

# Extended Description of Three Novel *Acinetobacter* Species of Possible Clinical Relevance, *Acinetobacter ursingii*, *Acinetobacter schindleri* and *Acinetobacter parvus*.

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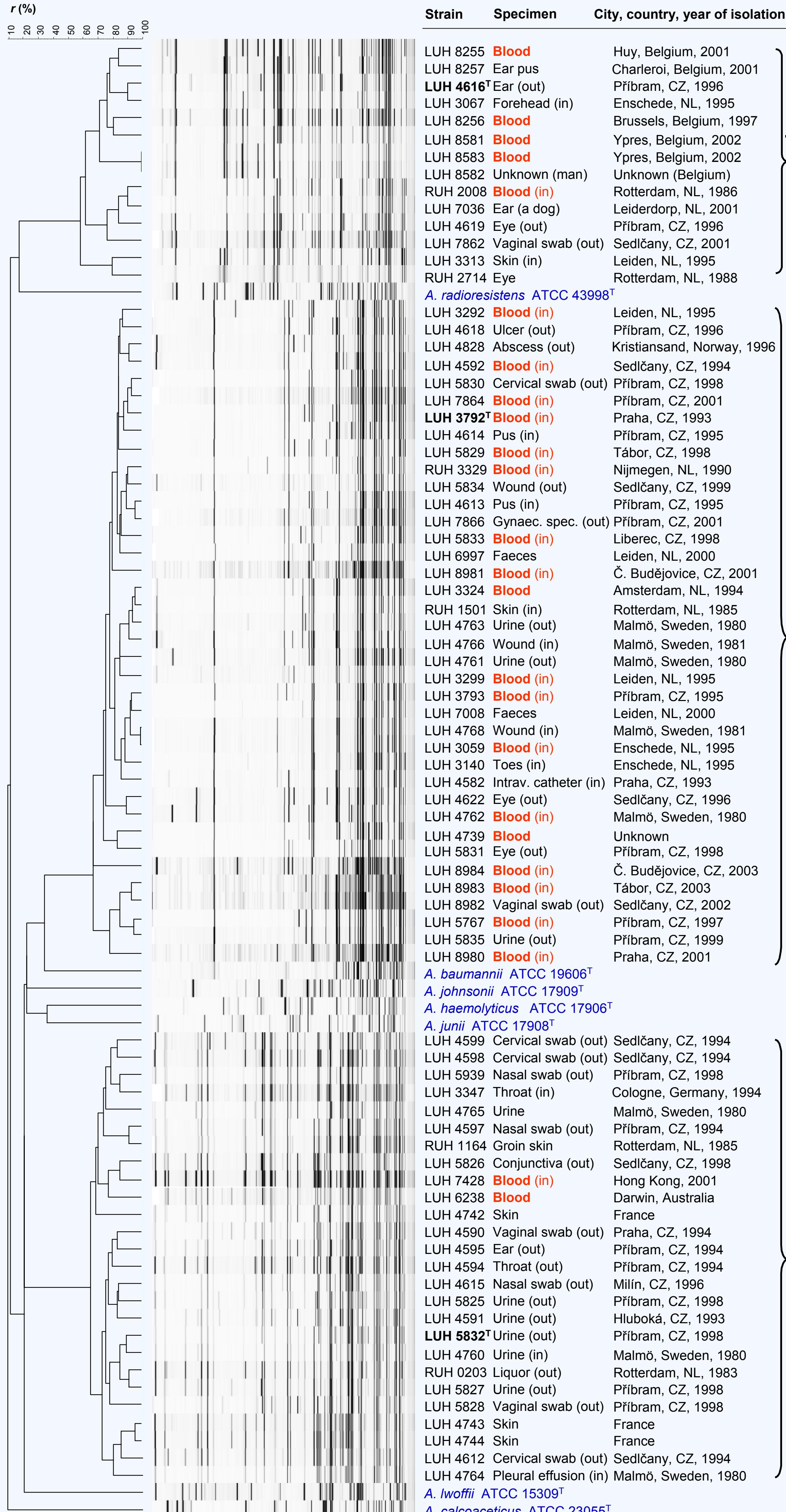


Fig. 1. Dendrogram of cluster analysis of AFLP fingerprints of the strains of *A. ursingii* (n=38), *A. schindleri* (n=26) and *A. parvus* (n=14), and of the type strains of 7 validated species of the genus *Acinetobacter*.

Fingerprints were generated using automated laser fluorescence detection and cluster analysis was performed with the BioNumerics software package using Pearson's product for similarity calculation and UPGMA for clustering. CZ, Czech Republic; NL, the Netherlands; in, inpatient; out, outpatient.

## Objective

Recently, three novel *Acinetobacter* species from human clinical specimens have been described, i.e., *Acinetobacter ursingii*, *Acinetobacter schindleri* and *Acinetobacter parvus* (4,5,6).

The aim of the study is to provide a description and identification criteria of the species using an extended set of strains.

## Results

AFLP (Fig. 1). *A. ursingii*, *A. schindleri* and *A. parvus* strains formed three distinct clusters at a grouping level of 67 %, 65 % and 58 %, respectively, which are above the 50 % level seen in previous studies for the delineation of *Acinetobacter* species (5).

Biochemical properties (Table 1) and colony morphology (Fig. 2). Striking features of *A. parvus* were its lack of metabolic activity and its small colony growth which is unusual in *Acinetobacter*.

ARDRA restriction profiles were characteristic for each species with few exceptions (Table 2).

Antibiotic susceptibility (Table 3). *A. schindleri* strains were mostly fully susceptible to the antibiotics tested whereas many *A. ursingii* strains showed intermediate susceptibility or resistance to some β-lactams and chloramphenicol. Notably, all but one *A. ursingii* strains had either no inhibition zones with penicillin or this zone was less than 10 mm, while all but one *A. schindleri* strains had inhibition zones >13 mm (range 14–25 mm).

Phenotypic tests allowed for presumptive identification of the novel species (Table 4), which can be improved by combination of these tests with ARDRA (Table 2).

## Strains

A total of 78 strains were investigated: *A. ursingii* (n=38), *A. schindleri* (n=26) and *A. parvus* (n=14) (Table 1). All but one strains were from human specimens; 18, 2 and 5 isolates of *A. ursingii*, *A. schindleri* and *A. parvus*, respectively, were from blood.

## Methods

AFLP™ fingerprinting (5)

Phenotypic characterization (4,5)

Susceptibility testing using disk diffusion (3)

Amplified rDNA restriction analysis (ARDRA) (1,5)

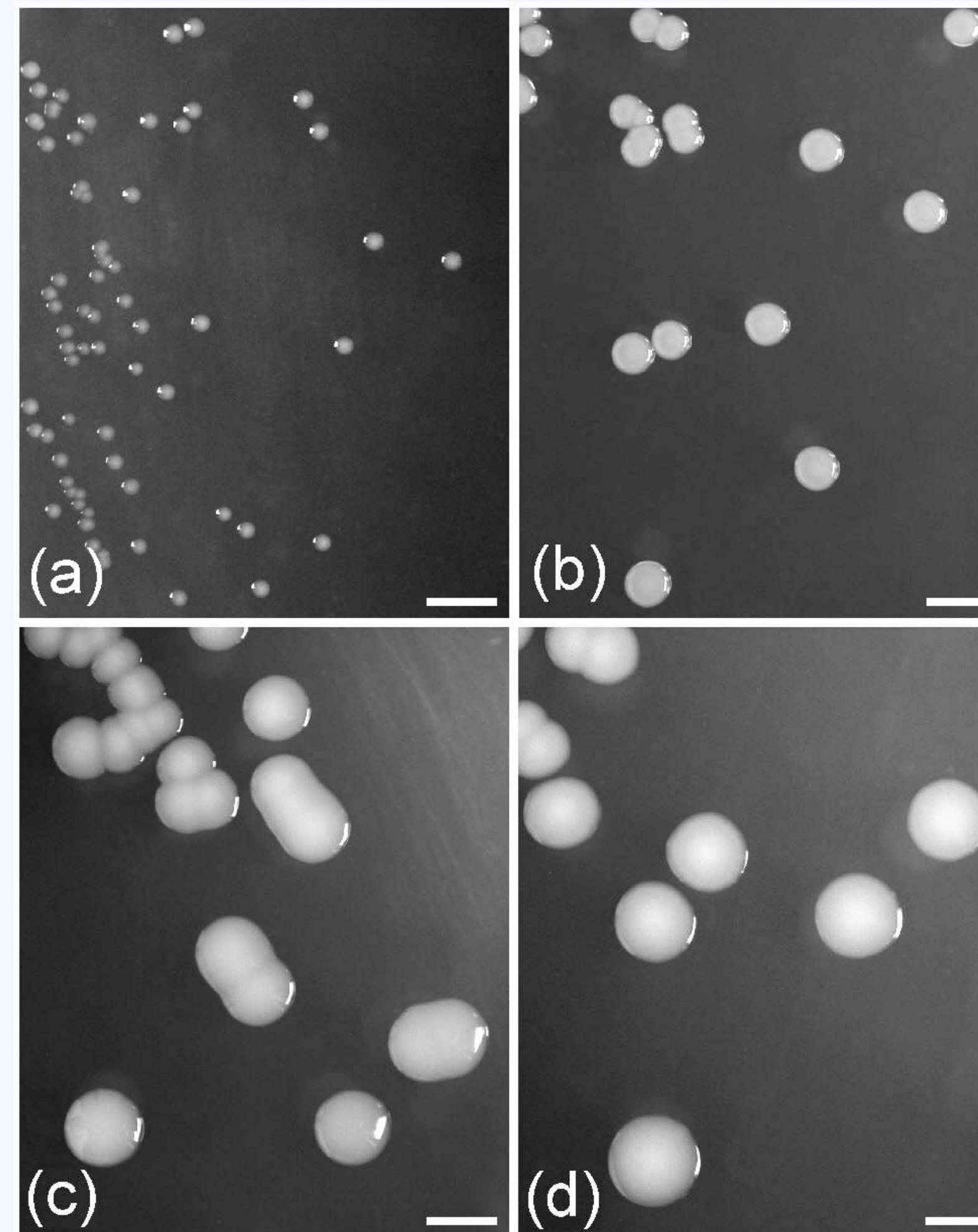


Fig. 2. Colonies of the type strains of (a) *A. parvus* (LUH 4616<sup>T</sup>), (b) *A. ursingii* (LUH 3792<sup>T</sup>), (c) *A. schindleri* (LUH 5832<sup>T</sup>) and (d) *A. iwoffii* (ATCC 15309<sup>T</sup>).

The strains were grown on Tryptic Soya Agar (Oxoid) at 30 °C for 24 h. Bar, 2 mm.

## Table 2. ARDRA patterns

The patterns designations as published previously (1,5). Typical combinations are in bold.

Species	Restriction pattern with enzyme					
	<i>Cfo I</i>	<i>Alu I</i>	<i>Mbo I</i>	<i>Rsa I</i>	<i>Msp I</i>	<i>Bfa I</i>
<i>A. ursingii</i>	1	4	3 or 1+3	5	3	
	1	4 or 2+4nw	3 or 1+3	4 or 4+5	3	
	1	4	3 or 1+3	2+5	3	
<i>A. schindleri</i>	1+5	2 or 2+4	1	2	2	10
	5	4	1	2	2	10
	5	New	1	2	2	New
<i>A. parvus</i>	1 or 1+5	2	1	2	3	

## Table 3. Antibiotic susceptibility

Susceptibilities of *A. parvus* were difficult to obtain due to poor growth, but were in the range of 71–100 % for these antibiotics. AMP, ampicillin; SAM, ampicillin-sulbactam; CAZ, ceftazidime; PIP, piperacillin; TET, tetracycline; CHL, chloramphenicol; KAN, kanamycin; GEN, gentamicin; NAL, nalidixic acid; OFX, ofloxacin; SXT, trimethoprim-sulfamethoxazole.

Species	Percentages of fully susceptible strains							
	AMP	SAM	CAZ	PIP	TET	CHL	KAN	GEN
<i>A. ursingii</i>	26	97	53	77	95	24	92	95
<i>A. schindleri</i>	100	100	100	88	92	100	100	92

# BHI from other manufacturers may give slightly different results.  
\* Weak growth of some strains.  
† Weak growth of most strains.