

Genomic Strategies Supporting Fungal Life in Acidic Mine Drainage Ecosystems

Helena Duarte*

Department of Environmental Mycological Genomics, University of Porto, Porto, Portugal

DESCRIPTION

Acidic mine drainage ecosystems arise from the exposure of sulfide minerals to oxygen and water, resulting in the production of sulfuric acid and the release of dissolved metals into surrounding environments. These habitats are characterized by extremely low potential of Hydrogen (pH) values, often ranging below pH 3, along with high concentrations of iron, aluminum, manganese, cadmium, and other toxic metals. Despite these harsh chemical conditions, diverse fungal communities persist in mine tailings, drainage channels, and contaminated sediments. Genomic investigations have revealed specialized molecular adaptations that enable fungal survival and activity in highly acidic and metal-rich environments.

One of the primary challenges in acidic mine drainage systems is proton toxicity. Excess hydrogen ions can disrupt intracellular pH balance, damage cellular structures, and impair enzyme function. Fungal genomes from these environments show enrichment of genes associated with proton transport and intracellular pH regulation. Membrane-bound Adenosine Triphosphate (ATP)-driven proton pumps play a central role in maintaining cytoplasmic stability by actively exporting excess protons from the cell.

Ion transport systems are highly developed in acid-adapted fungi. These organisms often possess expanded families of membrane transport proteins that regulate the movement of metal ions and other charged particles. Genomic analyses reveal increased representation of cation efflux transporters, which help reduce intracellular accumulation of toxic metals. Such systems are essential for maintaining cellular homeostasis in environments with extreme geochemical composition. Metal detoxification mechanisms are another key genomic feature. Acid mine drainage environments contain high concentrations of soluble metals that become more bioavailable under low pH conditions. Fungal species inhabiting these habitats frequently exhibit genes encoding metal-binding proteins capable of sequestering toxic ions. These proteins reduce chemical reactivity and prevent interference with essential cellular processes.

Oxidative stress is a major secondary effect of metal exposure. Transition metals can catalyze the production of reactive oxygen

species, leading to damage of proteins, lipids, and nucleic acids. Genomic studies show enrichment of antioxidant defense systems in acid-tolerant fungi. These include enzymes such as catalases, peroxidases, and superoxide dismutases, which collectively mitigate oxidative damage and support cellular survival under chemically reactive conditions. Cell wall composition plays a critical role in adaptation to acidic environments. The fungal cell wall acts as the first line of defense against external chemical stress. Genomic analyses indicate modifications in genes responsible for polysaccharide synthesis and cell wall remodeling. These adaptations may enhance binding of metal ions to the cell surface, reducing their penetration into the cytoplasm.

Biofilm formation is commonly observed in acidic mine drainage habitats. Fungal communities often grow as structured biofilms on rock surfaces, sediments, and mining infrastructure. Genomic data reveal genes associated with adhesion, extracellular matrix production, and community organization. Biofilms provide physical protection and facilitate nutrient exchange within microbial communities. Metabolic flexibility is essential for survival in nutrient-limited acidic systems. Organic carbon availability is often restricted, requiring fungi to utilize a wide range of substrates. Genomic studies reveal enzymes capable of degrading plant-derived compounds, microbial biomass, and industrial organic residues. Some fungi also exhibit metabolic pathways that allow utilization of dissolved organic molecules present in mine waters.

Iron metabolism is particularly significant in these ecosystems. Iron is abundant in acidic mine drainage and exists in both reduced and oxidized forms. Fungal genomes show the presence of genes involved in iron uptake, storage, and redox transformation. These systems allow fungi to regulate iron levels and potentially participate in biogeochemical cycling within contaminated environments. Population genomic studies indicate that fungal communities in acidic mine drainage systems are often highly specialized and genetically distinct from those in nearby uncontaminated environments. Strong selective pressure leads to the dominance of acid-tolerant lineages with specific genetic adaptations. Genome-wide analyses reveal signatures of selection acting on genes related to metal

Correspondence to: Helena Duarte, Department of Environmental Mycological Genomics, University of Porto, Porto, Portugal, E-mail: helena.duarte.acidfungi@up-pt.edu

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resistance, stress response, and membrane transport. Horizontal gene transfer has been identified as a potential contributor to adaptation in acidic mine drainage fungi. Genetic exchange with bacteria and other microorganisms may introduce novel metabolic capabilities, particularly those related to metal resistance and chemical transformation. Although relatively infrequent, such events may play a role in accelerating evolutionary adaptation in extreme environments.

Microbial interactions in acidic mine drainage ecosystems are highly dynamic. Fungi coexist with acidophilic bacteria and archaea that participate in sulfur and iron cycling. Genomic analyses indicate that fungi possess genes involved in interspecies interaction, signaling, and nutrient exchange. These relationships contribute to ecosystem stability and influence geochemical processes. Long-read sequencing technologies have improved the resolution of fungal genomes from contaminated

environments. These methods allow accurate assembly of repetitive regions and structural variations that are often associated with stress adaptation. Improved genomic resolution has revealed previously unrecognized genetic diversity within acid-tolerant fungal populations.

CONCLUSION

Overall, fungi inhabiting acidic mine drainage ecosystems demonstrate a wide range of genomic adaptations that enable survival under extreme chemical stress. Their genetic systems reflect long-term evolution in environments characterized by low pH, high metal concentrations, and limited nutrient availability. Continued genomic research will further clarify the biological mechanisms that support fungal persistence in these highly acidic environments and their role in ecosystem transformation.