Analysis of the temporal evolution of the infection by pathogenic fungis in plants. A new approach to *Verticillium* wilt of olive tree

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1. Introduction

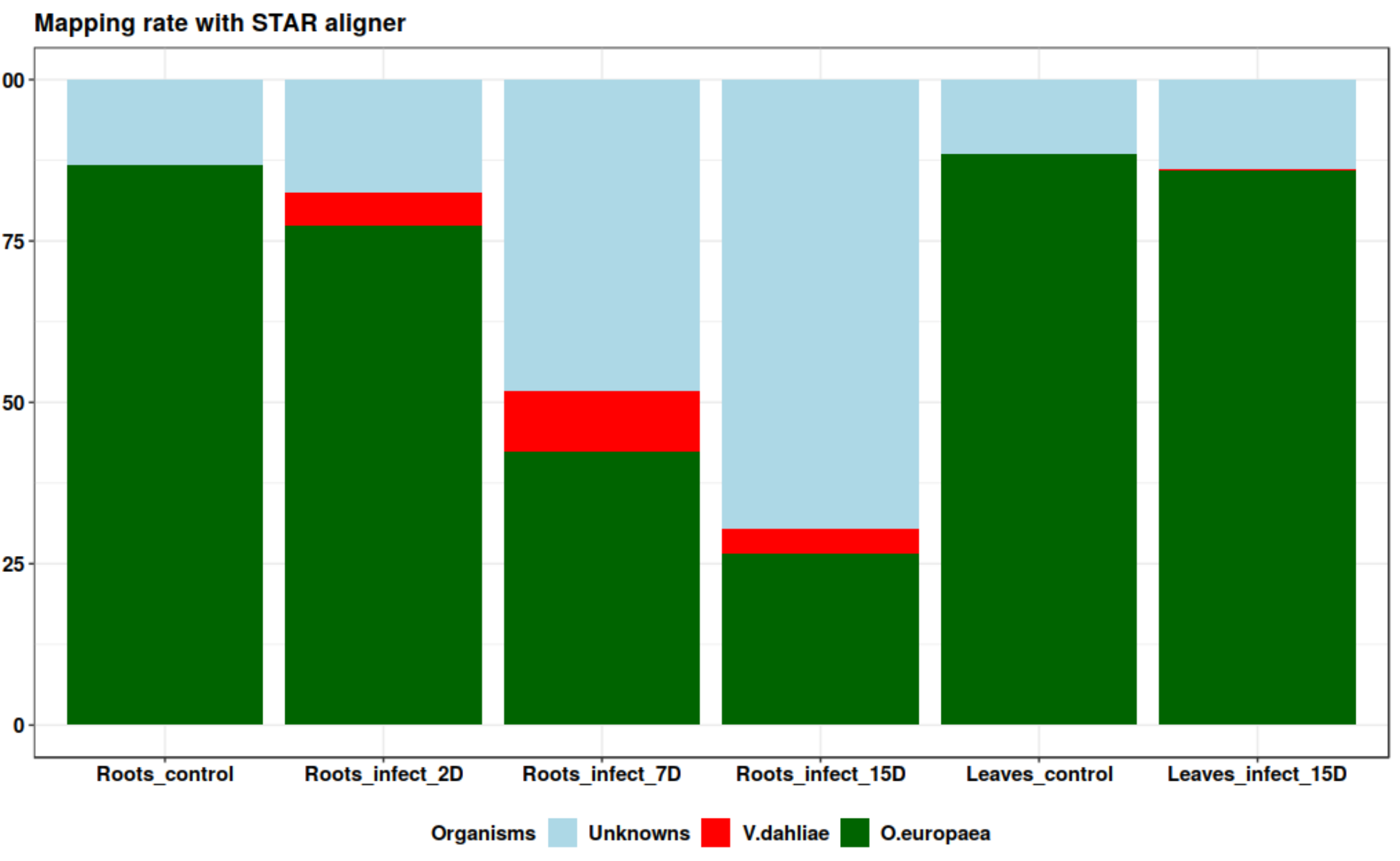
Most *omic* studies on pathogen-host interaction in plants mainly focus on the host and in the infectious agent, which is considered as the main factor in the infectious process. This approach hiddes the role of the great variety of microorganisms in environments as diverse as soils. With the development of metagenomics, new approaches have been explored. We have performed a robust classification using all available sequences to include the whole microbiome. Starting from public time series data of RNA-sequences of olive tree infected by *Verticillium dahliae* [1], we have analyzed the dynamic of the infection process as an integrated system.

2. *Verticillium* wilt

V. dahliae is a pathogenic fungus causing a severe wilt and many crops losses, including the olive tree present in Andalusia and the Mediterranean basin. At present, there is no effective treatment capable of reducing the impact and extent of these infections and, for this reason, many efforts are conducted to reveal the molecular bases of the infection and the resistance.

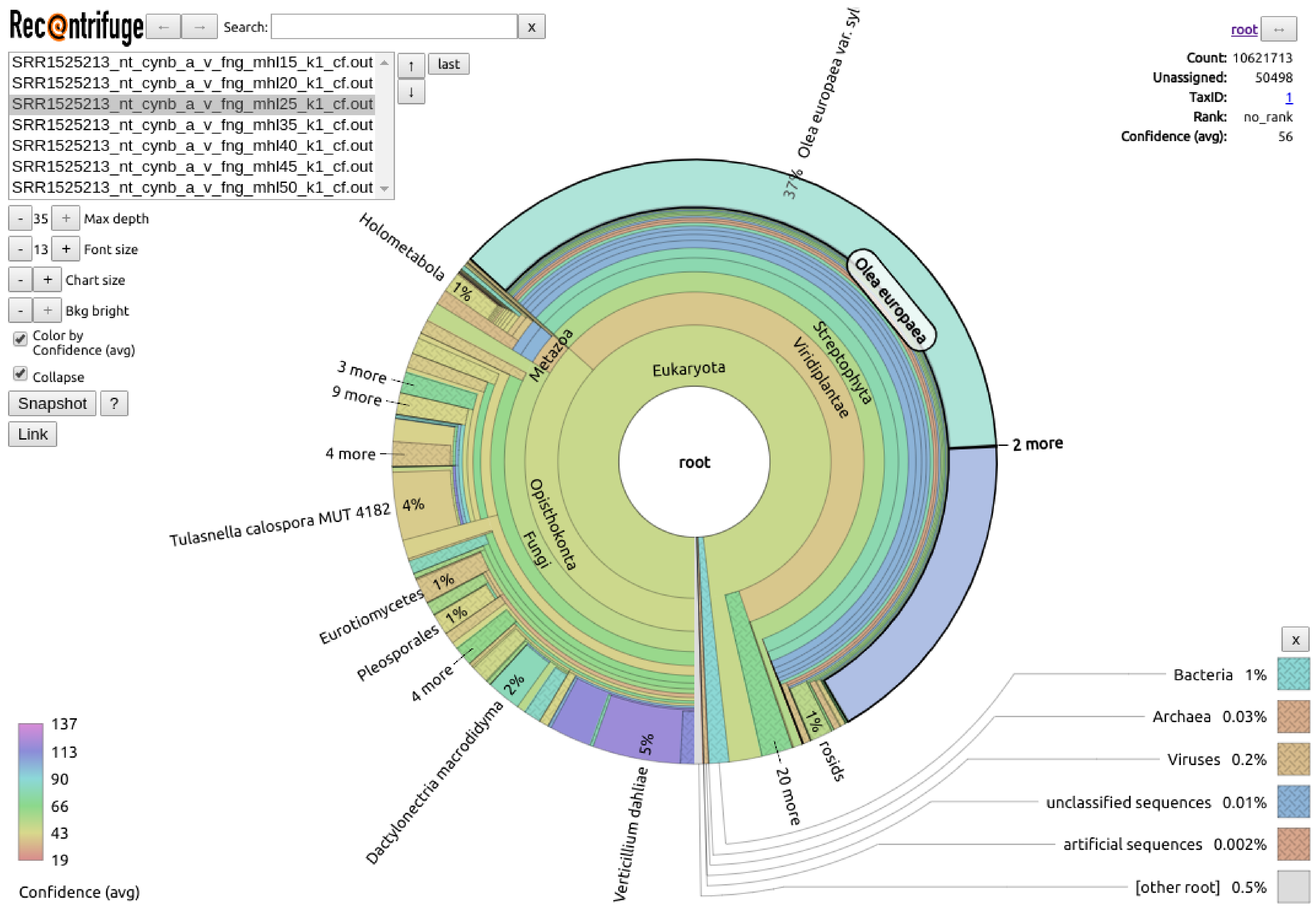
3. Alignment to a reference

In a classic RNA-seq pipeline one of the main steps is the alignment/mapping of reads to a reference. In our case, as the infection progresses, the mapping rate to our reference genomes, olive tree and *V. dahliae*, decreases considerably. This suggests carrying out the analysis from a metagenomic approach, what may help to uncover the dynamics of this complex system.



4. Meta-transcriptomic classification results

RNA-seq classification at each stage of the infection was carried out by **Centrifuge** [2] software using a massive database generated from NCBI nt and WGS [3]. The results were analyzed by **Recentrifuge** [4], a new metagenomic interactive tool which allows comparative analysis of multiple samples.



SRR1525213_nt_cynb_a_v_fng_mhl15_k1_cf.out
SRR1525213_nt_cynb_a_v_fng_mhl20_k1_cf.out
SRR1525213_nt_cynb_a_v_fng_mhl25_k1_cf.out
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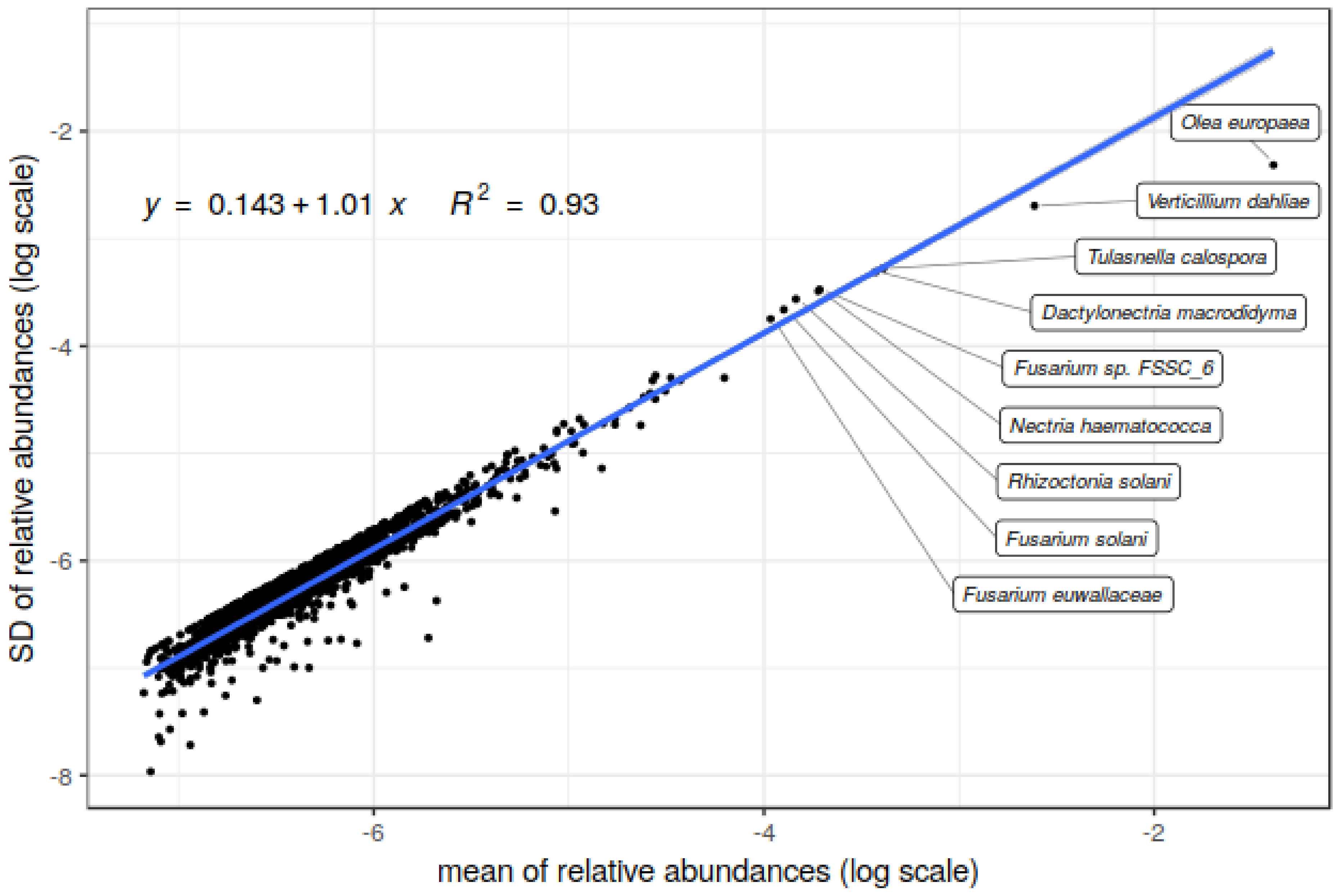
35 Max depth
13 Font size
☑ Color by Confidence (avg)
☑ Collapse

Count: 10621713
Unassigned: 50498
TaxID: 1
Rank: no_rank
Confidence (avg): 56

5. Taylor's Law and stability

Based on studies of microbial temporal variability [5], we have studied the relative variability of the mean abundance of each classified taxon at the species level to understand the stability of the community. This approach gives us an idea of the most abundant species and those that most change in the system over time.



6. Conclusions

1. Our metagemomic study of the infection as a system allows us to include a larger number of "lost" reads than in a classic study of RNA-seq.
2. We reconsider the role of the main pathogen, in this case *V.dahliae*, and the mechanism of infection by including the other opportunistic agents.
3. We plan to study host-pathogen interactions during the infection as a dynamic complex system.

7. References

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