

## **Postdoctoral position**

### **Title: Mining (meta-)genomes and (meta-)transcriptomes for metallophore biosynthetic genes or gene clusters**

#### **Context**

The **MesMic consortium (Metals in Environmental Systems Microbiology consortium)** is recruiting a collaborator in Bioinformatics and/or Computational Biology in the domain of microbial ecology at the Université de Pau et des Pays de l'Adour. The fellowships will have the duration of 12 months.

The post-doctoral position is part of the MeSMic (Metals in Environmental Systems Microbiology) project funded by E2S-UPPA (<https://iprem.univ-pau.fr/en/projects/thematic-hubs/mesmic.html>). The project brings together an interdisciplinary research team (genetics, molecular biology, physiology and microbial ecology, biogeochemistry, environmental and analytical chemistry), 6 PhD students and 7 post-doctorates and relies on a set of advanced instruments in analytical chemistry and environmental microbiology (<https://uppatech.univ-pau.fr/fr/plateaux.html>). More than 20 permanent researchers are collaborating on this project.

#### **Scientific context:**

In a natural environment, at pH where most life exists, microbial growth can be limited by the availability of metals. This limitation in the environment can have significant consequences on ecosystem functioning. To ensure their survival and their development, microorganisms have developed strategies for the recovery and absorption of metals from the surrounding environment (Hider and Kong 2010). The capture of metal is ensured by the synthesis of siderophores (iron) or more generically metallophores. The biosynthetic potential of metallophores does not appear to be equally distributed among organisms, environments or microbial life cycles, but rather is enriched within a number of prolific clades (Cimermancic et al. 2014, Smanski et al. 2016). One field of investigation aims at seeking for new metallophore biosynthetic genes to enlarge our view of their diversity in the microbial world and investigate these data in an eco-evolutionary perspective.

#### *References*

- Cimermancic, P, Marnix H Medema, J Claesen, K Kurita, Laura C Wieland Brown, K Mavrommatis, A Pati, Paul A Godfrey, M Koehrsen, J Clardy, Bruce W Birren, E Takano, A Sali, Roger G Lington, and Michael A Fischbach. (2014) Insights into Secondary Metabolism from a Global Analysis of Prokaryotic Biosynthetic Gene Clusters. *Cell* 158: 412-421.
- Hider, R. C., & Kong, X. (2010). Chemistry and biology of siderophores. *Natural Product Reports*, 27(5), 637-657.
- Hopwood, M, P Statham, SA Skrabal, and JD Willey. 2015. Dissolved iron (II) ligands in river and estuarine water. *Marine Chemistry* 173: 173-182.
- Smanski, MJ, DC Schlatter, and LL Kinkel. 2016. Leveraging ecological theory to guide natural product discovery. *Journal of Industrial Microbiology and Biotechnology* 43: 115-115-128.

#### **Position and assignments**

The post-doctoral fellow will work at the IPREM Institute (<https://iprem.univ-pau.fr/fr/index.html>) under the responsibility of Pr. B. Lauga and Pr R. Duran, and in collaboration with international partners (e.g. U. Wageningen, bioinformatics groups).

The post-doctoral fellow will bring all the bioinformatics expertise required for a fine investigation of metagenomic and metatranscriptomic data generated on field collected, microcosm generated samples and worldwide databases in order to i) establish an inventory of metallophore biosynthetic gene clusters (BGC), in microbial genomes and metagenomes from diverse environments, ii) infer their role in microbial assemblages by linking them to known metallophores and natural products, iii) conduct meta-analysis on the distribution of BGC across worldwide habitats in order to highlight any specific distribution and reveal if hot spots of genetic diversity exist for metallophore BGC. Our ultimate goals are i) to better understand the metabolic interactions occurring within complex multi-species microbial assemblages, ii) to evaluate, at the ecosystem level, how metallophores contribute to community assembly, functioning, and beyond, to ecosystems functioning. In parallel, teaching duties (64h) will accompany the research tasks.

## **Requirements**

We are seeking highly motivated postdoctoral research scientist with expertise in the analysis of (meta-)genomics/(meta-)transcriptomics data to work at IPREM. The ideal candidate should have a PhD in the fields of Bioinformatics or Computational Biology and microbial ecology, with research experience in NGS data analysis. A good background in microbial evolution and biostatistics would be appreciated.

## **Situation:**

The Université de Pau et des Pays de l'Adour campus is located in the charming city of Pau in southwestern France in a region bordering Spain. It benefits from exceptional resources due to its geographical location, close to the Pyrenees (1h drive) and the Atlantic coast (1h drive), with numerous air links from the airport and trains to Paris.

The IPREM is a Joint Research Unit CNRS / UPPA (UMR 5254) with 120 permanent staff and 140 PhD and Post-docs.

## **Application procedure**

Send by e-mail to [beatrice.lauga@univ-pau.fr](mailto:beatrice.lauga@univ-pau.fr) and [Robert.duran@univ-pau.fr](mailto:Robert.duran@univ-pau.fr) an application file including:

- CV
- cover letter
- Candidate's PhD abstract and publications
- List of jobs obtained after the PhD
- 2 letters of recommendation

Contact details (3 referees, including at least the PhD supervisor and the post-doc supervisor (if applicable))

## **Application deadline**

Mid-October 2022

## **Start**

Flexible but preferably before the end of November 2022