

TRANSCRIPTOMIC ANALYSIS OF THE INVASIVE STAGE OF THE PLATYHELMINTH *Fasciola hepatica*

Cancela, M¹, Dell'Oca, N², Da Silva, E.D¹, Rinaldi G², Roche L², Bizarro, C.V.¹,
Ferreira H.B.¹, Carmona C³, Tort J² and Zaha A¹

¹Centro de Biotecnología, UFRGS, Porto Alegre-Brasil

²Departamento de Genética. Facultad de Medicina. UDELAR

³Unidad de Biología Parasitaria. Facultad de Ciencias. UDELAR. Montevideo-
Uruguay

Fasciola hepatica is the etiological agent of fasciolosis, a world-wide zoonosis that affects mammals including humans. In agriculturally based countries, the infection of ruminants leads to important economic losses. Our goal is to understand host-parasite relationship and physiological process involved in parasitism in order to identify targets for drugs and vaccines design. For this reason, we started a transcriptomic-based analysis of the invasive stage of *F. hepatica* preparing full-length enriched cDNA libraries from newly excysted juvenile (NEJ). After cDNA synthesis and PCR amplification, we size fractionated and cloned three subpopulations of cDNAs: 400-800bp, 800-2000bp and >2000bp into TA cloning vectors. Plasmid DNA was sequenced and 2700 high quality sequences were analyzed and distributed in 477 different clusters, where 50% had significant similarity with sequences deposited in Genbank database. Antioxidants enzymes, cysteine proteinases and mucin-like proteins were highly redundant. Comparative analysis between NEJ and adult showed that 45% of NEJ clusters were not detected in adult parasite. This data suggested that a set of NEJ transcript are predominant or differentially expressed during infection of mammal host. Quantitative real time PCR confirmed that cDNA encoding a mucin-like protein and members of the legumain gene family were predominantly expressed in NEJ. These data support the hypothesis that important changes in gene expression take place during infection of mammal host. Functional genomic using RNAi will be a fundamental tool in order to identify gene function and to better understand parasite biology.

Support: CNPq, Dinacyt.

Keywords: NEJ, invasion, gene expression