



## **Genome assembly of the fungus *Leucoagaricus gongylophorus* cultivated by the ant *Atta colombica* using long-read MinION sequences**

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Assembling heterogenous (two very different sets of chromosomes) or polyploid (more than two sets of chromosomes) genomes can be challenging, but in a fast-developing world, new techniques and software are regularly developed. Leaf-cutting ants cultivate a polyploid fungus with an average of 7 different genomes which has proven to be difficult to assemble using regular short-read genome sequencing. In this study, I used the Oxford Nanopore Technologies MinION to produce long-read sequences of *Leucoagaricus gongylophorus* cultivated by the ant *Atta colombica*. I then used a series of different software packages to assemble genomes from long-read sequences (CANU and Nanopolish) as well as software to deal with heterogeneous and polyploid species (Redundans). The quality of the assemblies was tested by extracting a core set of single-copy genes using BUSCO. With this, I developed a pipeline to assemble fungal genomes accurately using long-read sequences. The resulting genome assembly is an improvement of the one currently available and gives new insights into this intriguing mutualism between ants and fungi. Furthermore, I was able to fully assemble the fungal mitochondrial genome with a high coverage ( $\pm 4000X$ ), which can be used to both understand the mechanistic of this fungus, but which can also be used for more accurate phylogenetic analyses. In conclusion, I was able to show cost-efficient methods and a pipeline to accurately assemble fungal genomes, that can be used for a wide variety of analyses.