

Table S2. The characteristics of strains of *A. pullorum* and *A. portensis*.

Characteristics	<i>A. pullorum</i>	<i>A. portensis</i>			
Strains	B301 ^T	AC 877 ^T	AC 1335	AC 1301	AC 1123
Catalase	+	+	+	+	+
Oxidase	-	-	-	-	-
Motility	-	-	-	-	-
Growth at 37 °C	-	-	-	-	-
Growth at 35 °C	+	ND	ND	ND	ND
Growth at 32 °C	+	ND	ND	ND	ND
Growth at 30 °C	+	+	+	+	+
Growth at 20 °C	+	+	+	+	+
Growth on R2A, 30 °C	+	+	+	+	+
Growth on TSA, 30 °C	+	+	+	+	+
0.5 % NaCl	+	+	+	+	+
1.5 % NaCl	+	+	+	+	+
3.0 % NaCl	-	+	+	+	+
6.0 % NaCl	-	-	-	-	-
Acidification of D-glucose	+	-	-	-	-
Hemolysis of horse blood	ND	-	-	-	-
Liquefaction of gelatin	-	-	-	-	-
Assimilation of					
Acetate	ND	+	+	+	+
trans-Aconitate	ND	-	-	-	-
Adipate	ND	-	-	-	-
β-Alanine	+	-	-	-	-
4-Aminobutyrate	ND	-	-	-	-
L-Arabinose	ND	-	-	-	-
L-Arginine	ND	-	-	-	-
L-Aspartate	ND	+	+	+	+
Benzoate	ND	-	-	-	-
2,3-Butanediol	ND	-	-	-	-
Citrate (Simmons')	+	+	+	+	+
Ethanol	ND	+	+	+	-
Gentisate	ND	-	+	-	-
D-Gluconate	ND	-	-	-	-
D-Glucose	+	-	-	-	-
L-Glutamate	ND	+	+	+	+
Histamine	ND	-	-	-	-
L-Histidine	+	+	+	+	+
4-Hydroxybenzoate	-	-	-	-	-
DL-Lactate	ND	+	+	+	+
L-Leucine	ND	-	-	-	-
D-Malate	+	ND	ND	ND	ND

Malonate	-	-	-	-	-
L-Ornithine	ND	-	-	-	-
L-Phenylalanine	ND	-	-	-	-
Putrescine	ND	-	-	-	-
D-Ribose	ND	-	-	-	-
L-Tartrate	ND	-	-	-	-
Tryptamine	ND	-	-	-	-
Genome					
Accession no.	JAAARQ00000 0000	LWRV00000 000	NA	NA	NA
Completeness (%)†	98.86	98.8	NA	NA	NA
Contamination (%)†	1.35	0.89	NA	NA	NA
Strain heterogeneity (%)†	14.29	0	NA	NA	NA
G+C content (%)§	37.0	36.6	NA	NA	NA
Contigs	3	123	NA	NA	NA
Largest contig (bp)§	3,059,385	141,290	NA	NA	NA
Total length§	3,102,684	2,897,281	NA	NA	NA
N50§	3,059,385	61,636	NA	NA	NA
L50§	1	16	NA	NA	NA
Genome coverage	316	206	NA	NA	NA
Protein-coding genes	2,835	2,649	NA	NA	NA
rRNA genes	21	3	NA	NA	NA
tRNA genes	80	64	NA	NA	NA

Characteristics are scored as: +, positive reaction; -, negative reaction, ND, not determined and NA, not available.

†These were determined using CheckM (1).

§The G+C contents, largest contig, total length, N50 and L50 were calculated using Quast (2).

Data for species are from references (3, 4).

References

1. Parks D, Imelfort M, Skennerton C, Hugenholtz P, Tyson G. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Research* 25:1043–1055.
2. Mikheenko A, Prjibelski A, Saveliev V, Antipov D, Gurevich A. 2018. Versatile genome assembly evaluation with QUAST-LG. *Bioinformatics* 34:i142-i150.
3. Carvalheira A, Gonzales-Siles L, Salvà-Serra F, Lindgren Å, Svensson-Stadler L, Thorell K, Piñeiro-Iglesias B, Karlsson R, Silva J, Teixeira P, Moore E. 2020. *Acinetobacter portensis* sp. nov. and *Acinetobacter guerrae* sp. nov., isolated from raw meat. *Int J Syst Evol Microbiol* doi:doi: 10.1099/ijsem.0.004311.:doi: 10.1099/ijsem.0.004311.
4. Elnar A, Kim M, Lee J, Han R, Yoon S, Lee G, Yang S, Kim G. 2020. *Acinetobacter pullorum* sp. nov., isolated from chicken meat. *J Microbiol Biotechnol* 30:526-532.