Article DOI: http://doi.org/10.3201/eid3008.240181



# Archaea in the Human Microbiome and Potential Effects on Human Infectious Disease

## Appendix

### Additional Information on *Methanobrevibacter* Species

*Methanobrevibacter* species demonstrate remarkable adaptability to engage with both hosts and the non-archaeal elements within their microbiomes. These members of the Methanobacteriaceae family (Methanobacteriota phylum), are characterized by their ability to perform methanogenesis from bacterial fermentation products, namely H2 and CO2. Formate and methanol could be further substrates, as their utilization is genetically encoded (*1*). In addition, *Methanobrevibacter* spp. exhibit various adaptations to the human gut, including the formation of adhesins (*2*), and the presence of genes encoding bile salt hydrolases (*3*). *Methanobrevibacter* species dominate the archaeal population in the gastrointestinal tracts (GITs) of various ruminant and non-ruminant animals, and are even associated with plants and their microbiomes (summarized in (*4*)). Although *Methanobrevibacter* species are very abundant in ruminants, to our knowledge they have not been reported to cause inflammation or disease in these animals, limiting interest primarily to the reduction of methane emissions (*5*). Not only in this aspect, *Methanobrevibacter* bacterial interactions are of high interest, which is why specific cocultures of bacteria (e.g., *Christensenella minuta*, *Bacteroides thetaiotaomicron*) (*6*–*8*) and *M. smithii* have been established, indicating a fine-tuned collaboration with effects on each other's metabolism. For instance, *C. minuta* shifted its metabolisms rather toward acetate than butyrate in the presence of *M. smithii*, which uses acetate for biomass production (*7*).

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