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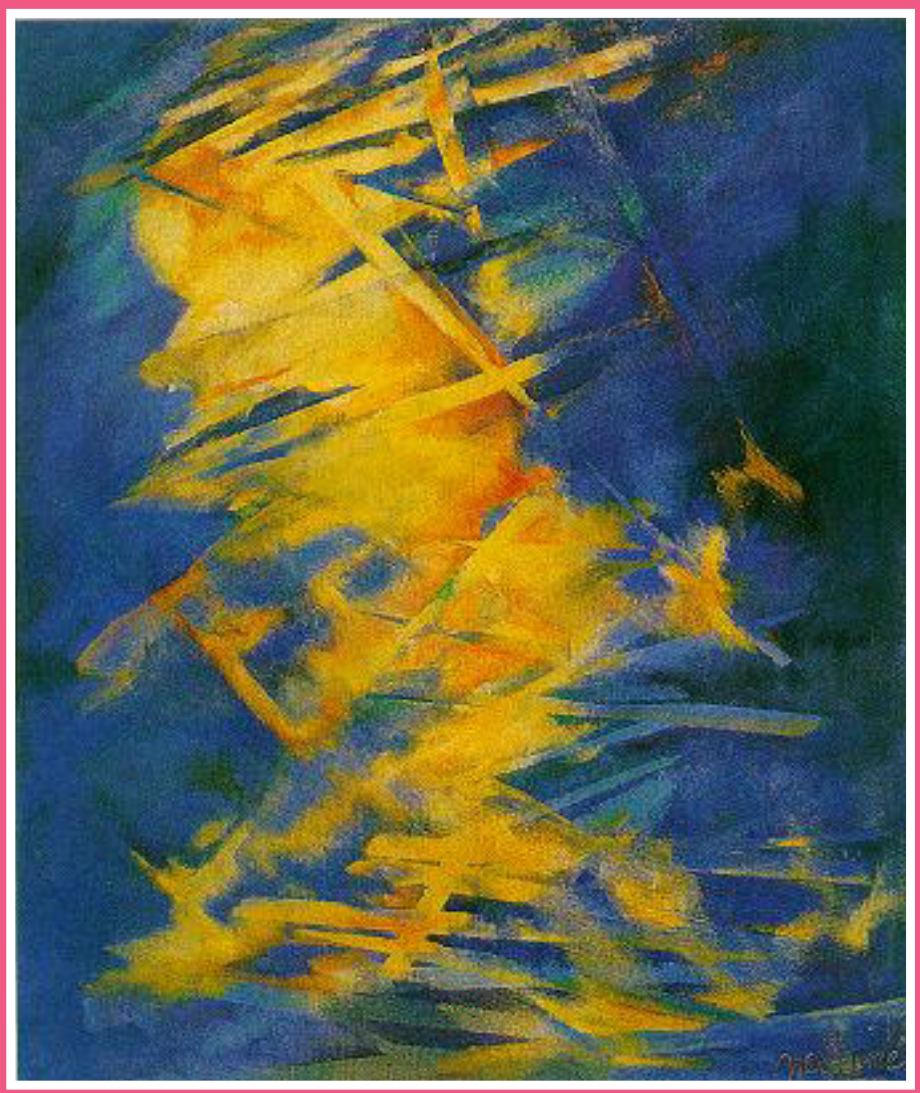

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La Tapa (Ver p. IV)
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REUNIÓN CONJUNTA DE SOCIEDADES DE BIOCIENCIAS

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LIII REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE INVESTIGACIÓN BIOQUÍMICA Y BIOLOGÍA MOLECULAR (SAIB)

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LXII ANNUAL MEETING OF ARGENTINE SOCIETY OF CLINICAL INVESTIGATION (SAIC)

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LA TAPA

María Esther Gené, **Imagen ígnea**, 1996.

Acrílico sobre tela, 110 x 95 cm. Cortesía de la Comisión Nacional de Energía Atómica, Predio TANDAR, Centro Atómico Constituyentes. Presidente de la Comisión Organizadora de la Exposición Permanente: Dr. A.J.G.Maroto.

María Esther Gené nació en Buenos Aires. Cursó Historia del Arte y Estética con Blanca Pastor y Nelly Perazo. Se inició en el taller de Centa Bertier y continuó su formación con Miguel Dávila. Participó del grupo de investigación plástica que dirigió Emilio Renart. Integró el Grupo Gen y formó el Grupo Fusión. Realizó numerosas exposiciones colectivas e individuales (Museos Municipal de Bellas Artes de Luján, Fernán Félix de Amador, de Arte Moderno de la Ciudad de Buenos Aires, Fundaciones San Telmo y Banco Mayo, Fundación Andreani, Patio Bullrich, Galería Kristel K., Salón ICCED de Pintura, entre otros). Sus obras se encuentran en colecciones privadas de Argentina, México, Alemania, España, Uruguay y EE.UU.

[1] Comisión Nacional de Energía Atómica. Artistas Plásticos con la CIENCIA, Centro Atómico Constituyentes, Predio TANDAR, Buenos Aires, 1999; En: *http://www2.cnea.gov.ar/xxi/artistas/artistasplasticos.htm*

taining their function, in contrast secreted proteins are highly divergent and poorly conserved in order to be able to interact with different hosts and environments.
Up to this date nine specialized bacterial SS have been characterized and thousands of secreted proteins have been identified in culture supernatants both with and without an assigned secretion mechanism. However, the experimental identification of SS remains challenging.
In this work we validated the detection of a given SS by comparing the evolutionary patterns between secreted proteins and elements of the SS in multiple organisms.
The OMA orthologous database was used to generate phylogenetic profiles (PP) across all the complete bacterial genomes. The PP of secreted proteins were compared against every element of the proteome using mutual information, PPs of protein constituents of the SS were found to score higher than proteins not related to the SS. High scoring proteins were used to conform a graph, where each edge represents a predicted coevolutionary interaction between PPs. The node connectivity is directly related to the number of different proteins secreted by a single SS, and putative complexes were analyzed by clustering the graph adjacency matrix, by doing so we were able to identify and group the core components of the type 2, 3, 4 and 6 SS from an unordered set of secreted proteins. Our results suggest that this methodology would be applicable in the detection of new SS, either by using pre existent data or by supernatant proteomic analysis.

(798) **USE OF VNTRS WITHIN CODING SEQUENCES TO GENOTYPE *TOXOPLASMA GONDII***

Rosalia Moretta (1), Paula Ruybal (2), Valentina Martin (1)
(1) Centro de Estudios en Salud y Medio Ambiente; CONICET, (2) IMPAM Instituto de Investigaciones en Microbiología y Parasitología Médica; CONICET.

Toxoplasma gondii is an intracellular protozoan with a worldwide prevalence in human and animal populations. Infection occurs as a result of ingestion of resistant forms present in meat products and exposure to cat faeces. In immunocompetent individuals is generally asymptomatic. Severe disease may occur in immunocompromised subjects and in congenital toxoplasmosis, which is caused by transplacental acquisition of Toxoplasma gondii.

Genetic diversity of *T. gondii* has been studied using a PCR-RFLP scheme based on nine molecular markers. These studies led to the description of a clonal population structure with three main lineages, designated as type I, II and III.

The aim of this study was to develop molecular markers that allowed the discrimination of genetic variants within each clonal linage and therefore describe *T. gondii* population variability closer to strain level.

We analyzed the genome of *Toxoplasma gondii* to identify genes containing variable number tandem repeats (VNTRs). The coding sequences of T. gondii ME49 genome (www.toxodb.org) were processed with Tandem Repeat Finder software. A panel of candidate markers was selected based on the following parameters: the repeat period (<9), the number of repeats copies (>20), the repeat module composition (to avoid single and dinucleotide runs) and the absence of introns within the repeat region.

The selected panel of eight molecular markers was analyzed in PRU (type II) and RH (type I) strains. As a first step, the variability of the PCR product size allowed us to differentiate PRU from ME49 (both type II strains) and RH from GT1 (both type I strains). Additionally, amplification products from PRU and RH strains were sequenced to study intra-lineage variability. Polymorphic markers between type I and type II strains presented specific arranges of the VNTR pattern. Nonetheless, those markers that didn´t present size polymorphisms were also conserved at the sequence level.

Keywords:Toxoplasmosis, Epidemiology, Minisatellites

(1027) **LABEL-FREE PROTEOMIC ANALYSIS OF THE HEXACHLOROCYCLOHEXANE-DEGRADING ACTINOBACTERIA *STREPTOMYCES* SP. M7**

José Sebastián Dávila Costa, Pedro Eugenio Sineli, Sergio Antonio Cuozzo
Planta Piloto de Procesos Industriales Microbiologicos (PROIMI-CONICET)

The increment of the global population and subsequently the increasing demand of food has promoted the use of pesticides such as hexachlorocyclohexane (HCH). HCH is a chlorinated pesticide used to protect crops from vector borne diseases. Large-scale production and the extensive use of this compound led to deterioration of environmental quality owing to its persistence in the environment. Over the last years, bacteria-mediated degradation of toxic organic compounds has become in an effective biotechnological process. *Streptomyces* sp. M7 was isolated from polluted sediments in the province of Tucumán, Argentina. Several physiological studies demonstrated the ability of M7 to remove HCH and highlighted the potential of this strain to be used in bioremediation processes. Degradation pathways for HCH and organochlorine compounds in general, are not fully elucidate in Actinobacteria. So far, a complete mechanism for the degradation of HCH was only proposed in *Sphingobium japonicum*. MS-based proteomics have become a powerful tool to elucidate and understand the mechanisms that underlie physiological processes. In the present work we used a MS-based, label-free, and quantitative proteomic approach as a starting point for understanding the degradation pathway for HCH in our strain. M7 proteome showed 293 proteins that were significantly up-regulated in the presence of HCH. Key enzymes involved in the dechlorination of HCH (LinA; LinB and LinC) were identified. In addition, 8 proteins assigned to the xenobiotic degradation category could be involved in the so called downstream degradation pathway of HCH. Proteomic results support the physiological capacity of *Streptomyces* sp. M7 to degrade hexachlorocyclohexane. In turn, the obtained results will allow to postulate a degradative pathway for this bacterium. Keywords: Biodegradation, *Streptomyces*, Proteomic

(1349) **HIGH QUALITY DRAFT GENOMES OF MEMBERS OF ACIDOBACTERIA SUBDIVISION 4 RESOLVED FROM TWO INDUSTRIAL WASTEWATER TREATMENT PLANT METAGENOME**

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(1) Instituto de Investigaciones en Ingeniería Genética y Biología Molecular (INGEBI-CONICET). Buenos Aires, Argentina. (2) Departamento de Fisiología, Biología Molecular y Celular, Facultad de Ciencias Exactas y Naturales. Universidad de Buenos Aires. Buenos Aires, Argentina.

The activated sludge (AS) technology, used worldwide for the treatment of municipal and industrial wastewater, relies on the self-assembly of a highly diverse and dynamic microbial community, where bacteria are responsible for the removal of most of the oxygen-demanding pollutants and nutrients. Our general aim is to gain understanding of AS functioning through the ecophysiology of key microbial players.

Shotgun sequencing of samples taken at different time from the aeration basins of two industrial full-scale wastewater treatment plant (WWTP), textile-dyeing (TD) and polymer synthesis (PS), was performed using Illumina HiSeq 1500. A total of 4.38 x 10^7 high quality paired end reads of 150bp (6.57 x 10^9 bp) were assembled. Differential coverage of scaffolds was used as a binning strategy, followed by %GC and tetranucleotide frequency. Paired end reads were tracked and reassembled, and contamination with foreign genomes was checked.

Out of forty-five genomes assembled into near-complete chromosomes, we focused primarily on two genomes of a stable and relatively abundant (ca. 9.8 % and 6.8%) member of this community, according to PCR amplification based on a specific region of the 16S rRNA gene and *in silico* abundance estimation. The genome from TD had 3.6 Mbp and 92.3% of completeness with 0.8% of contamination, while the genome from the PS had 2.7 Mbp with 77.2% of completeness and 0.05% of contamination. Phylogenetic reconstruction using 16S rRNA and 26 conserved genes sequences indicated both genomes belonged to Acidobacteria Subdivision 4,