

# Register list for 20 new names including *Aadella gelida* sp. nov.

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## Genus *Aadella*

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### Etymology

[Aa.del'la] N.L. fem. dim. n. *Aadella*, Named after AAD (Australian Antarctic Division)

### Nomenclatural type

Species *Aadella gelida*<sup>T5</sup>

### Description

The genus belongs to the family *Tantalellaceae*, order *Tantalellales*, class *Gorgyraia*, phylum *Omnitrophota*. The description is currently the same as for the nomenclatural type of the genus, the species *Aadella gelida*.

### Classification

*Bacteria* » *Omnitrophota* » “*Gorgyraia*” » “*Tantalellales*” » “*Tantalellaceae*” » *Aadella*

### References

Effective publication: Williams et al., 2021 [1]

### Registry URL

<https://seqco.de/i:33274>

## Genus *Gorgyraea*

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### Etymology

[Gor.gy'ra.e.a] N.L. fem. n. *Gorgyraea*, of Gorgyra, mythical denizen of the underworld in Greek mythology.

### Nomenclatural type

Species *Gorgyraea atricola*<sup>T5</sup>

### Description

The genus belongs to the family *Gorgyraeaceae*, order *Gorgyraeales*, class *Gorgyraia*, phylum *Omnitrophota*. The description is currently the same as for the nomenclatural type of the genus, the species *Gorgyraea atricola*.

### Classification

“*Gorgyraeales*” » “*Gorgyraeaceae*” » *Gorgyraea*

### References

Effective publication: Williams et al., 2021 [1]

### Registry URL

<https://seqco.de/i:33279>

## Genus *Tantalella*

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### Etymology

[Tan.ta'lel.la] N.L. fem. dim. n. *Tantalella*, Named for Tantalus (Gr. Tantalos), in Greek mythology, a mythical denizen of the underworld, condemned to being immersed in a lake.

### Nomenclatural type

Species *Tantalella remota*<sup>T5</sup>

**Description**

The genus belongs to the family *Tantalellaceae*, order *Tantalellales*, class *Gorgyraia*, phylum *Omnitrophota*. The description is currently the same as for the nomenclatural type of the genus, the species *Tantalella remota*.

**Classification**

*Bacteria* » *Omnitrophota* » “Gorgyraia” » “Tantalellales” » “Tantalellaceae” » *Tantalella*

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33288>

## Genus *Aceula*

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**Etymology**

[Ace.u'la] N.L. fem. dim. n. *Aceula*, from the name of the locality (Ace Lake).

**Nomenclatural type**

Species *Aceula laticola*<sup>T5</sup>

**Description**

The description for this genus is derived from Williams et al., 2021, and supplemented with additional information. Genome predictions designate this genus as heterotrophic and capable of the fermentation of glucose to acetyl-CoA through EMP pathway. Proteases and peptidases for the degradation of proteins to amino acids are present. Additionally, simple sugar transport and glycoside hydrolases are encoded by the genome and genes required for the synthesis of trehalose and glycogen are also present (Williams et al., 2021). A V-type ATPase, respiratory F-type ATPase and Rnf complex for ATP synthesis, and a Group 3d [NiFe] hydrogenase are present (Williams et al., 2021). All genes required for the tight-adherence complex and the production of a Type-4a pilus are present. The nomenclatural type for the genus is *Aceula laticola*, (genome designated 3300035698\_1100).

**Classification**

*Bacteria* » *Omnitrophota* » “Velamenicoccia” » “Zapsychrales” » “Aceulaceae” » *Aceula*

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33275>

## Genus *Saelkia*

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**Etymology**

[Sa.el'ki.a] N.L. fem. n. *Saelkia*, after saelkie or selkie, mythical water creature of Celtic and Norse folklore.

**Nomenclatural type**

Species *Saelkia tenebricola*<sup>T5</sup>

**Description**

This genus belongs to the family *Kaelpiaceae*, in the order *Kaelpiales*, however, their exact placement at the class-level within the phylum *Omnitrophota* is uncertain. As a monotypic genus, the description for the genus is the same as for the nomenclatural type, *Saelkia tenebricola*.

**Classification**

*Incertae sedis* (Bacteria) » “Kaelpiales” » “Kaelpiaceae” » *Saelkia*

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33286>

## Genus *Gygaella*

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**Etymology**

[Gy.ga.el'la] N.L. fem. dim. n. *Gygaella*, named for Gygaea (Gr. Gugaia), lake nymph from Greek mythology

**Nomenclatural type**

Species *Gygaella obscura*<sup>Ts</sup>

**Description**

The genus belongs to the family Gygaellaceae, order *Gygaellales*, class *Velamenicoccia*, phylum *Omnitrophota*. The available genome assembly belonging to this family was recovered from Ace Lake, Antarctica. The nomenclatural type for the genus is the species *Gygaella obscura*.

**Classification**

*Bacteria* » *Omnitrophota* » “*Velamenicoccia*” » “*Gygaellales*” » “*Gygaellaceae*” » *Gygaella*

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33281>

## Genus *Kaelpia*

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**Etymology**

[Ka.el'pi.a] N.L. fem. n. *Kaelpia*, after kaelpie or kelpie, mythical water creature of Celtic folklore.

**Nomenclatural type**

Species *Kaelpia aquatica*<sup>Ts</sup>

**Description**

This genus belongs to the family *Kaelpiaceae*, in the order *Kaelpiales*, however, their exact placement at the class within the phylum *Omnitrophota* is uncertain. The genomes of both species belonging to this genus encode V-type ATPase and Rnf complex for ATP synthesis, and a Group A3 [FeFe] hydrogenase. The nomenclatural type for the genus is the species *Kaelpia aquatica*.

**Classification**

*Incertae sedis* (Bacteria) » “*Kaelpiales*” » “*Kaelpiaceae*” » *Kaelpia*

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33283>

## Genus *Zapsychrus*

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**Etymology**

[Za.psy'chrus] Gr. pref. *za-*, intensifying prefix; Gr. adj. *psychros*, cold; N.L. masc. n. *Zapsychrus*, referring to an organism living in very cold conditions.

**Nomenclatural type**

Species *Zapsychrus exili*<sup>Ts</sup>

### Description

This genus belongs to the family *Zapsytranceae*, order *Zapsytrales*, class *Velaminicoccia*, phylum *Omnitrophota*. Available cell size data indicate small cells for members of the genus. Large ORFs are common in the genus. Some components of the tight-adherence complex is encoded in these genomes as well as genes for respiratory pathways. Assemblies originate from wastewater, a bioreactor, soil and groundwater. Where reported, assemblies were recovered from samples taken at circumneutral or slightly basic pH, microaerobic conditions and between 10 °C and 30 °C. The nomenclatural type for the genus is the species *Zapsytrus exilii*.

### Classification

*Bacteria* » *Omnitrophota* » “Velaminicoccia” » “Zapsytrales” » “Zapsytranceae” » *Zapsytrus*

### References

Effective publication: Williams et al., 2021 [1]

### Registry URL

<https://seqco.de/i:33301>

## Species *Aadella gelida*<sup>Ts</sup>

### Etymology

[ge.li'da] L. fem. adj. *gelida*, ice-cold; in reference to the very cold temperature of Ace Lake.

### Nomenclatural type

[NCBI Assembly: GCA\\_030765205.1](#)<sup>Ts</sup>

### Description

This species is the type for the genus *Aadella*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. Genome predictions designate this species as heterotrophic and capable of fermentation of glucose to acetyl-CoA through the EMP pathway. Proteases and peptidases for the degradation of proteins to amino acids is also encoded within the genome. Additionally, simple sugar transport and glycoside hydrolases are encoded by the genome and genes required for the synthesis of trehalose and glycogen are also present. The genome representative of this species encodes a V-type ATPase and an Rnf complex for ATP synthesis, and a Group 3b [NiFe] hydrogenase has been reported for this species. All components for a Type-4a pilus is encoded by the genome. The nomenclatural type for the species is the genome designated 3300035698\_848.

### Classification

*Bacteria* » *Omnitrophota* » “Gorgyraia” » “Tantalellales” » “Tantalellaceae” » *Aadella* » *Aadella gelida*<sup>Ts</sup>

### References

Effective publication: Williams et al., 2021 [1]

### Registry URL

<https://seqco.de/i:33273>

## Species *Aceula lacicola*<sup>Ts</sup>

### Etymology

[la.ci'co.la] L. masc. n. *lacus*, lake; L. n. suff. *-cola*, from *incola* the inhabitant; N.L. fem. n. *lacicola*, lake-dweller

### Nomenclatural type

[NCBI Assembly: GCA\\_030765785.1](#)<sup>Ts</sup>

### Description

This species is the type for the genus *Aceula*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. Genome predictions designate this species as heterotrophic and capable of the fermentation of glucose to acetyl-CoA through EMP pathway. A reversible acetyl-CoA synthetase may be indicative of acetogenesis in this species. Proteases and peptidases for the degradation of proteins to amino acids is also encoded within the genome. Additionally, simple sugar transport and glycoside hydrolases are encoded by the genome and genes required for the synthesis of trehalose and glycogen is also present (Williams et al., 2021). The genome representative of this species encodes a V-type ATPase, respiratory F-type ATPase and Rnf complex for ATP synthesis, and a Group 3d [NiFe] hydrogenase (Williams et al., 2021). All genes required for the tight-adherence complex and the production of a Type-4a pilus is present in the genome of this species, as well as genes coding for a conductive pilin. The nomenclatural type for the species is the genome designated 3300035698\_1100.

### Classification

*Bacteria* » *Omnitrophota* » “Velamenicoccia” » “Zapsychrates” » “Aceulaceae” » *Aceula* » *Aceula lacicola*<sup>Ts</sup>

### References

Effective publication: Williams et al., 2021 [1]

### Registry URL

<https://seqco.de/i:33276>

## Species *Aceula meridiana*

### Etymology

[me.ri.di.a'na] L. fem. adj. *meridiana*, of or belonging to the south; in reference to the southern continent of Antarctica.

### Nomenclatural type

[NCBI Assembly: GCA\\_030765185.1](#)<sup>Ts</sup>

### Description

This species belongs to the genus *Aceula*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. Genome predictions indicate that this species is likely heterotrophic, with a horse-shoe type TCA cycle, and several proteases and peptidases, along with ABC sugar transporters and glycoside hydrolases are predicted for this species. Genes required for the synthesis of trehalose and glycogen is also present, and fermentation of glucose to acetyl-CoA through the EMP pathway is likely. A V-type ATPase, respiratory F-type ATPase and Rnf complex are encoded for ATP synthesis, while Group 3d [NiFe] (Williams et al., 2021) and Group A3 [FeFe] hydrogenases are also encoded. Coupled with a reversible acetyl-CoA synthetase, acetogenesis is likely for this species. Genes required for the production of a Type-4a pilus and tight-adherence complex is encoded by the genome of this species. A very large ORF is present in this species. The type for this species is the genome designated 3300035698\_985.

### Classification

*Bacteria* » *Omnitrophota* » “Velamenicoccia” » “Zapsychrates” » “Aceulaceae” » *Aceula* » *Aceula meridiana*

### References

Effective publication: Williams et al., 2021 [1]

### Registry URL

<https://seqco.de/i:33277>

## Species *Gorgyraea atricola*<sup>Ts</sup>

### Etymology

[a.tri'co.la] L. masc. adj. *ater*, black, dark; L. n. suff. *-cola*, inhabitant; N.L. fem. n. *atricola*, inhabitant of the dark

**Nomenclatural type**

[NCBI Assembly: GCA\\_030765235.1](#)<sup>Ts</sup>

**Description**

This species is the nomenclatural type for the genus *Gorgyraea*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. The assembly representing this species has a genome of 1.74 Mb, with a %GC content of 41.71 %. This species encode for the Wood-Ljungdahl pathway, but the absence of genes for the reverse TCA cycle may indicate no capacity for autotrophic CO<sub>2</sub> fixation and rather that the Wood-Ljungdahl pathway in combination with the Rnf complex, functions in the reductive direction as an electron sink during homoacetogenic glucose fermentation. Several proteases and peptidases are encoded for the degradation of proteins to amino acids, some with signal peptides, while simple sugar transporters and glycoside hydrolases are also encoded by the genome. The ability to synthesize trehalose and glycogen is also feasible. A V-type ATPase and Rnf complex for ATP synthesis is present and a membrane-bound Group 4g [NiFe] hydrogenase is also encoded. Components for a Type-4a pilus and a very large ORF is encoded by the genome. The nomenclatural type for this species is the genome designated 3300035698\_32.

**Classification**

“Gorgyraeales” » “Gorgyraeaceae” » *Gorgyraea* » *Gorgyraea atricola*<sup>Ts</sup>

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33280>

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**Species *Gygaella obscura*<sup>Ts</sup>**

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**Etymology**

[ob.scu'ra] L. fem. adj. *obscura*, dark, hidden; referring to life at the bottom of Ace Lake

**Nomenclatural type**

[NCBI Assembly: GCA\\_030765485.1](#)<sup>Ts</sup>

**Description**

This species is the type for the genus *Gygaella*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. The estimated genome size for this species is 1.96 Mb. This species is predicted to be heterotrophic with an incomplete horse-shoe type TCA cycle, and code for proteases, peptidases and glycoside hydrolases, with ABC transporters for simple sugars presents. Several genes associated with acetogenesis, along with a V-type ATPase, a respiratory F-type ATPase (complex V) and an Rnf complex is encoded, and a Group A3 [FeFe] hydrogenase is present. A conductive pilin is present in the genome of this species and all genes associated with the production of a Type-4a pilus and the tight-adherence complex is present in this species. The nomenclatural type for this species is the genome recovered from Ace Lake, Antarctica, 3300035698\_1934.

**Classification**

*Bacteria* » *Omnitrophota* » “Velamenicoccia” » “Gygaellales” » “Gygaellaceae” » *Gygaella* » *Gygaella obscura*<sup>Ts</sup>

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33282>

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**Species *Kaelpia aquatica*<sup>Ts</sup>**

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**Etymology**

[a.qua'ti.ca] L. fem. adj. *aquatica*, living or found in the water.

**Nomenclatural type**

[NCBI Assembly: GCA\\_030765335.1](#)<sup>Ts</sup>

**Description**

This species is the nomenclatural type for the genus *Kaelpia*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. This species is predicted to be heterotrophic, with a horse-shoe type TCA cycle, and encodes to proteases and peptidases to degrade proteins to amino acids. Simple sugar ABC transporters and glycoside hydrolases, along with the ability to synthesize trehalose and glycogen is predicted, and genes for the fermentation of glucose to acetyl-CoA through EMP pathway is present. A V-type ATPase and Rnf complex for ATP synthesis is present, and a Group A3 [FeFe] hydrogenase is encoded by this genome. The genome also encodes a conductive pilin and all genes associated with the production of a Type-4a pilus is present. The nomenclatural type for the species is the genome 3300035698\_2000.

**Classification**

*Incertae sedis* (Bacteria) » “Kaelpiales” » “Kaelpiaceae” » *Kaelpia* » *Kaelpia aquatica*<sup>Ts</sup>

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33284>

## Species *Kaelpia imicola*

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**Etymology**

[i.mi'co.la] L. masc. adj. *imus*, bottom; L. n. suff. *-cola*, inhabitant; N.L. fem. n. *imicola*, bottom-dweller

**Nomenclatural type**

[NCBI Assembly: GCA\\_030765505.1](#)<sup>Ts</sup>

**Description**

This species belongs to the genus *Kaelpia*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. This species is predicted to be heterotrophic. Fermentation of glucose to acetyl-CoA through EMP pathway is likely, and the genome encodes a V-type ATPase and Rnf complex for ATP synthesis, and a Group A3 [FeFe] hydrogenase. The genome also encodes a conductive pilin and genes for the production of a Type-4a pilus. The type for this species is the genome designated 3300035698\_1655.

**Classification**

*Incertae sedis* (Bacteria) » “Kaelpiales” » “Kaelpiaceae” » *Kaelpia* » *Kaelpia imicola*

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33285>

## Species *Saelkia tenebricola*<sup>Ts</sup>

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**Etymology**

[ten.e'bri.co.la] L. fem. n. *tenebra*, darkness; L. n. suff. *-cola*, inhabitant; N.L. fem. n. *tenebricola*, a dweller of the dark

**Nomenclatural type**

[NCBI Assembly: GCA\\_030765145.1](#)<sup>Ts</sup>

**Description**

This species is the type for the genus *Saelkia*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. Genome predictions indicate that this species is likely heterotrophic, with an incomplete horse-shoe type TCA cycle, fermentation of glucose to acetyl-CoA through the EMP pathway, and codes for proteases and peptidases to degrade proteins to amino acids, simple sugar ABC transporters and glycoside hydrolases. The genome also codes for a V-type ATPase and Rnf complex for ATP synthesis, and a Group 4g [NiFe] hydrogenase. All genes required for the production of a Type-4a pilus and conductive pili are encoded by the genome. The nomenclatural type for this species is the genome 3300035698\_749.

**Classification**

*Incertae sedis* (Bacteria) » “Kaelpiales” » “Kaelpiaceae” » *Saelkia* » *Saelkia tenebricola*<sup>Ts</sup>

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33287>

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**Species *Tantalella remota*<sup>Ts</sup>**

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**Etymology**

[re.mo'ta] L. fem. adj. *remota*, remote, distant; referencing the remoteness of the locality.

**Nomenclatural type**

[NCBI Assembly: GCA\\_030765685.1](#)<sup>Ts</sup>

**Description**

This species is the nomenclatural type for the genus *Tantalella*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. Based on genome predictions, this species is heterotrophic and encodes several proteases and peptidases to degrade proteins to amino acids. Additionally, ABC transporters for transport of simple sugars and glycoside hydrolases are encoded by the genome, along with the ability to synthesize trehalose and glycogen. Fermentation of glucose to acetyl-CoA through the EMP pathway is likely. A V-type ATPase and an Rnf complex is encoded for ATP synthesis, and an incomplete horse-shoe type TCA cycle can be reconstructed from the genome. A Group 3b [NiFe] hydrogenase has been reported for this species. All components for a Type-4a pilus and a very large ORF are present in the genome. The nomenclatural type for the species is the genome designated 3300035698\_1097.

**Classification**

*Bacteria* » *Omnitrophota* » “Gorgyraia” » “Tantalellales” » “Tantalellaceae” » *Tantalella* » *Tantalella remota*<sup>Ts</sup>

**References**

Effective publication: Williams et al., 2021 [1]

**Registry URL**

<https://seqco.de/i:33289>

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**Species *Zapsychrus exili*<sup>Ts</sup>**

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**Etymology**

[ex.i'l.i] L. gen. n. *exili*, of an exile, refugee; referring to the isolation of Ace Lake, cut off from the Southern Ocean.

**Nomenclatural type**

[NCBI Assembly: GCA\\_030765585.1](#)<sup>Ts</sup>



### Description

This species is the nomenclatural type for the genus *Zapsychnus*. The estimated genome size is 2.1 Mb. Based on the description in Williams et al., 2021, an incomplete horse-shoe type TCA cycle is encoded by this genome, and this species is predicted to be heterotrophic. Glucose is predicted to be fermented through the EMP pathway. A Group 3d [NiFe] hydrogenase is predicted from the genome, and a V-type ATPase, respiratory F-type ATPase and Rnf complex for ATP synthesis is present. A reversible acetyl-CoA synthetase may be indicative of acetogenesis in this species. A conductive pilin is also encoded by the genome. All genes for a tight-adherence complex (Tad) and Type-4a pilus are present in the genome. The nomenclatural type for the species is the genome 3300035698\_1555, recovered from metagenomic sampling and sequencing of Ace Lake, Antarctica.

### Classification

*Bacteria* » *Omnitrophota* » “Velamenicoccia” » “Zapsychnales” » “Zapsychnaceae” » *Zapsychnus* » *Zapsychnus exili*<sup>TS</sup>

### References

Effective publication: Williams et al., 2021 [1]

### Registry URL

<https://seqco.de/i:33302>

## References

1. Williams et al. (2021). Shedding Light on Microbial “Dark Matter”: Insights Into Novel Cloacimonadota and Omnitrophota From an Antarctic Lake. *Frontiers in Microbiology*. DOI:10.3389/fmicb.2021.741077

## 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:2rggbgyb](https://seqco.de/r:2rggbgyb) submitted by **Allen, Michelle** and including 18 new names has been successfully validated.

Date of Priority: 2024-09-04 06:09 UTC

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