XVII INTERNATIONAL SYMPOSIUM ON
SCHISTOSOMIASIS
PERSPECTIVES ON SCHISTOSOMIASIS ELIMINATION
NOVEMBER 10-13TH 2024 | SALVADOR - BAHIA

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TITLE

CHARACTERIZATION OF BIOMPHALARIA GLABRATA'S MIRNAS: RHYTHMICITY AND DIFFERENTIAL EXPRESSION IN INTERACTION WITH ITS PARASITE SCHISTOSOMA MANSONI

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ABSTRACT

MiRNAs are short, single-stranded non-coding sequences that play crucial roles in the regulation of gene transcription in many biological processes such as embryonic development, cell proliferation or apoptosis. Even if miRNAs have been founded conserved in the Eumetazoan, some are dissociated or specific to a species or even to an individual. Indeed, some studies have identified isomiRNAs that can specifically respond to stress or potentially lead to new miRNAs within a species. miRNAs were known to regulate the host's internal defense system and immune cell response, which are a crucial process of host-parasite interactions. Herein, we describe the complete and constitutive set of miRNAs, referred to as the miRNome, in Biomphalaria glabrata snails, the primary intermediate host of the trematode parasite Schistosoma mansoni, the causative agent of schistosomiasis. The B. glabrata miRNome is characterized from the hemolymph, that is known as the main immune-related tissue of the snail, which contains hemocytes, the snail innate immune cells. Using a massive sequencing approach of small RNAs, we characterize their expression and specificity between strains of B. glabrata selected for their extreme compatibility phenotype with the parasite and differential geographical isolate. Our results uncover specific miRNAs and abundant isomiRNAs that are expressed exclusively in one strain or another, suggesting a specificity of the expression for the miRNAs derived by the local co-evolution with the parasite. As expected, expressed common core of miRNAs between naive strains have been founded and constitute thus a conserved cluster of miRNAs.
Others points remain to explore : what is the intrinsic expression of these miRNAs in immune cells but also in animal? Could their expression regulation be misinterpreted as a response to the parasite? The expression behavior of three miRNAs, bgl-miR-8-3p, bgl-miR-1985-5p, and bgl-miR-184-3p, was investigated over a 48-hour period in two tissues, hemolymph and head-foot, using qPCR. It was found that these miRNAs exhibit different dynamic expression patterns between the tissues and over time.

KEYWORDS

microRNA; Compatibility Polymorphism; Parasitology; Immunology

FINANCIAL SUPPORT

LabEx CeMEB, IHPE, Université de Perpignan Via Domitia, Agence Nationale de la Recherche (ANR-22-CPJ1-0056-01), BQR projects University of Perpignan (mimicSNAIL and HemoMIR)