

Table S1: Selection of *Bacteroidia* that produce propionate and respective plant polymers that can be utilized.

Organism	Strain	Isolated from	Acids produced	Polymeric substrates	Risc Group**	Reference
<i>Bacteroides</i>						
<i>B. cellulosilyticus</i>	CRE21	Human feces	A, P, S, F, L	CWS, cellulose (Avicel p101, Sigmacell 101), starch, pectin	1	[1]
<i>B. fragilis</i>	EN-2	Appendix abscess	S, A, P, L	*Starch	2	[2, 3]
<i>B. graminisolvens</i>	XDT-1	Methanogenic reactor	A, P, S, L, B	Xylan, starch, pectin	1	[4]
<i>B. intestinalis</i>	341	Human feces	Fu, A, P	-	1	[5, 6];
<i>B. luti</i>	UasXn-3	Methanogenic sludge	A, S, P, F	Cellulose, xylan, starch	1	[5]
<i>B. ovatus</i>	ATCC 8483	Human feces	A, P, S	Starch, pectin, xylan, arabinogalactan	2	[7, 8]
<i>B. propionificiens</i>	SV434	Methanogenic reactor	A, P, S	Starch	1	[9]
<i>B. propionigenes</i>	NSJ-90	Human feces	A, P, IV	Starch, Xylan	Nd.	[10]
<i>B. reticulotermitis</i>	Rs-03	Termite gut	S, A, P	Xylan, Starch, CMC, pectin	1	[11]
<i>B. thetaiotaomicron</i>	E50		A, P, S	*Starch, pectin, polygalacturonate, larch arabinogalactan	2	[3, 12, 13]
<i>B. xylanisolvens</i>	XB1A	Human feces	A, P, S	Xylan	1	[14]
<i>Butyricimonas</i>						
<i>B. faecalis</i>	H184	Human feces	P, A, IB, B, IV, V	-	Nd.	[15]
<i>Coprobacter</i>						
<i>C. fastidiosus</i>	NSB1	Infant feces	A, P, S	Nd.	1	[16]
<i>Dysgonomonas</i>						
<i>D. alginatilytica</i>	HUA-2	Alginate degrading consortium	L, S, A, P	Alginate	1	[17]
<i>D. capnocytophagoides</i>	CCUG 17996	Infected human gallbladder	P, L, S	Nd.	2	[18]
<i>D. mossii</i>	CCUG 43457	Human clinical sample	L, A, P	Nd.	1	[19]

Fermentimonas						
<i>F. caenicola</i>	ING2-E5B	Mesophilic biogas reactor	A, P	Soluble starch	1	[20]
Lentimicrobium						
<i>L. saccharophilum</i>	TBC1	Methanogenic sludge	A, M, P, F	starch	1	[21]
Odoribacter						
<i>O. splanchnicus</i>	1651/6	Human feces	A, P, IB, B	Nd.	2	[22, 23]
Paludibacter						
<i>P. propionigenes</i>	WB4	Anoxic rice-field soil	P, A, S	Soluble starch	1	[24]
<i>P. jianxiensis</i>	NM7	rice paddy field	A, P	Cellobiose, pectin, starch	1	[25]
Parabacteroides						
<i>P. acidifaciens</i>	426-9	Human feces	A, P, IB	Nd.	Nd.	[26]
<i>P. chartae</i>	NS31-3	Paper mill wastewater	L, P, F, A	Nd.	1	[27]
<i>P. johnsonii</i>	M-165	Human feces	S, A, P	Nd.		[28]
Petrimonas						
<i>P. mucosa</i>	ING2-E5A	Mesophilic biogas reactor	A, P	Soluble starch	1	[20]
Phocaeicola						
<i>P. paurosaccharolyticus</i>	WK042	Methanogenic reactor	A, P, S	Glycogen, starch, pectin	1	[29, 30]
<i>P. vulgatus</i>	ATCC 8482	Human feces	A, S, F, L, P	*Starch, larch arabinogalactan	1	[3, 30, 31]
Proteiniphilum						
<i>P. sachcharofermentans</i>	M3/6	Mesophilic biogas reactor	A, P	Soluble starch	1	[20]
Xylanibacter						
<i>X. ruminicola</i>	23	rumen	P, A, S		2	[32, 33]
<i>X. oryzae</i>	KB3	anoxic rice-field soil	A, P, S, M	Xylan, pectin, CMC	1	[34, 35]

Acids are listed in decreasing order according to relative amounts produced. Strains used in this study are written in bold. Abbreviations: acetate (A), propionate (P), succinate (S); lactate (L); malate (M), butyrate (B); isobutyrate (IB); isovalerate (IV), Fumarate (Fu), not determined (Nd.)

*Utilization has been confirmed for several strains. **According to German technical rule for biological agents 2015.

References

1. Robert C, Chassard C, Lawson PA, Bernalier-Donadille A. *Bacteroides cellulosilyticus* sp. nov., a cellulolytic bacterium from the human gut microbial community. *Int J Syst Evol Microbiol.* 2007;57:1516–20.
2. Chen M, Wolin MJ. Influence of heme and vitamin B₁₂ on growth and fermentations of *Bacteroides* species. *J Bacteriol.* 1981;145:466–71.
3. Salyers AA, Vercellotti JR, West SE, Wilkins TD. Fermentation of mucin and plant polysaccharides by strains of *Bacteroides* from the human colon. *Appl Environ Microbiol.* 1977;33:319–22.
4. Nishiyama T, Ueki A, Kaku N, Watanabe K, Ueki K. *Bacteroides graminisolvens* sp. nov., a xylanolytic anaerobe isolated from a methanogenic reactor treating cattle waste. *Int J Syst Evol Microbiol.* 2009;59:1901–7.
5. Hatamoto M, Kaneshige M, Nakamura A, Yamaguchi T. *Bacteroides luti* sp. nov., an anaerobic, cellulolytic and xylanolytic bacterium isolated from methanogenic sludge. *Int J Syst Evol Microbiol.* 2014;64:1770–4.
6. Bakir MA, Kitahara M, Sakamoto M, Matsumoto M, Benno Y. *Bacteroides intestinalis* sp. nov., isolated from human faeces. *Int J Syst Evol Microbiol.* 2006;56:151–4.
7. Macfarlane GT, Hay S, Macfarlane S, Gibson GR. Effect of different carbohydrates on growth, polysaccharidase and glycosidase production by *Bacteroides ovatus*, in batch and continuous culture. *J Appl Bacteriol.* 1990;68:179–87.
8. Horvath TD, Ihekweazu FD, Haidacher SJ, Ruan W, Engevik KA, Fultz R, *et al.* *Bacteroides ovatus* colonization influences the abundance of intestinal short chain fatty acids and neurotransmitters. *iScience.* 2022;25:104158.
9. Ueki A, Abe K, Kaku N, Watanabe K, Ueki K. *Bacteroides propionicifaciens* sp. nov., isolated from rice-straw residue in a methanogenic reactor treating waste from cattle farms. *Int J Syst Evol Microbiol.* 2008;58:346–52.
10. Sun X-W, Abdugheni R, Huang H-J, Wang Y-J, Jiang M-Z, Liu C, *et al.* *Bacteroides propionicigenes* sp. nov., isolated from human faeces. *Int J Syst Evol Microbiol* 2022.
11. Sakamoto M, Ohkuma M. *Bacteroides reticulotermis* sp. nov., isolated from the gut of a subterranean termite (*Reticulitermes speratus*). *Int J Syst Evol Microbiol.* 2013;63:691–5.
12. Kotarski SF, Salyers AA. Effect of long generation times on growth of *Bacteroides thetaiotaomicron* in carbohydrate-induced continuous culture. *J Bacteriol.* 1981;146:853–60.
13. Adamberg S, Tomson K, Vija H, Puurand M, Kabanova N, Visnapuu T, *et al.* Degradation of fructans and production of propionic acid by *Bacteroides thetaiotaomicron* are enhanced by the shortage of amino acids. *Front Nutr.* 2014;1:21.
14. Chassard C, Delmas E, Lawson PA, Bernalier-Donadille A. *Bacteroides xylanisolvens* sp. nov., a xylan-degrading bacterium isolated from human faeces. *Int J Syst Evol Microbiol.* 2008;58:1008–13.
15. Le Roy T, van der Smitten P, Paquot A, Delzenne N, Muccioli GG, Collet J-F, Cani PD. *Butyricimonas faecalis* sp. nov., isolated from human faeces and emended description of the genus *Butyricimonas*. *Int J Syst Evol Microbiol.* 2019;69:833–8.
16. Shkoporov AN, Khokhlova EV, Chaplin AV, Kafarskaia LI, Nikolin AA, Polyakov VY, *et al.* *Coprobacter fastidiosus* gen. nov., sp. nov., a novel member of the family

- Porphyromonadaceae* isolated from infant faeces. Int J Syst Evol Microbiol. 2013;63:4181–8.
17. Kita A, Miura T, Okamura Y, Aki T, Matsumura Y, Tajima T, *et al.* *Dysgonomonas alginatilytica* sp. nov., an alginate-degrading bacterium isolated from a microbial consortium. Int J Syst Evol Microbiol. 2015;65:3570–5.
 18. Hofstad T, Olsen I, Eribe ER, Falsen E, Collins MD, Lawson PA. *Dysgonomonas* gen. nov. to accommodate *Dysgonomonas gadei* sp. nov., an organism isolated from a human gall bladder, and *Dysgonomonas capnocytophagoides* (formerly CDC group DF-3). Int J Syst Evol Microbiol. 2000;50 Pt 6:2189–95.
 19. Lawson PA, Falsen E, Inganäs E, Weyant RS, Collins MD. *Dysgonomonas mossii* sp. nov., from human sources. Syst Appl Microbiol. 2002;25:194–7.
 20. Hahnke S, Langer T, Koeck DE, Klocke M. Description of *Proteiniphilum saccharofermentans* sp. nov., *Petrimonas mucosa* sp. nov. and *Fermentimonas caenicola* gen. nov., sp. nov., isolated from mesophilic laboratory-scale biogas reactors, and emended description of the genus *Proteiniphilum*. Int J Syst Evol Microbiol. 2016;66:1466–75.
 21. Sun L, Toyonaga M, Ohashi A, Tournalousse DM, Matsuura N, Meng X-Y, *et al.* *Lentimicrobium saccharophilum* gen. nov., sp. nov., a strictly anaerobic bacterium representing a new family in the phylum Bacteroidetes, and proposal of Lentimicrobiaceae fam. nov. Int J Syst Evol Microbiol. 2016;66:2635–42.
 22. Werner H, Rintelen G, Kunstek-Santos H. Eine neue buttersäurebildende *Bacteroides*-Art: *B. splanchnicus* n. sp [A new butyric acid-producing *bacteroides* species: *B. splanchnicus* n. sp.]. Zentralbl Bakteriol Orig A. 1975;231:133–44.
 23. Hardham JM, King KW, Dreier K, Wong J, Strietzel C, Eversole RR, *et al.* Transfer of *Bacteroides splanchnicus* to *Odoribacter* gen. nov. as *Odoribacter splanchnicus* comb. nov., and description of *Odoribacter denticanis* sp. nov., isolated from the crevicular spaces of canine periodontitis patients. Int J Syst Evol Microbiol. 2008;58:103–9.
 24. Ueki A, Akasaka H, Suzuki D, Ueki K. *Paludibacter propionicigenes* gen. nov., sp. nov., a novel strictly anaerobic, Gram-negative, propionate-producing bacterium isolated from plant residue in irrigated rice-field soil in Japan. Int J Syst Evol Microbiol. 2006;56:39–44.
 25. Qiu Y-L, Kuang X-Z, Shi X-S, Yuan X-Z, Guo R-B. *Paludibacter jiangxiensis* sp. nov., a strictly anaerobic, propionate-producing bacterium isolated from rice paddy field. Arch. Microbiol. 2014;196:149–55.
 26. Wang Y-J, Xu X-J, Zhou N, Sun Y, Liu C, Liu S-J, You X. *Parabacteroides acidifaciens* sp. nov., isolated from human faeces. Int J Syst Evol Microbiol. 2019;69:761–6.
 27. Tan H-Q, Li T-T, Zhu C, Zhang X-Q, Wu M, Zhu X-F. *Parabacteroides chartae* sp. nov., an obligately anaerobic species from wastewater of a paper mill. Int J Syst Evol Microbiol. 2012;62:2613–7.
 28. Sakamoto M, Kitahara M, Benno Y. *Parabacteroides johnsonii* sp. nov., isolated from human faeces. Int J Syst Evol Microbiol. 2007;57:293–6.
 29. Ueki A, Abe K, Ohtaki Y, Kaku N, Watanabe K, Ueki K. *Bacteroides paurosaccharolyticus* sp. nov., isolated from a methanogenic reactor treating waste from cattle farms. Int J Syst Evol Microbiol. 2011;61:448–53.
 30. García-López M, Meier-Kolthoff JP, Tindall BJ, Gronow S, Woyke T, Kyrpides NC, *et al.* Analysis of 1,000 type-strain genomes improves taxonomic classification of *Bacteroidetes*. Front Microbiol. 2019;10:2083.

31. Lück R, Deppenmeier U. Genetic tools for the redirection of the central carbon flow towards the production of lactate in the human gut bacterium *Phocaeicola (Bacteroides) vulgatus*. Appl Microbiol Biotechnol. 2022;106:1211–25.
32. Strobel HJ. Vitamin B12-dependent propionate production by the ruminal bacterium *Prevotella ruminicola* 23. Appl Environ Microbiol. 1992;58:2331–3.
33. Hitch TCA, Bisdorf K, Afrizal A, Riedel T, Overmann J, Strowig T, Clavel T. A taxonomic note on the genus *Prevotella*: Description of four novel genera and emended description of the genera *Hallella* and *Xylanibacter*. Syst Appl Microbiol. 2022;45:126354.
34. Ueki A, Akasaka H, Suzuki D, Hattori S, Ueki K. *Xylanibacter oryzae* gen. nov., sp. nov., a novel strictly anaerobic, Gram-negative, xylanolytic bacterium isolated from rice-plant residue in flooded rice-field soil in Japan. Int J Syst Evol Microbiol. 2006;56:2215–21.
35. Sakamoto M, Ohkuma M. Reclassification of *Xylanibacter oryzae* Ueki *et al.* 2006 as *Prevotella oryzae* comb. nov., with an emended description of the genus *Prevotella*. Int J Syst Evol Microbiol. 2012;62:2637–42.