

FORMULAIRE STAGE Recherche-M2 BBSG
(période de stage : du 5 janvier 2017 au 3 juillet 2017)

Titre du stage : Exploring an uncharted genome; characterising distant orthologues in the genome of *Drechmeria coniospora*

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 :

IBDM : Bianca Habermann (Computational biology)

CIML : Jonathan Ewbank (Innate immunity in *C. elegans*)

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Descriptif du stage :

To advance the characterisation of the interaction between *C. elegans* and the pathogen *Drechmeria coniospora* (e.g. [1,2]), the Ewbank lab has recently obtained the genome sequence of this nematophagous fungus [3]. Phylogenetic analysis indicates that *D. coniospora* represents an unexplored branch of the evolutionary tree. Indeed, using standard 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.

The Habermann lab has developed methods to identify remote orthologues [4,5], at the genome level. The proposed project will involve application of these methods, as well as Hidden Markov-Model (HMM) based algorithms as part of a detailed examination of the *D. coniospora* genome.

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 of advantage.

[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. doi: 10.1186/s12915-016-0256-3.

[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. doi: 10.1038/ni.2957.

[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. doi: 10.1371/journal.pgen.1006017

[4] 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. doi: 10.1186/1471-2105-15-263

[5] Bradshaw et al. HMMerThread: detecting remote, functional conserved domains in entire genomes by combining relaxed sequence-database searches with fold recognition. PLoS One. 2011 Mar 10;6(3):e17568. doi: 10.1371/journal.pone.0017568.