

The aim of this manuscript was to create a high-quality reference genome for the *Coccomyxa viridis* SAG 216-4 strain. The genome is a valuable resource for future studies on this ecologically widespread and versatile fungal lineage.

The analyses performed by the authors are of a high standard. However, I am missing a context as to why this data should be published as a scientific article rather than as a genome report. Except for the synteny graphs, all the data shown by the authors will be available upon their release on ENA.

The authors mentioned at lines 55-57 that "Coccomyxa and a genome sequence is available only for a single Coccomyxa species, namely Coccomyxa subellipsoidea C-169, which was isolated in Antarctica where it occurred on dried algal peat (Blanc et al., 2012)." However, I found seven Coccomyxa genomes on NCBI and two more on ENA. I consider that all these genomes should be taken into account and, in my opinion, even included in the analyses. This is because the authors already compared their strain with *Coccomyxa subellipsoidea* C-169. Given that more genomes are available, the authors should either include these additional genomes in their analyses or provide a new rationale for focusing solely on the comparison with *C. subellipsoidea* C-169.

Furthermore, since the comparison between strains was already initiated, I recommend conducting additional comparative analyses to match those performed for their strain, such as GC content, genome size, genome completeness, and the number of genes (as shown in Table 2). Does *C. subellipsoidea* C-169 also have signal proteins? Is the genome contaminated, etc.

If the authors decide to consider all the strains from ENA and NCBI, I suggest they also create a phylogeny using the Busco genes.

Furthermore, I would like the authors to address a few minor details:

1) Early diverging" is an incorrect term to refer to sister clades. While it is commonly used, the term inaccurately implies that these lineages evolved earlier than their sister groups. In reality, all extant lineages have evolved over the same amount of time, and no lineage is older than another. For a more detailed explanation, I recommend reading this blog post: [The Ancestors Are Not Among Us](#).

2) Lines 182-184: 'All software and tools used for the genome assembly and annotation are summarized in Table 1'  
This should be a supplementary table and the genome stats should be the Table 1.

3) 239-240 'BLAST analyses of six identified ITS sequences in the *C. viridis* SAG 216-4 assembly confirmed its species identity.  
I am curious if all ITS copies were identical. This is interesting to know and be documented.

4) About the KAT plots: Based on the KAT graph shape I see that the genome is haploid. Maybe is good to say this in the manuscript but also do KAT plots on the other genome/genomes.