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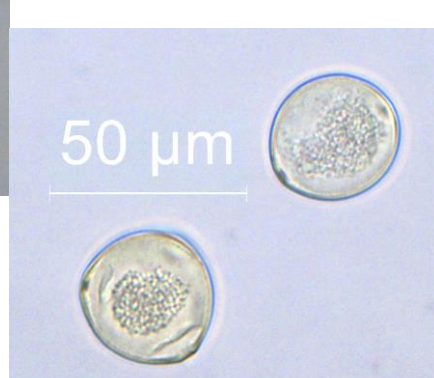
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Pollination is a vital process in the reproduction of most spermatophytes and requires the transfer of pollen to the plant carpel, which contains the ovule, so the fertilisation can occur. In this process, it is well known that many insects can be vectors for plant viruses by contamination of pollen with these pathogens when feeding, while there are a few reports of fungi associated with pollen. For example, pathogenic fungus can be spread with pollen, as it has been reported for *Citrus sinensis* pollen that may, in fact, play a role in the spread of the pathogen *Colletotrichum acutatum* in citrus orchards (Marques et al. 2013).

In order to understand whether fungi causal agents of rotten hazelnut can be transmitted via pollen, the fungal populations present on hazelnut pollen were analysed by metabarcoding.

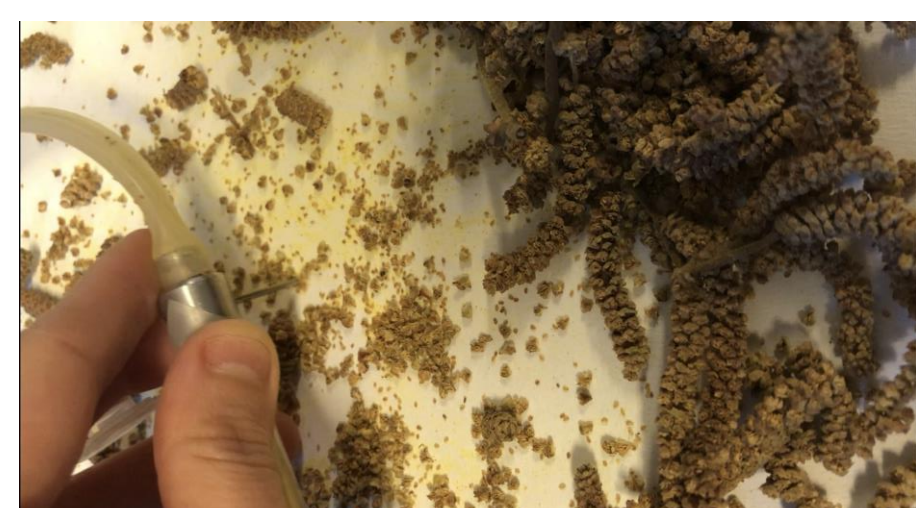


Hazelnut pollen



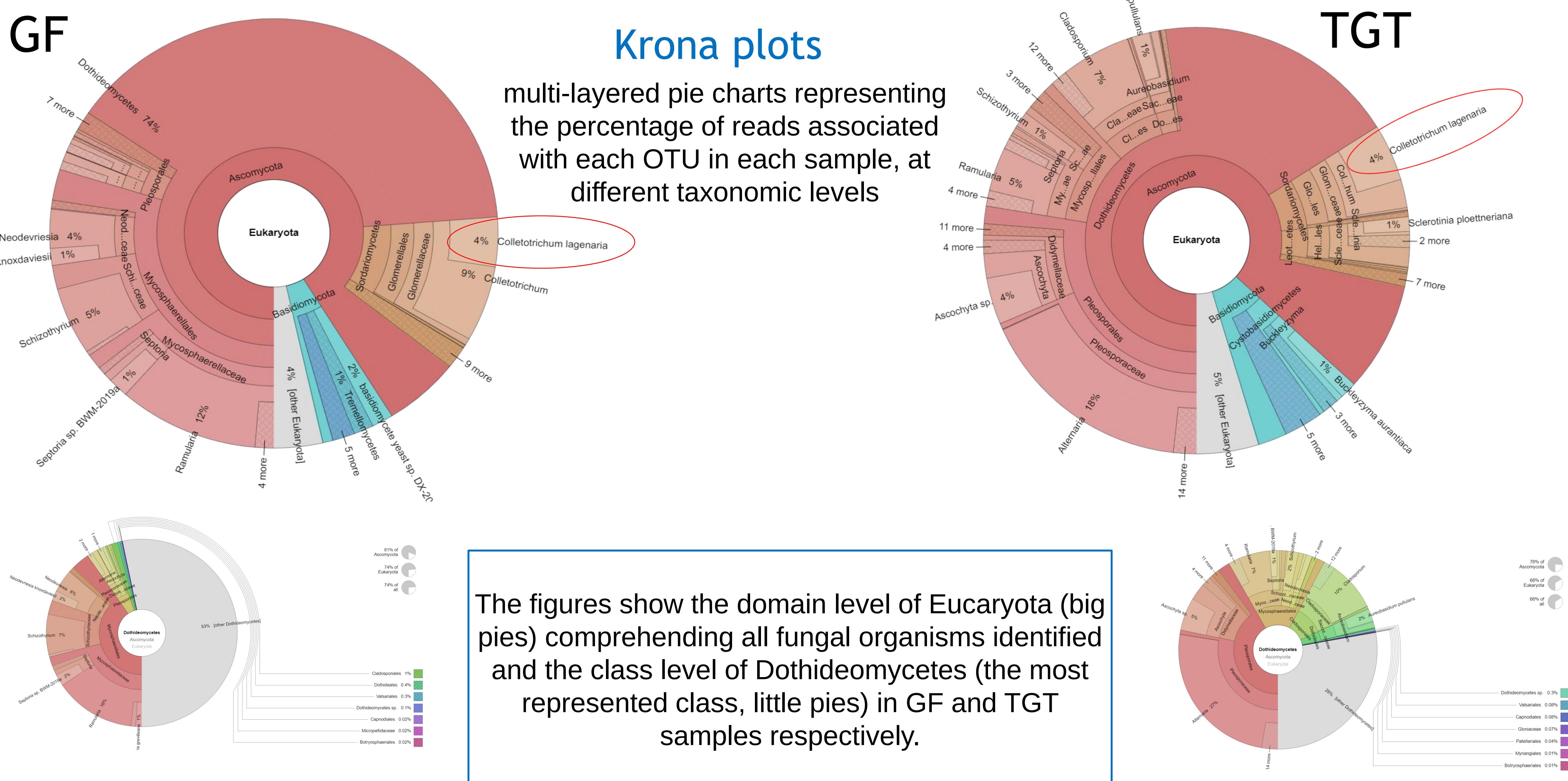
RESULTS

Pollen collected for DNA extraction



To this aim, DNA was extracted from microorganisms present on pollen of two commercial hazelnut “Tonda Gentile Trilobata” (TGT) and “Tonda di Giffoni” (GF) in a Piedmont orchard. A mild extraction was performed to avoid pollen breakage and plant DNA extraction.

Metabarcoding was performed by amplification of the fungal Internal Transcribed Spacer (ITS) region of rDNA followed by short-reads Illumina sequencing. Results are shown in Krona plots.



Preliminary analysis shows a high number of fungal microorganisms, many of which potential phytopathogens. The most represented species is *Colletotrichum lagenaria* (red circle) in both GF and TGT, but also other phytopathogenic species are present, as *Fusarium* sp. including *F. lateritium*, *Alternaria* sp. (especially in TGT), *Cladosporium* sp., *Ramularia* sp., in addition to different epiphyte/saprophyte fungi.