Report Short-Term Mission Epizone

Florencia Correa-Fiz

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The focus of this stay was on African swine fever (ASF). This African endemic disease has high mortality in pigs. The recent spread to Asia and the European Union posed a great threat to pig industry worldwide. With vaccines still not available new efforts should be made.

In our lab (CReSA) we are interested in the potential role of the gut microbiota composition on ASF as it has been associated to resistant to many diseases. The knowledge of the response of pigs to particular commensal bacteria isolated from resistant-to-ASF African warthogs could give light on the disease, and may open new avenues to fight against ASF. The phD student Jinya Zhang (also supported by short-term mission epizone) is performing experiments to study the host response on colon and ileum pig organoids to bacterial isolated from warthog feces. The effect of host response will be evaluated by sequencing RNA from these experiments.

The main objective of this stay at Wageningen University and Research was to interact and discuss with bioinformatics experts on RNA-seq pipelines. During these two weeks, I was able to accomplish all the proposed tasks. During the first week, we made some fruitful meetings with Jerry's group to discuss about Jinya's last results in the lab. We decided the planning of the organoids experiments as the set up procedure was already accomplished. However, since the transcriptomics data was not avaiblabe yet, we had some time to share the pipelines currently used at the host lab and decide the newest software to update them. Based on several discussions with the phD students Simen Fredriksen and Bart van deer Hee, we decided to use STAR software as RNA seq aligner (Fig. 1). To achieve to this decision, we test publicly available RNA-seq datasets and estimated several parameters including performance time, which was really reduced when leaving after updating this step. Quantification of the differential expression was done with DESeq2, although HTSeq was also tested (Figure 1). Although, the analysis with the data from Jinya's experiments was not done, the pipeline was set up and will be easily implemented with the real data in the future.

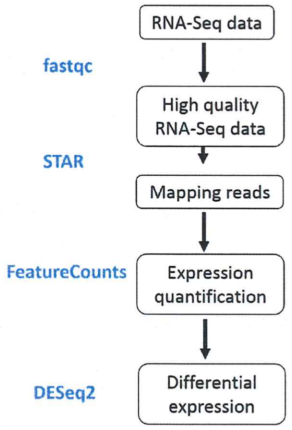

Figure 1. Description of the main steps on the RNA-seq pipeline. The software used for each step are depicted in blue.

Furthermore, I had the chance to share both metagenomics and 16s-metagenomics pipelines made in our institute with the host group, leading to very productive discussions. Moreover, during my stay I had the chance to discuss with Dr. Jerry Wells potential future collaborations regarding ASF. We elaborated a plan to check for possible grant applications.

In summary, I achieved all the proposed objectives and will certainly allow to characterize the host response through RNA-Seq by using this pipeline once the data is available. This stay has been successful and will be essential to complete Jinya's thesis work on ASFV and will be the initial point for further studies.

Florencia Correa Fiz

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building
122
Zodiac
De Elst 1
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