Supplementary Material

Apibacter adventoris gen. nov., sp. nov., a member of the phylum *Bacteroidetes* isolated from honey bees

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Table S1. Strain source information and full-length 16S rRNA identity to close relatives.

Strains: 1, *Empedobacter brevis* CCUG7320^T; 2, *Ornithobacterium rhinotracheale* LMG 9086^T; 3, *Chryseobacterium gleum* ATCC 35910^T; 4, *Flavobacterium aquatile* LMG 4008^T.

			16S rRNA identity (%) to						
Strain	**Host**	**Location**	**wkB301^T**	**wkB180**	**wkB309**	**1**	**2**	**3**	**4**
wkB301^T	*Apis dorsata*	University of Malaya, Kuala Lumpur, Malaysia	-	99.5	95.8	87.6	87.5	87.2	85.5
wkB180	*Apis dorsata*	HortPark, Singapore	99.5	-	95.9	87.6	87.5	87.1	85.4
wkB309	*Apis cerana*	Genting Highlands, Malaysia	95.8	95.9	-	88.4	87.5	86.3	85.7

Table S2. Deposited sequences from this study.

Gene	Length (bp)	GenBank accession no.
wkB301^T		
16S rRNA	1528	KT149221
alaS	2607	KT149224
atpA	1581	KT149227
dnaA	1431	KT149230
dnaN	1116	KT149233
ftsZ	1839	KT149236
fusA	2130	KT149239
groEL	1629	KT149242
gyrB	1938	KT149245
lepA	1794	KT149248
metK	1269	KT149251
nusG	546	KT149254
pfkA	993	KT149257
pyrG	1644	KT149260
recA	1014	KT149263
rplA	693	KT149266
rplB	822	KT149269
rpoB	3825	KT149272
rpsB	801	KT149275
sdhA	2016	KT149278
secA	3324	KT149281
wkB180		
16S rRNA	1529	KT149222
alaS	2607	KT149225
atpA	1581	KT149228
dnaA	1431	KT149231
dnaN	1116	KT149234
ftsZ	1839	KT149237
fusA	2130	KT149240
groEL	1629	KT149243
gyrB	1938	KT149246
lepA	1794	KT149249
metK	1269	KT149252
nusG	546	KT149255
pfkA	993	KT149258
pyrG	1644	KT149261
recA	1014	KT149264
rplA	693	KT149267

rplB	822	KT149270
rpoB	3825	KT149273
rpsB	801	KT149276
sdhA	2016	KT149279
secA	3324	KT149282
wkB309		
16S rRNA	1527	KT149220
alaS	2610	KT149223
atpA	1578	KT149226
dnaA	1431	KT149229
dnaN	1116	KT149232
ftsZ	1827	KT149235
fusA	2130	KT149238
groEL	1629	KT149241
gyrB	1938	KT149244
lepA	1821	KT149247
metK	1269	KT149250
nusG	546	KT149253
pfkA	993	KT149256
pyrG	1653	KT149259
recA	1023	KT149262
rplA	693	KT149265
rplB	822	KT149268
rpoB	3825	KT149271
rpsB	801	KT149274
sdhA	2016	KT149277
secA	3333	KT149280

Table S3. Antibiotic resistances of strains wkB301^T and wkB309. Strains were grown on heart infusion agar supplemented with 5% sheep blood at 35°C and 5% CO_2. Minimum inhibitory concentration strips were read after 2–3 days growth. Strips were manufactured by bioMérieux unless otherwise indicated.

Antibiotic	Minimum inhibitory concentration (µg)	
	wkB301^T	wkB309
Ampicillin	0.094	0.75
Chloramphenicol	1.5	8
Gentamicin	96	>256
Kanamycin (Liofilchem)	>256	128
Spectinomycin (Liofilchem)	1.5	8
Streptomycin (Liofilchem)	>256	6
Tetracycline	1	2

Table S4. Fatty acid profiles of strains wkB301^T, wkB309, and related *Flavobacteriaceae*.

Strains: 1, wkB301^T; 2, wkB309; 3, *Empedobacter brevis* CCUG7320^T; 4, *Ornithobacterium rhinotracheale* (multiple strains); 5, *Chryseobacterium gleum* (multiple strains). Unknown fatty acids and those comprising <1% of total are not listed. Values given as percentages; -, not detected. Distinguishing fatty acids are bolded.

Fatty acid	**1**	**2**	**3[a]**	**4[b]**	**5[c]**
Straight-chain					
$C_{14:0}$	<1	1.40	-	<1	-
$C_{16:0}$	**15.15**	**21.59**	4.0	2.9	1
$C_{18:0}$	1.04	<1	<1	-	-
Branched					
$C_{14:0}$ iso	<1	1.45	-	-	-
$C_{15:0}$ iso	23.24	15.44	24.5	57.4	35
$C_{15:0}$ anteiso	1.46	1.99	-	<1	<1
$C_{17:0}$ iso	1.84	1.32	<1	1.5	2
$C_{17:1}$ iso I and/or $C_{17:1}$ anteiso B	-	-	8.1	-	<1
Unsaturated					
$C_{15:1}$ω6*c*	-	-	2.2	-	-
$C_{16:1}$ω5*c*	-	-	5.5	-	-
$C_{16:1}$ω7*c* and/or $C_{16:1}$ω6*c*	9.58	<1	15.5	-	-
$C_{17:1}$ iso ω9*c*	-	-	1.7	-	20
$C_{18:1}$ ω9*c*	2.46	1.72		-	-
Hydroxy					
$C_{15:0}$ 2-OH	<1	<1	1.4	-	-
$C_{15:0}$ iso 3-OH	4.53	3.97	7.3	8.1	3
$C_{16:0}$ 2-OH	<1	1.63	-	-	-
$C_{16:0}$ 3-OH	**10.98**	**13.77**	3.5	2.8	1
$C_{16:0}$ iso 3-OH	<1	1.05	-	-	1
$C_{17:0}$ iso 3-OH	18.05	22.18	17.6	20.2	22
Summed feature $C_{15:0}$ iso 2-OH and/or $C_{16:1}$ω7*c* and /or $C_{16:1}$ω7*t*	-	-	-	-	12
Summed feature $C_{18:2}$ω6,9*c* and /or $C_{18:0}$ ante	4.00	5.51	-	-	-

[a] Data from Zhang *et al.* (2014).
[b] Data from Vandamme *et al.* (1994), 21 strains.
[c] Data from Bernardet *et al.* (2006), 5 strains.

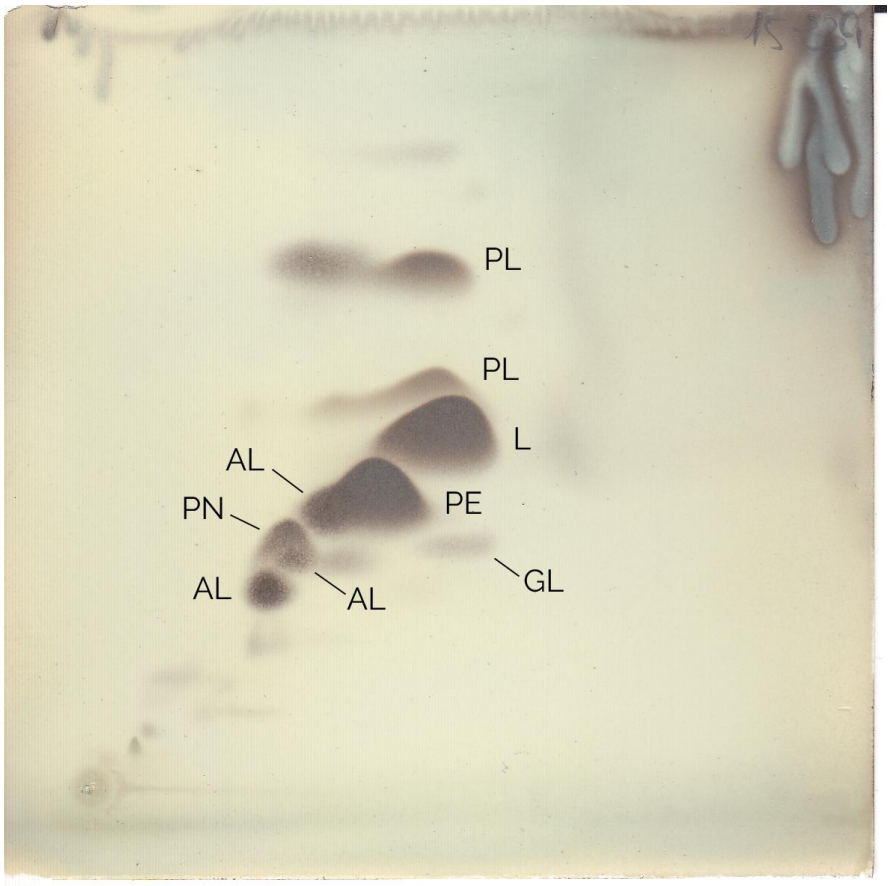

Figure S1. Polar lipid composition of strain wkB301^{T}, from two-dimensional silica gel thin layer chromatography (DSMZ, Braunschweig, Germany). AL, aminolipid; GL, glycolipid; L, lipid; PE, phosphatidylethanolamine; PL, phospholipid; PN, phosphoaminolipid.