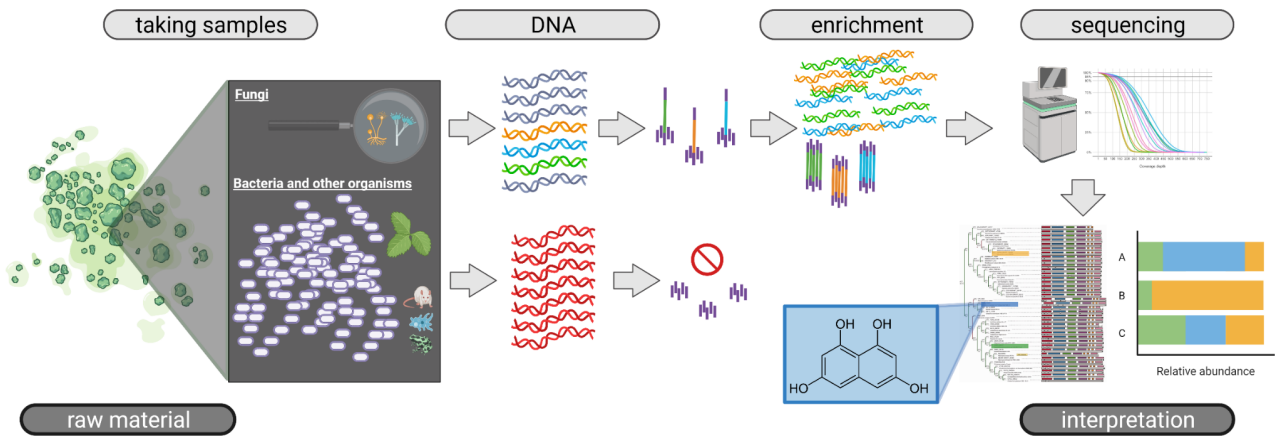


RICHFUN - enrichment and decoding of fungal biosynthetic clusters in low-abundant, plant-associated mycobionmes



Plants share space with multiple other organisms, many of them being unseen with the naked eye (microorganisms). Fungi can be present in much smaller volumes compared to bacteria, but their impact on the environment can still be crucial. Often silent, sometimes beneficial, sometimes harmful - the microscopic fungi produce many substances in order to survive.

Our project focuses on investigating environmental traces of what allows fungi to produce these compounds. Through molecular biology methods - hybridisation-based enrichment and next generation sequencing of DNA sampled from the environment - we want to investigate the presence and frequency of small parts of mycobionme (i.e. all environmental fungi) in detail. These sequences, the BGCs (biosynthetic gene clusters) are responsible for distinct substances individual fungi produce. As the produced substances are tied to the ancestral history (phylogeny) of BGC sequences, by comparing new sequences to parts of already known fungal BGCs, we will be able to predict what might be produced (biosynthetic potential). Hopefully, we will also be able to measure how frequently different producer variants occur in nature (relative abundance).

* figure created with BioRender