

Revised Supplement 1: Reference list for Figure 1.

Manuscript title: Process disturbances in agricultural biogas production – causes, mechanisms and effects on the biogas microbiome: A review

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References of Figure 1

¹Abt et al. 2010, ²Parizzi et al. 2012, ³Hahnke et al. 2016 and Tomazetto et al. 2018, ⁴Ueki et al. 2006 and Gronow et al. 2011, ⁵Grabowski et al. 2005, ⁶Chen and Dong 2005, ⁷Avgustin et al. 1997 and Purushe et al. 2010, ⁸Yamada et al. 2006 and Matsuura et al. 2015, ⁹Yamada et al. 2007 and Matsuura et al. 2015, ¹⁰Sun et al. 2016, ¹¹Suen et al. 2011, ¹²Hahnke et al. 2014 and Tomazetto et al. 2016, ¹³Mechichi et al. 1999, ¹⁴Koeck et al. 2015a and 2015b, ¹⁵Tomazetto et al. 2017, ¹⁶Fonknechten et al. 2010, ¹⁷Chen et al. 2010, ¹⁸Nishiyama et al. 2009, ¹⁹Sieber et al. 2010, ²⁰Pierce et al. 2008, ²¹Westerholm et al. 2011 and Müller et al. 2015, ²²Ueki et al. 2014, ²³Jackson et al. 1999 and McInerney et al. 2007, ²⁴Ma et al. 2017, ²⁵Harmsen et al. 1998 and Plugge et al. 2012, ²⁶Menes and Muxi 2002, Mavromatis et al. 2013 and Hania et al. 2016, ²⁷Qiu et al. 2014, ²⁸Baena et al. 2000 and Chertkov et al. 2010, ²⁹Chouari et al. 2005 and Pelletier et al. 2008, ³⁰Maus et al. 2016, ³¹Koeck et al. 2016, ³²Patil et al. 2015, ³³Barber et al. 2011, ³⁴Galagan et al. 2002, ³⁵Ma et al. 2006 and Zhu et al. 2012, ³⁶Maeder et al. 2006, ³⁷Kern et al. 2016, ³⁸Anderson et al. 2009, ³⁹Manzoor et al. 2016, ⁴⁰Maus et al. 2014, ⁴¹Kern et al. 2015, ⁴²Gunsalus et al. 2016, ⁴³Hahnke et al. 2018, ⁴⁴Nishiyama et al. 2009, ⁴⁵Hatamoto et al. 2014

References

1. Abt, B.; Foster, B.; Lapidus, A.; Clum, A.; Sun, H.; Pukall, R.; Lucas, S.; Del Rio, T.G.; Nolan, M.; Tice, H.; Cheng, J.-F.; Pitluck, S.; Liolios, K.; Ivanova, N.; Mavromatis, K.; Ovchinnikova, G.; Pati, A.; Goodwin, L.; Chen, A.; Palaniappan, K.; Land, M.; Hauser, L.; Chang, Y.-J.; Jeffries, C.D.; Rohde, M.; Göker, M.; Woyke, T.; Bristow, J.; Eisen, J.A.; Markowitz, V.; Hugenholtz, P.; Kyrpides, N.C.; Klenk, H.-P. (2010). Complete genome sequence of *Cellulomonas flavigena* type strain (134T). *Standards Genomic Sci* **2010**, 3, 15–25, doi.org/10.4056/sigs.1012662.
2. Parizzi, L.P.; Grassi, M.C.B.; Llerena, L.A.; Carazzolle, M.F.; Queiroz, V.L.; Lunardi, I.; Zeidler, A.F.; Teixeira, P.J.P.L.; Mieczkowski, P.; Rincones, J.; Pereira, G.A.G. The genome sequence of *Propionibacterium acidipropionici* provides insights into its biotechnological and industrial potential. *BMC Genomics* **2012**, 13, 562–582, doi.org/10.1186/1471-2164-13-562.
3. Hahnke, S.; Langer, T.; Koeck, D.E.; 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: 1466–1475, doi.org/10.1099/ijsem.0.000902.
4. Tomazetto, G.; Hahnke, S.; Wibberg, D.; Pühler, A.; Klocke, M.; Schlüter, A. *Proteiniphilum saccharofermentans* str. M3/6^T isolated from a laboratory biogas reactor is versatile in polysaccharide and oligopeptide utilization as deduced from genome-based metabolic reconstructions. *Biotechnol Rep* **2018**, 18, e00254, doi.org/10.1016/j.btre.2018.e00254.
5. 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, 1901–1907, doi.org/10.1099/ijms.0.008268-0.
6. 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, 1770–1774, doi.org/10.1099/ijms.0.056630-0.

7. Ueki, A.; Akasaka, H.; Suzuki, D.; Ueki, K. *Paludibacter propionigenes* 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.
8. Gronow, S.; Munk, C.; Lapidus, A.; Nolan, M.; Lucas, S.; Hammon, N.; Deshpande, S.; Cheng, J.-F.; Tapia, R.; Han, C.; Goodwin, L.; Pitluck, S.; Liolios, K.; Ivanova, N.; Mavromatis, K.; Mikhailova, N.; Pati, A.; Chen, A.; Palaniappan, K.; Land, M.; Hauser, L.; Chang, Y.-J.; Jeffries, C.D.; Brambilla, E.; Rohde, M.; Göker, M.; Detter, J.C.; Woyke, T.; Bristow, J.; Eisen, J.A.; Markowitz, V.; Hugenholtz, P.; Kyrpides, N.C.; Klenk, H.-P. Complete genome sequence of *Paludibacter propionigenes* type strain (WB4^T). *Standards Genomic Sci* **2011**, *4*, 36–44, doi.org/10.4056/sigs.1503846
9. Grabowski, A.; Tindall, B.J.; Bardin, V.; Blanchet, D.; Jeanthon, C. *Petrimonas sulfuriphila* gen. nov., sp. nov., a mesophilic fermentative bacterium isolated from a biodegraded oil reservoir. *Int J Syst Evol Microbiol* **2005**, *55*, 1113–1121.
10. Chen, S.; Dong, X. *Proteiniphilum acetatigenes* gen. nov., sp. nov., from a UASB reactor treating brewery wastewater. *Int J Syst Evol Microbiol* **2005**, *55*, 2257–2261.
11. Avgustin, G.; Wallace, R.J.; Flint, H.J. Phenotypic Diversity among ruminal isolates of *Prevotella ruminicola*, proposal of *Prevotella brevis* sp. nov., *Prevotella byantii* sp. nov., and *Prevotella albensis* sp. nov. and redefinition of *Prevotella ruminicola*. *Int J Syst Bacteriol* **1997**, *47*, 284–288.
12. Purushe, J.; Fouts, D.E.; Morrison, M.; White, B.A.; Mackie, R.I.; the North American Consortium for Rumen Bacteria; Coutinho, P.M.; Henrissat, B.; Nelson, K.E. (2010) Comparative genome analysis of *Prevotella ruminicola* and *Prevotella bryantii*: Insights into their environmental niche. *Microb Ecol* **2010**, *60*, 721–729, doi.org/10.1007/s00248-010-9692-8.
13. Yamada, T.; Sekiguchi, Y.; Hanada, S.; Imachi, H.; Ohashi, A.; Harada, H.; Kamagata, Y. *Anaerolinea thermolimosa* sp. nov., *Levilinea saccharolytica* gen. nov., sp. nov. and *Leptolinea tardivitalis* gen. nov., sp. nov., novel filamentous anaerobes, and description of the new classes *Anaerolineae* classis nov. and *Caldilineae* classis nov. in the bacterial phylum *Chloroflexi*. *Int J Syst Evol Microbiol* **2006**, *56*, 1331–1340.
14. Matsuura, N.; Tourlousse, D.M.; Ohashi, A.; Hugenholtz, P.; Sekiguchi, Y. Draft genome sequences of *Anaerolinea thermolimosa* IMO-1, *Bellilinea caldifistulae* GOMI-1, *Leptolinea tardivitalis* YMTK-2, *Levilinea saccharolytica* KIBI-1, *Longilinea arvoryzae* KOME-1, previously described as members of the class *Anaerolineae* (*Chloroflexi*). *Genome Announc* **2015**, *3*, e00975-15, doi.org/10.1128/genomeA.00975-15.
15. Yamada, T.; Imachi, H.; Ohashi, A.; Harada, H.; Hanada, S.; Kamagata, Y.; Sekiguchi, Y. *Bellilinea caldifistulae* gen. nov., sp. nov. and *Longilinea arvoryzae* gen. nov., sp. nov., strictly anaerobic, filamentous bacteria of the phylum *Chloroflexi* isolated from methanogenic propionate-degrading consortia. *Int J Syst Evol Microbiol* **2007**, *57*, 2299–2306.
16. Sun, L.; Toyonaga, M.; Ohashi, A.; Matsuura, N.; Tourlousse, D.M.; Meng, X.-Y.; Tamaki, H.; Hanada, S.; Cruz, R.; Yamaguchi, T.; Sekiguchi, Y. Isolation and characterization of *Flexilinea flocculi* gen. nov., sp. nov., a filamentous, anaerobic bacterium belonging to the class *Anaerolineae* in the phylum *Chloroflexi*. *Int J Syst Evol Microbiol* **2016**, *66*, 988–996, doi.org/10.1099/ijsem.0.000822.
17. Suen, G.; Weimer, P.J.; Stevenson, D.M.; Aylward, F.O.; Boyum, J.; Deneke, J.; Drinkwater, C.; Ivanova, N.N.; Mikhailova, N.; Chertkov, O.; Goodwin, L.A.; Currie, C.R.; Mead, D.; Brumm, P.J. The complete genome sequence of *Fibrobacter succinogenes* S85 reveals a cellulolytic and metabolic specialist. *PLoS ONE* **2011**, *6*(4), e18814, doi.org/10.1371/journal.pone.0018814
18. Hahnke, S.; Striesow, J.; Elvert, M.; Mollar, X.P.; Klocke, M. *Clostridium bornimense* sp. nov., isolated from a mesophilic, two-phase, laboratory-scale biogas reactor. *Int J Syst Evol Microbiol* **2014**, *64*, 2792–2797, doi.org/10.1099/ijms.0.059691-0.
19. Tomazetto, G.; Hahnke, S.; Koeck, D.E.; Wibberg, D.; Maus, I.; Pühler, A.; Klocke, M.; Schlüter, A. Complete genome analysis of *Clostridium bornimense* strain M2/40T: A new acidogenic *Clostridium* species isolated from a mesophilic two-phase laboratory-scale biogas reactor. *J Biotechnol* **2016**, *232*, 38–49, doi.org/10.1016/j.jbiotec.2015.08.001
20. Mechichi, T.; Labat, M.; Gracia, J.-L.; Thomas, P.; Patel, B.K.C. Characterization of a new xylanolytic bacterium, *Clostridium xylanovorans* sp. nov. *Syst Appl Microbiol* **1999**, *22*, 366–371.
21. Koeck, D.E.; Ludwig, W.; Wanner, G.; Zverlov, V.V.; Liebl, W.; Schwarz, W.H. *Herbinix hemicellulosilytica* gen. nov., sp. nov., a thermophilic cellulose-degrading bacterium isolated from a thermophilic biogas reactor. *Int J Syst Evol Microbiol* **2015a**, *65*, 2365–2371, doi.org/10.1099/ijms.0.000264.
22. Koeck, D.E.; Maus, I.; Wibberg, D.; Winkler, A.; Zverlov, V.V.; Liebl, W.; Pühler, A.; Schwarz, W.H.; Schlüter, A. Draft genome sequence of *Herbinix hemicellulosilytica* T3/55T, a new thermophilic cellulose degrading bacterium isolated from a thermophilic biogas reactor. *J Biotechnol* **2015b**, *214*, 59–60, doi.org/10.1016/j.jbiotec.2015.07.022

23. Tomazetto, G.; Hahnke, S.; Langer, T.; Wibberg, D.; Blom, J.; Maus, I.; Pühler, A.; Klocke, M.; Schlüter, A. The completely annotated genome and comparative genomics of the *Peptoniphilaceae* bacterium str. ING2-D1G, a novel acidogenic bacterium isolated from a mesophilic biogas reactor. *J Biotechnol* **2017**, *257*, 178–186, doi.org/10.1016/j.jbiotec.2017.05.027
24. Fonknechten, N.; Chaussonnerie, S.; Tricot, S.; Lajus, A.; Andreesen, J.R.; Perchat, N.; Pelletier, E.; Gouyvenoux, M.; Barbe, V.; Salanoubat, M. *Clostridium sticklandii*, a specialist in amino acid degradation: revisiting its metabolism through its genome sequence. *BMC Genomics* **2010**, *11*, 555–567, doi.org/10.1186/1471-2164-11-555.
25. Chen, S.; Niu, L.; Zhang, Y. *Saccharofermentans acetigenes* gen. nov., sp. nov., an anaerobic bacterium isolated from sludge treating brewery wastewater. *Int J Syst Evol Microbiol* **2010**, *60*, 2735–2738, doi.org/10.1099/ijs.0.017590-0.
26. Nishiyama, T.; Ueki, A.; Kaku, N.; Ueki, K. *Clostridium sufflavum* sp. nov., isolated from a methanogenic reactor treating cattle waste. *Int J Syst Evol Microbiol* **2009**, *59*, 981–986. doi: 10.1099/ijs.0.001719-0.
27. Sieber, J.R.; Sims, D.R.; Han, C.; Kim, E.; Lykidis, A.; Lapidus, A.L.; McDonnald, E.; Rohlin, L.; Culley, D.E.; Gunsalus, R.; McInerney, M.J. The genome of *Syntrophomonas wolfei*: new insights into syntrophic metabolism and biohydrogen production. *Environ Microbiol* **2010**, *12*, 2289–2301, doi.org/10.1111/j.1462-2920.2010.02237.x.
28. Pierce, E.; Xie, G.; Barabote, R.D.; Saunders, E.; Han, C.S.; Detter, J.C.; Richardson, P.; Brettin, T.S.; Das, A.; Ljungdahl, L.G.; Ragsdale, S.W. The complete genome sequence of *Moorella thermoacetica* (f. *Clostridium thermoaceticum*). *Environ Microbiol* **2008**, *10*, 2550–2573, doi.org/10.1111/j.1462-2920.2008.01679.x
29. Westerholm, M.; Roos, S.; Schnürer, A. *Tepidanaerobacter acetatoxydans* sp. nov., an anaerobic, syntrophic acetate-oxidizing bacterium isolated from two ammonium-enriched mesophilic methanogenic processes. *Syst Appl Microbiol* **2011**, *34*, 260–266, doi.org/10.1016/j.syapm.2010.11.018.
30. Müller, B.; Manzoor, S.; Niazi, A.; Bongcam-Rudloff, E.; Schnürer, A. Genome-guided analysis of physiological capacities of *Tepidanaerobacter acetatoxydans* provides insights into environmental adaptations and syntrophic acetate oxidation. *PLoS ONE* **2015**, *10*(3), e0121237, doi.org/10.1371/journal.pone.0121237
31. Ueki, A.; Watanabe, M.; Ohtaki, Y.; Kaku, N.; Ueki, K. Description of *Propionispira arcuata* sp. nov., isolated from a methanogenic reactor of cattle waste, reclassification of *Zymophilus raffinosivorans* and *Zymophilus paucivorans* as *Propionispira raffinosivorans* comb. nov. and *Propionispira paucivorans* comb. nov. and emended description of the genus *Propionispira*. *Int J Syst Evol Microbiol* **2014**, *64*, 3571–3577, doi.org/10.1099/ijs.0.063875-0.
32. Jackson, B.E.; Bhupathiraju, V.K.; Tanner, R.S.; Woese, C.R.; McInerney, M.J. *Syntrophus aciditrophicus* sp. nov., a new anaerobic bacterium that degrades fatty acids and benzoate in syntrophic association with hydrogen-using microorganisms. *Arch Microbiol* **1999**, *171*, 107–114.
33. McInerney, M.J.; Rohlin, L.; Mouttaki, H.; Kim, U.; Krupp, R.S.; Rios-Hernandez, L.; Sieber, J.; Struchtemeyer, C.G.; Bhattacharyya, A.; Campbell, J.W.; Gunsalus, R.P. The genome of *Syntrophus aciditrophicus*: Life at the thermodynamic limit of microbial growth. *PNAS* **2007**, *104*, 7600–7605.
34. Ma, S.; Huang, Y.; Wang, C.; Fan, H.; Dai, L.; Zhou, Z.; Liu, X.; Deng, Y. *Defluviitalea raffinosedens* sp. nov., a thermophilic, anaerobic, saccharolytic bacterium isolated from an anaerobic batch digester treating animal manure and rice straw. *Int J Syst Evol Microbiol* **2017**, *67*, 1607–1612, doi.org/10.1099/ijsem.0.001664
35. Harmsen, H.J.M.; Van Kuijk, B.L.M.; Plugge, C.M.; Akkermans, A.D.L.; De Vos, W.M.; Stams, A. JM *Syntrophobacter fumaroxidans* sp. nov., a syntrophic propionate-degrading sulfatereducing bacterium. *Int J Syst Bacteriol* **1998**, *48*, 1383–1387.
36. Plugge, C.M.; Henstra, A.M.; Worm, P.; Swarts, D.C.; Paulitsch-Fuchs, A.H.; Scholten, J.C.M.; Lykidis, A.; Lapidus, A.L.; Goltsman, E.; Kim, E.; McDonald, E.; Rohlin, L.; Crable, B.R.; Gunsalus, R.P.; Stams, A.J.M.; McInerney, M.J. Complete genome sequence of *Syntrophobacter fumaroxidans* strain (MPOB^T). *Standards Genomic Sci* **2012**, *7*, 91–106, doi.org/10.4056/sigs.2996379.
37. Menes, R.J.; Muxí, L. *Anaerobaculum mobile* sp. nov., a novel anaerobic, moderately thermophilic, peptide-fermenting bacterium that uses crotonate as an electron acceptor, and emended description of the genus *Anaerobaculum*. *Int J Syst Evol Microbiol* **2002**, *52*, 157–164.
38. Mavromatis, K.; Stackebrandt, E.; Held, B.; Lapidus, A.; Nolan, M.; Lucas, S.; Hammon, N.; Deshpande, S.; Cheng, J.-F.; Tapia, R.; Goodwin, L.A.; Pitluck, S.; Liolios, K.; Pagani, I.; Ivanova, N.; Mikhailova, N.; Huntemann, M.; Pati, A.; Chen, A.; Palaniappan, K.; Land, M.; Rohde, M.; Spring, S.; Göker, M.; Woyke, T.; Detter, J.C.; Bristow, J.; Eisen, J.A.; Markowitz, V.; Hugenholtz, P.; Klenk, H.-P.; Kyrpides, N.C. Complete genome sequence of the moderate thermophile *Anaerobaculum mobile* type strain (NGA^T). *Standards Genomic Sci* **2013**, *8*, 47–57, doi.org/10.4056/sigs.3547050
39. Hania, W.B.; Bouanane-Darenfed, A.; Cayol, J.-L.; Ollivier, B.; Fardeau, M.-L. Reclassification of *Anaerobaculum mobile*, *Anaerobaculum thermoterrenum*, *Anaerobaculum hydrogeniformans* as *Acetomicrobium*

- mobile* comb. nov., *Acetomicrobium thermoterrenum* comb. nov. and *Acetomicrobium hydrogeniformans* comb. nov., respectively, and emendation of the genus *Acetomicrobium*. *Int J Syst Evol Microbiol* 2016, 66, 1506–1509, doi.org/10.1099/ijsem.0.000910.
40. Qiu, Y.L.; Hanada, S.; Kamagata, Y.; Guo, R.B.; Sekiguchi, Y. *Lactivibrio alcoholicus* gen. nov., sp. nov., an anaerobic, mesophilic, lactate-, alcohol-, carbohydrate- and amino-acid-degrading bacterium in the phylum Synergistetes. *Int J Syst Evol Microbiol* 2014, 64, 2137–2145, doi.org/10.1099/ijse.0.060681-0.
 41. Baena, S.; Fardeau, M.-L.; Labat, M.; Ollivier, B.; Garcia, J.-L.; Patel, B.K.C. *Aminobacterium mobile* sp. nov., a new anaerobic amino-acid-degrading bacterium. *Int J Syst Evol Microbiol* 2000, 50, 259–264.
 42. Chertkov, O.; Sikorski, J.; Brambilla, E.; Lapidus, A.; Copeland, A.; Del Rio, T.G.; Nolan, M.; Lucas, S.; Tice, H.; Cheng, J.-F.; Han, C.; Detter, J.C.; Bruce, D.; Tapia, R.; Goodwin, L.; Pitluck, S.; Liolios, K.; Ivanova, N.; Mavromatis, K.; Ovchinnikova, G.; Pati, A.; Chen, A.; Palaniappan, K.; Land, M.; Hauser, L.; Chang, Y.-J.; Jeffries, C.D.; Spring, S.; Rohde, M.; Göker, M.; Bristow, J.; Eisen, J.A.; Markowitz, V.; Hugenholtz, P.; Kyrpides, N.C.; Klenk, H.-P. Complete genome sequence of *Aminobacterium colombiense* type strain (ALA-1^T). *Standards Genomic Sci* 2010, 2, 280–289, doi.org/10.4056/sigs.902116.
 43. Chouari, R.; Le Paslier, D.; Dauga, C.; Daegelen, P.; Weissenbach, J.; Sghir, A. Novel major bacterial candidate division within a municipal anaerobic sludge digester. *Appl Environ Microbiol* 2005, 71, 2145–2153, doi.org/10.1128/AEM.71.4.2145-2153.2005
 44. Pelletier, E.; Kreimeyer, A.; Bocs, S.; Rouy, Z.; Gyapay, G.; Chouari, R.; Rivière, D.; Ganesan, A.; Daegelen, P.; Sghir, A.; Cohen, G.N.; Médigue, C.; Weissenbach, J.; Le Paslier, D. “*Candidatus Cloacamonas Acidaminovorans*”: Genome sequence reconstruction provides a first glimpse of a new bacterial division. *J Bacteriol* 2008, 190, 2572–2579, doi.org/10.1128/JB.01248-07
 45. Maus, I.; Cibis, K.G.; Bremges, A.; Stolze, Y.; Wibberg, D.; Tomazetto, G.; Blom, J.; Sczyrba, A.; König, H.; Pühler, A.; Schlüter, A. Genomic characterization of *Defluviitoga tunisiensis* L3, a key hydrolytic bacterium in a thermophilic biogas plant and its abundance as determined by metagenome fragment recruitment. *J Biotechnol* 2016, 232, 50–60, doi.org/10.1016/j.jbiotec.2016.05.001
 46. Koeck, D.E.; Mechelke, M.; Zverlov, V.V.; Liebl, W.; Schwarz, W.H. *Herbivorax saccincola* gen. nov., sp. nov., a cellulolytic, anaerobic, thermophilic bacterium isolated via in sacco enrichments from a lab-scale biogas reactor. *Int J Syst Evol Microbiol* 2016, 66, 4458–4463, doi.org/10.1099/ijsem.0.001374.
 47. Patil, Y.; Junghare, M.; Pester, M.; Müller, N.; Schink, B. *Anaerobium acetethylicum* gen. nov., sp. nov., a strictly anaerobic, gluconate-fermenting bacterium isolated from a methanogenic bioreactor. *Int J Syst Evol Microbiol* 2015, 65, 3289–3296, doi.org/10.1099/ijsem.0.000410.
 48. Barber, R.D.; Zhang, L.; Harnack, M.; Olson, M.V.; Kaul, R.; Ingram-Smith, C.; Smith, K.S. Complete genome sequence of *Methanosaeta concilii*, a specialist in acetoclastic methanogenesis. *J Bacteriol* 2011, 193, 3668–3669, doi.org/10.1128/JB.05031-11
 49. Galagan, J.E.; Nusbaum, C.; Roy, A.; Endrizzi, M.G.; Macdonald, P.; Hugh, W.F.; Calvo, S.; Engels, R.; Smirnov, S.; Atnoor, D.; Brown, A.; Allen, N.; Naylor, J.; Stange-Thomann, N.; DeArellano, K.; Johnson, R.; Linton, L.; McEwan, P.; McKernan, K.; Talamas, J.; Tirrell, A.; Ye, W.; Zimmer, A.; Barber, R.D.; Cann, I.; Graham, D.E.; Grahame, D.A.; Guss, A.M.; Hedderich, R.; Ingram-Smith, C.; Kuettner, H.C.; Krzycki, J.A.; Leigh, J.A.; Li, W.; Liu, J.; Mukhopadhyay, B.; Reeve, J.N.; Smith, K.; Springer, T.A.; Umayam, L.A.; White, O.; White, R.H.; Conway de Macario, E.; Ferry, J.G.; Jarrell, K.F.; Jing, H.; Macario, A.J.L.; Paulsen, I.; Pritchett, M.; Sowers, K.R.; Swanson, R.V.; Zinder, S.H.; Lander, E.; Metcalf, W.W.; Birren, B. The genome of *M. acetivorans* reveals extensive metabolic and physiological diversity. *Genome Research* 2000, 12, 532–542.
 50. Ma, K.; Liu, X.; Dong, X. *Methanosaeta harundinacea* sp. nov., a novel acetate-scavenging methanogen isolated from a UASB reactor. *Int J Syst Evol Microbiol* 2006, 56, 127–131.
 51. Zhu, J.; Zheng, H.; Ai, G.; Zhang, G.; Liu, D.; Liu, X.; Dong, X. The genome characteristics and predicted function of methyl-group oxidation pathway in the obligate acetoclastic methanogens, *Methanosaeta* spp. *PLoS ONE* 2012, 7(5), e36756, doi.org/10.1371/journal.pone.0036756
 52. Maeder, D.L.; Anderson, I.; Brettin, T.S.; Bruce, D.C.; Gilna, P.; Han, C.S.; Lapidus, A.; Metcalf, W.W.; Saunders, E.; Tapia, R.; Sowers, K.R. The *Methanosarcina barkeri* genome: comparative analysis with *Methanosarcina acetivorans* and *Methanosarcina mazei* reveals extensive rearrangement within methanosarcinal genomes. *J Bacteriol* 2006, 188, 7922–7931.
 53. Kern, T.; Fischer, M.A.; Deppenmeier, U.; Schmitz, R.A.; Rother, M. *Methanosarcina flavescens* sp. nov., a methanogenic archaeon isolated from a full-scale anaerobic digester. *Int J Syst Evol Microbiol* 2016, 66, 1533–1538, doi.org/10.1099/ijsem.0.000894.
 54. Anderson, I.J.; Sieprawska-Lupa, M.; Lapidus, A.; Nolan, M.; Copeland, A.; Del Rio, T.G.; Hope, T.; Dalin, E.; Barry, K.; Saunders, E.; Han, C.; Brettin, T.; Detter, J.C.; Bruce, D.; Mikhailova, N.; Pitluck, S.; Hauser, L.; Land, M.; Lucas, S.; Richardson, P.; Whitman, W.B.; Kyrpides, N.C. Complete genome sequence of

- Methanoculleus marisnigri* Romesser et al. 1981 type strain JR1. *Standards Genomic Sci* **2009**, 1, 189–196, doi.org/10.4056/sigs.32535
55. Manzoor, S.; Schnürer, A.; Bongcam-Rudloff, E.; Müller, B. Complete genome sequence of *Methanoculleus bourgensis* strain MAB1, the syntrophic partner of mesophilic acetate-oxidising bacteria (SAOB). *Standards Genomic Sci* **2016**, 11; 80-89.
 56. Maus, I.; Stantscheff, R.; Wibberg, D.; Stolze, Y.; Winkler, A.; Pühler, A.; König, H.; Schlüter, A. Complete genome sequence of the methanogenic neotype strain *Methanobacterium formicicum* MF^T. *J Biotechnol* **2014**, 192, 40–41, doi.org/10.1016/j.jbiotec.2014.09.018
 57. Kern, T.; Linge, M.; Rother, M. *Methanobacterium aggregans* sp. nov., a hydrogenotrophic methanogenic archaeon isolated from an anaerobic digester. *Int J Syst Evol Microbiol* **2015**, 65: 1975-1980, doi.org/10.1099/ijms.0.000210.
 58. Gunsalus, R.P.; Cook, L.E.; Crable, B.; Rohlin, L.; McDonald, E.; Mouttaki, H.; Sieber, J.R.; Poweleit, N.; Zhou, H.; Lapidus, A.L.; Daligault, H.E.; Land, M.; Gilna, P.; Ivanova, N.; Kyrpides, N.; Culley, D.E.; McNerney, M.J. Complete genome sequence of *Methanospirillum hungatei* type strain JF1. *Standards Genomic Sci* **2016**, 11, 2–12, doi.org/10.1186/s40793-015-0124-8
 59. Hahnke, S.; Langer, T.; Klocke, M. *Proteiniborus indolifex* sp. nov., isolated from a thermophilic industrial-scale biogas plant. . *Int J Syst Evol Microbiol* **2018**, 68: 824-828, doi.org/10.1099/ijsem.0.002591.