

Titre du stage : Exploring an uncharted genome by comparative genomics: characterising distant orthologues in the genome of a pathogenic fungus.

Laboratoire (intitulé, adresse, site web) :

IBDM : <http://www.ibdm.univ-mrs.fr/equipe/computational-biology/>

CIML : <http://www.ciml.univ-mrs.fr/science/lab-jonathan-ewbank/>

Equipe :

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Descriptif du stage :

Discovering new ways to fight infectious disease in humans requires the study of host-pathogen interactions. These are so complex that simpler model systems are used. To advance our understanding of the interaction between the nematode *Caenorhabditis elegans* and the pathogen *Drechmeria coniospora* [1,2], the Ewbank lab has recently sequenced the genome of this nematophagous fungus [3]. Phylogenetic analysis indicates that *D. coniospora* represents an unexplored branch of the evolutionary tree. Indeed, using standard comparative genomics tools, more than 15% of the ca. 9,000 *D. coniospora* genes encode proteins that seem to be species-specific, as they do not share significant sequence similarity to other proteins in the databases. In this project, we aim to take a closer look at these species-specific proteins.

The Habermann lab is specialized on working with remotely conserved proteins [4] and is developing methods to detect distant orthologs [5]. In your Master project, you will be in charge of identifying remotely conserved orthologs of *D. coniospora* sequence orphans in other species, initially using in-house methods like morFeus [5] or the HH-suite from the Söding lab [6], but ideally also through the conception of new tools.

As an applicant, you will have scripting knowledge and should be familiar with the usage of the Linux/Unix-based command line. Programming skills in Python will be an advantage.

We offer a highly interdisciplinary, international and active research environment, where you will interact with both computational and wet-lab teams.

[1] Zugasti et al. A quantitative genome-wide RNAi screen in *C. elegans* for antifungal innate immunity genes. *BMC Biol.* 2016 Apr 29;14(1):35.

[2] Zugasti et al. Activation of a G protein-coupled receptor by its endogenous ligand triggers the innate immune response of *Caenorhabditis elegans*. *Nature Immunol.* 2014 Sep;15(9):833-8.

[3] Lebrigand et al. Comparative Genomic Analysis of *Drechmeria coniospora* Reveals Core and Specific Genetic Requirements for Fungal Endoparasitism of Nematodes. *PLoS Genet.* 2016 May 6;12(5):e1006017

[4] Habermann BH (2016). Oh Brother, Where Art Thou? Finding orthologs in the twilight and midnight zones of sequence similarity. *Evolutionary Biology* (Springer): pp393-419

[5] Wagner et al. morFeus: a web-based program to detect remotely conserved orthologs using symmetrical best hits and orthology network scoring. *BMC Bioinformatics.* 2014 Aug 6;15:263.

[6] Meier A, Söding J. 2015. Automatic Prediction of Protein 3D Structures by Probabilistic Multi-template Homology Modeling. *PLoS Comput Biol.* 11(10):e1004343.