**Effect of Sub-Stoichiometric Fe(III) Amounts on LCFA Degradation by Methanogenic Communities**

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**SUPPLEMENTARY INFORMATION**



**Figure S1.** Pictures of the Fe(III)-reducing enrichment cultures GS(5) after Fe(OH)3 reduction, showing the accumulation of a black precipitate that was attracted to a magnet (probably magnetite).



**(a)**

**(b)**

**(I)**

**(II)**

**(III)**

**(IV)**

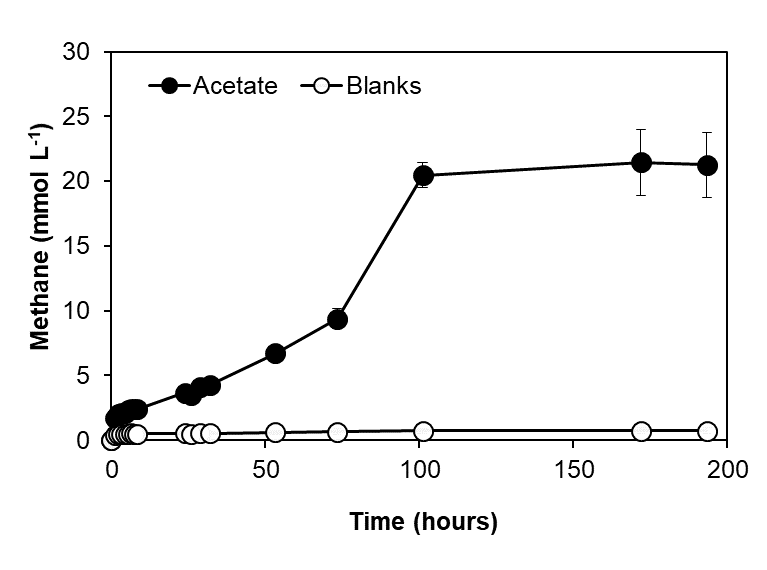
**(I)**

**(II)**

**(III)**

**(IV)**

**Figure S2.** Pictures of *Geobacter anodireducens* SD-1T (a) and *Geobacter bemidjiensis* DSM 16622T (b) batch incubations with ferric citrate and oleate (bottles I and II) or acetate (bottle III). Bottle IV is the negative control, prepared with oleate and Fe(III) (without inoculum).



**Figure S3.** Cumulative methane production from acetate measured in the SMA tests performed with the suspended sludge.

**Table S1.** Results of sequence alignment of the operational taxonomic units (OTU) assigned to *Geobacter* genus towards NCBI RefSeq\_RNA database, by using BLAST.

|  |  |  |
| --- | --- | --- |
| **Description** | **Identity (%)** | **Accession number** |
| *Geobacter anodireducens* SD-1T | 100.00 | NR\_126282.1 |
| *Geobacter soli* GSS01T | 99.60 | NR\_134039.1 |
| *Geobacter sulfurreducens* PCAT | 99.60 | NR\_075009.1 |
| *Geobacter sulfurreducens* | 99.60 | NR\_029179.1 |
| *Geobacter sulfurreducens* subsp. *ethanolicus* OSK2AT | 99.21 | NR\_132673.1 |
| *Geobacter metallireducens* GS-15T | 96.84 | NR\_075011.1 |
| *Geobacter pickeringii* G13T | 96.84 | NR\_025895.1 |
| *Geobacter metallireducens* GS-15T | 96.84 | NR\_025895.1 |
| *Geobacter grbiciae* TACP-2T | 96.84 | NR\_104561.1 |
| *Geobacter luticola* OSK6T | 96.44 | NR\_114303.1 |
| *Geobacter hydrogenophilus* H2T | 96.46 | NR\_025974.1 |
| *Geobacter daltonii* FRC-32T | 96.05 | NR\_074916.1 |
| *Geobacter daltonii* FRC-32T | 96.05 | NR\_116402.1 |
| *Geobacter toluenoxydans* TMJ1T | 96.05 | NR\_116428.1 |

**Table S2.** Proteins associated with fatty-acid degradation encoded in the genome of *Geobacter anodireducens* SD-1T. Protein annotation was obtained from the NCBI database (Sun et al. 2016). COG functional categories and EC numbers were obtained by running reGOGnizer **[EXCEL FILE]**.

**Table S3.** Proteins associated with fatty-acid degradation encoded in the genome of *Syntrophomonas zehnderi* strain OL-4T. Protein names and sequences were obtained from the Uniprot database, COG functional categories and EC numbers were obtained by running reGOGnizer **[EXCEL FILE]**.