

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

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Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Aadella</i>	[Aa.del'la] N.L. fem. dim. n. <i>Aadella</i> , Named after AAD (Australian Antarctic Division)	The genus belongs to the family <i>Tantalellaceae</i> , order <i>Tantalellales</i> , class <i>Gorgyraia</i> , phylum <i>Omnitrophota</i> . The description is currently the same as for the nomenclatural type of the genus, the species <i>Aadella gelida</i> .	<i>Tantalellaceae</i>	<i>Aadella gelida</i> ^{T5}	seqco.de/i:33274
Genus <i>Gorgyraea</i>	[Gor.gy'ra.e.a] N.L. fem. n. <i>Gorgyraea</i> , of Gorgyra, mythical denizen of the underworld in Greek mythology.	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 <i>Gorgyraea atricola</i> .	<i>Gorgyraeaceae</i>	<i>Gorgyraea atricola</i> ^{T5}	seqco.de/i:33279

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Tantalella</i>	[Tan.ta'le.la] N.L. fem. dim. n. <i>Tantalella</i> , Named for Tantalus (Gr. Tantalos), in Greek mythology, a mythical denizen of the underworld, condemned to being immersed in a lake.	The genus belongs to the family <i>Tantalellaceae</i> , order <i>Tantalellales</i> , class <i>Gorgyria</i> , phylum <i>Omnitrophota</i> . The description is currently the same as for the nomenclatural type of the genus, the species <i>Tantalella remota</i> .	<i>Tantalellaceae</i>	<i>Tantalella remota</i> ^{TS}	seqco.de/i:33288
Genus <i>Aceula</i>	[Ace.u'la] N.L. fem. dim. n. <i>Aceula</i> , from the name of the locality (Ace Lake).	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 <i>Aceula laticola</i> , (genome designated 3300035698_1100).	<i>Aceulaceae</i>	<i>Aceula laticola</i> ^{TS}	seqco.de/i:33275
Genus <i>Saelkia</i>	[Sa.el'ki.a] N.L. fem. n. <i>Saelkia</i> , after saelkie or selkie, mythical water creature of Celtic and Norse folklore.	This genus belongs to the family <i>Kaelpiaceae</i> , in the order <i>Kaelpiales</i> , however, their exact placement at the class-level within the phylum <i>Omnitrophota</i> is uncertain. As a monotypic genus, the description for the genus is the same as for the nomenclatural type, <i>Saelkia tenebricola</i> .	<i>Kaelpiaceae</i>	<i>Saelkia tenebricola</i> ^{TS}	seqco.de/i:33286

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Gygaella</i>	[Gy.ga.el'la] N.L. fem. dim. n. <i>Gygaella</i> , named for Gygaea (Gr. Gugaia), lake nymph from Greek mythology	The genus belongs to the family Gygaellaceae, order <i>Gygaellales</i> , class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . The available genome assembly belonging to this family was recovered from Ace Lake, Antarctica. The nomenclatural type for the genus is the species <i>Gygaella obscura</i> .	<i>Gygaellaceae</i>	<i>Gygaella obscura</i> ^{TS}	seqco.de/i:33281
Genus <i>Kaelpia</i>	[Ka.el'pi.a] N.L. fem. n. <i>Kaelpia</i> , after kaelpie or kelpie, mythical water creature of Celtic folklore.	This genus belongs to the family <i>Kaelpiaceae</i> , in the order <i>Kaelpiales</i> , however, their exact placement at the class within the phylum <i>Omnitrophota</i> 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 <i>Kaelpia aquatica</i> .	<i>Kaelpiaceae</i>	<i>Kaelpia aquatica</i> ^{TS}	seqco.de/i:33283
Genus <i>Zapsychrus</i>	[Za.psy'chrus] Gr. pref. <i>za-</i> , intensifying prefix; Gr. adj. <i>psychros</i> , cold; N.L. masc. n. <i>Zapsychrus</i> , referring to an organism living in very cold conditions.	This genus belongs to the family <i>Zapsychraceae</i> , order <i>Zapsychrates</i> , class <i>Velamnicoccia</i> , phylum <i>Omnitrophota</i> . 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 <i>Zapsychrus exilii</i> .	<i>Zapsychraceae</i>	<i>Zapsychrus exilii</i> ^{TS}	seqco.de/i:33301

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Aadella</i> <i>gelida</i> ^{Ts}	[ge.li'da] L. fem. adj. <i>gelida</i> , ice-cold; in reference to the very cold temperature of Ace Lake.	This species is the type for the genus <i>Aadella</i> . 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.	<i>Aadella</i>	NCBI Assembly: GCA_030765205.1 ^{Ts}	seqco.de/i:33273
Species <i>Aceula</i> <i>lacicola</i> ^{Ts}	[la.ci'co.la] L. masc. n. <i>lacus</i> , lake; L. n. suff. - <i>cola</i> , from <i>incola</i> the inhabitant; N.L. fem. n. <i>lacicola</i> , lake-dweller	This species is the type for the genus <i>Aceula</i> . 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.	<i>Aceula</i>	NCBI Assembly: GCA_030765785.1 ^{Ts}	seqco.de/i:33276

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Aceula meridiana</i>	[me.ri.di.a'na] L. fem. adj. <i>meridiana</i> , of or belonging to the south; in reference to the southern continent of Antarctica.	This species belongs to the genus <i>Aceula</i> . 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.	<i>Aceula</i>	NCBI Assembly: GCA_030765185.1 ^{Ts}	seqco.de/i:33277
Species <i>Gorgyraea atricola</i> ^{Ts}	[a.tri'co.la] L. masc. adj. <i>ater</i> , black, dark; L. n. suff. <i>-cola</i> , inhabitant; N.L. fem. n. <i>atricola</i> , inhabitant of the dark	This species is the nomenclatural type for the genus <i>Gorgyraea</i> . 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 ₂ 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.	<i>Gorgyraea</i>	NCBI Assembly: GCA_030765235.1 ^{Ts}	seqco.de/i:33280

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Gygaella</i> <i>obscura</i> ^{Ts}	[ob.scu'ra] L. fem. adj. <i>obscura</i> , dark, hidden; referring to life at the bottom of Ace Lake	This species is the type for the genus <i>Gygaella</i> . 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.	<i>Gygaella</i>	NCBI Assembly: GCA_030765485.1 ^{Ts}	seqco.de/i:33282
Species <i>Kaelpia</i> <i>aquatica</i> ^{Ts}	[a.qua'ti.ca] L. fem. adj. <i>aquatica</i> , living or found in the water.	This species is the nomenclatural type for the genus <i>Kaelpia</i> . 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.	<i>Kaelpia</i>	NCBI Assembly: GCA_030765335.1 ^{Ts}	seqco.de/i:33284
Species <i>Kaelpia</i> <i>imicola</i>	[i.mi'co.la] L. masc. adj. <i>imus</i> , bottom; L. n. suff. <i>-cola</i> , inhabitant; N.L. fem. n. <i>imicola</i> , bottom-dweller	This species belongs to the genus <i>Kaelpia</i> . 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.	<i>Kaelpia</i>	NCBI Assembly: GCA_030765505.1 ^{Ts}	seqco.de/i:33285

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Saelkia tenebricola</i> ^{Ts}	[ten.e'bri.co.la] L. fem. n. <i>tenebra</i> , darkness; L. n. suff. <i>-cola</i> , inhabitant; N.L. fem. n. <i>tenebricola</i> , a dweller of the dark	This species is the type for the genus <i>Saelkia</i> . 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.	<i>Saelkia</i>	NCBI Assembly: GCA_030765145.1 ^{Ts}	seqco.de/i:33287
Species <i>Tantalella remota</i> ^{Ts}	[re.mo'ta] L. fem. adj. <i>remota</i> , remote, distant; referencing the remoteness of the locality.	This species is the nomenclatural type for the genus <i>Tantalella</i> . 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.	<i>Tantalella</i>	NCBI Assembly: GCA_030765685.1 ^{Ts}	seqco.de/i:33289
Species <i>Zapsychrus exili</i> ^{Ts}	[ex.i'li] L. gen. n. <i>exili</i> , of an exile, refugee; referring to the isolation of Ace Lake, cut off from the Southern Ocean.	This species is the nomenclatural type for the genus <i>Zapsychrus</i> . 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.	<i>Zapsychrus</i>	NCBI Assembly: GCA_030765585.1 ^{Ts}	seqco.de/i:33302