**UMR CNRS 6023 Laboratoire Microorganismes : Génome et Environnement. (D. Debroas)**

**Directeur de thèse :** Eric Peyretaillade (MCU-HDR), co-directeur Ivan Wawrzyniak (IE CNRS)

eric.peyretaillade@uca.fr

**Study of non-coding RNAs roles in microsporidian host-parasite interaction.**

Non-coding RNAs (nncRNAs) are recognized as major players in the regulation of various cellular processes (Veneziano et al). However, no data is available on these molecules and their potential roles in host / pathogen interactions in microsporidi parasites found throughout the animal kingdom. Indeed, only a minimalist "core" of 15 ncRNAs, playing a role essentially in the spliceosome (snRNA), and various RNA processing processes (snoRNA), have been characterized (Belkorchia et al). The objective of this thesis will therefore be to ensure the characterization of the entire repertoire of non-coding RNAs that can be produced by these parasites during an infection process. To do this, the massive sequencing data of the total RNAs obtained (funding for the emergence project I-SITE CAP20-25) will be used using secondary and /or tertiary structure prediction tools. Subsequently, the distribution and role of these molecules in the host / parasite dialogue will be understood by studying their expression and regulation during the infestation process. The response of expression modulations of non-coding RNA of the host will also be evaluated in order to highlight the specific responses of the host and how the control of the host is performed by the parasite.

Veneziano *et al.* Current Deep Sequencing Data Analysis Approaches and Challenges. Hum Mutat. 2016 Dec;37(12):1283-1298.

Belkorchia *et al.* Comparative genomics of microsporidian genomes reveals a minimal non-coding RNA set and new insights for transcription in minimal eukaryotic genomes. DNA Res. 2017 Jun 1;24(3):251-260.