

POST-DOC OFFER

Laboratoire Interactions des Ecosystèmes Microbiens (LEMic), Institut Pasteur de la Guadeloupe, French West-Indies

Project title: Identification of *Naegleria fowleri* virulence-associated genes using a comparative genomics approach.

Candidate profile: Applicants must have a PhD and a solid background on eukaryotic genome research (from read assembly to functional annotation and visualization tools).

Rationale:

Naegleria fowleri (commonly referred to as the “brain-eating amoeba”) is a free-living amoeba (FLA) that causes a rare, but fatal, infection of the brain called primary amebic meningoencephalitis (PAM). In 2008, *N. fowleri* was responsible for the death of a 9-year-old boy who swam in one of geothermal baths of Guadeloupe. Since then, we frequently make surveys of *N. fowleri* in geothermal recreational waters of Guadeloupe. The results showed that this FLA is a common and widely distributed species in these hot waters. We recently showed that this amoeba is also widely distributed in the soil in Guadeloupe. As such, it represents a possible threat to the Guadeloupian but also for tourists, that frequently come in contact with raw water at recreational hot springs, as they are a very popular form of recreation. The number of cases of PAM is increasing throughout the world; this is probably due to global warming, global overpopulation, and increased industrial activities. Therefore, *N. fowleri* and resulting meningoencephalitis are not only a local problem but are of public health interest worldwide.

N. fowleri is very problematic due to the rapid onset and destructive nature of the disease as well as the lack of effective treatments. To develop more effective therapies as well as more rapid diagnostic tools, improved knowledge on *N. fowleri* pathogenic mechanisms are necessary. In order to identify *N. fowleri* virulence-associated genes, we aim to use a comparative genomics approach.

The genomes of the infectious *N. fowleri* (strain ATCC 30863 and 30894) and non-infectious *N. gruberi* (strain ATCC 30224) species are currently available. Nevertheless, they present a low genome similarity, hampering the finding of genes associated to virulence (or attenuation) phenomenon using a comparative genomics approach. The rDNA in the genus *Naegleria* is a circular plasmid from which thousands of copies are present in each cell. The internal transcribed spacers (ITS) and 5.8S rDNA are between the SSU and LSU rDNA. ITS and 5.8S rDNA sequences are the most used to study *Naegleria*. According to ITS and 5.8S rDNA sequences, the thermophilic and non-infectious *N. lovaniensis* strain is a close relative of *N. fowleri*. As such, we aim to identify potential *N. fowleri* virulence-associated genes by comparing the genomes of infectious *N. fowleri* and non-infectious *N. lovaniensis* strains. The genome of *N. lovaniensis* (strain ATCC 30569) was recently published.

To characterize the genomes of the *Naegleria* sp isolated in Guadeloupe, we used Illumina technology to sequence the two closely related *Naegleria* strains. For *N. fowleri*, DNA from 3 strains isolated in distinct geographical region and with different genotypes were used: AR12 (isolated in USA, genotype 2), PA34 (isolated in Australia, genotype 5) and GW_f (isolated in Guadeloupe, genotypes 2 and 3). For *N. lovaniensis*, 2 strains from distinct geographical region were studied: F9 (isolated in Belgium) and GW_lov (isolated in Guadeloupe). Strains AR12, PA34 and F9 were isolated in the 70's while all the others strains were isolated from hot springs in 2019; none of these genome sequences are published.

The aim of this Grant is to finalize the genome annotation of *N. fowleri* and *N. lovaniensis* species, and then conduct comparative genomics analyses (including the genomes already published).

Duration: 2 years (in case of attribution of Calmette & Yersin Post-doctoral scholarship)
<https://www.pasteur.fr/fr/enseignement/bourses-aides-mobilite/bourses-post-doctorales-calmette-yersin>

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Deadline for applications: 5th July 2020