



Sociedad Argentina de Microbiología General

VIII CONGRESO DE MICROBIOLOGIA GENERAL

4 AL 6 DE JULIO DE 2012-HOTEL 13 DE JULIO MAR DEL PLATA

LIBRO DE RESÚMENES

www.samige.org.ar

info@samige.org.ar

BD11 ARSENIC IN WATER WELLS IN TUCUMÁN, ARGENTINA. BACTERIAL COMMUNITY ANALYSIS AND RESISTANCE GENES SCREENING

Daniela Maizel¹, Emilce Viruel¹, Leandro A Sanchez¹, Adriana M Sales², Marcela A Ferrero¹.

¹PROIMI-CCT Tucumán-CONICET. ²Instituto de Química Analítica. Facultad de Bioquímica, Universidad Nacional de Tucumán.

danielamaizel@gmail.com

Arsenic is a toxic metalloid present in a variety of environments. It can be released by either natural weathering of rocks or by anthropogenic activities. Arsenic is found in the oxidation states +5 (arsenate), +3 (arsenite), 0 (elemental arsenic), and -3 (arsine). Contamination of drinking water supplies with inorganic soluble forms, arsenite and arsenate, has often been reported, thus arsenic has been identified as a major risk for human health in different parts of the world. The biogeochemical cycle of this element strongly depends on microbial transformation, which affects the mobility and distribution of arsenic species in the environment. Several bacteria involved in transformation processes comprising reduction, oxidation and methylation of arsenic species have been previously described.

Samples were obtained from four different water wells at "Los Pereyra", a village placed east Tucuman, known as a the region presenting the highest arsenic levels in drinking water in the province. The samples showed arsenic concentrations between 0.20 and 2.10 mg/L, higher than permitted level (0.10 mg/L) in drinking water (WHO; World Health Organization)

The aim of this study was to investigate bacterial communities associated to the arsenic cycle in drinking water of "Los Pereyra" and their growth conditions.

A cultivation-based approach involving organic electron donors was used in progressive arsenic enrichment cultures at different As(III) and As(V) concentrations. Bacterial communities able to grow up to 20 mM (arsenite) or 400 mM (arsenate) were obtained in aerobic and anaerobic enrichment cultures. Composition of arsenic resistant and metabolizing bacterial populations was analyzed by 16S rDNA DGGE electrophoresis. Cluster analysis (UPGMA) of DGGE profiles showed changes in bacterial communities depending on arsenic oxidation state (3+ or 5+) and their concentration.

In order to determine the presence of genes involved in arsenic tolerance or metabolism in the bacterial communities, a genetic screening was carried out using PCR amplification. The presence of *arrA* (anaerobic arsenate reductase) and *arsB* (aerobic arsenite reductase) genes in some enriched populations, allow us to confirm their hypothetical participation in the arsenic biogeochemical cycle and its arsenic tolerance.