Portfolio 4.1 – INTERNATIONAL WORKSHOP ON GENOME-MINING

To ensure that the bioinformatics tools we are developing for the analysis of nonribosomal peptides are disseminated and used as effectively as possible, we have designed and organized an international workshop that is regularly proposed. This 3-day workshop is primarily aimed at early career researchers, PhD students and post-docs who come to deepen their theoretical and practical knowledge of nonribosomal peptides, and to carry out their own bioinformatics analysis using the most up to date tools dedicated to microbial secondary metabolites. Among the tools are antiSMASH, NaPDos, MIBIG (developed by colleagues from Netherland and Denmark) and NORINE platform developed in Lille (https://norine.univ-lille.fr/NRP) . This international collaboration gives us the opportunity to offer the entire scientific community a wokflow that combine computational tools to optimize the search for microbial metabolites of interest. The attendees appreciate that this workshop teaches both theoretical and practical skills to rapidly identify, annotate and analyze secondary metabolite biosynthetic gene clusters in microbial genomes.

We all together co-supervise the workshop. Thus, as expert, Valérie LECLERE has a lecture on nonribosomal synthesis, highlighting its pecularities and Philippe JACQUES focuses on lipopeptides. They also help applicants for their analysis using NORINE during practical sessions. We rely on major publications, reviews and book chapters we published with this aim.

Leclère, V., Weber, T, Jacques, P. and Pupin, M. (2016) Bioinformatics tools for the discovery of new nonribosomal peptides. Chapter 14, In Evans, B., S. editor, NonRibosomal peptide and polyketide biosynthesis. *Methods Mol. Biol.* 1401, 209-232.

Pupin, M., Flissi, A., Jacques, P., and Leclère, V. (2018). Bioinformatics tools for the discovery of new lipopeptides with biocontrol applications. *Eur. J. Plant Pathol.*, 152, 993-1001

Flissi, A., Ricart, E., Campart, C., Chevalier, M., Dufresne, Y., Michalik, J., Jacques, P., Flahaut, C., Lisacek, F., Leclère, V. and Pupin, M. (2020) Norine: update of the nonribosomal peptide resource with a new pipeline to automatize massive sourcing and enhance annotations quality. *Nucl. Acids Res.* doi 10.1093/nar/gkz1000

Duban, M., Cociancich, S. and Leclère, V. (2022) Nonribosomal peptide synthesis definitely working out of the rules. Microorganisms. 10, 577. doi: 10.3390/microorganisms10030577

Flissi, A., Duban, M., Jacques, P., Leclère, V., and Pupin, M. (2023). Norine: bioinformatics methods and tools for the characterization of newly discovered NonRibosomal Peptides. *Methods Mol. Biol.* New York: Humana, New York, NY, pp. 303–318. https://link.springer.com/10.1007/978-1-0716-3214-7_16.

The two first editions (« *Bioinformatics tools for PKS and NRPS discovery : from genomic data to the products* ») were organised in 2013 and 2016 in ULille while the 2 following (« Genome-mining for Natural Products ») took place in Lyngby (Denmark) in 2018 and 2022. For the latter, we welcomed 34 applicants coming from 12 countries, mainly from Europe but also from USA and Columbia.

This workshop represents a nice opportunity for early career researchers to benefit from the skills of experts in a convivial atmosphere.

