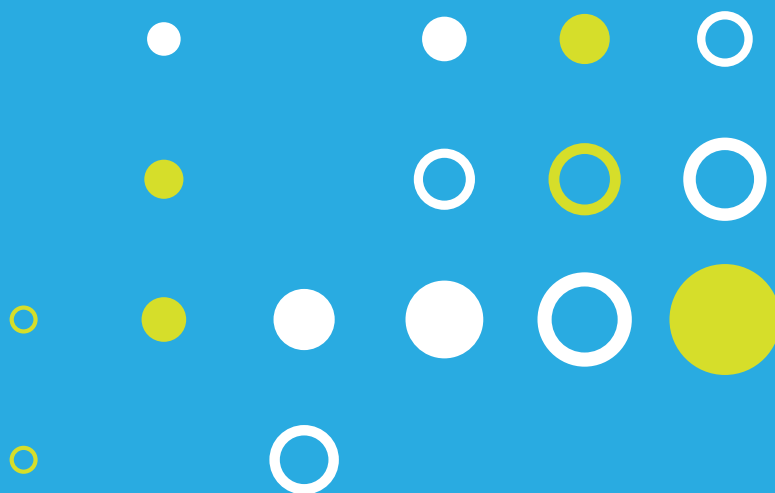


BIOCELL

n° 31

ISSN: 0327-9545 (print)
ISSN: 1667-5746 (online)

November 2007



SAIB

Sociedad Argentina de
Investigaciones en Bioquímica
y Biología Molecular

B I O C E L L

formerly ELECTRON MICROSCOPY AND CELL BIOLOGY

Official journal of the Sociedades Latinoamericanas de Microscopía Electrónica (SLAME), Iberoamericana de Biología Celular (SIABC), Federación Iberoamericana de Biología Celular y Molecular, and Sociedad Argentina de Investigaciones en Bioquímica y Biología Molecular (SAIB).

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CB-P32.
PARTICIPATION OF Agp1 PERMEASE IN THREONINE UPTAKE IN SACCHAROMYCES CEREVISIAE

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The old concept that yeast transports amino acids by multiple specific permeases and a general amino acid permease had to be modified with the demonstration that many individual amino acid permeases are capable of transporting several different amino acid. Most notable is the permease Agp1p that under appropriate conditions can transport virtually all the nonpolar amino acids. Physiological expression of "secondary" specificities can be manipulated by changes in growth medium and by mutation in other permeases. The relative contribution to the transport of a single amino acid by more than one permease is an area that has not been fully explored. In this paper we report experiments in which gap1 mutants defective individually in Agp1p, Agp2p, Agp3p, and Bap3p were used in investigating low-affinity leucine transport and transport of threonine. The cells grew in synthetic media with leucine or threonine 0.5 mM as the only nitrogen source. Our results show: 1) The LET2 gene appears to encode the most significant threonine transporter after Gap1p, 2) The following candidate genes are not allelic to LET2: GNP1, BAP3, AGP2 and AGP3 3) BAP3, and possibly AGP2, contribute to threonine transport in gap1 strains. Current phenotypic evidence favors the hypothesis that let2 is an allele of agp1. If this hypothesis is correct, low-affinity leucine transport is primarily due to Agp1p activity.

CB-P33.
PROTEIN C4 IS A PUTATIVE SMALL HEAT SHOCK PROTEIN IN THE INTESTINAL PARASITE GIARDIA LAMBLIA

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Giardia lamblia is a medical important protozoan with a low position in the eukaryotic lineage. *G. lamblia* trophozoites are transmitted through infected hosts by differentiation into cyst forms. By screening a *G. lamblia* WB 1267 cDNA expression library, we cloned the previously isolated gene Glorf-C4, considered specific of this organism. It encodes a 22 kDa protein that assembles in 60-66 kDa and high molecular mass complexes during the whole life cycle. 66 kDa complex formation is favored under some stress conditions. C4 localizes in cytosol of trophozoites and cysts and forms large spherical aggregates when it is overexpressed, without affecting viability and encystation. No homologous proteins nor conserved domains or features arise from sequence analysis of the predicted protein. Nevertheless, C4 presents local tertiary structure similarity with the α -crystallin domain of small heat shock proteins Hsp16.9B from *Triticum aestivum* and Hsp16.5 from the hyperthermophilic archaea *Methanococcus jannaschii*. Here, we discuss C4 putative role as a small heat shock protein in *G. lamblia* biology.

CB-P34.
IgA PRODUCTION AFTER ADMINISTRATION OF A PROBIOTIC

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Probiotics are live microorganisms that exert health beneficial actions to the host after their oral administration if they are given in suitable amounts. They have a stimulatory effect on humoral immunity by increasing the amount of available local and circulating IgA. However, it is possible that continuous administration might not be the optimal way to administer them. Our objective was to compare two doses of probiotics and study their effect on local immunity in rat intestine. For this purpose we used 27 rats that were divided in three groups: Control group (3 animals), Group A (15 animals) and group B (9 animals). Group A was given 1 ml of BIOFLORA (SIDUS Lab) and Group B 0,2 ml. Animals were sacrificed at 3,5,8,10 and 15 weeks of treatment and intestine was resected and processed by freezing technique. Immunofluorescence was performed in order to study the amount of IgA+ cells. Results: BIOFLORA stimulated the production of IgA secretory cells in group A with a peak at 3 days whereas in group B it did not exert significant effects with respect to control animals. The amount of IgA+ cells returned to basal values after 8 days of treatment. The results suggest that the increase in IgA secretory cells is dependent on the dose of probiotic and the period of treatment and that it is possible that a cyclic treatment would be a better way of administering the probiotic.

CB-P35.
ISOLATION AND MOLECULAR CHARACTERIZATIONS OF MARINE BACTERIA ISOLATED FROM BEAGLE CHANNEL

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Marine microorganisms play an important ecological role in the biological process of transformation of marine environment. Marine bacteria exhibit different hydrolytic enzymes that degrade fractions of organic matter in the sea. Marine microorganisms are the extremophiles carry out main a role in the biodegradation of the organic matter in diverse Antarctic ecosystems. Those culturing efforts have yielded new species within the divisions of γ - and α -Proteobacteria. The aims of this work were the isolation and taxonomy characterization of marine microorganisms from Antarctic region. Samples of benthonic organisms and seawater were taken from different coastal areas of the Beagle Channel (55°S; 67°W), Tierra del Fuego, Argentina. Samples were spread in LB medium and growth at 4 and 15°C. The 95 isolated colonies were characterized by 16S rDNA and gyrB PCR amplifications. Isolates were separated into groups according to their ARDRA profiles and RFLP analysis. 16S rDNA and gyrB gene were sequenced from one isolate from each group, and the phylogenetics trees were constructed. The gene sequences allowed us to determine their association with the class *Proteobacteria*; members of genera *Pseudomonas*, *Pseudoalteromonas*, *Serratia*, *Halomonas*, *Alteromonas*, *Psychrobacter*, *Shewanella*. These studies provide a new source of strains, genes, enzymes and metabolites for biotechnological applications.