Alicycliphilus

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2. KEYWORDS: *Alicycliphilus denitrificans*; facultative anaerobe; chemo-organotroph; alicyclic compounds degradation

3. ABSTRACT:

Short rods 1-2 µm long and 0.6 µm wide. **Motile**. **Gram-negative**. Nonsporulating. **Facultative anaerobe**. Nitrate is reduced to N_2. Mesophilic, with optimal growth at 28-30 °C, and pH 7.2-7.4 under aerobic or anoxic conditions. **Chemo-organotroph**, with strictly respiratory metabolism. Degrade aromatic and alicyclic compounds. Catalase- and cytochrome *c* oxidase positive. The respiratory quinone is **ubiquinone 8** and major fatty acids are $C_{16:1}$ *ω7c*, $C_{16:0}$, and $C_{18:1}$ *ω7c*. Major polar lipids are phosphatidylethanolamine, phosphatidylglycerol, and diphosphatidylglycerol. The type strain of the type species was isolated from a wastewater treatment plant, cultivated with cyclohexanol as sole carbon source and nitrate as electron acceptor.

4. DEFINING PUBLICATION:

Alicycliphilus, Mechichi, Stackebrandt and Fuchs, 2003, 149[VP]

5. ETYMOLOGY:

Alicycliphilus [a.li.cyc.li'phi.lus. Gr. adj. *aliphos* fat; Gr. n. *kyklos*, circle or ring; N.L. adj. *alicyclo* referring to circular fat-like organic compounds; Gr. masc. n. *philos* friend; N.L. adj. *Alicycliphilus* alicyclic compound-liking, referring to the substrates used for the isolation of this organism].

6. GENERIC DEFINITION:

Short rods 1-2 µm long and 0.6 µm wide. **Motile**. **Gram-negative**. Nonsporulating. **Facultative anaerobe**. Nitrate is reduced to N_2. Mesophilic, with optimal growth at 28-30 °C, and pH 7.2-7.4 under aerobic or anoxic conditions. **Chemo-organotroph**, with strictly respiratory metabolism. Degrade aromatic and alicyclic compounds. Catalase- and cytochrome *c* oxidase positive. The respiratory quinone is **ubiquinone 8** and major fatty acids are $C_{16:1}$ *ω7c*, $C_{16:0}$, and $C_{18:1}$ *ω7c*. Major polar lipids are phosphatidylethanolamine, phosphatidylglycerol, and diphosphatidylglycerol. The type strain of the type species was isolated from a wastewater treatment plant, cultivated with cyclohexanol as sole carbon source and nitrate as electron acceptor.

The DNA G+C content (mol %) is 66 (HPLC) or 67.9 (genome analysis, GenBank).

Type species: *Alicycliphilus denitrificans*, Mechichi, Stackebrandt and Fuchs, 2003, 149^{VP}

Number of species with validated names: 1.

7. FAMILY CLASSIFICATION:

Comamonadaceae (fbm00182)

8. FURTHER DESCRIPTIVE INFORMATION:

8.1. *Alicycliphilus* strains

A single species is described within the genus *Alicycliphilus*, *Alicycliphilus denitrificans* (Mechichi et al., 2003), based on a single strain (K601^{T}), which was originally classified in the genus *Pseudomonas* (Dangel et al., 1988). An additional member of *Alicycliphilus denitrificans* was reported by Weelink et al. (2008) based on the isolate BC, which shares 100% 16S rRNA gene sequence similarity and 74.5±3.5% DNA-DNA hybridization similarity with strain K601^{T} (Oosterkamp et al., 2013). The average nucleotide identity values between strains K601^{T} and

BC calculated with both BLAST (ANIb) and MUMmer (ANIm) are 98.71% and 99.60%, respectively. Since both are above the threshold of 95% for circumscribing species (Goris et al., 2007), strain BC can be confirmed as *Alicycliphilus denitrificans* member. This conclusion is strengthened by the tetranucleotide frequency correlation coefficient value of 0.9995, which is above the boundary of 0.99 used for species delineation (Oosterkamp et al., 2013, Richter and Rosselló-Mora, 2009).

Several other strains of *Alicycliphilus denitrificans* have been described (Solís-González and Loza-Tavera, 2019), namely strain BQ1, which shares 99% 16S rRNA gene similarity and 96.14% ANI value with strain K601^{T} (Oceguera-Cervantes et al., 2007, Solís-González and Loza-Tavera, 2019). Other strains, such as BQ8, B1, ADC-16 and KN Bun08 were included in this species based on the high 16S rRNA gene sequence similarity values (≥ 98%) shared with strain K601^{T} (Dullius et al., 2011, Morohoshi et al., 2016, Ntougias et al., 2015, Oceguera-Cervantes et al., 2007).

8.2. Cell morphology:

The cells of *Alicycliphilus denitrificans* strain K601^{T} are Gram-negative, non-spore forming, motile short rods, 0.6 µm wide and 1-2 µm long (Dangel et al. 1988, Mechichi et al., 2003, Weelink et al 2008). A similar cell morphology is observed in other species members, strains BC and KN Bun08 (Dullius et al., 2011, Oosterkamp et al., 2013, Weelink et al., 2008).

8.3. Colonial and cultural characteristics:

On solid agar medium (Luria-Bertani agar), after 48 h of incubation at 30 ºC, the type strain of *Alicycliphilus denitrificans* forms circular (up to 4 mm diameter), convex, white colonies (Vaz-Moreira et al., 2017). Under the same conditions, *A. denitrificans* BQ1 forms small (1-2 mm diameter) creamy colonies with a pale pink-coloured centre (Solís-González and Loza-Tavera, 2019).

8.4. Nutrition and growth conditions:

The type strain of *Alicycliphilus denitrificans* grows well in mineral medium with a wide variety of single carbon sources, without vitamins requirement (Dangel et al., 1988, Mechichi et al., 2003) under aerobic and anoxic conditions. It also grows well in complex media such as Luria-Bertani agar, under aerobic conditions. The mineral medium used for routine cultivation of *A. denitrificans* strain K601^T contains per liter of distilled water: 1.08 g KH_2PO_4, 5.6 g K_2HPO_4, 0.54 g NH_4Cl, 0.15 g $CaCl_2.2H_2O$, 0.2 g $MgSO_4{\cdot}7H_2O$, 1 mL trace element solution SL-10 (Widdel et al., 1983), 1 mL selenite/tungstate solution (Tschech and Fuchs, 1987), 1 mL vitamin solution VL-7 (Pfennig, 1978), and 1 mM cyclohexanol as carbon source. For growth under anoxic conditions, 1.27 g $NaNO_3$ is supplied as the final electron acceptor and the medium is flushed with oxygen-free nitrogen (Mechichi et al., 2003).

Under both aerobic and anoxic conditions, the optimal growth of the type strain of *A. denitrificans* occurs at 28-30 °C, and pH 7.2–7.4 (Mechichi et al., 2003). Under anoxic conditions and with cyclohexanol as a single source of carbon and energy, no growth occurs below 4 °C or pH 6.3 and above 40 °C, or pH 9.1 (Dangel et al., 1988).

8.5. Metabolism:

The type strain of *Alicycliphilus denitrificans* is a facultative anaerobe. Nitrate is reduced to nitrite, which is further reduced to nitrogen. It is not able to use sulfate, sulfite, fumarate or chlorate as electron acceptor (Mechichi et al., 2003, Oosterkamp et al., 2013). In contrast, strain BC is capable of chlorate reduction, besides of oxygen and nitrate (Oosterkamp et al., 2013, Weelink et al., 2008). The capacity of strain BC to use chlorate as electron acceptor relies on the fact that the key genes of chlorate reduction are located on a mega-plasmid (pAlide01), which is absent in strain K601^T (Oosterkamp et al., 2013). *A. denitrificans* comprises chemo-organotrophs able to assimilate carbon sources that include organic acids and aromatic and alicyclic compounds (Dangel et al., 1988, Mechichi et al., 2003). *A. denitrificans* members differ in the profile of carbon sources metabolized, as well as in the diversity of terminal electron acceptors used (Oosterkamp et al., 2013, Solís-González and Loza-Tavera, 2019).

A. denitrificans strain K601^T degrades cyclohexanol both aerobically and anaerobically with nitrate as electron acceptor (Dangel et al., 1988). Strain KN Bun08 also reported as capable of using cyclohexanol, demonstrated this property under aerobiosis (Dullius et al., 2011, Solís-González and Loza-Tavera, 2019). Cyclohexanol mineralization may involve the formation of intermediaries such as cyclohexanone, 2-cyclohexenone, 3-hydoxycyclohexanone, 1,3-cyclohexanedione, and 5-oxocaproic acid, which can enter the beta-oxidation pathway, as proposed by different authors (Dangel et al., 1989, Oosterkamp et al., 2013). In contrast with the abovementioned *A. denitrificans* strains, strain BC cannot use cyclohexanol, neither aerobically nor anaerobically, including when chlorate is supplied as final electron acceptor (Oosterkamp et al., 2013, Weelink et al., 2008).

A. denitrificans degrade benzene and toluene with oxygen, but not under denitrifying conditions. Probably through the activity of a phenol monooxygenase, benzene and/or toluene are hydroxylated to (methyl-)phenol and subsequently to (methyl-)catechol, which seems to be further degraded through the meta-cleavage pathway into acetyl-CoA that can enter the citric acid cycle (Oosterkamp et al., 2013). Strain BC also contains all the genes essential for ortho-cleavage of catechol, in contrast to strain K601^T, where based on the genome analysis this pathway seems to be incomplete (Oosterkamp et al., 2013).

Strain BC, but not strain K601^T, is also capable of benzene and toluene degradation using chlorate as electron acceptor (Oosterkamp et al., 2013, Weelink et al., 2008). Such capability seems to depend on the production of oxygen from chlorate that, as electron acceptor, is reduced to chloride, supporting in this way oxygen-dependent pathways (Oosterkamp et al., 2013, Weelink et al., 2008).

Strain KN Bun08 is able to degrade acetone using both oxygen and nitrate as final electron acceptors, whereas strain BC only grows with this substrate in the presence of nitrate (Dullius et al., 2011, Oosterkamp et al., 2015). Through the activity of an ATP-dependent acetone-carboxylase enzyme, also present in strain K601^T, acetone is transformed into acetoacetate and AMP (Dullius et al., 2011). Further degradation steps may include the activity of an AMP-dependent synthetase/ligase, which converts acetoacetate to acetoacetyl-CoA, cleaved into two acetyl-CoA by an acetyl-CoA acetyltransferase (Dullius et al., 2011, Oosterkamp et al., 2015). According to Oosterkamp and collaborators (2015), poly-beta-hydroxybutyrate accumulation by strain BC growing with acetone may be due to a putative aldehyde dehydrogenase, which catalyzes the transformation of the surplus acetoacetate into that energy and carbon storage compound.

In contrast to *A. denitrificans* K601^T and BC, strains BQ1 and BQ8 under aerobic conditions are able to grow and degrade Hydroform, a commercial surface-coating polyurethane (Oceguera-Cervantes et al. 2007; Solís-González and Loza-Tavera, 2019). The activity of these strains on Hydroform was evidenced by the formation of holes, as observed by scanning electron microscopy, and by the increase carbonyl and amine signals, measured by Fourier transform infra-red spectroscopy (Oceguera-Cervantes et al. 2007; Solís-González and Loza-Tavera, 2019). Also strain BQ8 demonstrates polymer degrading activity against the ester and urethane groups of polyurethane foams synthesized from adipic acid or phthalic anhydride, probably due to the action of extra-cellular and membrane bound esterases (Pérez-Lara et al., 2016, Solís-González and Loza-Tavera, 2019).

Strain BQ1, but not strains BC and K601^T, is able to degrade N-methylpyrrolidone, an additive of Hydroform, under aerobic conditions (Solís-González et al., 2018). Based on the reactions of the proteins encoded by the six-gene operon *nmp*ABCDEF found in this strain, N-methylpyrrolidone is putatively hydrolysed into gamma-N-methylaminobutyric acid, deaminated to succinic-semialdehyde, and finally converted into succinate through the activity of a N-methylhydantoin amidohydrolase, an amino acid oxidase and a semialdehyde dehydrogenase, respectively (Solís-González et al., 2018, Solís-González and Loza-Tavera, 2019)

8.6. Chemotaxonomic characteristics:

According to Mechichi et al. (2003), the predominant fatty acids of *A. denitrificans* strain K601^T are $C_{16:1}$ $\omega 7c$ (37%), $C_{16:0}$ (24%), and $C_{18:1}$ $\omega 7c$ (21%). Other fatty acids occurring in smaller amounts include $C_{10:0}$ 3-OH, $C_{12:0}$, $C_{15:0}$, and $C_{17:0}$ cyclo. According to Oosterkamp et al. (2013), the fatty acid methyl ester patterns of strains BC and K601^T are similar. Based on the type strain K601^T analysis, the major respiratory quinone is ubiquinone 8 and the major polar lipids are phosphatidylethanolamine, phosphatidylglycerol, and diphosphatidylglycerol (Vaz-Moreira et al., 2017).

8.7. Genome:

The complete genome of the *Alicycliphilus denitrificans* type strain K601^T is available under the DDBJ/EMBL/GenBank accession no. CP002657 (chromosome) and CP002658 (plasmid). The complete genome has 5.1 Mbp, with a chromosome with approximately 5.0 Mbp and a plasmid with 75.5 kbp. In total 4899 genes codify 4696 proteins (Oosterkamp et al., 2013).

The complete genome of the strain BC is available under the DDBJ/EMBL/GenBank accession no. CP002449 (chromosome), CP002450 (megaplasmid), and CP002451 (plasmid). The genome is slightly smaller than the genome of the type strain, with 4.8 Mbp, comprising a chromosome with 4.6 Mbp, a megaplasmid with 119.7 kbp, and a plasmid with 79.0 kbp. In total 4709 genes codify 4542 proteins (Oosterkamp et al., 2013).

The draft genomes of several other strains, as well as metagenome assembled genomes, allocated to *Alicycliphilus* are available at the DDBJ/EMBL/GenBank (Table 1).

<Table 1 near here>

8.8. Ecology:

Members of the genus *Alicycliphilus* have been isolated mainly from enrichment cultures of samples collected from polluted habitats. *Alicycliphilus denitrificans* strain K601^{T} was recovered from anaerobic sewage sludge from a municipal wastewater treatment plant in Konstanz (Germany) enriched in mineral medium with cyclohexanol and nitrate as electron donor and acceptor, respectively (Dangel et al. 1988). Strain BC was co-isolated with organisms closely related with *Zoogloea resiniphila*, *Mesorhizobium* sp. and *Stenotrophomonas acidaminiphila*, from a benzene-degrading, chlorate-reducing enrichment culture with mixed material from a wastewater treatment plant and soil samples obtained from a location contaminated with benzene (Weelink et al., 2008, Weelink et al., 2007). Strains BQ1 and BQ8 were recovered from an enrichment culture in mineral medium with flexible foam pieces of a commercial polyester polyurethane collected from the ground in an open-air refuse dump in Mexico (Oceguera-Cervantes et al., 2007). The acetone-degrading strain KN Bun08 was recovered from sediment of a small tarn in Germany, enriched with butanone and nitrate as the sole source of carbon and energy and electron acceptor, respectively (Dullius et al., 2011). Strain ADC-16 was isolated from an activated sludge intermittently aerated pulse fed bioreactor treating municipal wastewater and operating under high organic loading conditions, together with other anthracene-degrading organisms, closely related with species such as *Microbacterium arabinogalactanolyticum*, *Shinella zoogloeoides*, and *Paracoccus huijuniae* (Ntougias et al., 2015).

The Cr(VI)-reducing and resistant strain SC15, according to the authors affiliated to the genus *Alicycliphilus*, was isolated from direct dilution and spread plating of water collected in the Igarapé do Quarenta stream, an affluent of Rio Negro (Amazon, Brazil), in an area of discharge of domestic sewage and industrial effluents (Teles et al., 2018). Other Cr(VI)-reducing and resistant organisms co-isolated with strain SC15 were related to genera such as *Bacillus*, *Vagococcus*, *Acinetobacter*, *Enterobacter*, *Proteus* and *Acidovorax* (Teles et al., 2018). Also strain B1, an N-acylhomoserine lactone (quorum-sensing signalling molecule) producing organism, was isolated after dilution and spread plating of an activated sludge sample collected in the wastewater treatment plant of an electronic component factory in Japan (Morohoshi et al., 2016, Okutsu et al., 2015).

The co-occurrence network analysis of nitrite-reductase *nir*S gene-based Illumina sequencing data, identified *Alicycliphilus*, together with *Dechlorospirillum*, *Dechloromonas*, *Pseudogulbenkiania*, and *Paracoccus* as the keystone taxa in the denitrifying bacterial communities of different Chinese urban lakes (Zhang et al., 2018). Based on similar sequencing data, *Alicycliphilus* was found as the dominant genus of the denitrifying bacterial communities of activated sludge of different wastewater treatment plants located in north and west areas of China, followed by *Paracoccus*, *Thauera* or *Pseudomonas* (Zhang et al., 2019).

Organisms affiliated to *Alicycliphilus* have been also identified through metagenomic assembly. Examples are the genomes of the strains 69-12 and Bin_7_3, recovered from the metagenomes of a thiocyanate ramp bioreactor in South Africa and wastewater from an advanced water purification facility in California, respectively (Table 1).

9. ENRICHMENT/ISOLATION PROCEDURES:

Alicycliphilus denitrificans strain K601^T was isolated from an enrichment culture established from anaerobic sewage sludge from a German municipal sewage plant with 1 mM cyclohexanol as sole carbon source and 5 mM nitrate as electron acceptor (Dangel et al., 1988). Infusion bottles containing the mineral medium described above for routine cultivation were gassed with N_2, sealed with Latex rubber septa and inoculated with 10% (v/v) of anaerobic samples. Cultures were incubated at 28-30 °C. After five transfers into fresh culture medium three pure cultures were obtained by repeatedly applying agar shake series (Dangel et al., 1988, Weelink et al., 2007).

Strain BC was isolated from an enrichment culture established from mixed material from a wastewater treatment plant and soil samples obtained from a location contaminated with benzene. Cultures were incubated in 120-mL serum bottles containing 40 mL strictly anaerobic AW-1-sulfate medium at 30 °C, 50 rpm. Benzene and chlorate were supplied as a 20 mM water-saturated and a 0.4 M $NaClO_3$ stock solution, respectively. For strain isolation, samples of the stable enrichment culture were serially diluted and spread on AW-1-sulfate medium with 0.125 g L^{-1} fermented yeast extract, 0.25 mM benzene and 10 mM chlorate, as nutrient supplement and electron donor and acceptor, respectively. Colonies were picked from the highest dilutions and transferred to fresh plates. This procedure was repeated four times (Weelink et al., 2008).

10. MAINTENANCE PROCEDURES:

Stock cultures of the type strain of *Alicycliphilus denitrificans* can be obtained by growing in the mineral medium described above using 125 mL infusion bottles (75 mL) under anaerobic conditions at 28 °C, stored at room temperature and subcultured weekly (Dangel et al., 1989).

Alicycliphilus denitrificans can be also maintained on complex solid media such as Luria–Bertani agar for short periods or in nutritive broth with 15% (v/v) glycerol at -80 ºC.

11. DIFFERENTIATION OF THE GENUS *ALICYCLIPHILUS* FROM OTHER GENERA:

The closest related genera to *Alicycliphilus* is *Oryzisolibacter* (see gbm01828). Differentiating characteristics between *Alicycliphilus denitrificans* K601^T and *Oryzisolibacter propanilivorax* EPL6^T are given in Table 1 of the *Oryzisolibacter* chapter (see gbm01828). Other related genera include *Diaphorobacter* (see gbm01826), *Acidovorax* (see gbm00943), *Pseudoacidovorax*, *Melaminivora* (see gbm01827), *Comamonas* (see gbm00945) and *Simplicispira*. The relatively close taxonomic relatedness between genera within the family *Comamonadaceae* (Willems, 2014) together with the wide metabolic versatility of the organisms affiliated to these last taxa make it difficult to differentiate *Alicycliphilus* based on phenotypic and chemotaxonomic traits.

12. TAXONOMIC COMMENTS:

Based on the 16S rRNA gene sequence analysis, *Alicycliphilus denitrificans* is a member of the family *Comamonadaceae* (see fbm00182). *Oryzisolibacter propanilivorax* is the nearest neighbour species, sharing 97.0% 16S rRNA gene pairwise sequence similarity with the type strain of *Alicycliphilus denitrificans.*

Slightly lower values (96.8-96.2%) are shared between the type strain of *Alicycliphilus denitrificans* and those of the four validly named species of *Diaphorobacter*, as well as with *"D. ruginosibacter"* strain BN30. In addition, the type strain of *Alicycliphilus denitrificans* shares between 96.7 and 96.1 % 16S rRNA gene pairwise sequence similarity with the type strains of specific species of the genera *Acidovorax (Ac. wautersii*, *Ac. caeni*, *Ac. soli*, *Ac. kalamii*, *Ac. citrulli*, *Ac. cattleyae*, *Ac. orizae*, *Ac. avenae*, *Ac. valerianellae*), *Pseudoacidovorax* (*P. intermedius*), *Melaminivora* (*M. alkalimesophila*), *Comamonas* (*C. humi*, *C. zonglianii*), and *Simplicispira* (*S. limi*, *S. lacusdiani*). Lower values are shared between *Alicycliphilus denitrificans* strain K601^{T} and the type strains of the other nine *Acidovorax* (94.9-95.9%), twenty-one *Comamonas* (93.8-95.7%), five *Simplicispira* (94.9-95.9%), and one *Melaminivora* (95.7%) validly named species.

13. LIST OF SPECIES OF THE GENUS *ALICYCLIPHILUS*:

1. ***Alicycliphilus denitrificans*** Mechichi, Stackebrandt and Fuchs, 2003, 149^{VP}

denitrificans [de.ni.tri'fi.cans. L. prep. *de* away from; L. n. *nitrum* soda; N.L. n. *nitrum* nitrate; N.L. v. *denitrifico* to denitrify; N.L. part. adj. *denitrificans* denitrifying].

In addition to the characteristics given in the genus description, the type strain shows the following properties:

Under both aerobiosis and denitrifying conditions, it uses L-lactate, pyruvate, propionate, L-malate, crotonate, and fumarate but not benzoate, resorcinol, 2-aminobenzoate, 3-hydroxybenzoate, hydroxyquinol.

Under aerobic conditions, it uses aniline, indole, vanillic acid, acetate, 4-hydroxybenzoate, *m*-cresol, *o*-cresol and *p*-cresol, but not 4-aminobenzoate, 2-naphthoate, biphenyl 2-carboxylate, gentisate, protocatechuate, 3-fluorobenzoate, and 3-chlorobenzoate.

Under denitrifying conditions, it uses monocarboxylic acids (C2–C7), adipate, pimelate, 5-oxocaproate, 2-oxoglutarate, and succinate, but not aniline, phenol, 2-hydroxybenzoate, 4-hydroxybenzoate, *m*-cresol, *o*-cresol, *p*-cresol, vanillate, naphthoate, indole, 1,2-

cyclohexanediol, 1,2-cyclohexanedione, 2-hydroxycyclohexanone,1,4-cyclohexanedione, cyclohexane, formate, D-glucose, D-fructose, D-xylose, and aliphatic alcohols (C1–C8).

The DNA G+C content (mol %) is 66 (HPLC) or 67.9 (genome analysis, GenBank).

Type strain: K601 (=DSM 14773 =CIP 107495)

GenBank accession number (16S rRNA): AJ418042

GenBank accession number (genome): CP002657.1 (chromosome) and CP002658.1 (plasmid pALIDE201)

RELATED ARTICLES:

gbm00943

gbm00945

gbm01826

gbm01827

gbm01828

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Table 1. Examples of draft and metagenome assembled genomes (MAG) of *Alicycliphilus* available at DDBJ/EMBL/GenBank, at the moment of writing.

Organism	Origin	Accession number	No. scaffolds/ contigs	Size (Mbp)	GC content (%)	Genes	Proteins
Strain B1	Industrial wastewater plant, Japan	GCA_000974645.1	59	7.5	67.3	7083	5927
Strain BQ1	Decomposed soft foam, Nezahualcoyotl, Mexico	GCA_002250385.2	12	4.7	69.0	4374	4253
Strain CD02	Sludge from N_2O producing bioreactor, USA	GCA_002894355.1	52	4.8	68.3	4462	4298
MAG 69-12	Thiocyanate ramp bioreactor, Cape Town, South Africa	GCA_001897775.1	96	4.6	68.5	4289	3956
MAG Bin_7_3	Advanced water purification facility, California, USA	GCA_008017235.1	297	3.0	66.2	3124	2950
MAG UBA880	Wood, New York, USA	GCA_002294305.1	141	3.0	66.7	n.a.	n.a.
MAG UBA2076	Metal, New York, USA	GCA_002331945.1	267	2.3	67.3	n.a.	n.a.
MAG UBA3448	Metal/plastic, New York, USA	GCA_002378445.1	108	2.4	65.8	n.a.	n.a.
MAG UBA4115	Wood, New York, USA	GCA_002383145.1	265	2.9	65.5	n.a.	n.a.
MAG UBA6560	Metal/plastic, New York, USA	GCA_002434305.1	13	3.5	68.8	n.a.	n.a.
MAG UBA6761	Metal, New York, USA	GCA_002331945.1	244	2.2	65.6	n.a.	n.a.
MAG UBA7619	Metal/plastic, New York, USA	GCA_002484205.1	20	4.7	68.9	n.a.	n.a.

n.a., not available