# Master 2 internship project Year 2019-2020

# Laboratory/Institute: IAB

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**Team:** Immunologie Analytique des Pathologies Chroniques Head of the team: Patrice MARCHE

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

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## Program of the Master's degree in Biology:

□ Physiology, Epigenetics, Differentiation, Cancer □ Neurosciences and Neurobiology

Planta International

# <u>Title of the project</u>: Study of the effect of stressors on pollinator health using molecular mass fingerprints and proteomics

Objectives (up to 3 lines):

The objectives of this Master 2 internship project will be to investigate the effects of different types of stressors (abiotic and/or biotic) on the health status of a pollinator using complementary mass spectrometry approaches (MALDI-Biotyping and LC-ESI-MS/MS).

#### Abstract (up to 10 lines):

Pollinator decline presents a real issue that could have a significant impact on our environment and economy. This decline would be due to the environmental conditions in which the pollinators live. Many researchers worldwide are dealing with this issue and trying to clarify how the environmental stressors (abiotic and/or biotic) could impact the health and fitness of pollinators. Nevertheless, more studies need to be conducted to better elucidate the physiological effects of the stressors on he health status of pollinators We propose to use proteomics approaches to follow this status through a simple « blood collection ». The first strategy will be to perform molecular mass fingerprints using MALDI-Biotyping, a strategy used routinely in clinical microbiology. This will be complemented by searching potential biomarkers of the impact of stressors through Top-down and Bottom-up proteomics. This may serve to help the beekeepers and other sanitary services to adjust the beekeeping practices.

## Methods (up to 3 lines):

You will (i) analyze the haemolymph (bee blood) of one pollinator using MALDI molecular mass fingerprints, (ii) create models using bioinformatics tools, (iii) study the peptidome/proteome changes using LC-ESI-MS/ MS and (iv) analyze the biological pathways and the proteome pattern using dedicated proteomic tools.

#### Up to 3 relevant publications of the team:

- Arafah K, Voisin S, Masson V, Alaux C, Le Conte Y, Bocquet M, Bulet P: A MALDI-MS 1. Biotyping-like method to address the honeybee health status through computational modelling. Submitted to PNAS
- 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), 1700368. https://doi.org/ 10.1002/pmic.201700368

Pisani C, Voisin S, Arafah K, Durand P, Perrard M-H, Guichaoua M-R, Bulet P, Prat O: *Ex Vivo* Assessment of Testicular Toxicity Induced by Carbendazim and Iprodione, Alone or in a Mixture. ALTEX - Altern. Anim. Exp. 2016, 33 (4), 393–413. https://doi.org/10.14573/altex.1601253

Requested domains of expertise (up to 5 keywords):

Mass spectrometry and Chromatography, Bioinformatics, Infection, Immunity, Pollinator