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## **Partnership between *Methanobrevibacter smithii* clades and different microbial taxa in the human gut**

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*Methanobrevibacter smithii* is considered the predominant archaeal representative in the human gastrointestinal tract and recently, this archaeal species has been reported to comprise two species-level clades named *M. smithii* and *Candidatus M. intestini*. The high occurrence of *M. smithii* might be due to its ability to establish interactions with several gut bacteria. However, it is not yet clear if there is a unique partnership between these two *M. smithii* clades and different microbial taxa. To elucidate this, in this study, fecal samples from a total of 94 participants with the age range between 46 and 86 years old were recruited at the Medical University of Graz irrespective of their medical conditions. DNA was then extracted and sent for shotgun sequencing. Raw shotgun reads were processed using ATLAS for obtaining MAGs and also mapped against Unified Human Gastrointestinal Genome (UHGG) database using Kraken and then processed with Bracken. The correlation between the two *M. smithii* clades and top 800 most abundant bacterial taxa was calculated using Spearman correlation and bacterial species were chosen based on adjusted  $p < 0.01$ . In total, it was possible to assemble high-quality MAGs (completeness  $> 90\%$ , contamination  $< 1\%$ ) in 7 (6 *M. smithii*, and 1 *Ca. M. intestini*) out of 94 samples (7.4%). According to the co-occurrence network analysis, *M. smithii* has a strong negative correlation with *Blautia* spp. as well as *Streptococcus* spp. and a positive correlation with *Bacteroidaceae* members, while *Candidatus M. intestini* showed mostly unique positive correlations with specific members of *Oscillospiraceae* and *Christensenellaceae* family, while also sharing positive correlations with different members of these bacterial taxa with *M. smithii*. Notably, these two archaeal clades also strongly correlate to one another. According to these observations, these species might grow together and distinctive microbial taxa might support or hinder their presence and growth.