Register list for 17 new names including Skiveiella danica sp. nov.

Submitted by Fischer Petersen, Jette

Genus *Aalborgicola*

Etymology

[Aal.bor.gi'co.la] **N. L. neut. n.** *Aalborg*, the city of Aalborg; **L. suff.** *-cola*, inhabitant; **N.L. masc. n.** *Aalborgicola*, an inhabitant of Aalborg

Nomenclatural type

Species *Aalborgicola defluviihabitans*^{Ts}

Description

Genus of species found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
Most species are predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta*.
All species (except Aalborgicola danicus) have the potential to reduce nitrate with *narGHI* along with the reduction of nitrate to nitric oxide with *nirS*. Lastly it also had nitrous oxide reductase, *nosZ* predicted.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Aalborgicola*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44106

Genus *Aalborgiella*

Etymology

[Aal.bor.gi.el'la] **N.L. fem. dim. n.** *Aalborgiella*, bacterium named after the city Aalborg where the MAG had been retrieved

Nomenclatural type

Species *Aalborgiella aggregata*^{Ts}

Description

Genus of rod shaped bacteria found in activated sludge. Type species is Aalborgiella aggregata.
Type species(Aalborgiella aggregata) is a rod shaped bacterium (1.4± 0.3 x 0.4±0.1 µm) abundant in activated sludge globally. Based on FISH analysis it seems to grow along filaments in activated sludge.
Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for transportation of branched amino acids.
Presence of *narGHI* genes showed potential to reduce nitrate.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Aalborgiella*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44101

Genus *Defluviibacillus*

Etymology

[De.flu.vi.i.ba.ci'llus] **L. neut. n.** *defluvium*, sewage; **L. masc. n.** *bacillus*, rod-shaped bacterium; **N.L. masc. n.** *Defluviibacillus*, indicating a rod-shaped bacterium from sewage

Nomenclatural type

Species *Defluviibacillus avedoerensis*$^{\mathrm{Ts}}$

Description

A genus of rod shaped bacteria found in activated sludge. Type species is Defluviibacillus avedoerensis.
The type species is a rod shaped bacteria (2.1± 0.4 x 0.6±0.1 µm) abundant in activated sludge globally.
Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for transportation of polar amino acids and branched amino acids.
Presence of *narGHI* genes showed potential to reduce nitrate along with potential for further conversion via *norB* . It also had the potential to reduce nitrite to nitric oxide via nitrite reductase, *nirS.*
Defluviibacillus avedoerensis had predicted all genes of the three pathways (polyP, glycogen and PHA) associated with Pao metabolism.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Defluviibacillus*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44099

Genus *Egaibacter*

Etymology

[E.ga.i.bac'ter] **N. L. masc. n.** *Egaa*, the city Egaa where the MAG had been retrieved; **N.L. masc. n.** *bacter*, bacterium; **N.L. masc. n.** *Egaibacter*, indicating a bacterium found in Egaa

Nomenclatural type

Species *Egaibacter danicus*$^{\mathrm{Ts}}$

Description

Genus of bacteria found in activated sludge.
Species generally have the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
They can also utilize branched chain amino acids (livFGHKM).
Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*.
Potential to reduce nitrate with narGHI along with the reduction of nitrate to nitric oxide with nirS.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Egaibacter*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44121

Genus *Skiveiella*

Etymology
[Ski.ve.i.el'la] **N.L. fem. dim. n.** *Skiveiella*, named after the city Skive where the MAG had been retrieved

Nomenclatural type
Species *Skiveiella danica*Ts

Description
Genus found in actived sludge. Type species is Skiveiella danica

Classification
Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Skiveiella*

References
Effective publication: Petersen et al., 2025 [1]

Registry URL
https://seqco.de/i:44104

Species *Aalborgicola bjergmarkensis*

Etymology
[bjerg.mar.ken'sis] **N.L. masc. adj.** *bjergmarkensis*, of the city of Bjergmarken, from where the MAG was obtained

Nomenclatural type
NCBI Assembly: GCA_016708725.1 Ts

Description
Bacterium found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
The *gtsABC+malK* transporters of of glucose uptake was also predicted.

Potential to reduce nitrate with narGHI. Lastly it also had nitrous oxide reductase, nosZ predicted.

Classification
Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Aalborgicola* » *Aalborgicola bjergmarkensis*

References
Effective publication: Petersen et al., 2025 [1]

Registry URL
https://seqco.de/i:44112

Species *Aalborgicola danicus*

Etymology

[da'ni.cus] **L. masc. adj.** *danicus*, Danish

Nomenclatural type

NCBI Assembly: GCA_016703945.1 Ts

Description

Bacterium found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
Can utilize branched chain amino acids (*livFGHKM*).
Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, acs, acetate kinase, ackA, and phosphate acetyltransferase, pta.
Potential to reduce nitrate with *napAB* along with the reduction of nitrate to nitric oxide with nirS. Lastly it also had nitrous oxide reductase, nosZ predicted.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Aalborgicola* » *Aalborgicola danicus*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44114

Species *Aalborgicola defluviihabitans*Ts

Etymology

[de.flu.vii.ha'bi.tans] **L. neut. n.** *defluvium*, sewage; **L. pres. part.** *habitans*, inhabiting; **L. masc. part. adj.** *defluviihabitans*, pertaining to the habitat where the MAG was sequenced from.

Nomenclatural type

NCBI Assembly: GCA_016705575.1 Ts

Description

Bacterium found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta.*
Potential to reduce nitrate with *narGHI* along with the reduction of nitrate to nitric oxide with *nirS.* Lastly it also had nitrous oxide reductase, *nosZ* predicted.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Aalborgicola* » *Aalborgicola defluviihabitans*Ts

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44105

Species *Aalborgicola lynettensis*

Etymology

[ly.net.ten'sis] **N.L. masc. adj.** *lynettensis*, of the city of Lynetten, from where the MAG was obtained

Nomenclatural type

NCBI Assembly: GCA_016719405.1 ^{Ts}

Description

Bacterium found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
Can utilize branched chain amino acids (*livFGHKM*)
Potential to reduce nitrate with *narGHI*. Lastly it also had nitrous oxide reductase, *nosZ* predicted.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Aalborgicola* » *Aalborgicola lynettensis*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44113

Species *Aalborgiella aggregata*^{Ts}

Etymology

[ag.gre.ga'ta] **L. fem. part. adj.** *aggregata*, joined together

Nomenclatural type

NCBI Assembly: GCA_016708645.1 ^{Ts}

Description

Rod shaped bacterium (1.4± 0.3 x 0.4±0.1 µm) abundant in activated sludge globally. Based on FISH analysis it seems to grow along filaments in activated sludge. Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for transportation of branched amino acids. Presence of *narGHI* genes showed potential to reduce nitrate.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Aalborgiella* » *Aalborgiella aggregata*^{Ts}

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44100

Species *Defluviibacillus avedoerensis*^{Ts}

Etymology

[a.ve.doe.ren'sis] **N.L. masc. adj.** *avedoerensis*, of the city Avedoere from which the MAG is retrieved from

Nomenclatural type

NCBI Assembly: GCA_016703665.1 ^{Ts}

Description

Rod shaped bacteria (2.1± 0.4 x 0.6±0.1 µm) abundant in activated sludge globally.
Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for transportation of polar amino acids and branched amino acids.
Presence of *narGHI* genes showed potential to reduce nitrate along with potential for further conversion via *norB* . It also had the potential to reduce nitrite to nitric oxide via nitrite reductase, *nirS.*
Defluviibacillus avedoerensis had predicted all genes of the three pathways (polyP, glycogen and PHA) associated with Pao metabolism.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Defluviibacillus* » *Defluviibacillus avedoerensis*^{Ts}

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44098

Species *Egaibacter danicus*^{Ts}

Etymology

[da'ni.cus] **L. masc. adj.** *danicus*, Danish

Nomenclatural type

NCBI Assembly: GCA_016707075.1 ^{Ts}

Description

Bacterium found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
Glucose uptake of via the *gtsABC+malK* transporter was also predicted.
Can utilize branched chain amino acids (*livFGHKM*).
Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*.
Potential to reduce nitrate with *narGHI* along with the reduction of nitrate to nitric oxide with *nirS*.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Egaibacter* » *Egaibacter danicus*^{Ts}

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44120

Species *Rhodoferax bjergmarkensis*

Etymology

[bjerg.mar.ken'sis] **N.L. masc. adj.** *bjergmarkensis*, of the city of Bjergmarken, from where the MAG was obtained

Nomenclatural type

NCBI Assembly: GCA_016708345.1 ^{Ts}

Description

Bacterium found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
Can utilize branched chain amino acids (*livFGHKM*).
Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, and acetate kinase, *ackA*
Potential to reduce nitrate with narGHI along with the reduction of nitrate to nitric oxide with *nirS*. Lastly it also had nitrous oxide reductase, nosZ predicted.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Rhodoferax* » *Rhodoferax bjergmarkensis*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44117

Species *Rhodoferax mariagerensis*

Etymology

[ma.ri.a.ge.ren'sis] **N.L. masc. adj.** *mariagerensis*, of the city of Mariager where the MAG was obtained

Nomenclatural type

NCBI Assembly: GCA_016719055.1 ^{Ts}

Description

Bacterium found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
Can utilize branched chain amino acids (*livFGHKM*) and polar amino acids (ABC.PA.A, ABC.PA.P, ABC.PA.S).
Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta*.
Potential to reduce nitrate with *narGHI*

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Rhodoferax* » *Rhodoferax mariagerensis*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44118

Species *Rhodoferax odensensis*

Etymology

[o.den.sen'sis] **N.L. masc. adj.** *odensensis*, pertaining to Odense, a city in Denmark where the original sample was collected

Nomenclatural type

NCBI Assembly: GCA_016718405.1 Ts

Description

acterium found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
Can utilize branched chain amino acids (*livFGHKM*).
Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta*.
Potential to reduce nitrate to nitric oxide with *nirS*. Lastly it also had nitrous oxide reductase, *nosZ* predicted.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Rhodoferax* » *Rhodoferax odensensis*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44116

Species *Rhodoferax randersensis*

Etymology

[ran.der.sen'sis] **N.L. masc. adj.** *randersensis*, from the city Randers where the MAG had been retrieved

Nomenclatural type

NCBI Assembly: GCA_016718155.1 Ts

Description

Bacterium found in activated sludge.
Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.
Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta*.
Potential to reduce nitrate with *narGHI* along with the reduction of nitrate to nitric oxide with *nirS*. Lastly it also had nitrous oxide reductase, *nosZ* predicted.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Rhodoferax* » *Rhodoferax randersensis*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44115

Species *Skiveiella danica*$^{\mathrm{Ts}}$

Etymology

[da.ni'ca] **L. fem. adj.** *danica*, Danish

Nomenclatural type

NCBI Assembly: GCA_016721925.1 $^{\mathrm{Ts}}$

Description

Bacteria found in activated sludge. Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for transportation of polar amino acids.
Presence of *narGHI* genes showed potential to reduce nitrate.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Skiveiella* » *Skiveiella danica*$^{\mathrm{Ts}}$

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44103

References

1. Petersen et al. (2025). Diversity and physiology of abundant Rhodoferax species in global wastewater treatment systems. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2024.126574

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:ftcpaei9** submitted by **Fischer Petersen, Jette** and including 17 new names has been successfully validated.

Date of Priority: 2025-08-28 09:33 UTC
DOI: 10.57973/seqcode.r:ftcpaei9