TABLE 1. Distribution of bacterial 16S rRNA genes by cloning and sequencing for CH4- oxidation MEC test

|  |  |  |
| --- | --- | --- |
| Class | Species (No. of clones) | GenBank accession no (% identity)  |
| Cloacimonetes# | *Candidatus Cloacimonas* sp. (n=3)\* | KP258984 (94%) or AF338764 (99%) |
| Delta-Proteobacteria | *Geobacter sulfurreducens* (n=53)*Geobacter pickeringii* (n=28)*Geobacter* spp. (n=5)\* | AE017180 (98%)CP009788 (95%)AE017180 (92%) |
| Bacteroidia | *Bacteroidales* (n=1)\*\*\**Paludibacter propionicigenes* (n=1) | CP006772 (94%) or GU083566 (99%)CP002345 (97%) or GU455014 (99%) |
| Spirochaetes | *Spirochaetaceae* (n=1)*\*\** | HQ689204 (88%) |

#candidate phylum

\*genus

\*\*family

\*\*\*order

***Candidatus Cloacimonas acidaminovorans***

Solli et al. A metagenomic study of the microbial communities in four parallel biogas reactors. Biotechnology for Biofuels 2014, 7:146

**Spirochaetaceae bacterium enrichment culture**

Cheng et al. Enrichment and dynamics of novel syntrophs in a methanogenic hexadecane-degrading culture from a Chinese oilfield. FEMS Microbiol. Ecol. 2013. 83 (3), 757-766.

**GU083566**

Kiely et al. Long-term cathode performance and the microbial communities that develop in microbial fuel cells fed different fermentation endproducts. Bioresour. Technol. 2011. 102 (1), 361-366

**GU455014**

Zhang et al. Understanding short-chain fatty acids accumulation enhanced in waste activated sludge alkaline fermentation: kinetics and microbiology. ES&T 2010 44 (24), 9343-9348.

TABLE 2. Distribution of archael 16S rRNA genes by cloning and sequencing for CH4- oxidation MEC test

|  |  |  |
| --- | --- | --- |
| Class | Species (No. of clones) | GenBank accession no (% identity)  |
| Methonomicrobia  | *Methanocorpusculum labreanum* (n=60)*Methanocorpusculum sinense* (n=1)*Methanocorpusculum* spp. (n=3)\**Methanosaeta concilii* (n=12)*Methanosaeta* spp.(n=2)\* | NR074173 (99%)NR104804 (98%)NR074173 (92%)CP002565 (99%)CP002565 (92%) |
| Thermoplasmata | *Candidatus Methanoplasma termitum* (n=6)*Methanomassiliicoccus luminyensis* (n=3) | CP010070 (97%)NR118098 (95%) |

\*genus

***Candidatus Methanoplasma termitum***

K. Lang, J. Schuldes, A. Klingl, A. Poehlein, R. Daniel, A. Brune, New mode of energy metabolism in the seventh order of methanogens as revealed by comparative genome analysis of “Candidatus methanoplasma termitum”. Appl. Environ. Microbiol. 81, 1338–1352 (2015).

Evans et al. Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. Science October 2015 350:6259 434-438

TABLE 3. Distribution of 16S rRNA genes by pyrosequencing for CH4-MEC test

|  |  |  |
| --- | --- | --- |
| Class | Genus | Biofilm(n=1629) |
| Actinobacteria | *Corynebacterium* | 31 |
| Alpha-Proteobacteria  | *Bradyrhizobium* | 9 |
| Beta-Proteobacteria | *Ralstonia**Thiobacillus*  | 76 |
| Delta-Proteobacteria | *Desulfococcus**Desulfovibrio**Geobacter\***Pelobacter**Syntrophobacter* | 1261120 (69%)67 |
| Bacilli | *Exiguobacterium* | 12 |
| Bacteroidia | *Alistipes**Dysgonomonas\*\** | 556 (3.4%) |
| Chlorobia | *Chlorobium* | 16 |
| Clostridia | *Caldicellulosiruptor* | 8 |
| Cytophagia | *Flammeovirga*  | 5 |
| Flavobacteria | *Dokdonia**Krokinobacter* | 2140 |
| Mollicutes | *Acholeplasma* | 11 |
| Spirochaetes | *Spirochaeta* *Treponema*  | 1933 |
| Synergistia | *Thermanaerovibrio\*\*\**  | 66 (4.1%) |
| Thermolithobacteria | *Thermolithobacter* | 33 |

- (not found or less than 4 sequences)

**Species**

*\* Geobacter sulfurreducens* (1102), *Geobacter uraniireducens* (9), *Geobacter uraniumreducens* (5)

\*\* *Dysgonomonas gadei*

\*\*\* *Thermanaerovibrio acidaminovorans*