

Master 2 internship project Year 2020-2021

Laboratory/Institute: IAB

Director: Pierre HAINAUT

Team (until December 2020): Immunologie Analytique des Pathologies Chroniques

Head of the team: Dr Patrice Marche

Team (from January 2021th): Dept of Signaling Through Chromatin, group RNA and Epigenetics

Head of the team: Dr André Verdel

Name and status of the scientist in charge of the project: Dr Philippe BULET

HDR: yes

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Program of the Master's degree in Biology:

- | | |
|---|---|
| <input checked="" type="checkbox"/> Immunology, Microbiology, Infectious Diseases | <input type="checkbox"/> Integrative Structural Biology |
| <input type="checkbox"/> Physiology, Epigenetics, Differentiation, Cancer | <input type="checkbox"/> Neurosciences and Neurobiology |
| <input type="checkbox"/> Planta International | |

Title of the project: Mass spectrometry as innovative tool to investigate the effects of multiple stressors' exposure on bee health

Objectives (up to 3 lines):

The main objective of this Master 2 internship project will be to investigate the effects of different types of stressors (abiotic and/or biotic) on bee health status using hyphenated mass spectrometry approaches (molecular profiling and proteomics).

Abstract (up to 10 lines):

Pollinator decline presents a real issue that could have a significant impact on environment and economy. Over the last decade, researchers and organisations are dealing with this issue and trying to clarify how the environmental stressors (abiotic and /or biotic) could influence the pollinators. Nevertheless, more extensive investigations need to be conducted to better elucidate the physiological effects of the stressors on pollinators and especially perturbations of the proteomes. We are studying the stressor impact on the haemolymph (insect blood) as the targeted tissue, which may be considered as the mirror of the pollinator health. Proteomics investigations will allow to decipher the altered biological pathways while molecular profiling will allow to have a unique mass fingerprint of the pollinator haemolymph and to elaborate specific models to estimate the stressor impact on bee health. This internship is part of the PoshBee EU project.

Methods (up to 3 lines):

You will have to (i) analyze the haemolymph using MALDI mass fingerprints, (ii) create models using bioinformatics tools, (iii) study the proteome changes by LC-MS/MS and (iv) analyze the biological pathway deregulation using dedicated Bottom-Up proteomics approaches.

Up to 3 relevant publications of the team:

1. Arafah K, Voisin SN, Masson V, Alaux C, Le Conte Y, Bocquet M, Bulet P. MALDI–MS Profiling to Address Honey Bee Health Status under Bacterial Challenge through Computational Modeling. *Proteomics* 2019, doi: 10.1002/pmic.201900268
2. Masson V, Arafah K, Voisin S, Bulet P. Comparative Proteomics Studies of Insect Cuticle by Tandem Mass Spectrometry: Application of a Novel Proteomics Approach to the Pea Aphid Cuticular Proteins. *Proteomics*. 2018;18(3-4):10.1002/pmic.201700368. doi:10.1002/pmic.201700368
3. Guschinskaya N, Ressenkoff D, Arafah K, et al. Insect Mouthpart Transcriptome Unveils Extension of Cuticular Protein Repertoire and Complex Organization. *iScience*. 2020;23(2):100828. doi:10.1016/j.isci.2020.100828

Requested domains of expertise (up to 5 keywords):

Biology, Mass spectrometry, Chromatography (HPLC), Bioinformatics, Immunology

Language of writing:

French, English