Proposition de stage

Parcours Master 2 « Microbiologie, Environnement, Santé »

1. **Laboratoire / Entreprise d'accueil :**

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2. **Description du stage** (2 pages maximum) **:**

Titre : Capture de microorganisme par culture haut débit

Mots clés : Microbiote, Culture, Haut-débit

Contexte et objectifs généraux :

Sequencing is a great asset in the toolbox of any microbiologist willing to study the ecology. However, the conclusion of the observations based on sequencing -especially based on sequencing the 16S rRNA genes- can be challenging due to the lack of information linked to each sequence. To go further in the interpretation, we propose to use the second anaerobic high-throughput culturing station in Europe. This device will allow us to retrieve cells from the initial samples (stored at -80°C in a special anaerobic medium) and sequence their 16S rRNA gene. Recent results in the team and elsewhere (Lagkouvardos et al., 2017) suggest that 80% of the bacteria can be grown as isolates.

Projet de stage :
Here we aim to generate the Hudson RapidPick colony picker placed in an anaerobic chamber to sequence individually the 16S rRNA of hundreds of bacteria isolates. The method will be developed during the internship.
More specifically, we will use the gut bacteria of pigs as a model to perform the following:
- Plate microbes from the pig feces on 15 plates filled with the YCFA medium
- Use the robot to automatically pick 250 colonies per plate and store them in 384 well plates (so 10 plates)
- Use the robot to perform a colony PCR on the 10 plates and obtain the 16S of each of the 3750 isolates.

Les objectifs de ce stage M2 sont :
- Calibrate the robot to avoid cross-contamination during colony PCR
- design a method using colony-PCR for high throughput screening (either based on individual tags or smart pooling of the isolates).
- Sequence the PCR products (a sequencing platform on site will make this step quick and easy)

- Analyze the sequences (we will use the DADA2 pipeline), and look for interesting microbial species (for this demo we will use the samples and the sequences from the PIGLETBIOTA project, which identifies microbes of interest in piglets at weaning).
- If the schedule allows it, we will design a multiplexing strategy for the sequencing step.

Bibliographie *:*

Lagkouvardos I, Overmann J, Clavel T. 2017. Cultured microbes represent a substantial fraction of the human and mouse gut microbiota. Gut Microbes. Sep 3;8:493–503. Epub 2017/04/19.

Sélection d'autres publications de l'équipe sur le sujet:

Effect of chronic and acute heat challenges on fecal microbiota composition, production and thermoregulation traits in growing pigs. Le Sciellour M, Zemb O, Hochu I, Riquet J, Gilbert H, Giorgi M, Billon Y, Gourdine JL, Renaudeau D.,J Anim Sci. 2019 Jul 2. pii: skz222. doi: 10.1093/jas/skz222.

Effect of dietary fiber content on nutrient digestibility and fecal microbiota composition in growing-finishing pigs. Le Sciellour M, Labussière E, Zemb O, Renaudeau D. PLoS One. 2018 Oct 24;13(10):e0206159. doi: 10.1371/journal.pone.0206159. eCollection 2018.

Ce stage peut-il se poursuivre par une thèse ? :
If the student is highly interested, we will discuss the possibilities of a PhD on the subject, potentially combined with inoculation of re-assembled microbial communities in animals.