

CONTEXT AND GOALS

Lignicolous Marine Fungi are defined as those able to obtain energy, organic matter and physical support from colonizing wood. These fungi are the main wood decomposers in salt marshes, mangroves, and estuaries, therefore an important member of the marine ecologic mechanisms.

They are sought and exploited for their **biotechnological potential**, due to the production of bioproducts with applications in various industries such as pharmaceuticals, food, agriculture, among others.

Despite their importance and potential, their diversity is still **poorly known**, especially in Portuguese ecosystems.

Novel and **uncharacterized** species may express relevant biological activities, not yet known.

The main objective of this study was:

Identify and isolate lignicolous marine fungi from Portugal;



RESULTS

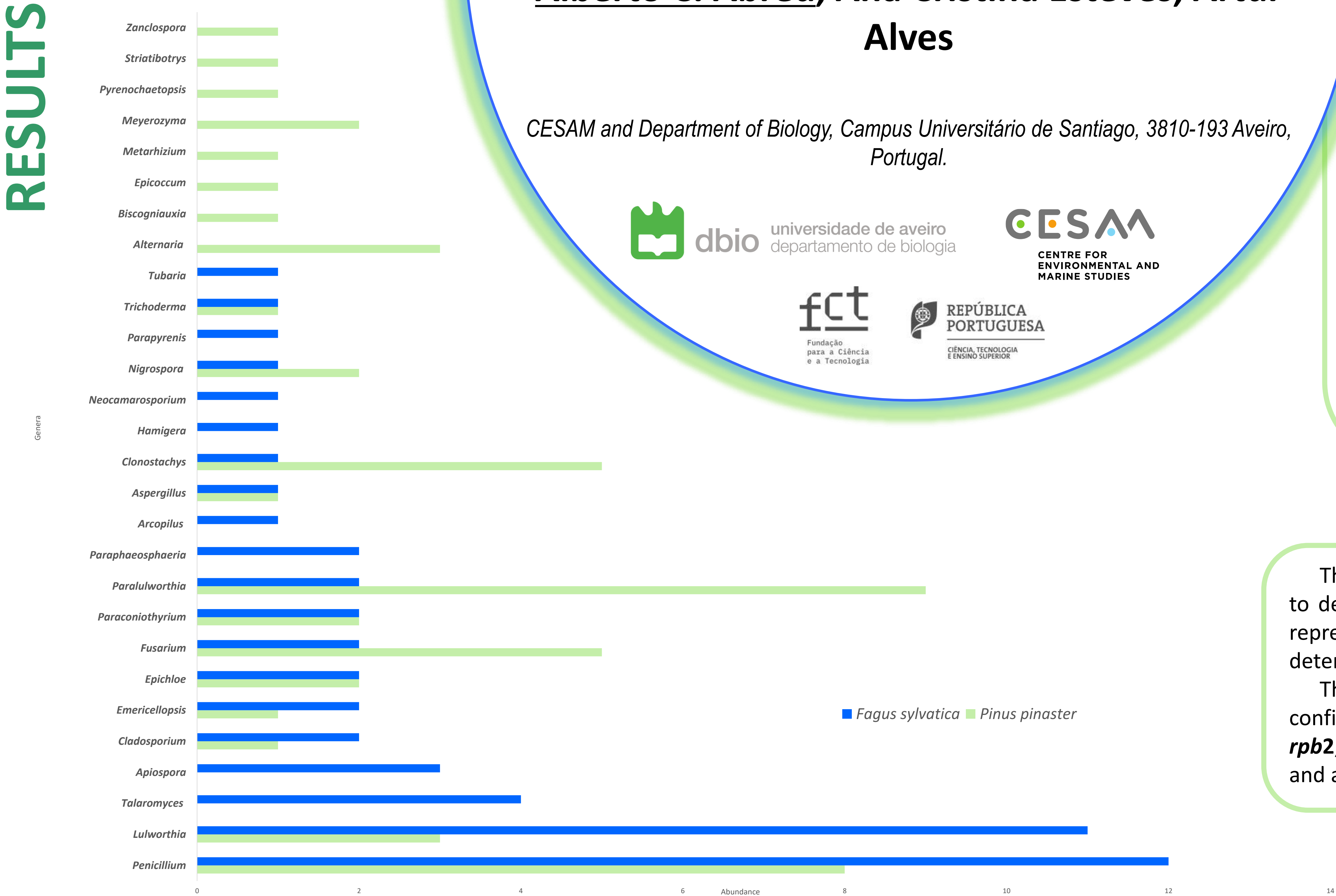


Figure 1 – Grouped bars chart of the representative isolates from *Fagus sylvatica* and *Pinus pinaster* woodbaits ordered by genus abundance.

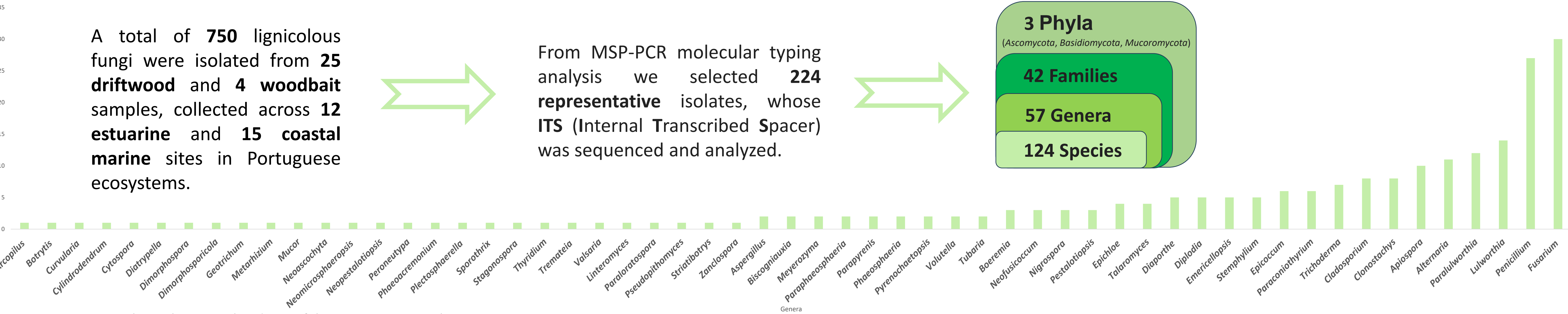


Figure 2 - Graphic with genera abundance of the representative isolates

FINAL REMARKS

The predominant lignicolous genus was ***Fusarium*** genus, representing **13%** of all species identified. But the most frequent species isolated was ***Lulworthia atlantica*** (6.25%), a common lignicolous marine fungus.

Around 31% of the isolates identified may represent **undescribed fungal taxa**. This result confirms that lignicolous marine fungi are an under explored group and these ecosystems conceal a large unknown diversity.

The high variety of species may be explained by the diversification of sampling sites, both coastal marine and estuarine, as well as the different wood substrates associated with different fungal communities.



- 1 DNA Extraction
- 2 MSP-PCR with primer (GTG)5 and analysis of the Genetic Fingerprinting patterns
- 3 PCR amplification of the ITS region of fungal rRNA gene cluster
- 4 Sanger Sequencing
- 5 Taxonomic Affiliation

METHODS

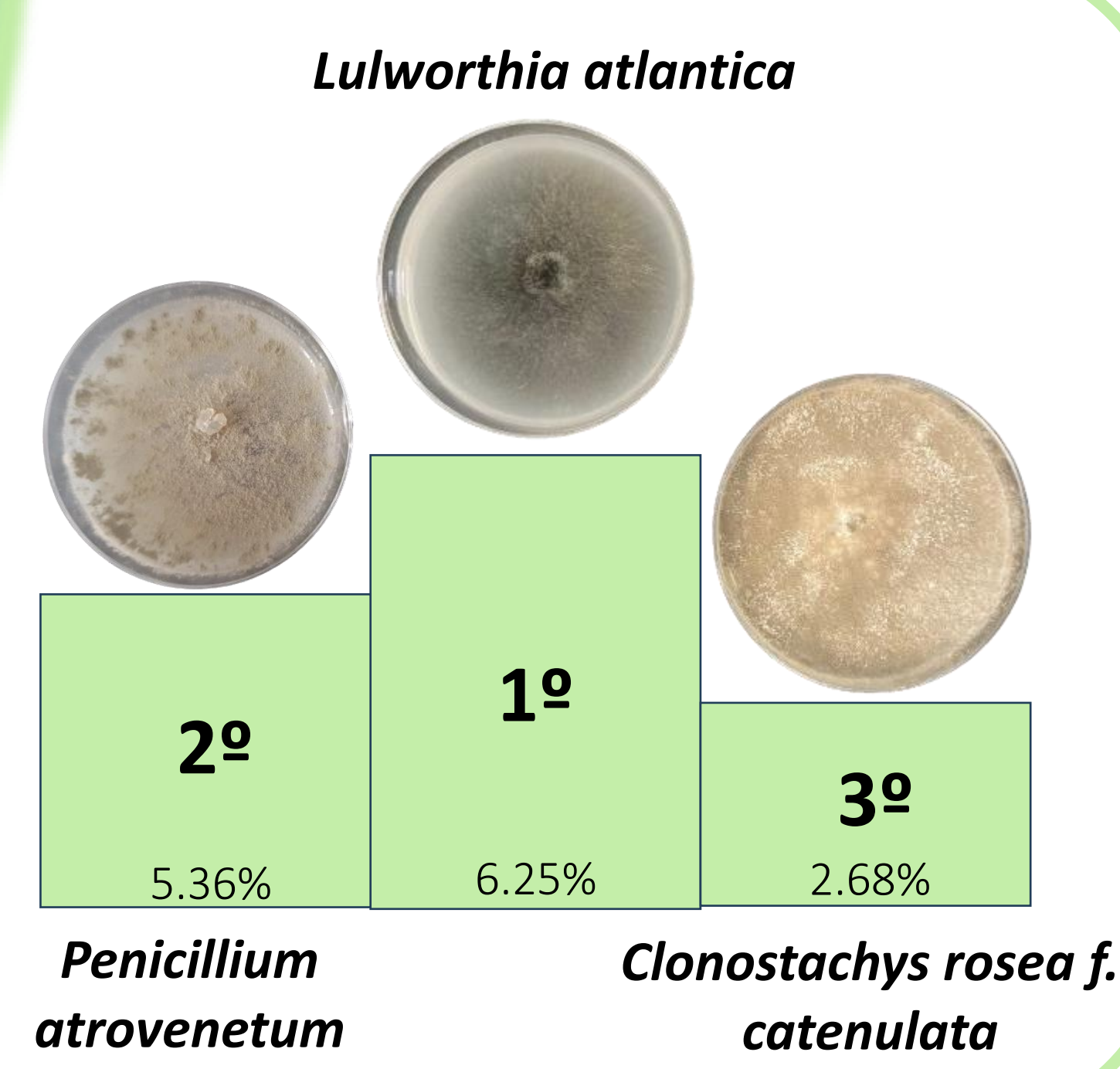


Figure 3 – The three most abundant isolated species.

The analysis of the **ITS** region alone did not allow to determine the species identity of **70** of the **224** representative isolates. It was only possible to determine its genus.

These isolates may represent novel species. To confirm this, secondary barcodes such as ***tub2***, ***tef1***, ***rpb2***, ***act***, ***cal***, ***his*** and ***gapdh*** are being sequenced and analyzed.