

# Genomic Adaptation of Fungi in Seagrass Meadow Sediment Ecosystems

Sofia Almeida\*

Department of Coastal Microbial Genomics, University of Algarve, Faro, Portugal

## DESCRIPTION

Seagrass meadow ecosystems represent highly productive coastal environments that provide habitat stability, nutrient cycling functions, and sediment stabilization in shallow marine waters. Beneath the dense vegetation of seagrass species, sediments accumulate organic matter derived from plant detritus, marine organisms, and suspended particulates. These sediments form chemically active zones where microbial life thrives under fluctuating oxygen availability, variable salinity, and dynamic organic carbon inputs. Fungal communities inhabiting seagrass sediments play essential roles in decomposition, nutrient recycling, and interaction with surrounding microbial populations. Genomic studies of these fungi reveal specialized adaptations that enable survival in sedimentary environments influenced by both marine and terrestrial inputs. One of the defining characteristics of seagrass sediment ecosystems is the presence of oxygen gradients. Surface layers may be oxygen-rich due to diffusion from overlying water and photosynthetic activity of seagrass roots, while deeper layers often become anoxic. Fungal genomes from these environments show enrichment of genes involved in facultative metabolic strategies that allow organisms to switch between aerobic and anaerobic energy production. This metabolic flexibility enables fungi to persist across vertical sediment gradients with varying oxygen availability. Carbon availability in seagrass sediments is relatively high compared with many other marine environments due to continuous deposition of plant material. However, much of this carbon is structurally complex and requires enzymatic breakdown. Genomic analyses reveal that sediment-associated fungi possess extensive arrays of carbohydrate-active enzymes capable of degrading cellulose, hemicellulose, and lignin-like compounds derived from seagrass tissues. These enzymes contribute significantly to organic matter turnover within coastal ecosystems.

Nitrogen cycling is another important ecological function influenced by fungal activity in seagrass sediments. Genomic studies indicate the presence of genes associated with nitrogen assimilation, transformation, and recycling. These pathways allow fungi to utilize diverse nitrogen sources, including organic nitrogen compounds released during decomposition processes.

Variation in nitrogen metabolism genes among fungal populations suggests adaptation to localized nutrient availability within sediment layers. Salinity fluctuations represent a major environmental challenge in coastal sediment ecosystems. Seagrass meadows experience tidal cycles, freshwater inputs, and evaporation-driven changes that influence salt concentrations. Fungal genomes from these habitats show expansion of genes involved in osmotic regulation, including ion transporters and compatible solute synthesis pathways. These systems help maintain cellular stability under changing salinity conditions.

Sediment compaction and particle heterogeneity also shape fungal adaptation. Fungi must navigate complex physical structures composed of sand, silt, and organic debris. Genomic studies identify genes associated with hyphal growth regulation, adhesion, and extracellular matrix production. These traits facilitate penetration of sediment matrices and establishment of stable colonization zones. Microbial interactions within seagrass sediments are highly diverse. Fungi coexist with bacteria, archaea, and microeukaryotes in densely populated communities. Genomic analyses reveal genes involved in interspecies communication, competition, and cooperative metabolism. These interactions influence nutrient cycling dynamics and overall sediment ecosystem function.

Sulfur cycling is particularly important in deeper sediment layers where oxygen is limited. Anaerobic microbial processes generate sulfide compounds that can be toxic to many organisms. Fungal genomes show the presence of detoxification systems and enzymes involved in sulfur compound transformation. These adaptations allow fungi to survive in chemically reduced conditions while contributing to sulfur cycling processes. Biofilm formation is commonly observed among sediment-associated fungi. Genomic studies identify genes responsible for adhesion, extracellular polymer production, and structural organization of microbial communities. Biofilms provide protection against environmental stress and enhance nutrient retention within sediment microhabitats.

Population genomic analyses indicate that fungal communities in seagrass sediments exhibit spatial heterogeneity influenced by sediment depth, plant density, and water movement. Genetic differentiation among populations reflects adaptation to

**Correspondence to:** Sofia Almeida, Department of Coastal Microbial Genomics, University of Algarve, Faro, Portugal, E-mail: sofia.almeida.seagrassfungi@ualg-pt.edu

**Received:** 01-Jun-2026, Manuscript No. FGB-26-42491; **Editor assigned:** 03-Jun-2026, PreQC No. FGB-26-42491 (PQ); **Reviewed:** 17-Jun-2026, QC No. FGB-26-42491; **Revised:** 24-Jun-2026, Manuscript No. FGB-26-42491 (R); **Published:** 01-Jul-2026, DOI: 10.35248/2165-8056.26.16.317

**Citation:** Almeida S (2026). Genomic Adaptation of Fungi in Seagrass Meadow Sediment Ecosystems. *Fung Genom Biol.* 16:317.

**Copyright:** © 2026 Almeida S. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

microenvironmental variation. Some fungal lineages are restricted to specific sediment layers, while others show broader distribution across the sediment column. Epigenetic regulation plays a role in controlling gene expression in response to sediment conditions. Chemical modifications to Deoxyribonucleic Acid (DNA) and chromatin structure allow fungi to adjust metabolic activity without altering genetic sequences. These mechanisms support rapid responses to changes in oxygen availability, salinity, and nutrient concentration.

Horizontal gene transfer has been observed in some sediment-associated fungal genomes, though it occurs at relatively low frequency. Genetic exchange with bacteria may introduce new metabolic capabilities related to nutrient utilization and environmental stress response. Such events contribute to evolutionary innovation in complex microbial communities. Advances in metagenomic sequencing have revealed that fungal

diversity in seagrass sediments is significantly higher than previously recognized. Many uncultured fungal lineages have been identified, suggesting the presence of extensive hidden diversity. Functional gene analyses indicate that these organisms contribute to decomposition, nutrient cycling, and ecosystem stability.

## CONCLUSION

Overall, fungi inhabiting seagrass sediment ecosystems exhibit a combination of metabolic flexibility, stress tolerance, and ecological interaction that supports survival in dynamic coastal environments. Their genomes reflect long-term adaptation to gradients of oxygen, salinity, and nutrient availability. Continued genomic investigation will further enhance understanding of fungal roles in coastal sediment processes and their contribution to marine ecosystem functioning.