

CONTRIBUTION TO THE KNOWLEDGE OF THE DIVERSITY OF ECTOMYCORRHIZAL FUNGI OF NATIVE FORESTS OF URUGUAY



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- The ectomycorrhizal fungi (ECM) of Uruguay have been relatively little studied and most of the knowledge about them comes from studies on cultivated exetic species.
- A total of 8683 OTUs belonging to Kingdom Fungi were obtained by ITS (ITS1F primer) sequencing.

them comes from studies on cultivated exotic species, such as the commercial *Eucalyptus* and *Pinus* spp., and other ornamental species.

- The native forests of Uruguay occupy approximately 5% of the country's surface and have a diversity of more than 200 species of trees and shrubs. Some of these species belong to families reported as hosts of ECM fungi.
- The objective of this work is to make an approximation to the diversity of ECM fungi in native riparian forests in different geographical areas of Uruguay.



- In total, 3824 sequences were assigned to 167 OTUs from 20 ECM fungal lineages using FunGuild.
- The most represented lineages, according to the number of OTUs, were: /entoloma (37), /cantharellus (18), /cortinarius (18), /tomentella-telephora (17), /boletus (13), /sebacina (11), /inocybe (10), and /ramaria (9) (Fig. 2).
- Other common lineages, such as /amanita, /clavulina, /hebeloma, /hysterangium, /laccaria, /russula-lactarius /tomentellopsis, and /tulasnella, were observed.
- The /cantharellus and /cortinarius lineages are cited for the first time for the Uruguay, and for /entoloma and /cantharellus some OTUs may not be ECM fungi.
- 61% (102/167) of the OTUs could not be assigned to species and some are doubtful.

Figure 1. The localization of the 35 sampled sites in native riparian forests.





Figure 2. Number of OTUs obtained by lineage of ECM fungi.

 Soil sampling was carried out in 35 riparian forests from all geographical areas of the country to make an approximation to the diversity of ECM fungi in native forests of Uruguay (Fig. 1).

- For each sample, DNA was extracted from 1g of soil (PowerSoil kit) and a metagenomic study was carried out by sequencing the ITS gene using PacBio.
- For each of the total OTUs (8683) belonging to Kingdom Fungi the functional group was determined using FunGuild.

CONCLUSIONS

Despite the small number of samples studied and that no ECM-directed sampling was done, many species assignable to ECM lineages were found. Work is currently being carried out to refine the identification of species present and associate the diversity found with physico-chemical and plant-diversity characteristics of the forests.