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First description of bacterial populations at shallow hydrothermal vents

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The study of hydrothermal systems has generated a wealth of information demonstrating that the processes that take place in these sites correspond partially to inorganic chemical reactions, but that there is also the generation of organic compounds. In addition, it has proved that a large portion of hydrothermal biogeochemical processes involve the activity of chemosynthetic microorganisms. Here we present the first characterization of bacteria associated with shallow hydrothermal vents that are not associated with active volcanism.

This study aims to establish the identity of bacterial communities associated with hydrothermal activity in the Mexican Pacific west coast. For this purpose, five sampling campaigns were conducted in two shallow hydrothermal vent systems (Bahia Concepcion and Punta de Mita) in 2006, 2007, 2008 and 2009. Sediment samples were taken from the first 5 cm depth in two zones (with venting influence and no influence) and a comparative analysis of 16S rRNA gene sequencing of bacterial communities in sediments from both study areas was performed.

The analyzed clones allowed describing nine Phyla: Alpha-, Delta-, Epsilon- and Gamma-proteobacteria, Aquaficae, Chloroflexi, Bacteroidetes, Firmicutes and Heterokontophyta (the chloroplast of a eukaryote). The highest sequences percentages (30% in Bahía Concepción and 57% in Punta de Mita) were microorganisms that have not yet been cultivated, so nothing is known about their ecological and metabolic characteristics. These sequences are grouped as "Unclassified".

In the Punta de Mita cladogram four Phyla were observed. In the control area, within the proteobacteria group, two Alpha- (clone G3-46 and Ahrensia sp. string HDW-32), one Delta-(clone UncDee36) and four unclassified clones were recorded. Similarly, in the vent area, one Alpha- (clone ctg_CGOAB55) and one Delta- (clone PI_4t8g) to Chloroflexi sp. (string MSB-3D4), Hydrogenivirga sp. (Aquaficae, string 128-5-R1-6) (within the group of proteobacteria) were identified; also observed was one not yet cultivated bacteria (clone a2b008). The latter two (Hydrogenivirga and clone a2b008) are related to hydrothermal vents.

In the Bahia Concepcion cladogram seven Phyla were observed. The control area was characterized by the Firmicutes Phylum with four species: Bacillus sp. (string MI_A64), B. taeanensis (string BH030017), B. flexus (string D10) and B. megaterium (string CP4). In the vent area seven phylogenetic groups were recognized: within proteobacteria grup there were four Alpha- (clone MD3.11, Paracoccus denitrificans clone PD1222, Phaeobacter sp. clone NH521 and clone JM9_B4), two Delta- (clone 88FS and Desulfosarcina sp. chain CB11140), three Bacteroidetes (Flavobacterium sp. clone ARTE12_255, and one clone Tokio.16S.Bac.40 SI-13) and Phaeodactylum tricornutum complete chloroplast genome sequence (Heterokontophyta). The bacteria associated with hydrothermal vents were: Sulfurospirillum sp. clone pCIRB-75 (Epsilon-proteobacteria), one endosymbiont (unidentified) of a flaky shell and one sulfur-oxidizing bacterium (clone OD1116), these two last are classified as Gamma-proteobacteria.

It is important to note that the all bacteria, except one, associated with hydrothermal environments that were identified in both study areas are typical of deep hydrothermal vents, so it could be inferred that despite the pressure and temperature differences there are similarities in microorganism species adapted to the physicochemical conditions of submarine hydrothermal systems.