Acinetobacter bohemicus sp. nov.,

widespread in natural soil and water ecosystems in the Czech Republic



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AIM

To define the taxonomic status of a phenetically distinct group of 25 environmental Acinetobacter strains which did not belong to any of the known species.

STRAINS

The 25 strains were isolated from soil and water samples collected in natural ecosystems of the Czech Republic (Fig. 1) via selective enrichment in a vigorously aerated mineral medium with acetate. All strains were genotypically unique at the strain level, as revealed by Apal macrorestriction analysis.

An additional large set of reference strains belonging to all known validly named species and genomic species was used in comparative analyses.

100

81

RESULTS and CONCLUSION

The 25 strains formed a genotypically and phenotypically coherent group clearly distinct from the other *Acinetobacter* species based on the results of the following analyses:

- comparative sequence analyses of the *rpoB* and *gyrB* genes (Fig. 2 and Fig. 3)
- whole-cell **MALDI-TOF MS** profiling (Fig. 4 and Fig. 5)
- nutritional and physiological characterization (Table 1).
- Three selected strains formed a distinct branch within the genus based on **16S rRNA cluster analysis** (Fig. 6).

BLAST-based average nucleotide identity (ANIb) values (calculated using JSpecies V1.2.1; www.imedea.uib.es/jspecies) between the whole genome sequence of ANC 3994^T (NCBI accession no. APOH00000000) and those derived from other 32 *Acinetobacter* (genomic) spp. were ≤77.3%.

Fig. 2. Rooted neighbour-joining tree based on the partial nucleotide sequence of the *rpoB* 100 gene (positions 2915-3775) of 25 A. *bohemicus* sp. nov. strains and the representatives of all known Acinetobacter spp. Bootstrap percentages (>70%) after 1000 simulations are shown. Bar, 5% sequence divergence.



Fig. 3. Unrooted neighbour-joining tree based on the partial nucleotide sequence of the gyrB gene (positions 435-1190) of 25 A. bohemicus sp. nov. strains and the representatives of most other Acinetobacter spp.

'A. puyangensis' BQ4-1 A. radioresistens CCM 3588^T A. soli CCUG 590231 *A. ursingii* NIPH 137[⊤] *A. nectaris* SAP 763.2[⊤] **A. boissieri** SAP 284.1[⊤] **A. junii** CCM 2376[™] Genomic sp. 6 LMG 1026 A. haemolyticus CCM 2358^T *A. towneri* CCM 7201[⊤] **A. tandoii** CCM 7199^T *A. rudis* CIP 110305[™] *A. brisouii* ANC4119[⊤] *A. gerneri* CCM 7197[⊤] A. bereziniae LMG1003T A. guillouiae LMG 988[™] *A. baylyi* CIP 107474[⊤] *A. bouvetii* CCM 7196[⊤] *A. Iwoffii* CCM 5581[⊤] A. schindleri NIPH 1034^T **A. indicus** CCM 7832[⊤] Genomic sp. 15TU NIPH 2171 A. johnsonii LMG 999^T A. baumannii ATCC 19606^T A. nosocomialis LMG 10619^T 'Close to 13TU' NIPH 973 **A. pittii** LMG 1035[⊤] A. calcoaceticus ATCC 23055^T Between 1 and 3' NIPH 817 A. beijerinckii NIPH 838^T *A. parvus* NIPH 384[⊤] Genomic sp. 14BJ NIPH 1847 Genomic sp. 13BJ/14TU ATCC 17905 *A. venetianus* ATCC 31012[™] Genomic sp. 17 NIPH 1867 A. gyllenbergii NIPH 2150[⊤] A. tjernbergiae CCM 7200[™] Genomic sp. 16 ATCC 17988 Genomic sp. 15BJ CIP 110321 ANC 4253 ANC 4315 **ANC 4248 ANC 4313** ANC 4278

All strains could be identified as the same new species using both phenotypic testing and MALDI-TOF MS profiling (Table 1, Fig. 4, and Fig. 5).

We conclude that the **25 strains represent a novel environmental species**, for which the name Acinetobacter bohemicus sp. nov. is proposed.



Characteristic	A. bohemicus (n = 25)	A. johnsonii (n = 20)	A. Iwoffii (n = 14)	A. junii (n = 15)	A. beijerinckii (n = 16)	
Growth at 37 °C	-	25	+	+	÷	
Growth at 35 °C	-	+	+	+	+	
Hemolysis	70	25	-	47	+	
Utilization of						
DL-Lactate	+	+	93	93	-	
Citrate (Simmons)	-	85	14	80	+	
L-Aspartate	+	75	-	27	+	
Azelate	-	-	+	-	-	
L-Histidine	+	-	-	93	+	
Malonate	+	50	7	-	+	
Phenylacetate	-	-	71	-	-	Table 1. Pheno
4-Hydroxybenzoate	88	15	-	-	-	nov. from pher non-glucose-ox
L-Arginine	+	70	-	93	-	
L-Leucine	-	-	-	20	88	Tests were perfor
2,3-Butanediol	+	60	7	-	-	evaluated after si other tests after t days (hemolysis c positive; -, all stra percentages of st
Benzoate	92	95	86	87	-	
Adipate	-	-	79	-	-	

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4). Utilizat	ion tests	were				

Acinetobacter bohemicus sp. nov.

Acinetobacter bohemicus (bo.he'mi.cus. N.L. masc. adj. bohemicus, pertaining to Bohemia (a major historical region of the Czech Republic), where multiple strains of this organism were isolated.

The species description is based on the characterization of 25 strains isolated from soil or water in natural ecosystems. Colonies on Tryptic Soy Agar (Oxoid) after 24 h incubation at 30°C are 1.0– 2.0 mm in diameter, circular, convex, smooth and slightly opaque with entire margins. Growth occurs in Brain-Heart Infusion (Oxoid) at temperatures ranging from 25°C to 30°C but not at 35°C. Acid is not produced from D-glucose and gelatin is not hydrolysed. Weak haemolysis on agar media supplemented with sheep erythrocytes is observed in most strains. Acetate, 4-aminobutyrate, L-arginine, L-aspartate, 2,3-butanediol, ethanol, L-glutamate, L-histidine, DLlactate, and malonate are utilized as sole sources of carbon with growth visible in 4 days of incubation. No growth on transaconitate, adipate, β-alanine, L-arabinose, azelate, citraconate, Dgluconate, D-glucose, glutarate, histamine, phenylacetate, Lphenylalanine, L-leucine, levulinate, L-ornithine, putrescine, Dribose, tricarballylate, or trigonelline occurs in 10 days. Various numbers of strains utilize benzoate (93% of the strains), gentisate (4%), 4-hydroxybenzoate (89%), L-tartrate (11%), or tricarballylate (4%). Tests of citrate (Simmons) or D-malate utilization are either negative, weakly positive or difficult to interpret.

The type strain is ANC 3994^T (= CIP 110496^{T} = CCM 8462^{T} = CCUG 63842[†]), isolated from the wetland mud of a deciduous forest in Křivoklátsko (a national protected landscape area and UNESCO biosphere reserve, located in the central Bohemia; GPS coordinates: 50°6'23.215"N, 13°56'39.027"E) in May 2011. The strain is weakly hemolytic and grows on benzoate and 4hydroxybenzoate but does not assimilate gentisate, L-tartrate or tricarballylate.

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