**Supplementary material: Material and Methods**

**Sampling**

The samples was made up of 7 sets of leaf samples from temperate-climate tree species collected during the summer (France, Madera) and 4 sets of leaf samples from tropical-climate tree species collected during the dry season (Thailand, Reunion Island)(Table S1). In these two climate zones three different biomes were sampled (deciduous forest, chaparral and rain forest) (Table S1). To limit any bias in the collection process, leaves were collected from a minimum of two branches on each tree at 1.5–2 m height. Whenever possible, a southern exposure orientated towards the sun was chosen. Leaves were wrapped in sealed plastic bags and stored at ambient temperature during the collection period. Finally, 15 g (corresponding to 30 % of the sample) were taken from the mix and washed to obtain leaf surface bacteria.

**DNA extraction**

The leaves were washed inside containers with a 1:50 diluted sterile wash solution (1 M Tris–HCL, 500 mM ethylenediamine tetraacetic acid, and 1.2% Triton diluted in sterile water (Redford and Fierer, 2009)) and the container was shaken for 5 min prior to incubation at room temperature for 2 hours. The wash solutions were then centrifuged at 2,000×g for 10 min. The supernatant was discarded and the DNA was extracted from the pellets as previously described (Le Goff et al., 2011).

**Identification of OTUs by 454-pyrosequencing**

The identification of dominant bacterial communities from all the reactors at steady-state was obtained by 454-pyrosequencing of the V4–V5 regions of the 16S rRNA gene (Molecular Research Laboratory, TX, USA). Sequence data derived from the sequencing was processed using a proprietary analysis pipeline (Molecular Research Laboratory, TX, USA). Operational taxonomic units (OTUs) were defined after removal of singleton sequences and clustering at 3% divergence on the 16S rDNA sequence (Edgar, 2010). OTUs were then taxonomically classified using BLASTn against a curated GreenGenes database (DeSantis et al., 2006).

**Nucleotide sequence accession numbers**

Sequence data associated with this study have been deposited in GenBank's Short Read Archive (SRA) under the accession number PRJNA273803.

**Fermentation**

For aerobic thermophilic growth, leaves were kept for two months in a flask maintained at 55°C. Relative humidity close to 100% was obtained with a soaked cotton pad. We incubated 12 leaf samples at 55°C in the dark, under both aerobic and anaerobic conditions, 9 and 3 samples respectively.

For anaerobic thermophilic growth, leaves were kept for three months at 55°C in sealed flasks flushed with nitrogen to maintain anaerobic conditions in a bicarbonate buffered solution. The activity of the anaerobic microbial communities was assessed by measuring the production of hydrogen, volatile fatty acids and carbon dioxide after 22, 43, 71 and 80 days of incubation (Aceves-Lara et al., 2008). The biogas production was measured using differences in pressure. The biogas composition (CH4, CO2, H2, and N2) was analyzed by gas chromatography (GC-14A, Shimadzu) (Aceves-Lara et al., 2008). The volatile fatty acids (VFA) were determined in the aqueous phase by gas chromatography (GC800, Fisons Instruments).

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