'Candidatus Peptacetobacter felis' sp. nov., a novel bile acid-converting bacterial species isolated from the feces of healthy cats in the United States

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Keywords: *Peptacetobacter* sp., culturomics, bile acid, whole genome sequencing, taxonogenomic

GenBank genome accession number: JBLOUI000000000.1
GenBank 16S rRNA accession number: PV358556

Abbreviations:

MALDI-TOF MS: Matrix-Assisted Laser Desorption/Ionization Time of Flight Mass Spectrometry

WGS: Whole genome sequencing

COG: Clusters of Orthologous Genes

MAG: metagenome assembled genomes

OMCL: Orthologous Markov Clustering

ABSTRACT

Six strains of a novel anaerobic bacterial taxa exhibiting bile acid-transforming activity were isolated from fecal samples of clinically healthy cats living in Oakland, California. 16S rRNA sequencing and phylogenetic analysis indicate that strain AB800^{T} belongs to the genus *Peptacetobacter*, with *Peptacetobacter hiranonis* strain JCM 10541 (98% coverage, 99.7% identity) as its closest relative. Whole genome sequencing shows an average nucleotide identity (ANI) of less than 96% (95.73% ANI, 90.53% AF) with the closest validly named species being *Peptacetobacter hiranonis DGF055142*. The size is about 2.58 Mb, containing 2,355 predicted coding sequences and 2,450 annotated genes. Phenotypic characterisation, and comprehensive genomic analysis, including ANI, digital DNA-DNA hybridization (dDDH) and core genome phylogenetic analysis, placing the strain AB800^{T} on a separate branch, supported the classification of a novel species, strain AB800^{T} (DSM 120482 = LMG 34035) with the proposed name '*Candidatus Peptacetobacter felis'* sp. nov., derived from "*felis"* the latin name of cat *felis catus*. These findings expand our understanding of host-associated bile acid converters and provide promising candidates for probiotic development.

INTRODUCTION

Comprehensive characterisation of the gut microbiome in companion animals and identification of live bacterial taxa are essential for developing next-generation microbial supplements, live biotherapeutic products, and advancing veterinary health [1, 2]. Yet, much of its diversity remains unexplored, especially at the species level. Among the critical microbial processes in the gut, bile acid metabolism plays a central role in regulating host physiology, microbial community structure and interactions, and intestinal homeostasis [3, 4]. In both humans and animals, gut microbes convert primary bile acids into secondary bile acids, modulating lipid absorption, intestinal signalling, and colonisation resistance effects mediated through host receptors such as FXR and TGR5 [5–7]. In dogs and cats, bile acid metabolism has been shown to have profound health implications, with alterations in bile acid profiles linked to gastrointestinal disorders and dysbiosis [5, 8].

To address this knowledge gap, culturomics, a high-throughput, culture-based microbial discovery method, has emerged as a powerful tool [9, 10]. By combining selective anaerobic cultivation, MALDI-TOF MS profiling, and whole genome sequencing, culturomics enables the isolation of novel gut microbes and the functional exploration of their metabolic capabilities [11, 12]. While metagenomics offers broad surveys of genomics content, only culture-based techniques provide direct insight into physiology, metabolic activity, and potential therapeutic applications. The gastrointestinal tracts of healthy cats and dogs provide a rich anaerobic environment that supports diverse microbial consortia involved in key transformations, such as protein fermentation and bile acid conversion [1, 13]. Protein-rich diets common to companion animals enhance microbial fermentation potential, but may also lead to the accumulation of ammonia and other intermediates that disrupt gut stability[14, 15]. In this context, bile acid-transforming bacteria may help stabilise

68 the microbial community and maintain gut homeostasis[5, 16]. One of the main bacteria reported
69 to modulate bile acid levels in companion animals with chronic enteropathy is *Pepetacetobacter*
70 *(Clostridium) hiranonis* [17].
71 The *Peptacetobacter* genus is classified in the *Peptostreptococcaceae* family and includes a group
72 of rod-shaped Gram-positive, obligatory anaerobic bacteria. There are two members of the genus
73 *Peptacetobacter*: *Peptacetobacter hiranonis* and *Peptacetobacter hominis*. The first species
74 isolated from this genus was initially classified as *Clostridium* based on the 16s rRNA similarity
75 and DNA-DNA hybridisation analysis [18]. Then, in 2020, the second species was isolated with a
76 ~95% 16S rRNA gene similarity, and exhibited ANI values of 66–76% (< 96%) and dDDH values
77 of 17–35% (< 70%), far below accepted genus and species thresholds. The whole-genome
78 phylogenomics further demonstrated that these organisms belonged to a distinct lineage, separated
79 from *Clostridium sensu stricto*, leading to the establishment of the genus *Peptacetobacter*, with *P.*
80 *hominis* as the type species and *P. hiranonis* reclassified accordingly ([19].
81 Here, we report the isolation and characterisation of a novel bile acid-transforming species from
82 the feces of healthy cats: '*Candidatus Peptacetobacter felis'* sp. nov., expanding the genus
83 *Peptacetobacter* to three species. Using a culturomics framework, we identified and analysed these
84 strains through phenotypic, phylogenetic, chemo-taxonomic, and genomic methods. This
85 discovery enhances our ability to conduct additional studies to better understand the bile acid
86 microbiome axis in companion animals. It offers novel candidates for the development of precision
87 probiotics to improve gastrointestinal health and metabolic stability in dogs and cats.
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91 **SAMPLE COLLECTION AND ISOLATION**

92 Fecal samples were collected from five different healthy cats living in Oakland, California, USA,
93 in 2022. Strain AB800^{T} was isolated from a fecal sample obtained from an 8-year-old, spayed
94 domestic short-haired cat. AB403 was isolated from a fecal sample obtained from a 2-year-old,
95 spayed female domestic short-haired cat. AB804 was isolated from a fecal sample obtained from
96 a 7-year-old, spayed female domestic short-haired cat. AB807 and AB808 were isolated from the
97 same 6-year-old, neutered male American short-haired cat. Strain AB811 was cultivated from a
98 fecal sample obtained from a 1-year-old, spayed female domestic long-haired cat.

99 Freshly collected samples were transported in BIOME-Preserve AS-930 (Anaerobe Systems,
100 Morgan Hill, CA) transport media in a one-to-one ratio and processed as part of the AnimalBiome
101 culturomics process [20]. Culture and isolation were carried out between September 2022 and
102 February 2023. In an AS500 Anaerobic chamber (Anaerobe Systems, Morgan Hill, CA), the
103 sample was serially diluted, and the diluted samples were plated on Brain Heart Infusion Agar
104 with Horse Blood and Taurocholate (BHIY-HT) (Anaerobe Systems, Morgan Hill, CA) and
105 incubated anaerobically for 48 hours at 37°C. The grown colonies of strain AB800^{T} were
106 repeatedly subcultured on homemade Columbia agar with 5% sheep blood until pure isolates were
107 obtained. Colony identification of the strain was carried out using MALDI Biotyper smart System
108 RUO microflex LT/SH smart with the BIDAL database v12 (Bruker Daltonics, Bremen, Germany)
109 as previously described [20].

110

111 **MORPHOLOGICAL, PHENOTYPICAL, AND BIOCHEMICAL CHARACTERISTICS**

112 After isolation, a pure culture of strain AB800^{T} was morphologically characterised by phase-
113 contrast microscopy and Gram staining. Motility was assessed by wet mount, and biochemical

114 profiling was conducted using API ZYM, API 50 CH, and API Rapid ID 32A strips (bioMérieux).
115 The ribosomal protein MALDI-TOF MS spectra profiling was obtained using MALDI Biotyper
116 smart System RUO microflex LT/SH smart with the software flexAnalysis 3.4 (Bruker Daltonics,
117 Bremen, Germany).
118 On both Chocolate agar (Fig. 1a1) and Brain Heart infusion agar (Fig. 1a2) (Anaerobe Systems,
119 Morgan Hill, CA), strain AB800^T exhibits white-grayish colonies in the form of a star measuring
120 approximately 1 to 2 mm in diameter. The wet mount reveals a non-motile bacterial cell, while the
121 Gram stain shows Gram-positive bacilli with no endospore formation detected (Fig. 1b2). The
122 electron microscopy characterisation shows that strain AB800^T cells measure approximately 0.7–
123 1 µm in width and 3.2–8 µm in length (Fig.1 b1). Growth of AB800^T is optimal on a Chocolate
124 agar (Anaerobe Systems, Morgan Hill, CA) plate at 37 °C in strict anaerobic conditions . The
125 Protein profile characterized by the mass spectra (Fig. 1c) obtained by MALDI-TOF Mass
126 spectrometry, shows a reproducible spectrum among multiple replicates composed of the cytosolic
127 and main ribosomal proteins. This spectrum is unique and composed of peaks within the 2,000 to
128 15,000 m/z range.

129 The enzymatic activity evaluation shows that strain AB800^T exhibits positive activity for N-acetyl-
130 β-D-glucosaminidase, acid phosphatase, alkaline phosphatase, naphthol-AS-BI-
131 phosphohydrolase, proline aminopeptidase, and esterase lipase (C8). Negative activity was
132 observed for β-glucosidases, β-galactosidase, valine, leucine arylamidases, lipase (C14), α-
133 chymotrypsin, and trypsin. Regarding carbohydrates, strain AB800^T can metabolise D-glucose and
134 D-mannose but shows no activity towards sucrose or sorbitol. Strain AB800^T shows no activity
135 for urea utilisation, nitrate reduction, indole production, and gelatin hydrolysis (Table 1)

136 **SEQUENCING AND GENOMIC ANALYSIS**

137 The total nucleic acid of strain AB800^{T} AB403, AB804, AB807, AB808, and AB811 was extracted
138 using the ZymoBIOMICS™ DNA Miniprep Kit for bacterial cells (Zymo Research, Irvine, CA,
139 USA) as previously described [20]. The concentration of the nucleic acid was measured using a
140 Qubit 4 Fluorometer (Thermo Fisher Scientific, Waltham, MA, USA). The strains AB800^{T},
141 AB403, AB804, AB807, AB808, and AB811 were sequenced using Illumina technology by
142 SeqCenter (Pittsburgh, PA, United States) as described in their protocol. Illumina sequencing
143 libraries were prepared using the tagmentation-based and PCR-based Illumina DNA Prep kit and
144 custom IDT 10 bp unique dual indices (UDI) with a target insert size of 280 bp. No additional
145 DNA fragmentation or size selection steps were performed. Illumina sequencing was performed
146 on an Illumina NovaSeq X Plus sequencer in one or more multiplexed shared-flow cell runs,
147 producing 2x151 bps paired-end reads. Demultiplexing, quality control, and adapter trimming
148 were performed with bcl-convert1 (v4.2.4).

149

150 **PHYLOGENY AND GENOME FEATURES**

151 Sequencing reads were screened for quality control using Fastqc v0.12.1 [21] and filtered with a
152 Phred score >30. We assembled them using SPAdes genome assembler v3.15.5 [22] implemented
153 in shovill (https://github.com/tseemann/shovill) with default parameters. The final scaffolds were
154 screened for quality using CheckM2 v1.0.2 [23] and taxonomically confirmed using GTDB-Tk
155 v2.4.0 (RefDB version r220) [24] and a Blastn search using BLASTN 2.17.0+ [25] against the 16S
156 rRNA database (NCBI). We annotated the genomes using Prokka v1.14.6 [26]. The genome was
157 searched for antimicrobial resistance and virulence genes using Abricate
158 (https://github.com/tseemann/abricate) (version 1.0.0) and the NCBI AMRFinderPlus [27],

ARGANNOT [28], ResFinder [28, 29], CARD [30], and MEGARes [31] databases downloaded in November 2025. In addition, we conducted a screening for metabolism pathways associated with bile acid metabolism using gapseq (version 1.3.1) [32] and searched for complete and incomplete pathways.

The strain AB800^T was assembled into 149 contigs, totalling 2.58 Mb in genome size. Compared with the other five strains, AB800^T is in the upper range of genome size, ranging from 2.43 to 2.86 Mb across all strains. The strain AB800^T encodes 2,355 coding sequences and 2,450 total genes, values that fall centrally within the variation seen among other related strains (2,165–2,624 CDS; 2,261–2,719 genes). The strain carries 16 rRNA genes, 78 tRNA genes, and one tmRNA, with three annotated repeat regions, reflecting the typical genomic architecture present across the set. Regarding antimicrobial resistance determinants, strain AB800^T harbors both tetB(P) and tetA(P) genes among the tetracycline group of genes, while no macrolide (ermQ) or lincosamide (lnuP) genes are detected. This resistance gene profile is shared with the strains AB0403, AB804, and AB811. However there were no genes associated to virulence. The genes associated with bile acid metabolism are broadly conserved across all genomes examined, and strain AB800^T encodes the complete set of core *bai* genes, including *baiN_1, baiN_2, baiB, baiE, baiCD_1, baiCD_2, baiF, baiH* and *baiA2*. As in the other strains, *baiN_3, baiN_4* and *baiN_5* are absent (Table 2)

178 The 16S rRNA gene sequence of strain AB800^{T}, when blasted against the 16S ribosomal RNA
179 database, showed 97% coverage and 99% identity to *P. hiranonis JCM 10541*. The maximum
180 likelihood phylogenetic inference with a General Time-Reversible (GTR) model shows strain
181 AB800^{T} to be a close parent of *P. hiranonis JCM10541(NR178263.1)* and *P. hiranonis strain TO-*
182 *931 (NR028611.1),* with a bootstrap of 98% and a midpoint rooting topology (Fig. 2: a). Genomic
183 taxonomic classification using Gtdbtk v2 showed that the closest species is *Peptacetobacter*
184 sp900539645 (GCA_900539645.1) with 98.67% ANI, *Peptacetobacter hiranonis*
185 *(GCF_008151785.1)*, ANI= 94.46%, AF=0.81, and *Peptacetobacter hominis*
186 *(GCF_006861675.1)*, ANI=80.74, AF=0.45. The DNA-DNA-Hybridization analysis with GGDC
187 showed that the closest from the database is *Peptacetobacter hiranonis DSM 13275* with dDDH =
188 67.7% (Suppl.Data: Table1). The Core-genome-based phylogeny showed strain AB800^{T} to be
189 close to or belong to the *Peptacetobacter* cluster but on a separate branch, as *P. hiranonis* and
190 close to the metagenome assembled genomes (MAG) of *Peptacetobacter* (*Pepetacetobacter* sp.
191 bin-44 and *Pepetacetobacter* sp. DOME MAG 11184) (Fig. 2: b). The closest species genomes
192 and other genomes were retrieved from NCBI, and ANI and AF were computed directly using
193 FASTANI (version 1.34) [33]. The results indicated that the closest are *Pepetacetobacter* sp.
194 DOME MAG11184 and *Pepetacetobacter* sp. bin-44 (ANI=98.72%, AF=81.95%, ANI=98.67%,
195 AF=74.17%). The closest known isolate is *Peptacetobacter hiranonis* DGF055145 (ANI=95.73%,
196 AF=81.95%) with ANI < 96%, making strain AB800^{T} a 'candidatus' new species of the genus
197 *Peptacetobacter* (Fig. 3). The 16S rRNA and the genome of strain AB800^{T} were deposited in
198 Genbank with the respective accession numbers PV358556 and NZ_JBLOUI000000000.1

199

200 **COMPARATIVE GENOMIC**

201 A pangenome analysis using OMCL clustering showed that strain AB800^{T} shared only 1331 gene
202 clusters with *Peptacetobacter hiranonis* and *Peptacetobacter hominis* (core genome) while
203 conserving 500 genes as unique. It shares 405 with *Peptacetobacter hiranonis* and only 67 with *P.*
204 *hominis*, confirming that strain AB800^{T} is closer to *P. hiranonis* than *P. hominis* (Fig. 4: a). The
205 metabolic pathway analysis revealed that, while only *P. hiranonis* and strain AB800^{T} possess the
206 bile acid 7-alpha and 7-beta dehydroxylation pathways, only strain AB800^{T} lacks the
207 deconjugation pathways, as shown in Fig. 4: b.
208

209 **DESCRIPTION OF *PEPTACETOBACTER SP*. NOV**

210 *'Candidatus Peptacetobacter felis'* (fe.lis. L. gen. n. felis, referring to the Latin name of cat, felis
211 catus, the species from which it was isolated).
212 A bile acid-converting, Gram-positive, non-motile, obligate anaerobic rod-shaped bacterium
213 isolated from the feces of a healthy cat living in Oakland, California. *Peptacetobacter felis AB800^{T}*
214 can be grown on Columbia blood agar, Chocolate agar, and Brain Heart infusion agar (with optimal
215 growth on Chocolate agar at 37 °C after 48h. On agar plates, it exhibits white-grayish colonies in
216 the form of a star measuring approximately 1 to 2 mm in diameter. Regarding enzymatic activity,
217 *'Candidatus Peptacetobacter felis'* AB800^{T} shows the ability to hydrolyze specific peptide and
218 amino sugar substrates and active phosphatase and esterase systems, which translates to positive
219 results for naphthol-AS-BI-phosphohydrolase, leucine arylamidase, N-acetyl-β-D-
220 glucosaminidase, alkaline phosphatase, esterase (C4), esterase lipase (C8), and acid phosphatase.
221 On the other hand, strain AB800^{T} does not exhibit activity for cystine arylamidase, trypsin, lipase
222 (C14), valine arylamidase, α-mannosidase, α-fucosidase, α-chymotrypsin, β-glucosidase, or β-
223 galactosidases, showing limited glycosidic activity and proteolytic activity in comparison with

224 other *Peptacetobacter* taxa. Regarding carbohydrate, amino acid, and salt activity, *'Candidatus*
225 *Peptacetobacter felis' AB800^T* is urea- and L-tryptophan-negative, suggesting the absence of
226 urease and tryptophanase activities. For carbon sources, the strain AB800^T can use D-saccharose
227 (sucrose) and D-glucose, but does not use amygdalin, D-melibiose, D-mannitol, D-sorbitol, L-
228 rhamnose, L-arabitol, or inositol. In summary, *'Candidatus Peptacetobacter felis' AB800^T* is
229 particularly characterized by its esterase and phosphatase reactivity, but in general by its specific
230 enzyme activities and limited substrate spectrum among the tested compounds. Even though the
231 16S RNA similarity search and phylogeny did not show a clear delineation between the strain
232 *'Candidatus Peptacetobacter felis' AB800^T* and other *P. hiranonis*, Genomic taxonomic
233 classification using Gtdbtk v2 showed that the closest species is Peptacetobacter sp900539645
234 (GCA_900539645.1) with 98,67% ANI, which is a MAG. However, the nearest known isolate is
235 *Peptacetobacter hiranonis DGF055145* (ANI=95.73%, AF=81.95%), with ANI < 96% and dDDH
236 = 67.7% (< 70%), and Peptacetobacter hiranonis DSM 13275, making *Peptacetobacter sp.*
237 *AB800T,* a new species of the genus *Peptacetobacter*. The genome is 2,577,873 bp, comprises 149
238 contigs, has a GC content of 31%, and has been deposited in GenBank under BioProject accession
239 number PRJNA1200056. *'Candidatus Peptacetobacter felis'* AB800^T was deposited in two
240 international collections with the following accession numbers: *Candidatus Peptacetobacter felis*
241 AB800^T (=DSM 120482= LMG 34035
242
243
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245 **Ethical statement**

246 The fecal sample used to isolate *'Candidatus Peptacetobacter felis'* strain AB800^T, as well as the
247 strains AB403, AB804, AB808, AB807, and AB811, were all non-invasively obtained and donated
248 by the cats' owners with informed consent of the research that will be carried out.

249 **Author Contributions:**

250 ND: Conceived the idea, isolated the strains AB800^T, AB804, AB807, AB808, and AB811,
251 designed the experiments, supervised the characterization experiments, analyzed and validated the
252 data, created the figures, drafted the manuscript, and performed review and preparation. HHG:
253 Conceived the idea, validated the data, reviewed, and prepared the manuscript. KDM: Assembled
254 the genomes, analyzed the data, conducted comparative genomic analyses, drafted the manuscript,
255 and contributed to editing and review. GJ: Prepared the data and deposited the genomes to NCBI,
256 reviewed the manuscript, and contributed to editing. ZM: Isolated strains AB0403, deposited the
257 strains in the international collections (DSMZ and BCCM), and performed phenotypic
258 characterization. SL: Performed the strain purification and cryobanking, DNA extraction, and
259 prepared the DNA for sequencing

260 **Funding**

261 This study was supported by internal funding from Animal Biome.

262 **Conflict of Interest**

263 Niokhor Dione, Zara Marfori, Guillaume Jospin, and Holly Ganz are employees of and/or have
264 equity in Animal Biome, a company that develops microbiome-based diagnostics and next-
265 generation probiotic products for companion animals. These authors affirm that this affiliation did
266 not influence the study design, data analysis, interpretation of results, or the conclusions presented
267 in this manuscript. All other authors declare no competing financial or non-financial interests.

268 **Acknowledgments**

269 We thank the owners of the cats, LizG, Marie, Bwett, Mitz, and Willow, for donating the fecal
270 material used for isolation. We also thank the Animal Biome Microbial Discovery team for
271 assistance with anaerobic culturing and phenotypic characterization, and Seqcenter for sequencing
272 our genomes.

273

274 **Supplementary Material**

275 Supplementary Table 1: DNA-DNA Hybridisation table from GGDC

276 **Data Availability Statement**

277 The genomes of strains AB800^{T} , as well as the five strains reported in this study, were submitted
278 and referenced in the NCBI database with the accession numbers JBLOUI000000000 for
279 *'Candidatus Peptacetobacter felis'* AB800^{T}, and the temporary BioSample accession numbers for
280 AB0403, AB804, AB807, AB808, and AB811 are SAMN53260830, SAMN53260831,
281 SAMN53260832, SAMN53260833, SAMN53260834, respectively.

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List of Figures

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420 AB800$^{\mathbf{T}}$ possess the bile acid 7-alpha and 7-beta-dehydroxylation pathways, only strain AB800$^{\mathbf{T}}$
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422 **Tables:**

423

424 **Table 1:** Phenotypic characteristics of strain AB800^{T}, including morphology, enzymatic, amino acids, salts, utilization and activity,
425 carbon sources of strain AB800^{T} in comparison with existing members of the genus *Peptacetobacter*, TO-931^{T}, HD-17, and
426 ZHW00191^{T}

427

Substrates tested	*Peptacetobacter Felis* AB800^{T}	*Peptacetobacter hiranonis* TO-931^{T}	*Peptacetobacter hiranonis* HD-17	*Peptacetobacter hominis* ZHW00191^{T}
Basic characteristics				
Cell diameter (µm)		0.8 × 1.6–10	0.8 × 1.6–10	0.7–1 × 3.2–8
Oxygen requirement	Strict Anaerobe	Strict anaerobe	Obligate anaerobe	Obligate anaerobe
Gram stain	+	+	+	+
Motility	non-motile	non-motile	non-motile	non-motile
Endospore formation	-	+	+	-
Enzyme				
Alkaline phosphatase	+	NA	NA	+
Esterase (C 4)	+	NA	NA	w
Esterase Lipase (C 8)	+	NA	NA	+
Lipase (C 14)	-	NA	NA	NA
Leucine arylamidase	+	NA	NA	NA
Valine arylamidase	-	NA	NA	NA
Cystine arylamidase	-	NA	NA	NA
Trypsin	-	NA	NA	NA

α-chymotrypsin	-	NA	NA	NA
Acid phosphatase	+	NA	NA	+
Naphthol-AS-BI-phosphohydrolase	+	NA	NA	NA
α-galactosidase	-	NA	NA	-
ß-galactosidase	-	NA	NA	NA
ß-glucuronidase	-	NA	NA	NA
α-glucosidase	-	-	-	-
ß-glucosidase	-	NA	NA	NA
N-acetyl-ß-glucosaminidase	+	+	+	+
α-mannosidase	-	NA	NA	NA
α-fucosidase	-	NA	NA	NA
Amino acids / Salts / Carbon source	-	NA	NA	NA
Urea	-	NA	NA	NA
L-Tryptophan	-	NA	NA	NA
D-Glucose	+	+	+	+
D-Mannitol	-	-	-	w (acid)
Inositol	-	NA	NA	NA
D-Sorbitol	-	-	-	-
L-Rhamnose	-	-	-	-
D-Saccharose	+	+	+	-
D-Melibiose	-	NA	NA	NA

Amygdalin	-	NA	NA	NA
L-Arabitol	-	NA	NA	NA
Temperature range (°C)	37	30–50 (optimum ≈37)	30–50 (optimum ≈37)	25–45 (optimum 37–42)
pH range	NA	6.5–9.0 (optimum 7.5–8.0)	6.5–9.0 (optimum 7.5–8.0)	5.5–10.0 (optimum 6.5–7.0)
NaCl tolerance	NA	Up to ~1% (reported low)	Up to ~1% (reported low)	0–2% (optimum 0%)
Proline aminopeptidase	NA	+	+	+
Bile acid 7α-dehydroxylating activity	NA	High activity	High activity	NA
Origin	feline gut	Human gut	Human gut	Human gut

NA = Not available / not tested / data not reported ; **w** = Weak reaction ; **+** = Positive reaction / activity present ;
– = Negative reaction/activity absent

430 **Table 2:** Genomic features of all strains of strain AB403, strain AB800^T, strain AB804, strain AB807, strain AB808, strain AB811,
431 including antimicrobial resistance genes and genes involved in metabolism pathways.
432

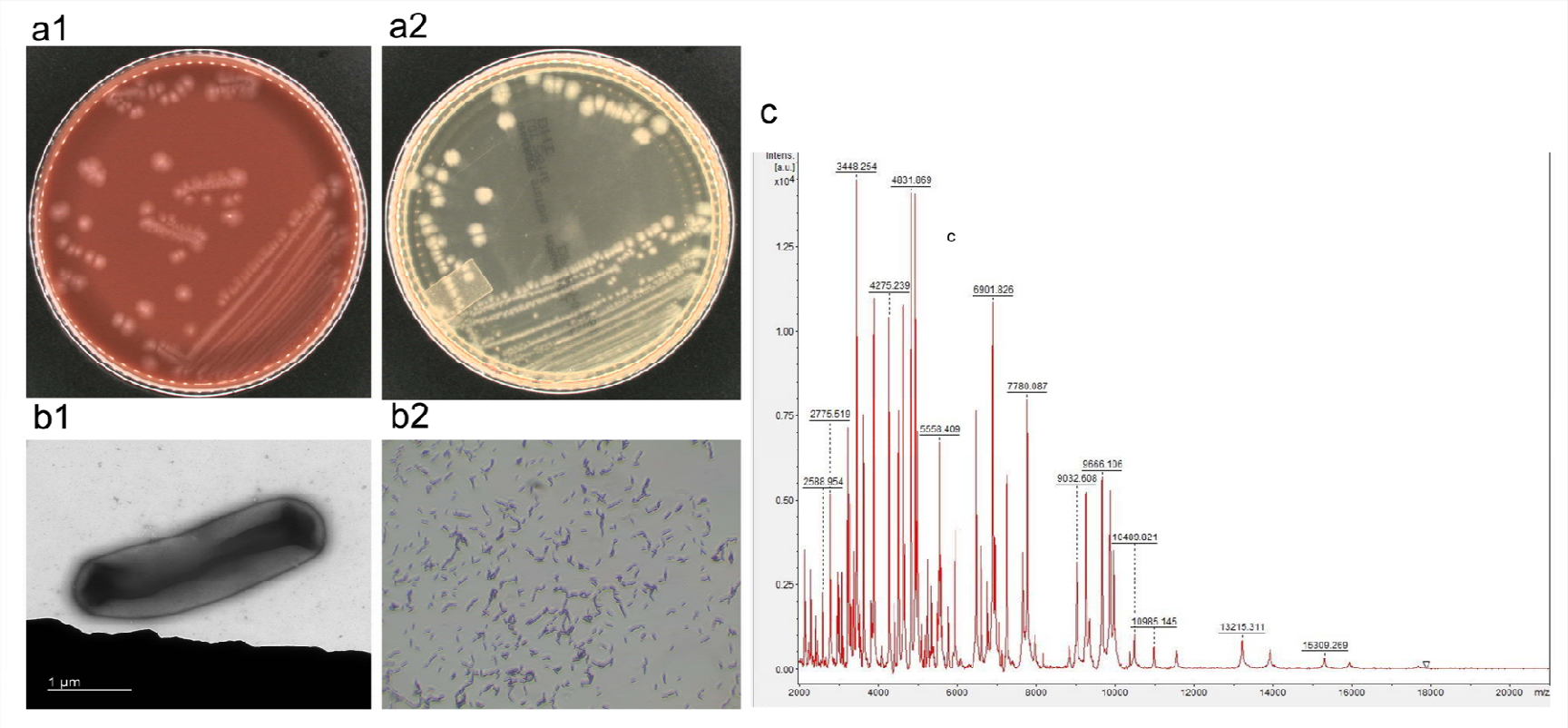
	Description	**AB0403**	AB800^T	**AB804**	**AB807**	**AB808**	**AB811**
Genome features							
contigs		189	149	221	179	182	199
bases	Size	2518813	2583354	2529093	2692535	2857951	2430653
CDS	number of coding sequences	2206	2355	2299	2507	2624	2165
gene	Number of genes	2297	2450	2390	2599	2719	2261
rRNA	-	16	16	17	16	20	17
repeat_region	-	3	3	3	2	3	3
tRNA	-	74	78	73	75	74	78
tmRNA	-	1	1	1	1	1	1
Resistance Genes							
(Tet)tetA-P	Tetracycline resistance gene	-	-	-	-	-	-
(Tet)tetB-P	Tetracycline resistance gene	+	+	+	-	-	+
ERMQ	Macrolide resistance gene	-	-	-	-	-	-
LnuP	Lincosamide resistance gene	-	-	-	-	-	-
tetA(P)	Tetracycline resistance gene	+	+	+	-	-	+
Bile acid metabolism genes							
baiN_2	3-dehydro-bile acid delta(4,6)-reductase	+	+	+	+	+	+
baiN_1	3-dehydro-bile acid delta(4,6)-reductase	+	+	+	+	+	+
baiB	Bile acid-coenzyme A ligase	+	+	+	+	+	+
baiE	Bile acid-coenzyme A ligase	+	+	+	+	+	+
baiCD_1	3-oxocholoyl-CoA 4-desaturase	+	+	+	+	+	+
baiCD_2	3-oxocholoyl-CoA 4-desaturase	+	+	+	+	+	+
baiF	Bile acid-CoA transferase	+	+	+	+	+	+

baiH	7-beta-hydroxy-3-oxochol-24-oyl-CoA 4-desaturase	+	+	+	+	+	+
baiA2	Bile acid 7-alpha dehydratase	+	+	+	+	+	+
baiN_3	3-dehydro-bile acid delta(4,6)-reductase	-	-	-	-	-	-
baiN_4	3-dehydro-bile acid delta(4,6)-reductase	-	-	-	-	-	-
baiN_5	3-dehydro-bile acid delta(4,6)-reductase	-	-	-	-	-	-

+ = Presence of genes ; – = Absence of genes

435 **List of Supplementary data**

436 **Supplementary Table 1**: DNA-DNA Hybridization table from GGDC with strain AB800^{T} as the



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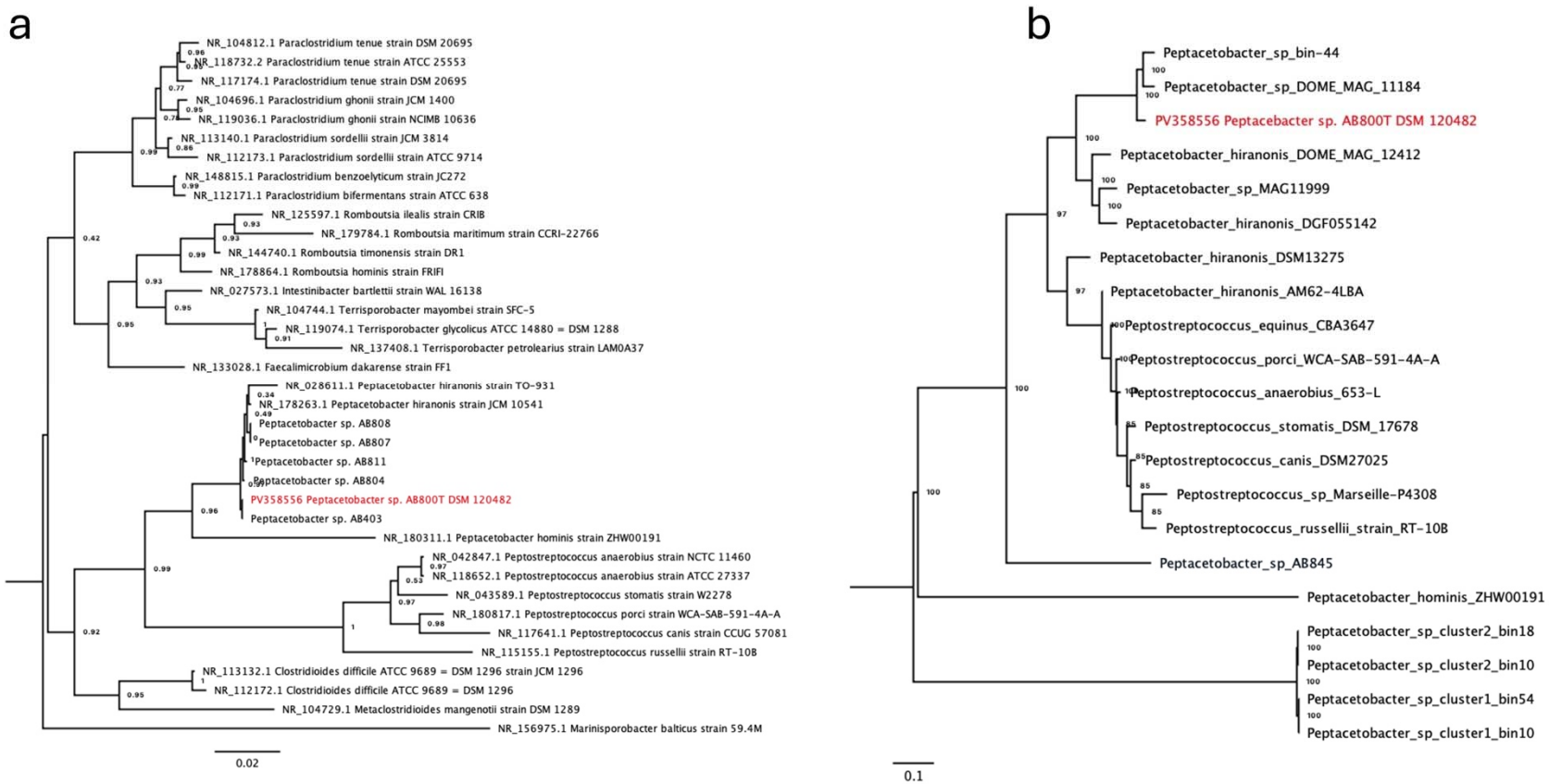

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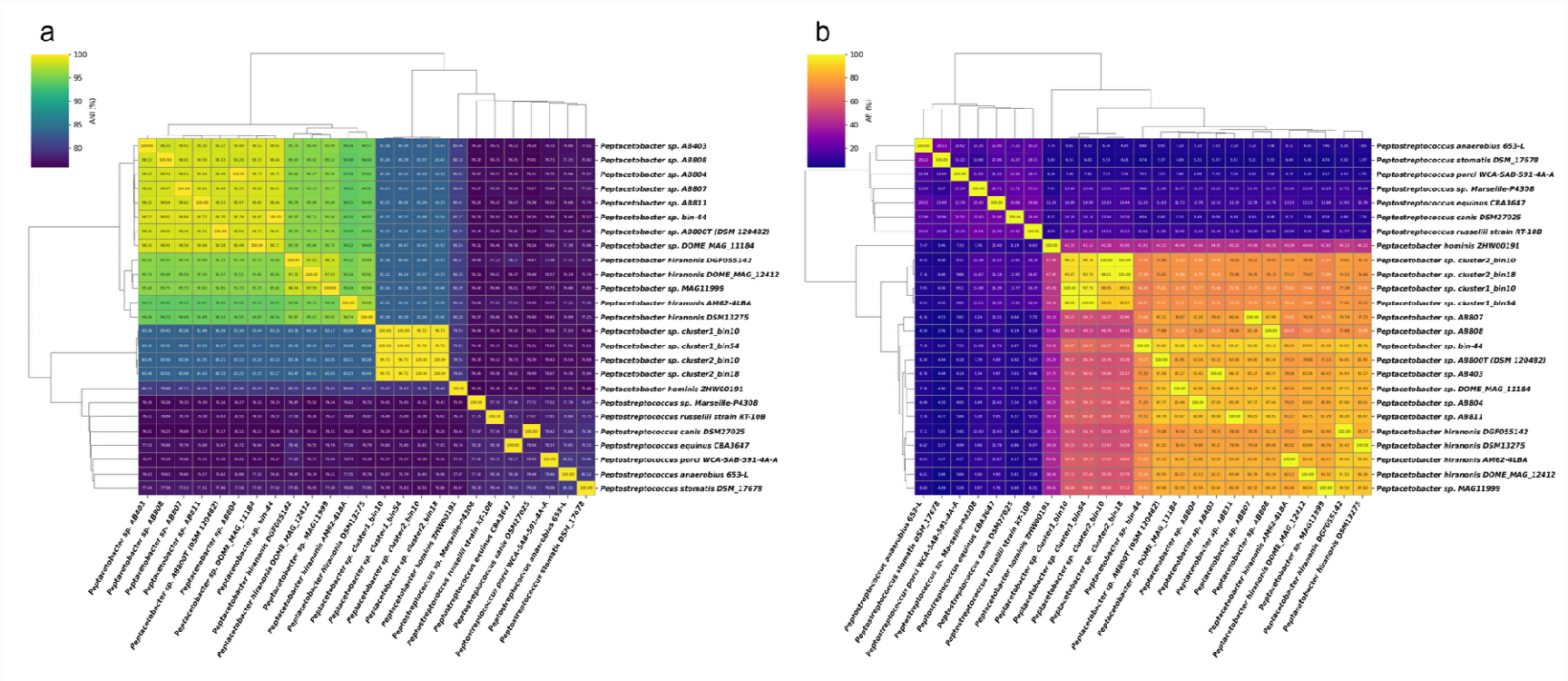

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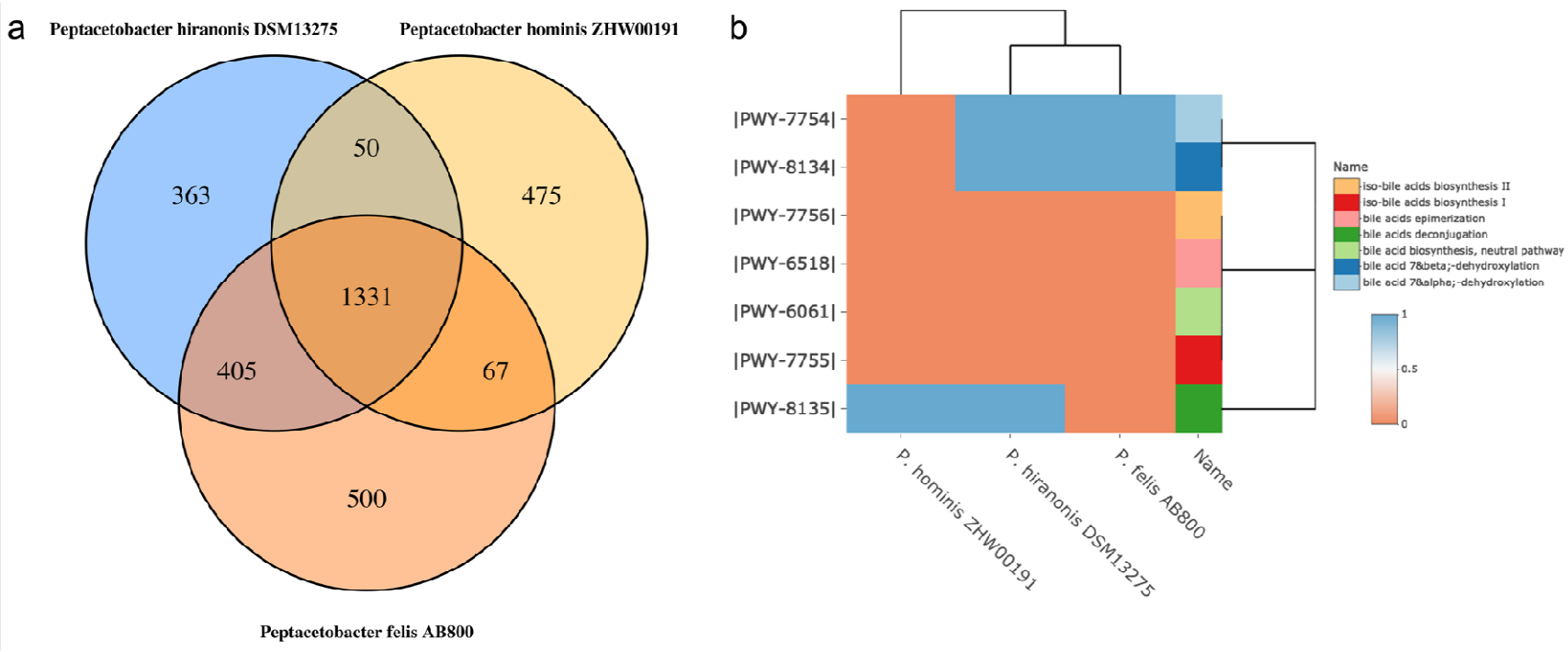

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