

Fig. S1

Detail of the experimental plates. A, B in the laboratory being prepared, C in situ at -15m depth.

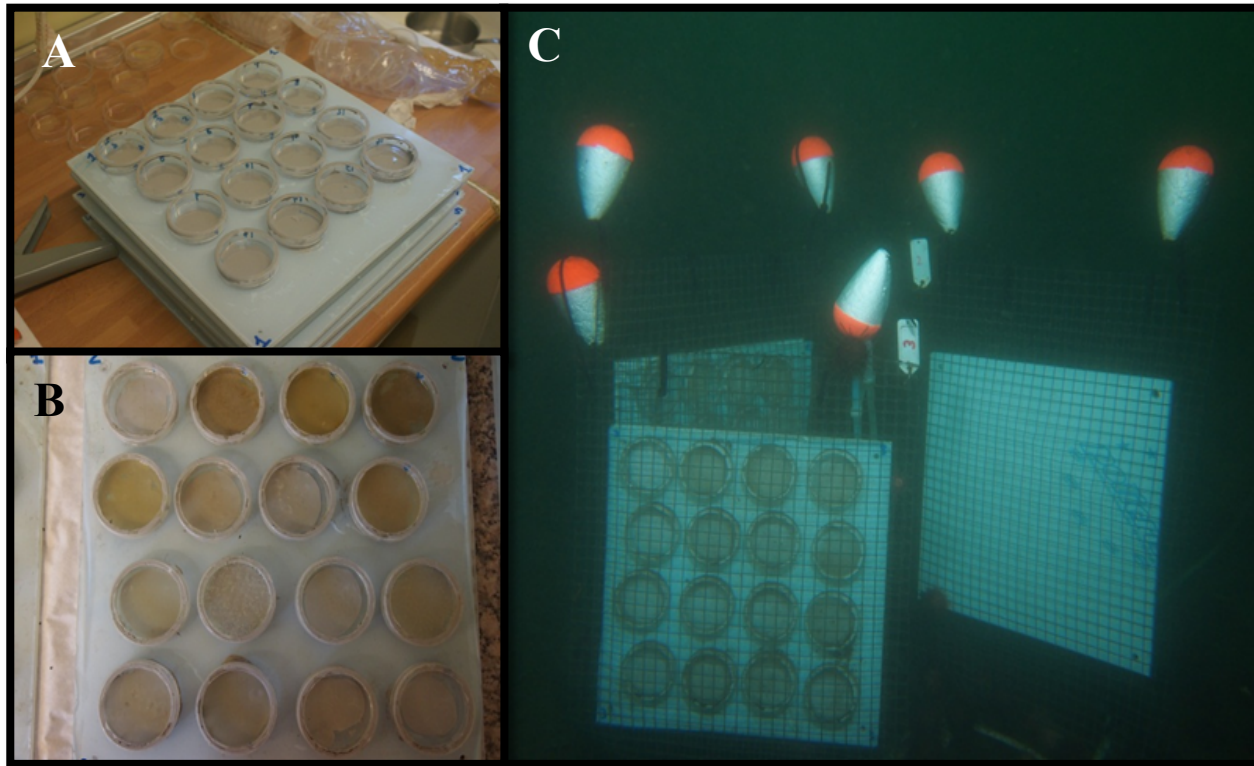


Table S1

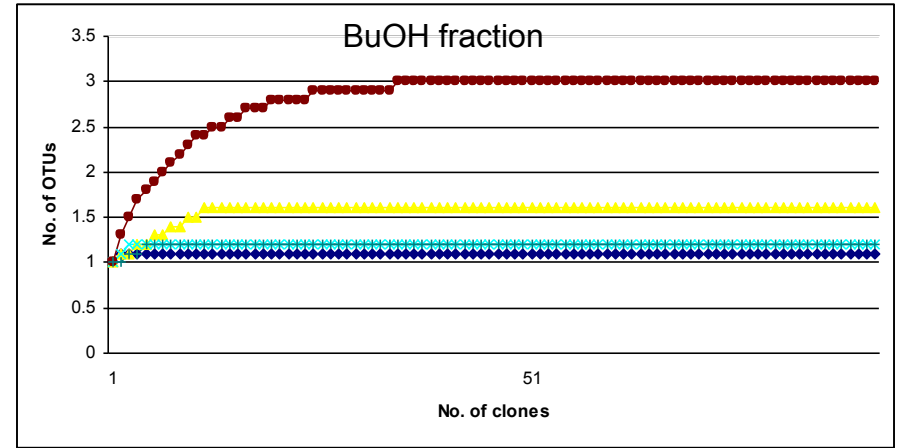
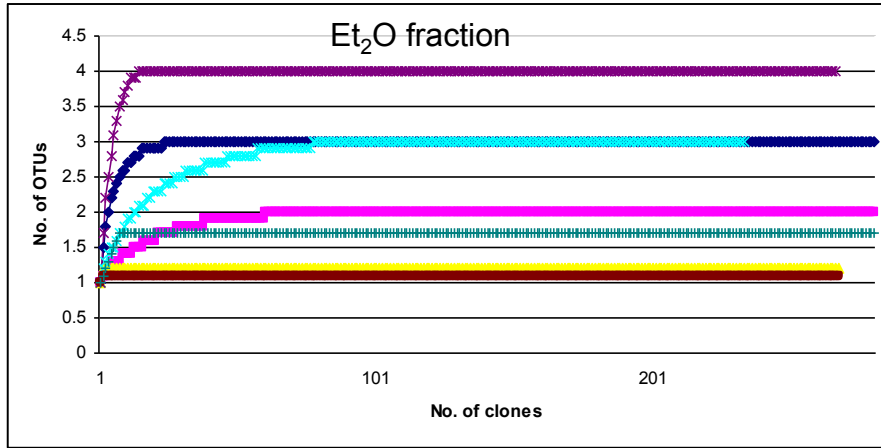
Oligonucleotide sequences used in this study.

Specificity	Primers	Sequence (5' to 3')	Product length (bp)	Reference
Bacteria	16S-F	AGAGTTTGATCCTGGCTCAG	1000	Lane 1991
Bacteria	16S-R	CACGAGCTGACGACAGCC	1000	Lane 1991
Archaea	20F	TTCCGGTTGATCCYGCCRG	1372	Massana et al. 1997
Archaea	U1392R	ACGGGCGGTGTGTRC	1372	Massana et al. 1997
Eukarya	Euka1F	CTGGTTGATCCTGCCAG	500	Lefranc et al. 2005
Eukarya	Euk502R	TGATCCTTCTGCAGGTTACCT AC	500	Amann et al. 1990

Fig. S2

Rarefaction curves determined for 18S rRNA and 16S rRNA gene clones. Rarefaction curves indicate the observed OTUs at a genetic distance of 3%.

Eukaryotes



Bacteria

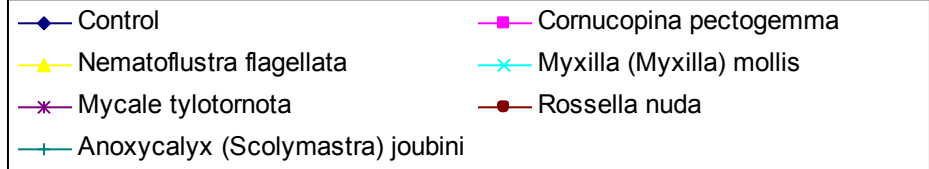
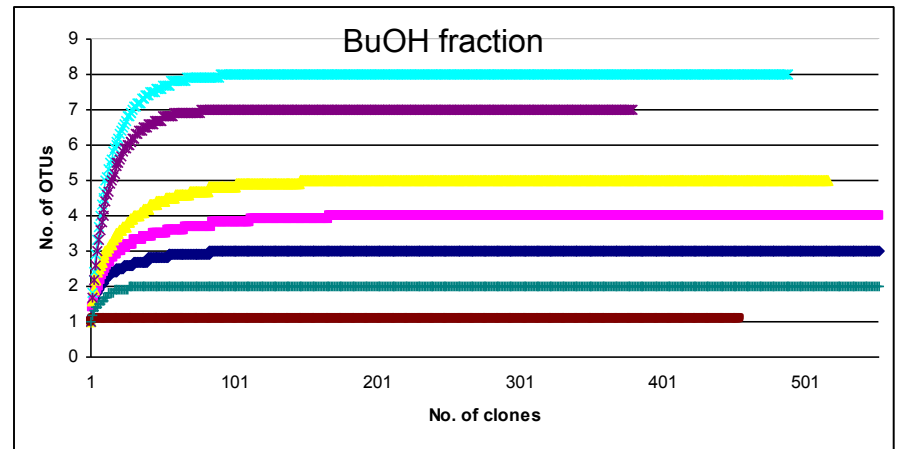
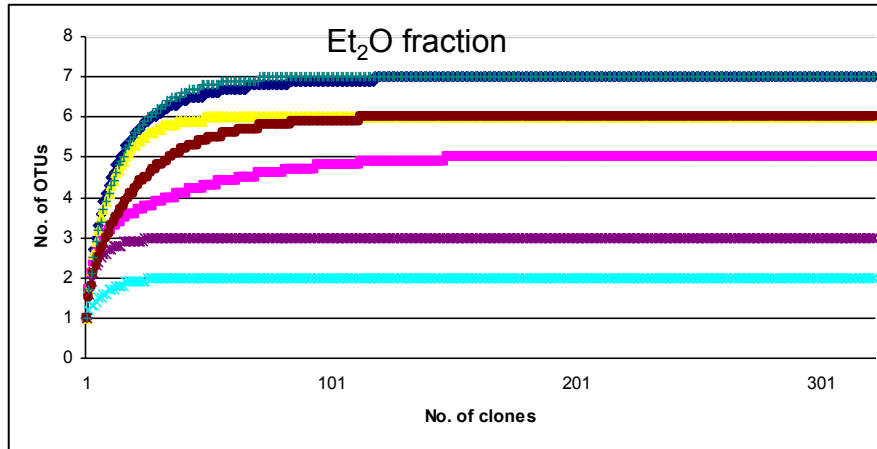


Fig. S3

Phylogenetic consensus trees of microbial community DNA in Phytigel samples derived from 16S rRNA and 18S rRNA gene sequences data. Clones attached to gels with Et2O-extracts.

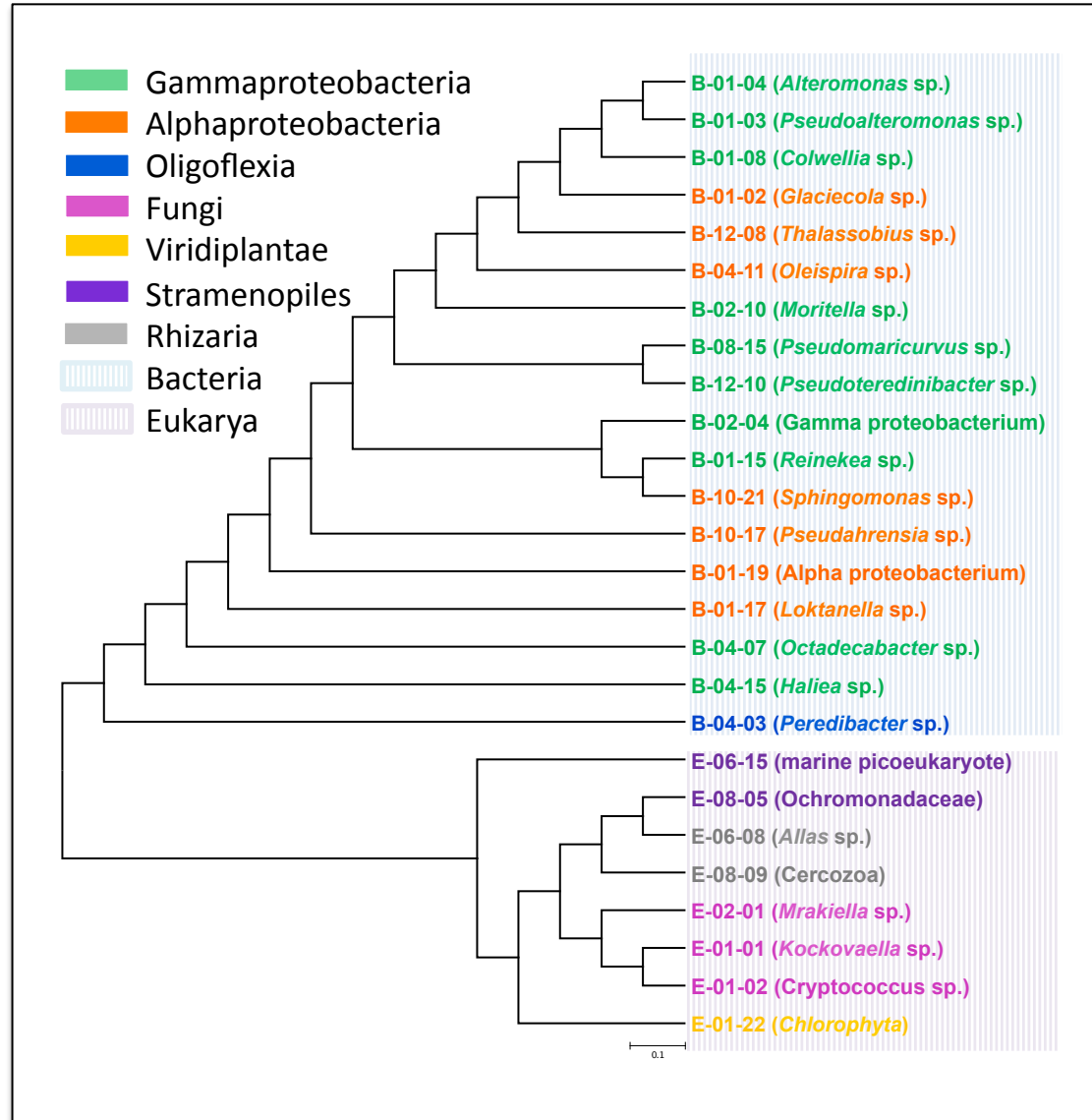


Fig. S4

Phylogenetic consensus trees of microbial community DNA in Phytigel samples derived from 16S rRNA and 18S--- rRNA gene sequences data. Clones attached to gels with BuOH-extracts.

