



X CONGRESO ARGENTINO DE MICROBIOLOGIA GENERAL SAMIGE

2 al 4 de Julio de 2014
Hotel 13 de Julio
Mar del Plata, Argentina

www.samige.org.ar
info@samige.org.ar

UNA MIRADA MÁS PROFUNDA DENTRO DE LOS EXTREMOFILOS: ANÁLISIS DEL GENOMA DE UNA NUEVA ESPECIE DE ARQUEA TERMOACIDÓFILA

A DEEPER LOOK INTO EXTREMOPHILES: ANALYSIS OF THE DRAFT GENOME OF A NOVEL THERMOACIDOPHILIC ARCHAEON

Sofía Urbieto¹, Nicolás Rascovan², Camila Castro¹, Alejandra Giaveno³, Martín Vazquez², Edgardo Donati¹

¹CINDEFI (CCT La Plata-CONICET, UNLP), Facultad de Ciencias Exactas, Universidad Nacional de La Plata. ²Instituto de Agrobiotecnología de Rosario (INDEAR), CONICET, Predio CCT, Rosario, Argentina. ³IDEPA (CCT Comahue-CONICET, UNCo), Facultad de Ingeniería, Universidad Nacional del Comahue

castro.camila@biotec.org.ar

Copahue geothermal area is located on the Northwest corner of Neuquén, crowned by Copahue volcano (30000 m o.s.l. in Cordillera de los Andes). The constant volcanic activity has determined the extreme environments found in the area, specially the existence of many high-temperature, acidic, sulphur-rich ponds and hot springs. Such habitats are populated by extremophilic microorganisms well adapted to develop under hard physicochemical conditions and the lack of organic carbon sources. In acidic high temperature environments archaea are important members of the communities, however many of the species are yet unknown and uncharacterized.

Acidianus copahuensis is a thermoacidophilic archaeon (phylum *Crenarchaeota*, order *Sulfolobales*) that has been isolated from various hot springs in Copahue. *A. copahuensis* is a facultative chemolithoautotroph that grows optimally at 75°C and pH 2.5. It is capable of autotrophic growth; aerobically using iron and different sulfur compounds as energy sources, and anaerobically using H₂ and S as electron donors and Fe(III) or S as final electron acceptors. It can also grow heterotrophically using yeast extract or glucose.

In this work we present the first analysis of the genome sequence of *A. copahuensis*, obtained using a whole-genome shotgun (WGS) strategy with a 454-FLX Titanium pyrosequencer. The draft genome is 2,454,023 bases in length and the G+C content is 35.63 mol%. According to RAST annotation a total of 2,548 coding sequences (CDSs) and 52 structural RNAs (49 tRNAs, 3 rRNA) were predicted. A 47% of the CDSs were classified as coding for hypothetical proteins and 20% for known enzymes.

The genome of *A. copahuensis* revealed specific genes that could be associated with the metabolic activities of this organism. The key enzymes for sulphur compounds oxidation described for other acidophilic archaea, such as sulfur oxygenase-reductase (SOR) and thiosulfate-quinone oxidoreductase (TQO), were detected in *A. copahuensis*. Iron oxidation as an energy source was also represented in the genome by some of the fox cluster enzymes. *A. copahuensis* presents genes coding for proteins of the five major terminal oxidase complexes of *Sulfolobales*, so far reported in only two species. As regards autotrophic metabolism, carbon fixation through the 3-hydroxypropionate–4-hydroxybutyrate cycle could be inferred by the presence of the key enzymes of this pathway. An interesting discovery is the presence of genes encoding for arsenite oxidase (aioAB), not common in *Sulfolobales*. This could be related with the use of arsenite as an energy source or the arsenic bioremediation potential of *A. copahuensis*.

The present analysis confirms the presence of key enzymes that allow *A. copahuensis* survival in the environmental conditions of Copahue and make it a good candidate for biomining of sulphide minerals. Further analysis would be required to for a better understanding of this archaeon extreme metabolic features.