



Introduction

Microorganisms found in the marine deep subsurface serve as model organisms to gain insights into survivability and the limits of life. Within these environments there is a lack of knowledge about the extent and diversity of fungal populations in subsurface environments.

The Mariana forearc is characterized by mud volcanoes that are undergoing active serpentinization, a water rock reaction leading to the episodic release of ultra high pH fluids that are considered inhospitable to most microorganisms. These volcanoes play an important role in the cycling of volatiles and other elements between the surface, deep lithosphere, and mantle. Understanding the fungal community that is found in this system can provide insight into how fungi interact with carbon in serpentinizing systems and subduction zones through their potential to breakdown refractory carbon, the biomineralization of carbonate minerals, and the input of necromass to the total carbon pool.

Objective

Objective: Understand the roles of fungi on biogeochemical cycling in high pH crustal fluids of the Mariana forearc serpentinite mud volcanoes utilizing culture-dependent methods

Functional Annotations

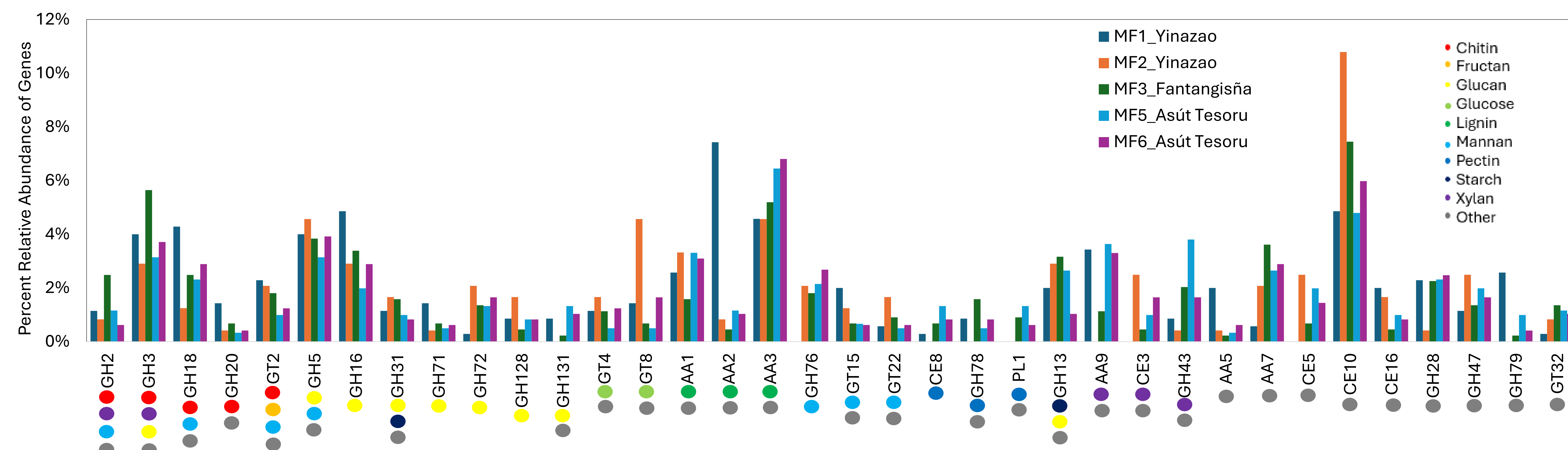


Figure 3. Functional annotation of the most abundant Carbohydrate-Active Enzyme (CAZyme) families and their substrates. Only the families representing a relative abundance of 1.25% or greater for at least one of the five isolates are included. AA: auxiliary activities, CE: carbohydrate esterases, GH: glycoside hydrolases, GT: glycosyl transferases.

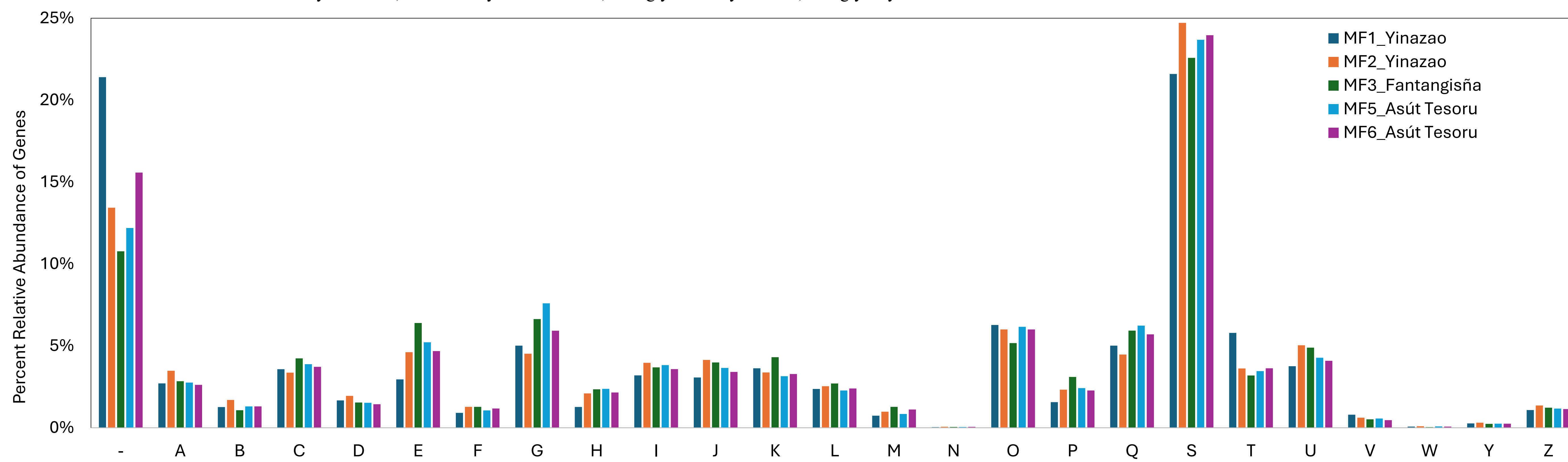


Figure 4. Functional annotation with Clusters of Orthologous Genes (COG) Categories: (-) COG not assigned, (A) RNA processing and modification, (B) Chromatin structure and dynamics, (C) Energy production and conversion, (D) Cell cycle control, cell division, chromosome partitioning, (E) Amino acid transport and metabolism, (F) Nucleotide transport and metabolism, (G) Carbohydrate transport and metabolism, (H) Coenzyme transport and metabolism, (I) Lipid transport and metabolism, (J) Translation, ribosomal structure and biogenesis, (K) Transcription, (L) Replication, recombination and repair, (M) Cell wall/membrane/envelope biogenesis, (N) Cell motility, (O) Posttranslational modification, protein turnover, chaperones, (P) Inorganic ion transport and metabolism, (Q) Secondary metabolites biosynthesis, transport and catabolism, (S) Function unknown, (T) Signal transduction mechanisms, (U) Intracellular trafficking, secretion, and vesicular transport, (V) Defense mechanisms, (W) Extracellular structures, (Y) Nuclear structure, (Z) Cytoskeleton.

Study Site

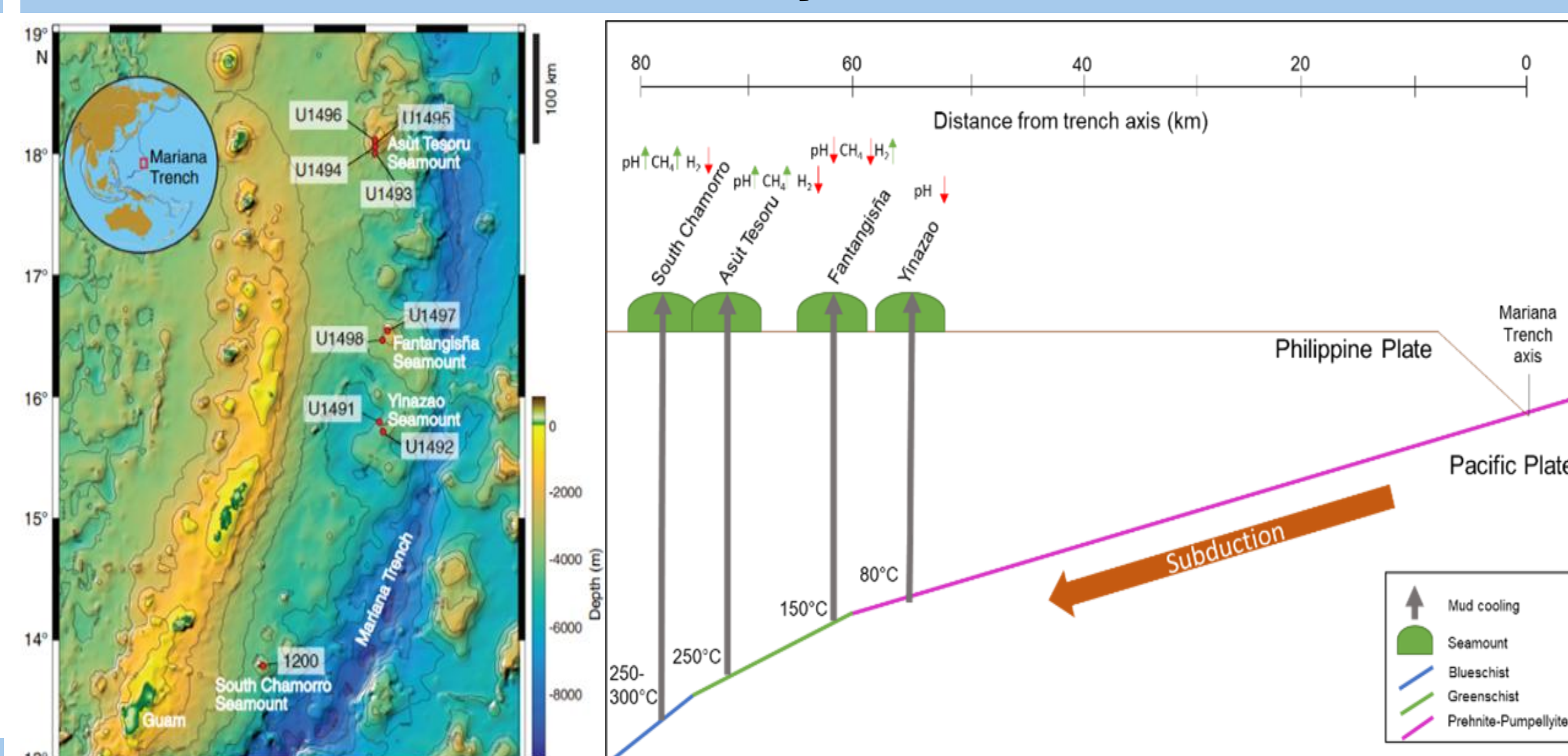


Figure 1. A) Map of IODP Expedition 366 four serpentinite mud volcanoes on the Mariana Forearc. From Fryer et al. 2018¹. B) Cross section schematic of the Mariana Forearc system depicting geology of the subducting plate, distance to the trench and water. Modified from Fryer, 2012².

Methods

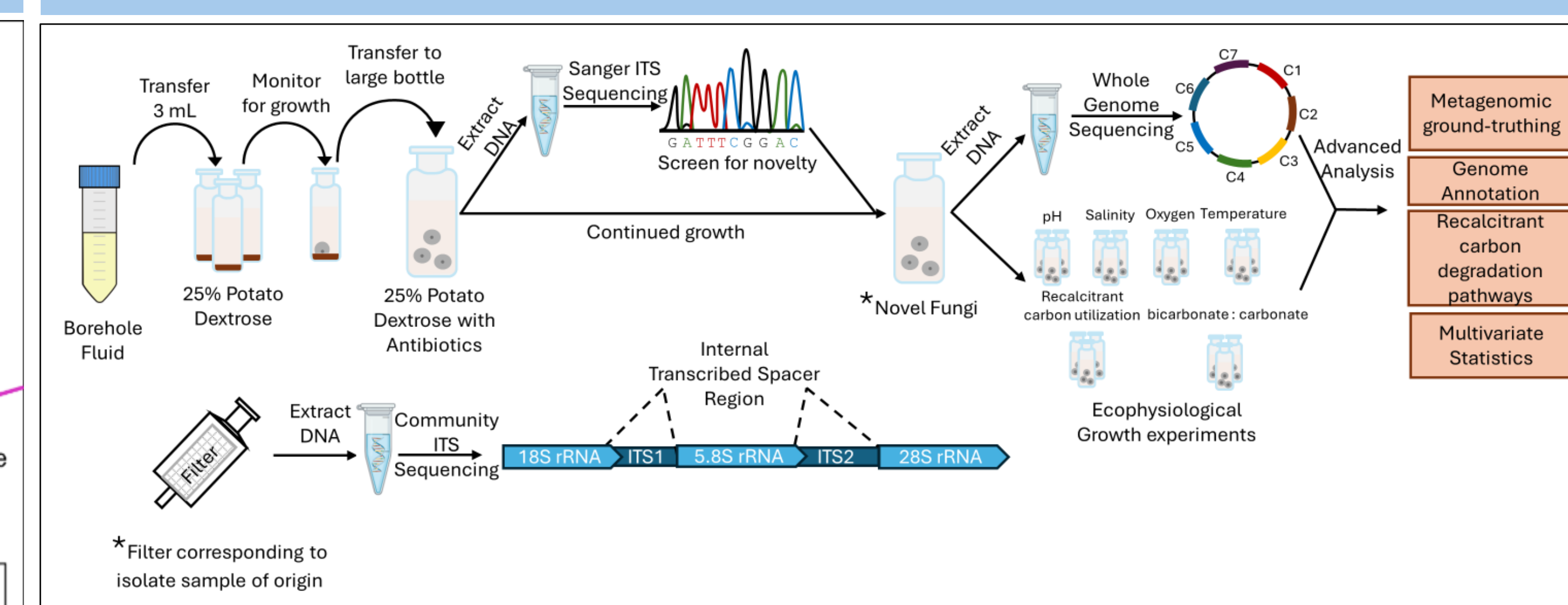


Figure 2. Workflow of sample analysis.

Fungal Imaging

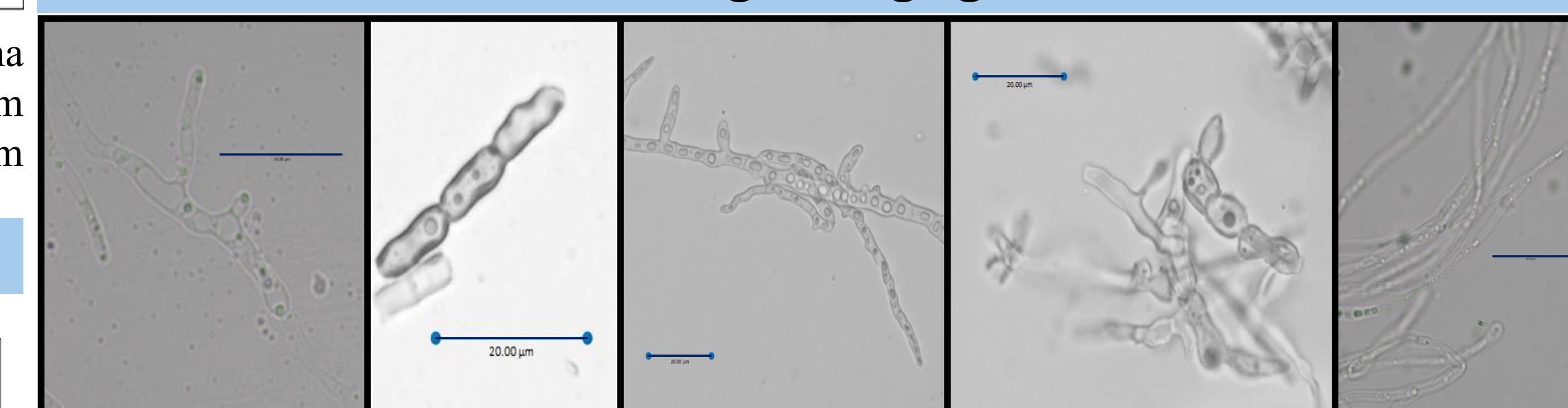


Figure 5. Microscope images of fungal isolates. The blue scale bar in each photo is 20.00µm. A) MF1 B) MF2 C) MF3 D) MF5 E) MF6

Discussion

- MF1 is most closely related to *Trametes versicolor*, found in terrestrial soils and plants, but has also been found in marine sediments³
- MF2 is most closely related to *Stromiopsis sp.*, found as a saprobe on *Harpephyllum sp.* in China, and *Phyllanthus emblica* in Thailand⁴ and *Mangifera indica L.* in Japan⁵
- MF3 is most closely related to *Cladosporium sp.*, found in soils, but have also been found in marine water and sediments³
- MF5 is most closely related to *Gnomoniopsis sp.*, found in terrestrially in leaf litter and plants⁶
- MF6 is most closely related to *Incrucipulum capitatum*, found in leaf litter in Japan⁷
- CAZyme genes of highest relative abundance were related to degradation of chitin, glucan, lignin, and xylan.
- Genes related to pectin degradation were common among all isolates except for MF2
- After unknown and unassigned genes, transport and metabolic COG categories have the highest percent relative gene abundance (E, G, O, Q)
- Lowest relative gene abundance are in motility (N), nuclear structure (Y), and extracellular structures (W).
- Kyoto Encyclopedia of Genes and Genomes (KEGG) database annotation showed genes related to aromatic hydrocarbon degradation

Next Steps

- Ecophysiological testing of isolates under different conditions (e.g., temperature, salinity, pH, light, oxygen, carbon availability)
- Functional annotation (e.g., metabolic pathways, and their relationship to biogeochemical cycling; stress response genes for survival strategies)

Acknowledgements and References

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