ENRICHMENT OF SULFIDOGENIC BACTERIA FROM THE HUMAN INTESTINAL TRACT

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Hydrogen sulfide is formed in the human intestinal tract as the end product of the anaerobic microbial degradation of sulfur compounds present in mucus, bile or proteins. Since human gut microbial sulfur metabolism has been poorly characterized, we aimed to identify and isolate the microorganisms involved in sulfide formation. Fresh fecal samples from one healthy donor and one diagnosed with irritable bowel syndrome were used as inocula for enrichments that were supplemented with sulfate or sulfite as electron acceptors in combination with different electron donors. After two transfers, cultures with high sulfide production were selected and the phylogenetic composition of the enriched microbial communities was determined. Sulfite respiration and cysteine degradation were the dominant sulfidogenic processes, and the most abundant bacteria enriched belonged to Bilophila and Clostridium cluster XIVa. Different isolates were obtained and remarkably included a novel sulfite reducer, designated strain 2C. Strain 2C belongs to the Veillonellaceae family of Firmicutes phylum and showed limited (91%) 16S rRNA gene sequence similarity with that of known Sporomusa species and hence may represent a novel genus. This study indicates that bacteria that utilize sulfite and organic sulfur compounds rather than merely sulfate are relevant for human intestinal sulfur metabolism.