



# MaCuMBA

Marine Microorganisms: Cultivation Methods for Improving their  
Biotechnological Applications

**Project number:** 311957

**Start of the project (duration):** August 1<sup>st</sup>, 2012 (48 months)

Collaborative Project  
Seventh Framework Programme  
Cooperation, KBBE

## *Deliverable D2.24*

A list of isolated microorganisms for further cultivation optimization,  
sequencing and screening.

**Organisation name of lead contractor:** UBO-LM2E

**Due date of deliverable:** M36

**Actual submission date:** M36

**Revision:** V.I

Project co-funded by the European Commission within the Seventh Framework Programme (2007-2013)	
Dissemination Level	
<b>PU</b> Public	
<b>PP</b> Restricted to other programme participants (including the Commission Services)	<b>X</b>
<b>RE</b> Restricted to a group specified by the consortium (including the Commission Services)	
<b>CO</b> Confidential, only for members of the consortium (including the Commission Services)	

**All rights reserved**

This document may not be copied, reproduced or modified in whole or in part for any purpose without the written permission from the MaCuMBA Consortium. In addition to such written permission to copy, reproduce or modify this document in whole or part, an acknowledgement of the authors of the document and all applicable portions of the copyright must be clearly referenced.

## List of reviewers

Issue	Date	Implemented by
v.1	07-20-2015	S.L'Haridon and G. Le Blay

**Indicate any document related to this deliverable (report, website, ppt etc) and give file name**

*\* Please attach deliverable documents and any additional material if needed.*

## Summary

**Objective(s):** The objective was to provide a list of isolates for which interesting phylogenetic affiliations based on their 16S rRNA gene sequences has been revealed, or isolates coming from difficult to sample area, or microorganisms which could have potential biotechnological features.

**Rationale:** We have used different approaches to isolate these new microorganisms depending on the sampling area. For the pelagic environment and other aerobic environments, the dilution to extinction method was employed using the Cocagne Platform. For anaerobic environments, a first enrichment was processed and positive enrichments were streaked on solid medium for isolation.

**Results:** Twenty one hyperthermophilic autotrophic methanogens have been isolated from the world's deepest known hydrothermal vent sites known at the Caiman Through (Depth 4965 m; Beebe vent field). Their 16S rRNA gene sequences, showing less than 94 % of identity with the sequence of *Methanothermococcus okinawensis* strain IH1<sup>T</sup>, suggests that they belong to a new genus. Analyses of their optimal growth conditions (temperature, pH, salinity) are presently on going.

A hyperthermophilic heterotrophic Archaea from the genus *Thermococcus* has been also isolated from this deepest vent, it belongs to a new species with interesting piezophilic behaviours. Preliminary experiments indicate an optimal hydrostatic pressure of 50 MPa. The strain is under complete characterization and its genome is about to be sequenced.

An anaerobic thermophilic bacteria has been isolated from the centre of the haakon Mosby Mud Volcano located in the Barents Sea and represents a new genus in the *Bacteroidetes* phylum. We are presently trying to improve the cultivation efficiency of this strain in order to deposit it in an open collection.

Three new anaerobic halophilic archaeal strains SLHTYRO, SLHKRYOS, SLHTHETIS belonging to the genus *Methanohalophilus* have been isolated from 3 different deep anoxic brine lakes Tyro, Kryos, and Thetis. They represent the first methanogenic strains isolated from this area. The genomes of these 3 strains are going to be sequenced with the genome of the two type species *M. portucalensis* strain FDF-1<sup>T</sup> and *M. halophilus* strain Z-7982<sup>T</sup>.

A new thermophilic anaerobic heterotrophic bacteria belonging to the genus *Kosmotoga* has been described as *Kosmotoga pacifica* strain SLHLJ1<sup>T</sup> (L'Haridon, 2014), the genome is going to be sequenced.

A new anaerobic sulphate reducing bacterial species affiliated to the genus *Desulfovibrio* has been isolated from hydrothermal vent samples from the Indian Ocean. The strain is under complete characterization. The genome is going to be sequenced.

Two new species, *Phaeobacter leonis* strain 306<sup>T</sup> (Gaboyer, 2013) and *Halomonas lionensis* strain RHS90<sup>T</sup> (Gaboyer, 2014), isolated from sediments of Gulf of Lions in the Mediterranean Sea have been described.

Sixteen strains belonging to the *Actinobacteria* phylum have been isolated from Brittany coastal sea water and from the Mediterranean Sea. The antibacterial activity against *Vibrio anguillarum* strain 90-11-287 of these sixteen strains will be soon tested.

Around one hundred mesophilic aerobic bacterial strains from Brittany coastal sea water have been isolated by the dilution to extinction method on the Cocagne platform. They show an interesting phylogenetic affiliation with less than 95 % of identity with cultivable microorganisms 16s rRNA gene sequences present in GenBank databases. Most of the strains belong to the Alpha and Gamma classes of the *Proteobacteria* phylum. We are presently improving their culture efficiency by using different sources and organic matter concentrations in order to fully characterize some very interesting new isolates.

**Partner(s) involved in Deliverable production:** Specify the list of MaCuMBA partners and other contributors that have worked on this Deliverable (just the name of the organisations, not the name of the persons).