**Preliminary landscape of *Candidatus* Saccharibacteria in the human microbiome**

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Une image contenant texte, Logiciel multimédia, logiciel, capture d’écran

Description générée automatiquement

Figure S1: **Coculture image of *Candidatus* Saccharibacteria associated with its host *Schaalia odontolytica.*** A fecal sample positive to *Candidatus* Saccharibacteria was filtered at 0.22µm, then ultracentifuged as previously described 24. The filtrate was cultured with *S. odontolytica* then subcultured 4 times every 24 hours. We realized standard PCR of these cultures (A) and then sequenced the PCR products by Sanger sequencing. Blast results confirm the detection of *Candidatus* Saccharibacteria in these cultures and showed 100% coverage and 99.78% identity with *Candidatus* Saccharibacteria (B). Exosymbionts were observed using scanning electron microscopy. (C) An uninfected *S. odontolytica* culture. (D) Infected *S. odontolytica* showing deformed bacilli with an exosymbiont. These micrographs were used as a positive control in this study.

**Table S1. Summary table of primers and probes used to perform standard PCR and RT–PCR, respectively.**

|  |  |  |  |
| --- | --- | --- | --- |
| PCR types | Primer and probe names | Sequences | References |
| Standard PCR | 1177R | GACCTGACATCATCCCCTCCTTCC | Brinig et al., 2003 |
| Standard PCR | 580F | AYTGGGCGTAAAGAGTTGC | Hugenholtz et al., 2001 |
| RT–PCR | SacchariF | GGCTTATAGCGCCCAATAG | Ibrahim et al., 2021 |
| RT–PCR | SacchariR | CGGATATAAACCGAACTGTC | Ibrahim et al., 2021 |
| RT–PCR | SacchariP | 6-FAM-CATAGACGGCGCTGTTTGGCAC-TAMRA | Ibrahim et al., 2021 |

**Table S2. Kruskal-Wallis statistical tests of the relative abundance of CPR-positive samples using 16S amplicon sequencing.**



**Table S3. Summary table of nucleotide sequences cleaned and assembled using ChromasPro obtained using Sanger sequencing.**

Sequences were compared with the NCBI NR database using the BLASTn program (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>).

