

## Contagious Bovine Pleuropneumonia Causative Agent: its Sequencing, Assembly and Annotation

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*Mycoplasma mycoides mycoides subsp. Small Colony* (MmmSC) is a small bacterium affecting cattle and causing the contagious bovine pleuropneumonia (CBPP), the deadliest cattle disease in Africa. This project aims at sequencing and annotating the genome of MmmSC strain Afade, one of the first *Mycoplasma mycoides* that has been directly extracted from African cattle.

The sequencing was realised with the Illumina MiSEQ 300PE technology, and a first quality control (Schmieder and Edwards, 2011) showed that although the quality of the reads and the sequence length distribution were perfect, the number of reads, as well as the duplication level, was way too high. Those being obvious signs of over sequencing, the genome assembler (Chevreux *et al.*, 1999) cannot produce any decent assembly with so many reads and an estimated coverage of 1500x. Several methods

for downsampling were tried and the assembly was done with different coverage. The best one was obtained with a coverage assessment of 100x and the downsampling was finally done with a simple shell script that discarded 80% of the reads. 106 contigs and a N50 of 22,554 were obtained. Those contigs were mapped against a reference genome (MmmSC strain Gladysdale, an Australian strain of the bacterium) and merged with a python script. The annotation work is still ongoing.

### References

- Schmieder R and Edwards R (2011) Quality control and pre-processing of metagenomic datasets. *Bioinformatics*, **27**, 863-864. <http://dx.doi.org/10.1093/bioinformatics/btr026>
- Chevreux B, Wetter T, Suhai S (1999) Genome Sequence Assembly Using Trace Signals and Additional Sequence Information. *Computer Science and Biology: Proceedings of the German Conference on Bioinformatics (GCB)* **99**, 45-56.