Acinetobacter bohemicus sp. nov. widespread in natural soil and water ecosystems in the Czech Republic ¶

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Table S1

ANIb and TETRA values between the genome sequence of *A. bohemicus* ANC 3994[T] (NCBI accession no. APQI00000000) **and those of other *Acinetobacter* spp.***

Strain	Genome NCBI accession no.	ANIb	TETRA
A. calcoaceticus CIP 81.8[T]	APQI00000000	74.56	0.89157
A. baumannii CIP 70.34[T]	APRG00000000	74.68	0.88142
A. baylyi CIP 107474[T]	APPT00000000	73.92	0.8553
A. beijerinckii CIP 110307[T]	APQL00000000	74.75	0.93003
A. bereziniae CIP 70.12[T]	APQG00000000	75.85	0.95812
A. bouvetii CIP 107468[T]	APQD00000000	75.89	0.7743
A. brisouii ANC 4119[T]	APPR00000000	74.11	0.85958
A. gerneri CIP 107464[T]	APPN00000000	75.46	0.90918
A. guillouiae CIP 63.46[T]	APOS00000000	76.24	0.9677
A. gyllenbergii CIP 110306[T]	ATGG00000000	74.59	0.9502
A. haemolyticus CIP 64.3[T]	APQQ00000000	74.49	0.92913
A. indicus ANC 4215[T]	ATGH00000000	75.99	0.70178
A. johnsonii CIP 64.6[T]	APON00000000	77.37	0.95338
A. junii CIP 64.5[T]	APPX00000000	74.71	0.9089
A. lwoffii NIPH 512[T]	AYHO00000000	76.16	0.79975
A. nectaris CIP 110549[T]	AYER00000000	72.41	0.83092
A. nosocomialis NIPH 2119[T]	APOP00000000	74.6	0.88416
A. parvus CIP 108168[T]	APOM00000000	74.87	0.85689
A. pittii CIP 70.29[T]	APQP00000000	74.68	0.88488
A. radioresistens CIP 103788[T]	APQF00000000	73.85	0.66743
A. rudis CIP 110305[T]	ATGI00000000	73.82	0.90666
A. schindleri CIP 107287[T]	APPQ00000000	75.64	0.82136
A. soli CIP 110264[T]	APPU00000000	73.42	0.80399
A. tandoii CIP 107469[T]	AQFM00000000	76.62	0.96167
A. tjernbergiae CIP 107465[T]	AYEV00000000	74.99	0.93131
A. towneri CIP 107472[T]	APPY00000000	77.27	0.9134
A. ursingii CIP 107286[T]	APQA00000000	74.55	0.92074
A. venetianus CIP 110063[T]	APPO00000000	74.67	0.90213
Genomic sp. 6 CIP a165	APOK00000000	74.73	0.95459
Genomic sp. 13BJ/14TU CIP 64.2	APRT00000000	74.7	0.94846
Genomic sp. 14BJ NIPH 1847	APRR00000000	74.41	0.83205
Genomic sp. 15BJ CIP 110321	AQFL00000000	74.88	0.95244
Genomic sp. 15TU NIPH 2171	APRS00000000	76.03	0.80482
Genomic sp. 16 CIP 70.18	APRN00000000	74.69	0.94258
Genomic sp. 17 NIPH 1867	APRO00000000	74.86	0.95074
Genomic sp. 'Close to 13TU' NIPH 973	APOO00000000	74.79	0.90382
Genomic sp. 'Between 1 & 3' NIPH 817	APPF00000000	74.57	0.88391

* Average nucleotide identity based on BLAST(ANIb) and the tetranucleotide frequency correlation coefficient (TETRA) values (means of reciprocal values) were calculated using the JSpecies web program with default settings (http://www.imedea.uib.es/jspecies).
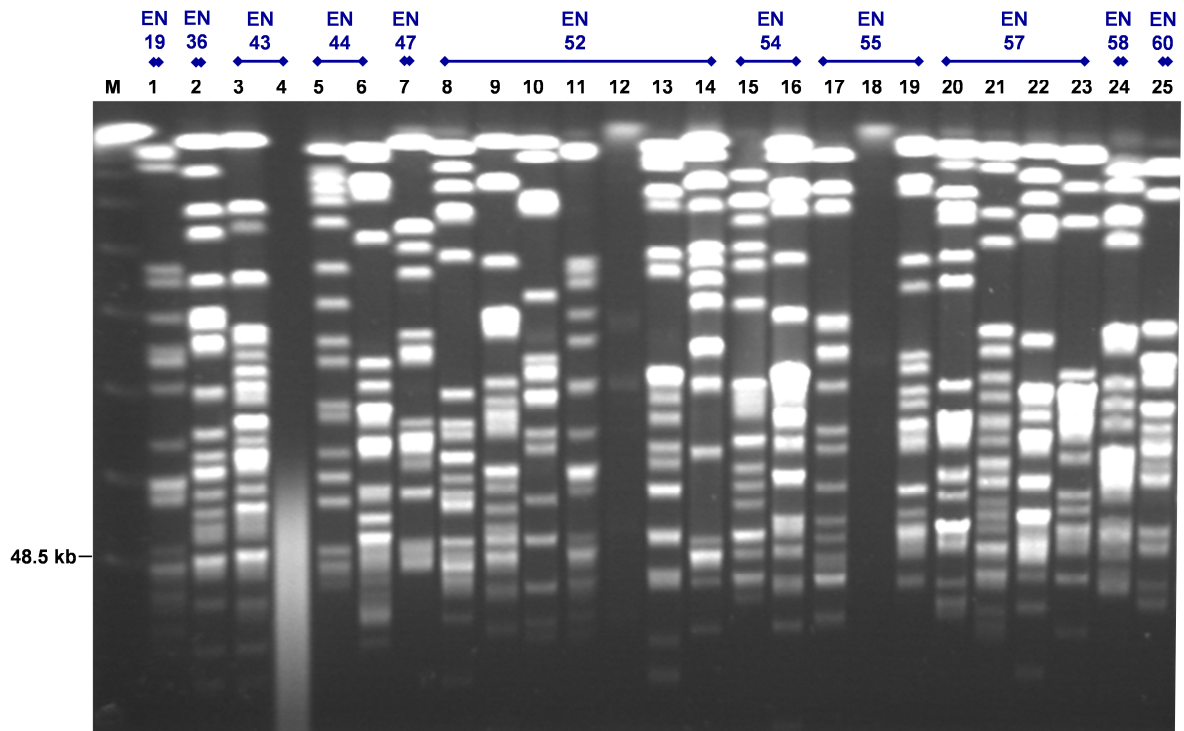
Figure S1. Genomic DNA restriction endonuclease patterns demonstrating the genotypic distinctness of the 25 *Acinetobacter bohemicus* strains studied. ApaI macrorestriction analysis by pulsed-field gel electrophoresis was carried out as described [Nemec *et al.* (2008) J. Antimicrob. Chemother. 62, 484–489]. Environmental sample (EN) codes (Table 1) are indicated above the strain identifiers which are given above the lanes (1, ANC 3994[T]; 2, ANC 4153; 3, ANC 4182; 4, ANC 4183; 5, ANC 4187; 6, ANC 4189; 7, ANC 4160; 8, ANC 4245; 9, ANC 4246; 10, ANC 4248; 11, ANC 4250; 12, ANC 4252; 13, ANC 4253; 14, ANC 4254; 15, ANC 4278; 16, ANC 4283; 17, ANC 4286; 18, ANC 4288; 19, ANC 4290; 20, ANC 4311; 21, ANC 4312; 22, ANC 4313; 23, ANC 4315; 24, ANC 4321; and 25, ANC 4476). Strains with repeatedly uncleaved or smeared DNA (ANC 4183, ANC 4252, and ANC 4288) have unique *rpoB* and/or *gyrB* sequences (Fig. 1). Lane M, molecular size markers (48.5 kb ladder).
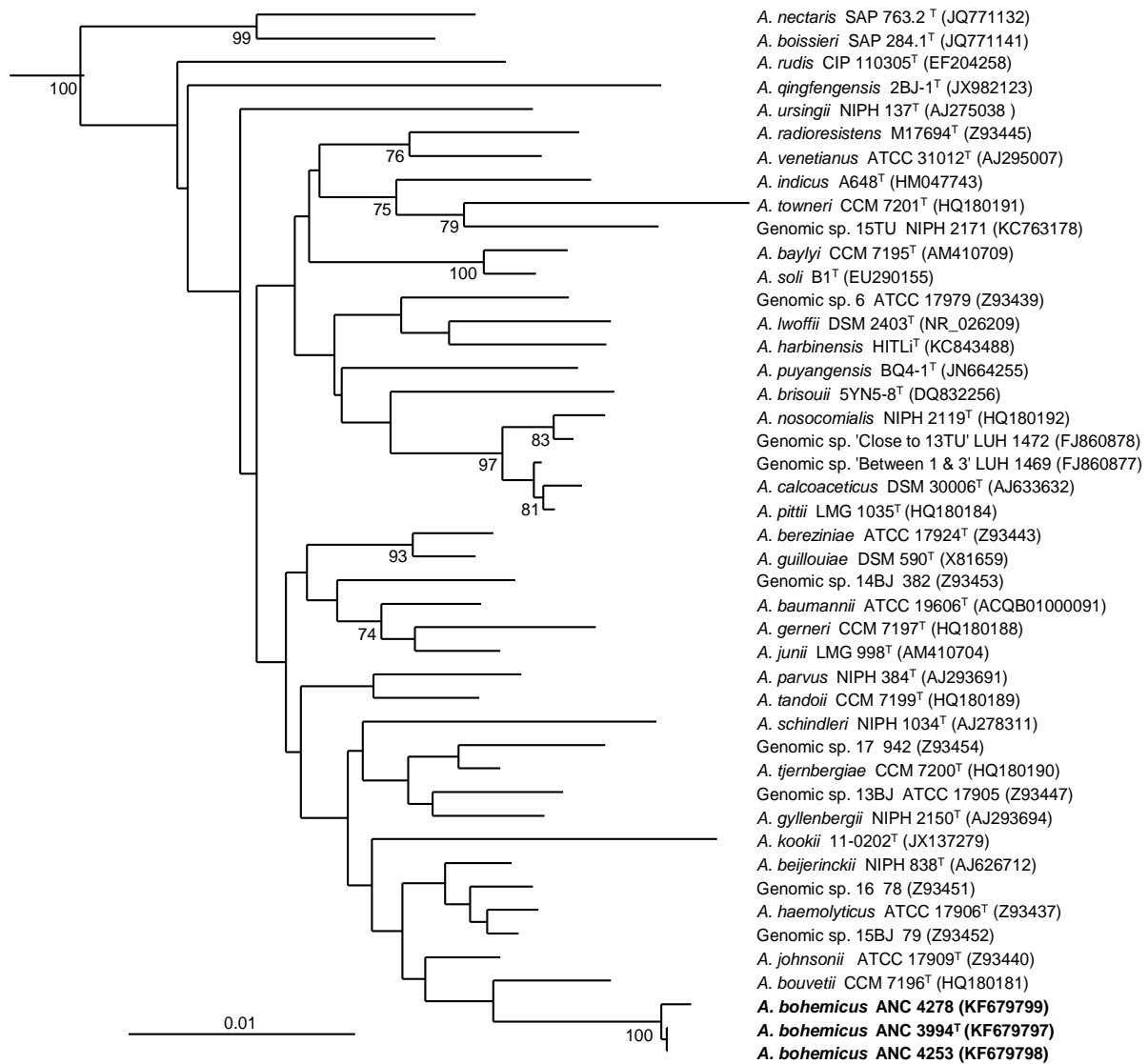
Figure S2. Rooted neighbor-joining tree based on 16S rRNA gene sequences, showing the relationships between strains of *Acinetobacter bohemicus* and other members of the genus *Acinetobacter*. The analysis was carried out on the regions corresponding to positions 174 through 1422 of the 16S rRNA gene of *Escherichia coli* using the BioNumerics 6.6 software (Applied Maths) and the parameters specified previously [Nemec *et al.* (2011) Res. Microbiol. 162, 393–404]. The sequence of *Moraxella lacunata* ATCC 17967[T] (NCBI accession no. AF005160) was used as the outgroup. Bootstrap percentages (>70%) after 1000 resamplings are shown. NCBI accession numbers are given in parentheses. Bar, 0.01 substitutions per nucleotide site. The cluster encompassing the three *A. bohemicus* strains was supported by a bootstrap value of 95% using maximum parsimony analysis based on of the same dataset.