Report on STM to Host-Microbe Interactomics Group/Wageningen University and Research, Wageningen, 14/03/2019—10/06/2019 Jinya Zhang

Thanks to the support of EPIZONE short term mission, I visited Host-Microbe Interactomics Group/Wageningen University and Research, Wageningen, Netherland during 14/03/2019—10/06/2019. I have learnt techniques in working with organoids and strict anaerobic bacteria that are routinely applied at Dr. Jerry Well's lab. I have achieved majority of my objectives (1-7 items), while some parts couldn't, due to certain circumstances explained below (item 8).

A brief description of the main tasks performed:

- 1. Establish organoid from three different tissues: ileum, colon and tonsil. I learned this technique in detail: isolating stem cell from these set of tissues, stimulate or induce proliferation to different cell types, culture organoids in 3D and 2D.
- 2. Work in strict anaerobic chamber. We cultured different bacteria isolated from warthog feces under strict anaerobic condition, to follow the growth. Anaerobic chamber facility is totally different from normal flow cabinet. And there are several things to keep in mind, to make sure no oxygen exists, neither contamination.
- 3. WST (Cell Viability & Proliferation) assay: in order to test the effect of bacteria supernatant on organoid, WST assay was conducted. We tried different concentration to select a good dilution ratio. This WST assay was done on both ileum and colon tissues.
- 4. Bioinformatic analysis: I learned how to work with CLC bench to analyse microbiota compositon from warthog feces. And do some downstream analysis with R studio: Random forest analysis, differential analysis.... It help me a lot to have a deep and more accurate understanding of bioinformatics through a gsoftware with a graphical interface.
- 5. I had the chance to attend the host-microbiome interaction class for the master supported by HMI group. It is of great interest for my thesis work the understanding on how the immune system responses to the bacteria/microbiota. I learned some ideas about how to design experiment.
- 6. Whole genome sequence of selected isolates: we sent for sequencing the whole genome of bacteria isolated from warthogs (in total 22 strains), in order to identify new species and predict the function (antivirus or antibacterial..) based on the genome. Result are ongoing.
- 7. In HMI group, there are students, technicians and professors expert in different techniques. I had the chance to interact and learnt a lot from them. For example: basic work flow for CRISPR technique, analysis with R, also the way to think and design experiment.
- 8. I was not able to finish the aims proposed in the application for the STM EPIZONE, due to a bacterial contamination in organoid culture. However, we are planning a new short stay during this same year to accomplish all the tasks proposed. Moreover, this short stay was useful for start a collaboration with this HMI group. Once the stimulation experiments are done, we will be able to perform the proposed RNA seq analysis to analyze the host response.

