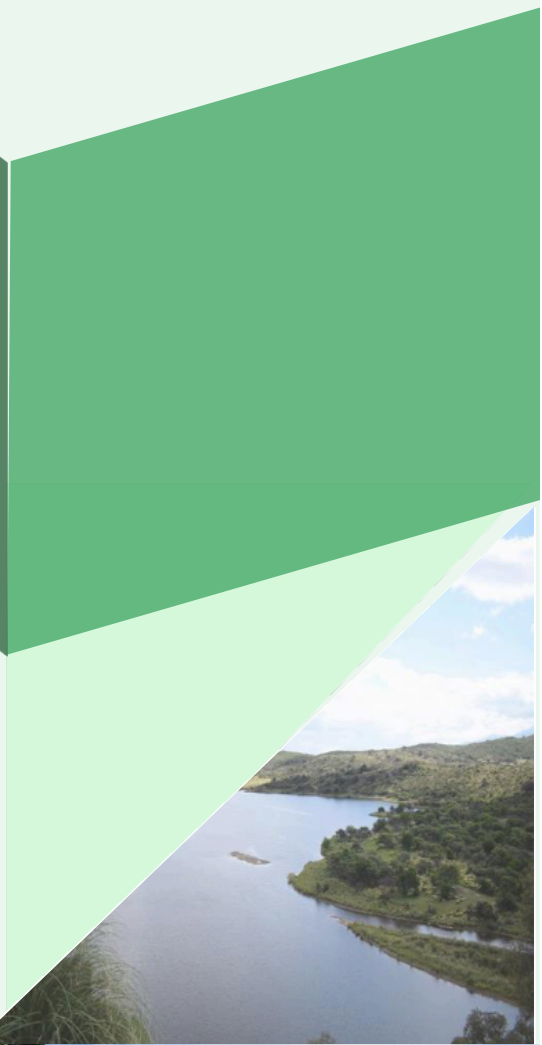
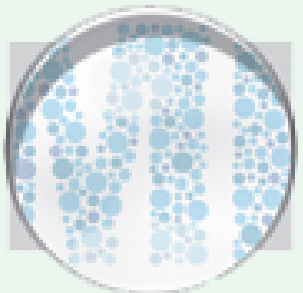


XIII CONGRESO ARGENTINO
DE MICROBIOLOGÍA GENERAL



SAMIGE



Asociación Civil de Microbiología General

2018

San Luis, Argentina

Diseño gráfico Lic. María Fernanda Castro

COMISIÓN DIRECTIVA SAMIGE 2015-2018:

Presidente: **Oswaldo Yantoro**
Vice-Presidente: **Eleonora García Véscovi**
Secretaria: **Diana Vullo**
Pro-Secretario: **Claudio Valverde**
Tesorera: **Daniela Russo**
Pro-Tesorero: **Leonardo Curatti**
Presidente saliente: **Néstor Cortez**

COMISIÓN ORGANIZADORA LOCAL SAMIGE 2018-San Luis

Liliana Beatriz Villegas, INQUISAL-UNSL
María Fernanda Castro, INQUISAL-UNSL
Claudio Daniel Delfini, INQUISAL-UNSL
José Oscar Bonilla, INQUISAL-UNSL
César Américo Almeida, INQUISAL-UNSL
Luis Escudero, INQUISAL-UNSL
Patricia Gisela Silva, UNSL
Martín Masuelli, INFAP-UNSL
Eugenia Menoyo, IMASL-UNSL
Maria Cecilia Della Vedova, INQUISAL-UNSL

COMISIÓN EVALUADORA:

César Almeida
Leonardo Curatti
Marcela Ferrero
Eleonora García Véscovi
Eugenia Menoyo
Alejandra Pereyra
Patricia Silva
Daniela Russo
Claudio Valverde
Liliana Villegas
Diana Vullo
Oswaldo Yantorno

Código de Resumen: BF-004

Sección: Biotecnología y Fermentaciones

Modalidad: Poster

DEGRADATION OF SUGARCANE VINASSE BY AN AUTOCHTHONOUS FUNGUS: MOLECULAR IDENTIFICATION

Luciana M Del Gobbo¹, Macarena M Rulli², Liliana B Villegas³, Verónica L Colin².

¹Universidad Nacional de Tucumán, Facultad de Bioquímica, Química y Farmacia.

²Planta Piloto de Procesos Industriales Microbiológicos (PROIMI-CONICET). ³Instituto de Química San Luis (INQUISAL-CONICET).

lucianadelgobbbo@gmail.com

Various fungus-based processes can be applied to degrade sugarcane vinasse, an acid effluent (pH=3.5–5.0) from sugar-alcohol industry which contains a high chemical oxygen demand (COD) and biochemical oxygen demand (BOD). Previous studies demonstrated the potential of a native fungus from the province of Tucumán (strain V1) to degrade a vinasse sample. In the present study, the molecular identification of this strain was carried out. In addition, it was evaluated the effectiveness of the microbial treatment conducted during 15 d. Mycelium in the exponential growth phase was harvested by centrifugation and total DNA extraction was performed using DNA Kit, MOBIO. Amplification of the rDNA ITS1-5.8S-ITS2 regions was carried out using ITS1 and ITS4 primers and 18S rDNA sequences were compared with partial 18S rDNA sequences published in the GenBank using the BLAST tool from the National Center for Biotechnology Information (NCBI). Finally, a phylogenetic tree was constructed using the neighbor-joining method. Regarding the microbiological treatment, 200 mL of vinasse were inoculated with fungus spores at a final concentration of 1×10^6 UFC/mL, and was incubated at 30°C (150 rpm) for 15 d. Vinasse samples without inoculation were used as abiotic controls (AC). Growth kinetics (measured as biomass production), pH changes, and the removal percentages of COD and BOD was determined each 72 h in the microbiologically treated vinasse (TV) and in AC, by using standard methods for the examination of wastewater. The fungus strain was identified as *Aspergillus* sp. V1 and it was closely related to *Aspergillus terreus* ATCC MYA-4898 (99%). As expected in the AC, no significant growth was detected until the end of the assay. For TV it was observed the maximum growth at 9th d of cultivation (biomass higher than 5 g/l). The TV for 3 d did not show a significant increase in the pH with respect to AC, which remained unchanged throughout the entire experiment (pH = 4.1). However, at 6th d of incubation, pH was significantly increased until a value close to neutral (6.7 ± 0.5). At 12th d of cultivation, it was detected the maximum COD and BOD removal, with percentages of 59% and 89%, respectively. At that point in time, only a 10% and a 30% was removed from AC. Based on these results, a removal of COD and BOD of 49% and 59%, respectively, can be attributed to the metabolism of *Aspergillus* sp. V1. This could involve a significant reduction in the toxicity of the effluent mediated by the action of this strain.

Supported by MINCyT-CAPES (BR/14/09) and CONICET.