- **Identification of metabolic pathways involved in carbon sources respiration under anaerobic conditions *in silico* and validation of prediction *in vitro* using *Dickeya dadantii* model strain.**

Encadrement : Feth el Zahar Haichar, Prof INSA Lyon, Équipe Chromatine et Régulation de la pathogénie
Stephanie Heux, DR INRAE Toulouse, Toulouse Biotechnologie Institute, INSA Toulouse

Contexte et Objectifs

Plant roots modulate anaerobic respiration both indirectly and directly. Indeed, it is well known that roots increase the anaerobic volume of the soil by consuming oxygen, exude different carbon sources that may act as TEAs, and compete with the microbial community for certain elements, such as nitrate, thereby diminishing its availability to microbes (Lecomte *et al.,* 2018). Therefore, the **demonstration of whether C sources could be used as alternative TEAs and the elucidation of the underlying genetic pathways holds a great potential to help understand microbial dynamics and evolutionary strategies to adapt and persist in the environment and cope with oxygen depletion**. This question is more relevant in the case of **pathogenic bacteria** which face many specific challenges to colonise and/or infect hots (Mendes *et al*., 2013) and are constantly exposed to changing environmental conditions. It is the case of *Dickeya dadantii*

For *Dickeya,* **an emergent pathogen in Europe**, is the causative agent of soft rot in a wide variety of plants including **economically important crops and many ornamental plants** (Ma *et al.,* 2017)*.* Certain species of *Dickeya* can live as epiphytes or as saprophytes in soils and ground waters until they encounter a susceptible host, such as plants (Reverchon and Nasser, 2013; Chen *et al*., 2019). During these periods, **bacteria experiences low oxygen availability**. This factor represents, in plant tissue for example, **one of the key factors in the development of soft-rot diseases** (Reverchon and Nasser, 2013).

Beside general information of anaerobic respiration in rhizobacteria, **understanding anaerobic respiratory pathways involved in pathogenic bacteria persistence and colonization will allow us to better understand their pathogeny**, and thus better counter it. Actually, we identified some C sources used in anaerobic conditions as TEA. <u>The aim of this project</u> is to **(i) test *in silico* using *D. dadantii* metabolic model the capacity of this strain to respire different C sources, (ii) characterize the metabolic pathways involved in the anaerobic respiration on these C sources and (iii) validates *in vitro* the predicted results.**

We are looking for a student with programming skills and, more specifically, knowledge of python code in order to use the metabolic model.
The training period is from January to June 2024. If you are interested in this subject, please send your CV to
feteh-el-zahare.haichar@insa-lyon.fr