

[INSDC Nucleotide: CP119326.1](#)^{Ts}

Description

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_833. Genomic metrics include ANI (87.3), AAI (82.62) and dDDH d4 (29.7). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 73 CAZymes, 13 of them involved in lignocellulose degradation. In addition, putative genes for protocatechuate and phtalate catabolism were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Caulobacterales* » *Caulobacteraceae* » *Brevundimonas* » *Brevundimonas colombiensis*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24108>

Species *Brevundimonas phytovorans*

Etymology

[phy.to.vo'rans.] Gr. neut. n. *phyton*, plant; L. pres. part. *vorans*, devouring, destroying; N.L. fem. part. adj. *phytovorans*, plant-devouring

Nomenclatural type

[INSDC Nucleotide: CP119309.1](#)^{Ts}

Description

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_1865. Genomic metrics include ANI (91.28), AAI (87.92) and dDDH d4 (40.3). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 39 CAZymes, 6 of them involved in lignocellulose degradation. In addition, putative genes for protocatechuate and phthalate catabolism were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Caulobacterales* » *Caulobacteraceae* » *Brevundimonas* » *Brevundimonas phytovorans*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24099>

Species *Chryseobacterium colombiense*

Etymology

[co.lom.bi.en'se.] N.L. neut. adj. *colombiense*, belonging to Colombia

Nomenclatural type

[INSDC Nucleotide: CP119310.1](#)^{Ts}

Description

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_1654. Genomic metrics include ANI (88.96), AAI (95) and dDDH d4 (36.2). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 139 CAZymes, 41 of them involved in lignocellulose degradation. In addition, putative genes for PUR hydrolysis were found within the MAG.

Classification

Bacteria » *Bacteroidota* » *Flavobacteriia* » *Flavobacteriales* » *Weeksellaceae* » *Chryseobacterium* » *Chryseobacterium colombiense*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24098>

Species *Pseudomonas phytovorans*

Etymology

[phy.to.vo'rans.] Gr. neut. n. *phyton*, plant; L. pres. part. *vorans*, devouring, destroying; N.L. fem. part. adj. *phytovorans*, plant-devouring

Nomenclatural type

[INSDC Nucleotide: CP119325.1](#)^{Ts}

Description

A genus established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_876. Genomic metrics include ANI (92.18), AAI (95) and dDDH d4 (47). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 87 CAZymes, 16 of them involved in lignocellulose degradation. In addition, putative genes for PUR hydrolysis were found within the MAG.

Classification

Bacteria » Pseudomonadota » Gammaproteobacteria » Moraxellales » Pseudomonadaceae » Pseudomonas » Pseudomonas phytovorans

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

<https://seqco.de/i:24109>

References

1. Díaz-García et al. (2024). Andean soil-derived lignocellulolytic bacterial consortium as a source of novel taxa and putative plastic-active enzymes. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2023.126485

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List seqco.de/r:-kiq_w89 submitted by Díaz-García, Laura and including 16 new names has been successfully validated.

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