Description of *Pseudochrobactrum* gen. nov., with the two species *Pseudochrobactrum asaccharolyticum* sp. nov. and *Pseudochrobactrum saccharolyticum* sp. nov.

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Two Gram-negative, rod-shaped, oxidase-positive, non-spore-forming, non-motile bacteria (CCUG 46016^T and CCUG 33852^T), isolated from a knee aspirate of a 66-year-old man and an industrial glue, respectively, were studied for their taxonomic position. On the basis of chemotaxonomic data [i.e. major ubiquinone (Q-10), major polar lipids (phosphatidylethanolamine, phosphatidylglycerol and phosphatidylcholine) and major fatty acids (C_{18:1}ω7c and C_{19:0} cyclo ω8c)] and 16S rRNA gene sequence similarity, both strains belong to the *Alphaproteobacteria*. The presence of spermidine and putrescine as the predominant polyamines in CCUG 46016^T were in agreement with its phylogenetic affiliation in the vicinity of the genus *Ochrobactrum*. 16S rRNA gene sequence similarities between both strains and established species within the genera *Bartonella*, *Ochrobactrum* and *Brucella* were less than 95 %. Although both organisms showed highest 16S rRNA gene sequence similarity to members of *Brucella*, phenotypic features (including chemotaxonomic features) were more like those of members of the genus *Ochrobactrum*. Sequence comparison of the *recA* genes confirmed the separate phylogenetic position of the two strains. On the basis of DNA–DNA pairing results and physiological and biochemical data, the two strains can be clearly differentiated from each other and from all known *Ochrobactrum* species. It is evident that these organisms represent two novel species in a new genus, *Pseudochrobactrum* gen. nov., for which the names *Pseudochrobactrum asaccharolyticum* sp. nov. (the type species, type strain CCUG 46016^T = CIP 108977^T) and *Pseudochrobactrum saccharolyticum* sp. nov. (type strain CCUG 33852^T = CIP 108976^T) are proposed.

The genus *Ochrobactrum* was first described by Holmes *et al.* (1988). At present, the genus comprises five species:

Abbreviation: PME, phosphatidylmonomethylethanolamine.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains CCUG 46016^T and CCUG 33852^T are AM180485 and AM180484, respectively, and those of the partial *recA* sequences of strains CCUG 46016^T and CCUG 33852^T are AM118081 and AM118082.

A multiple sequence alignment of partial *recA* gene sequences and a two-dimensional TLC of the polar lipids of CCUG 46016^T are available as supplementary material in IJSEM Online.

Ochrobactrum anthropi Holmes *et al.* 1988, *Ochrobactrum intermedium* Velasco *et al.* 1998, *Ochrobactrum tritici* Lebuhn *et al.* 2000, *Ochrobactrum grignonense* Lebuhn *et al.* 2000 and *Ochrobactrum gallinifacis* Kämpfer *et al.* 2003. The status of '*Ochrobactrum lupini*' (Trujillo *et al.*, 2005) is not yet clear.

On the basis of 16S rRNA gene sequence data, members of the genus *Brucella* are most closely related to members of the genus *Ochrobactrum*; however, they clearly differ on the basis of serology, Western blot profiles and protein patterns (Velasco *et al.*, 1998). An overview of the genus *Brucella* is

provided by Moreno & Moriyon (2001). Bacteria of the genus *Bartonella* are aerobic, fastidious, oxidase-negative, slow-growing organisms. Currently, 19 species are recognized, all of which are associated with mammalian hosts and can be differentiated on the basis of genetic analyses (Breitschwerdt & Kordick, 2000; Bermond *et al.*, 2002; Pitulle *et al.*, 2002; Zeaiter *et al.*, 2002). Based on 16S rRNA gene sequence comparisons, members of the genus *Bartonella* also fall into the *Alphaproteobacteria*, with species of *Brucella*, *Rhizobium* and *Agrobacterium* as closest relatives. In general, the genus *Bartonella* is relatively homogeneous, with members exhibiting greater than 95 % similarity among aligned 16S rRNA gene sequences.

Strain CCUG 46016^T was isolated on blood agar at 37 °C from a knee aspirate of a 66-year-old man in Uddevalla, Sweden. Strain CCUG 33852^T was isolated on blood agar at 37 °C from an industrial glue in Göteborg, Sweden. Both strains formed beige-coloured colonies on blood agar. Subcultivation was done on tryptone soy agar (TSA) at 28 °C for 48 h. On this agar, both organisms were able to grow at 15–45 °C, but not at 10 or 50 °C. Growth at 30 °C was also observed on nutrient agar, MacConkey agar and R2A agar (all from Oxoid).

Gram-staining was performed as described by Gerhardt *et al.* (1994). Cell morphology was observed under a Zeiss light microscope at $\times 1000$, with cells grown for 3 days at 28 °C on TSA. The 16S rRNA gene was analysed as described by Kämpfer *et al.* (2003). Phylogenetic analysis was performed using the ARB (Strunk *et al.*, 2000; Ludwig *et al.*, 2004) and MEGA version 2.1 (Kumar *et al.*, 2001) software packages after multiple alignment of data by CLUSTAL X (Thompson *et al.*, 1997). The sequenced lengths of the 16S rRNA genes of strains CCUG 46016^T and CCUG 33852^T were 1457 bp and 1401 bp, respectively (GenBank accession nos AM180485 and AM180484, respectively). Nucleotide sequence similarities were below 95 % with all species of the genera *Bartonella* (94.2 and 94.3 %, respectively), *Brucella* (94.6–94.8 %) and *Ochrobactrum* (93.8–94.6 %) with validly described names. The phylogenetic tree shown in Fig. 1 results from a neighbour-joining reconstruction modified after comparison with maximum-parsimony and maximum-likelihood trees and with the use of different datasets as reported previously (Albert *et al.*, 2005). The multifurcation shown in the tree represents branching orders that could not be resolved by the multiple reconstructions as recommended by Ludwig *et al.* (1998). In all calculations, both sequences appeared on a single phylogenetic branch, indicating their independent affiliation.

Partial *recA* sequences of some *Ochrobactrum* type strains and strains of *Brucella* species were amplified by PCR with primers *recA*-BrucOchro-f (5'-ATGTCTCAAATTCATT-GCGAC-3') and *recA*-BrucOchro-r (5'-AGCATCTTCTT-CCGGTCCGC-3') to generate a 1065 bp fragment. Partial *recA* sequences (909 bp) of strains CCUG 46016^T and CCUG 33852^T were amplified by PCR with primers *RecA*-PsOchro-f (5'-AAGGCTCTGGACGCGGCACT-3')

Fig. 1. 16S rRNA gene sequence phylogenetic neighbour-joining tree reconstruction showing the affiliation of *Pseudochrobactrum* species to their closest relatives. The tree topology shows the consensus of neighbour-joining, maximum-parsimony and maximum-likelihood algorithms with different datasets, as implemented in the ARB software package (Ludwig *et al.*, 2004). In cases where the branching order was irresolvable, a multifurcation was drawn (Ludwig *et al.*, 1998). Bar, 5 % sequence dissimilarity.

and *RecA*-PsOchro-r (5'-CGCAAGGTCAGTTCAATCTC-AT-3').

Subsequent sequencing and sequence comparison analyses of the *recA* genes revealed multiple sequence variations within *recA* among the investigated strains (see the multiple sequence alignment available as Supplementary Fig. S1 in IJSEM Online). The similarity between *recA* sequences of CCUG 46016^T and CCUG 33852^T was 91 % over 909 nt. Lower similarity values were observed with species of *Brucella* (80.1–81.0 %), *Ochrobactrum* (80.7–81.4 %) and *Bartonella* (76.3 %). CCUG 46016^T and CCUG 33852^T shared several motifs within *recA* that were absent from sequences in species of *Bartonella*, *Brucella* and *Ochrobactrum* (Supplementary Fig. S1).

Strains CCUG 46016^T and CCUG 33852^T were found as separate branches in the phylogenetic tree of *recA* sequences (909 nt) (Fig. 2). The tree was constructed using the online accessible bioinformatics tools of HUSAR (available from <http://genius.embnet.dkfz-heidelberg.de/menu/w2h/w2hdkfz>) from CLUSTAL W using CLUSTREE neighbour-joining and the Kimura two-parameter model; 1000 bootstrap resamplings were performed. The tree was rooted using the sequence of *Mesorhizobium loti* MAFF 303099 as an outgroup.

Results of chemotaxonomic analyses are given in the genus description. The following compounds were analysed: respiratory quinones (Tindall, 1990; Altenburger *et al.*, 1996), polyamines (Busse & Auling, 1988; Busse *et al.*, 1997), polar lipids (Ventosa *et al.*, 1993) and fatty acids (Kämpfer & Kroppenstedt, 1996). The presence of the quinone system ubiquinone Q-10 (97 %) supports affiliation of CCUG 46016^T and CCUG 33852^T to the *Alphaproteobacteria*, where the majority of species have Q-10 as the major quinone (Lechner *et al.*, 1995; Yokota *et al.*, 1992). In addition, CCUG 46016^T contained small amounts of Q-9 (3 %). Strain CCUG 46016^T contained the following polyamines [in $\mu\text{mol (g dry weight)}^{-1}$]: spermidine, 63.8; putrescine,

Fig. 2. Phylogenetic tree reconstruction with *recA* sequences (909 nt) using CLUSTREE neighbour-joining analysis and the Kimura two-parameter model. Bar, 0.1 divergent residues per site. The significance of each branch is indicated by a bootstrap value from 1000 repetitions. The tree was rooted using the sequence of *Mesorhizobium loti* MAFF 303099 as an outgroup.

11.6; diaminopropane, 3.8; spermine, 0.5; and cadaverine, 0.1. This profile is similar to those reported for species of *Ochrobactrum* (Lechner *et al.*, 1995; Hamana & Takeuchi, 1998; Kämpfer *et al.*, 2003), but distinct from the polyamine patterns of members of the genera *Rhizobium*, *Mesorhizobium*, *Sinorhizobium*, *Aminobacter*, *Pseudaminobacter*, *Phyllobacterium* and *Mycoplana*, which have been shown to contain *sym*-homospermidine in at least minor amounts (Busse & Auling, 1988; Hamana & Takeuchi, 1998; Kämpfer *et al.*, 1999). The polar lipid profiles of CCUG 46016^T (TLC available as Supplementary Fig. S2 in IJSEM Online) and CCUG 33852^T (not shown) were almost identical and were similar to those of species of the related genera *Aminobacter*, *Pseudaminobacter*, *Ochrobactrum* (Kämpfer *et al.*, 1999, 2003), *Brucella* (Thiele *et al.*, 1971; H.-J. Busse, unpublished results), *Sinorhizobium* (Geiger *et al.*, 1999) and *Mesorhizobium* (Choma & Komanićka, 2002). The absence of unknown aminolipid AL2 shown to be present in *O. gallinifaecis* Iso 196^T, *O. anthropi* LMG 7991 (Kämpfer *et al.*, 2003), *O. anthropi* CCUG 24695^T and *O. intermedium* LMG 3301^T (B. Huber and H.-J. Busse, unpublished results) distinguishes CCUG 46016^T and CCUG 33852^T from *Ochrobactrum* species. Phosphatidylmethylethanolamine shared almost identical chromatographic behaviour with the unknown aminolipid AL1. The existence of two lipids at almost the same position in the two-dimensional TLC (spot between phosphatidylglycerol and phosphatidylethanolamine; available as supplementary material in IJSEM Online) could be clearly identified when the plate was first sprayed with ninhydrin reagent and afterwards with molybdenum blue reagent. Only the lower part of the ninhydrin-positive spot stained blue with molybdenum blue reagent. Polar lipid profiles did not clearly distinguish CCUG 46016^T and CCUG 33852^T from two analysed *Brucella* strains (results not shown). However, the content of phosphatidylmonomethylethanolamine (PME) might be a distinguishing characteristic. In *Brucella* species, this lipid was not detectable or was present only in minor amounts,

whereas it was a major compound in the polar lipid profiles of CCUG 46016^T and CCUG 33852^T. However, the suitability of PME as a distinguishing trait would have to be substantiated by analysis of additional strains. Unfortunately, no information is available on polar lipids in *Bartonella* nor could strains of this genus be made available for our study. The fatty acid profiles of strains CCUG 46016^T and CCUG 33852^T (Table 1) revealed mainly C_{19:0} cyclo ω 8c (7.3–14.3%), C_{18:1} ω 7c (74.6–74.9%), C_{16:0} (1.9–5.6%) and C_{18:0} (7.4–10.9%). The presence of C_{19:0} cyclo ω 8c appears to be useful for differentiation of CCUG 46016^T and CCUG 33852^T from *Brucella* and *Bartonella* species. Whereas *Brucella* species were shown to contain this fatty acid either only in traces (*Brucella canis*; Dees *et al.*, 1981) or as a predominant compound (>34% in the four other species; Dees *et al.*, 1980; 1981; Coloe *et al.*, 1984), it was completely absent in fatty acid profiles of *Bartonella* species (Welch *et al.*, 1992; Regnery *et al.*, 1992; Daly *et al.*, 1993). However, this observation has to be considered with care because the data for *Brucella* and *Bartonella* species were obtained from biomass grown on blood-supplemented media.

Results of the physiological characterization are given in the species description and in Table 2. Methods used have been described previously (Kämpfer *et al.*, 1991). Both organisms can be clearly differentiated on the basis of several tests. A comparison with the physiological profiles of *Bartonella* species is difficult. As pointed out by Breitschwerdt & Kordick (2000), biochemical profiles of *Bartonella* species are fairly neutral. Members of the genus *Brucella* are biochemically quite heterogeneous.

The G + C content for strain CCUG 46016^T was determined as described by Ziemke *et al.* (1998). DNA–DNA hybridization experiments were performed with CCUG 46016^T and type strains of all *Ochrobactrum* species using the method described by Ziemke *et al.* (1998), except that, for nick translation, 2 μ g DNA was labelled during a 3 h incubation at 15 °C. Strain CCUG 46016^T showed relatively low DNA–DNA relatedness to *O. anthropi* LMG 3331^T (46%), *O. intermedium* LMG 3301^T (42%), *O. tritici* LMG 18957^T (47%), *O. grignonense* DSM 13338^T (53%) and *O. gallinifaecis* Iso 196^T (38%). DNA–DNA hybridization values between strains CCUG 46016^T and CCUG 33852^T were 41.9%. Pooled standard deviations of all hybridization experiments were between 3.9 and 7.9%.

From the results of 16S rRNA gene and *recA* sequencing and from the physiological characteristics, it is evident that strains CCUG 46016^T and CCUG 33852^T differ from each other and from all species of the genera *Bartonella*, *Brucella* and *Ochrobactrum*. For this reason, a new genus with two novel species is proposed.

Description of *Pseudochrobactrum* gen. nov.

Pseudochrobactrum (Pseud.och.ro.bac'trum. Gr. adj. *pseudes* false; N.L. neut. n. *Ochrobactrum* a bacterial genus name; N.L. neut. n. *Pseudochrobactrum* false *Ochrobactrum*).

Table 1. Major fatty acid composition (%) of strains CCUG 46016^T and CCUG 33852^T and type strains of the genus *Ochrobactrum*

Strains: 1, CCUG 46016^T; 2, CCUG 33852^T; 3, *O. gallinifaecis* Iso 196^T; 4, *O. intermedium* LMG 3301^T; 5, *O. anthropi* LMG 3331^T; 6, *O. grignonense* DSM 13338^T; 7, *O. tritici* LMG 18957^T; 8, '*O. lupini*' LUP21 (data from Trujillo *et al.* 2005). All strains were grown on TSA at 28 °C for 48 h prior to fatty acid analysis. For unsaturated fatty acids, the position of the double bond is located by counting from the methyl (ω) end of the carbon chain; *cis* and *trans* isomers are indicated by the suffixes *c* and *t*, respectively. –, Not detected.

Fatty acid	1	2	3	4	5	6	7	8
Saturated								
C _{12:0}	–	0.7	–	–	–	–	–	–
C _{14:0}	–	–	0.7	–	–	–	–	–
C _{16:0}	5.5	1.9	8.9	3.7	6.6	2.9	3.7	4.2
C _{17:0}	–	–	–	3.1	1.4	1.7	0.9	1.6
C _{18:0}	11.0	7.4	3.7	4.1	8.8	7.2	9.6	3.0
Unsaturated								
C _{13:1} at 12–13	–	–	–	–	0.6	0.7	–	–
C _{17:1ω6c}	–	–	–	1.1	–	0.5	–	1.4
C _{18:1ω7c}	74.9	74.6	28.8	25.8	45.6	31.6	77.9	70.8
C _{18:3ω6c} (6,9,12)	–	0.5	–	–	–	–	–	–
11-methyl-C _{18:1ω7t}	–	–	1.6	1.5	1.0	1.0	–	–
C _{20:1ω7c}	–	–	–	–	–	0.8	–	–
C _{20:2ω6,9c}	–	–	1.1	0.9	0.5	0.8	–	–
Hydroxylated								
C _{18:1} 2-OH	–	–	1.5	1.8	0.6	0.5	1.4	6.2
C _{18:0} 3-OH	–	–	–	–	–	0.5	–	1.0
Summed feature 3*	0.8	–	3.7	0.7	1.1	1.0	0.7	2.3
Cyclopropane acids								
C _{17:0} cyclo	–	–	2.9	–	0.8	–	–	–
C _{19:0} cyclo ω 8c	7.3	14.3	47.2	57.4	32.7	50.2	5.9	4.3
Unknown 13.957†	–	–	–	–	–	0.2	–	–
Unknown 14.959†	0.6	0.9	–	–	0.3	0.7	–	–

*Summed features are groups of two or three fatty acids that cannot be separated by GLC with the MIDI system. Summed feature 3 contains C_{16:1 ω 7c} and/or C_{15:0} iso 2-OH.

†Unknown fatty acids have no name listed in the peak library file of the MIDI system and therefore cannot be identified; they are referred to by their equivalent chain length.

Cells are non-motile, non-spore-forming rods (approx. 2 μ m in length). Gram-negative and oxidase-positive, showing an oxidative metabolism. The quinone system consists mainly of Q-10. Polyamine patterns comprise spermidine and putrescine as major compounds and 1,3-diaminopropane and spermine in minor amounts. Predominant polar lipids are phosphatidylethanolamine, phosphatidylmonomethylethanolamine, phosphatidylglycerol, diphosphatidylglycerol and phosphatidylcholine. Additionally, moderate amounts of phosphatidylmethylethanolamine and unknown aminolipid AL1 and small amounts of unknown phospholipid PL1 and five unknown lipids (L1–L5) are detected. Fatty acid profiles contain large amounts of C_{18:1 ω 7c} and moderate amounts of C_{18:0} and C_{19:0} cyclo ω 8c. Negative for a *Brucella abortus*- and *Brucella melitensis*-specific antigen (according to the assay of Bailly *et al.*, 1992). In *recA* sequence analyses,

most closely related to species of *Brucella* (80%) and *Ochrobactrum* (81%), followed by *Bartonella* (76%). Species of the genus can be differentiated from *Bartonella* species by a positive oxidase reaction, non-fastidious growth and utilization of several organic acids (Table 2). The type species is *Pseudochrobactrum asaccharolyticum*.

Description of *Pseudochrobactrum asaccharolyticum* sp. nov.

Pseudochrobactrum asaccharolyticum (a.sac.cha.ro.ly'ti.cum. Gr. pref. *a* not; Gr. n. *saccharon* sugar; N.L. neut. adj. *lyticum* able to lyse from Gr. adj. *lutikos* able to loose; N.L. neut. adj. *asaccharolyticum* not digesting sugar).

Shares all characteristics listed in the genus description. Good growth occurs on R2A agar, TSA, nutrient agar and

Table 2. Physiological characteristics of strains CCUG 46016^T and CCUG 33852^T and type strains of the genus *Ochrobactrum*

Strains: 1, CCUG 46016^T; 2, CCUG 33853^T; 3, *O. gallinifaecis* Iso 196^T; 4, *O. intermedium* LMG 3301^T; 5, *O. anthropi* LMG 3331^T; 6, *O. grignonense* DSM 13338^T; 7, *O. tritici* LMG 18957^T. +, Positive; –, negative; (+), weakly positive; pNA, para-nitroanilide; pNP, para-nitrophenyl. All strains were positive for hydrolysis of L-alanine pNA and weak hydrolysis of bis-pNP phosphate. All strains were negative for hydrolysis of aesculin, pNP β-D-galactopyranoside, pNP β-D-glucuronide, pNP α-D-glucopyranoside, pNP β-D-glucopyranoside, pNP phosphorylcholine and 2-deoxythymidine-5'-pNP phosphate. All strains were also positive for assimilation of acetate, oxoglutarate, L-alanine, L-proline and L-serine. All strains were negative for assimilation of p-arbutin, salicin, putrescine, L-phenylalanine, L-tryptophan, 3-hydroxybenzoate, adipate, itaconate, mesaconate, phenylacetate, α-D-melibiose and azelate. Hydrolysis of aesculin and pNP β-D-galactopyranoside and assimilation of oxoglutarate, L-serine, phenylacetate and α-D-melibiose were also tested using a different method by Holmes *et al.* (1988) with *O. anthropi*; results were in agreement with those of this study. Adipate assimilation was also tested using a different method by Velasco *et al.* (1998) with *O. intermedium*; results were in agreement with those of this study.

Test	1	2	3	4	5	6	7
Hydrolysis of:							
pNP phenylphosphonate	–	–	–	–	–	–	(+)
L-Glutamate γ-3-carboxy-pNA	–	–	–	+	(+)	–	(+)
L-Proline pNA ^{a*}	+	+	+	(+)	+	+	(+)
Assimilation of:							
Gluconate	–	–	+	+	+	+	+
L-Arabinose ^b , D-glucose, D-mannose, D-xylose	–	+	+	+	+	+	+
D-Fructose	–	+	–	+	+	+	+
DL-3-Hydroxybutyrate ^b	–	+	–	+	+	+	+
D-Galactose ^b	–	+	+	+	+	+	+
D-Ribose ^b , propionate ^b , fumarate ^b , glutarate, DL-lactate, L-malate ^b , pyruvate ^b , ornithine ^b	–	+	+	+	+	+	+
i-Inositol ^b , D-sorbitol ^b	–	–	–	+	+	+	+
L-Rhamnose ^b , citrate ^{bc}	–	–	–	+	+	+	+
4-Aminobutyrate, β-alanine ^b	–	+	(+)	+	+	+	+
cis-Aconitate	+	+	–	+	+	+	+
D-Maltose ^{bc} , adonitol ^{ab}	–	–	–	+	+	–	+
N-Acetyl-D-glucosamine ^b	–	+	–	+	+	–	+
Sucrose ^{bc}	–	–	–	–	+	–	+
D-Trehalose	–	+	–	–	+	–	+
Maltitol	–	–	–	–	+	–	–
D-Mannitol	–	–	–	–	+	+	+
trans-Aconitate ^b	–	–	–	(+)	–	–	–
D-Cellobiose ^{ab}	–	–	–	+	+	–	–
N-Acetyl-D-galactosamine	–	–	–	+	(+)	+	+
Suberate ^b	–	–	–	–	–	–	+
L-Aspartate ^b	–	+	+	+	+	+	–
4-Hydroxybenzoate	–	–	–	(+)	(+)	–	+
L-Histidine ^b	–	+	+	+	+	+	(+)
L-Leucine ^b	–	–	–	+	+	+	(+)

*Tested using a different method in another study for the type strains of the species listed; results were in agreement with those of this study. a, Leubhn *et al.* (2000) with *O. grignonense*, *O. intermedium*, *O. tritici* and *O. anthropi*; b, Holmes *et al.* (1988) with *O. anthropi*; c, Velasco *et al.* (1998) with *O. intermedium*.

MacConkey agar at 25–30 °C. Beige, translucent and shiny colonies with entire edges form within 24 h on blood agar, with a diameter of approximately 2 mm. Carbon source utilization (none of the sugars were utilized) and hydrolysis of chromogenic substrates (including differentiating characters for all *Ochrobactrum* species) are indicated in Table 2.

Type strain is CCUG 46016^T (=CIP 108977^T), isolated

from a knee aspirate of a 66-year-old man. The G+C content of strain CCUG 46016^T is 50.9 mol%.

Description of *Pseudochrobactrum saccharolyticum* sp. nov.

Pseudochrobactrum saccharolyticum (sac.cha.ro.ly'ti.cum. Gr. n. *saccharon* sugar; N.L. neut. adj. *lyticum* able to lyse

from Gr. adj. *lutikos* able to loose; N.L. neut. adj. *saccharolyticum* digesting sugar).

Good growth occurs on R2A agar, TSA, nutrient agar and MacConkey agar at 25–30 °C. Beige, translucent and shiny colonies with entire edges form within 24 h on blood agar, with a diameter of approximately 2 mm. Carbon source utilization (several sugars were utilized) and hydrolysis of chromogenic substrates (including differentiating characters for all *Ochrobactrum* species) are indicated in Table 2.

The type strain is CCUG 33852^T (= CIP 108976^T), isolated from an industrial glue.

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