

Genomic Organization and Adaptive Evolution of Fungi in Urban Concrete Microhabitats

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DESCRIPTION

Urban environments contain a wide range of artificial substrates that create unique ecological niches for microbial life. Among these, concrete structures represent one of the most widespread and chemically distinctive habitats. Bridges, buildings, tunnels, sidewalks, and drainage systems provide surfaces that are continuously exposed to atmospheric conditions while also interacting with moisture, pollutants, and mineral leaching processes. Fungal communities inhabiting concrete microhabitats exhibit specialized genomic features that allow survival in alkaline, desiccating, and chemically variable conditions. Genomic studies of these fungi reveal how life adapts to human-made environments that differ fundamentally from natural ecosystems. Concrete is primarily composed of calcium silicates, calcium hydroxide, and various aggregates that create a highly alkaline environment. Fresh or aging concrete structures often exhibit pH values that exceed 10, creating conditions that are inhibitory to many microorganisms. Fungal genomes from these environments show enrichment of genes involved in alkaline tolerance, including proton transport systems that regulate intracellular potential of Hydrogen (pH). These mechanisms enable fungi to maintain cytoplasmic stability despite external alkalinity.

Ion exchange processes play an important role in concrete-associated fungal survival. The porous structure of concrete allows movement of water and dissolved ions, including calcium, sodium, and magnesium. Genomic analyses reveal expanded families of membrane transporters that regulate ion influx and efflux. These transport systems help fungi maintain ionic balance and prevent toxic accumulation of alkaline-earth metals. Desiccation resistance is another key adaptation in urban concrete microhabitats. Concrete surfaces frequently undergo cycles of drying and rehydration depending on rainfall, humidity, and environmental exposure. Fungal genomes from these habitats often contain genes associated with water retention, including those responsible for producing compatible solutes such as trehalose and glycerol. These compounds stabilize proteins and membranes during dehydration events, allowing cellular recovery when moisture becomes available.

Temperature fluctuations in urban environments can be extreme due to heat absorption by concrete surfaces during daytime and rapid cooling at night. Fungi inhabiting these substrates possess genomic adaptations related to thermal stress management. Heat-shock protein families are frequently expanded, supporting protein folding and repair during temperature extremes. Cold-responsive regulatory systems also assist in maintaining metabolic function during cooler periods. Exposure to pollutants is a defining feature of urban ecosystems. Concrete surfaces are often in contact with atmospheric contaminants such as heavy metals, hydrocarbons, and particulate matter. Fungal genomes from these environments show enrichment of detoxification pathways, including enzymes involved in degradation or sequestration of toxic compounds. These systems allow fungi to persist in chemically contaminated settings.

Hydrocarbon degradation is particularly relevant in urban environments with traffic-related pollution. Some concrete-associated fungi possess genes encoding enzymes capable of breaking down complex organic pollutants derived from fossil fuel combustion. These metabolic capabilities contribute to environmental remediation processes within urban ecosystems. Biofilm formation is a widespread strategy among fungi colonizing concrete surfaces. The porous nature of concrete provides microspaces where biofilms can develop and persist. Genomic studies identify genes involved in adhesion, extracellular matrix production, and community organization. Biofilms provide protection from environmental stress and enhance nutrient retention in nutrient-poor urban environments.

Nutrient limitation is a significant challenge in concrete microhabitats. Organic carbon sources are scarce, requiring fungi to rely on atmospheric deposition, dust particles, and trace organic matter. Genomic analyses reveal enzymes capable of utilizing diverse substrates, including plant-derived compounds and microbial residues deposited on surfaces. This metabolic flexibility supports survival in nutrient-deficient conditions. Microbial interactions in urban concrete ecosystems involve fungi, bacteria, algae, and lichens. These organisms often coexist in complex communities that influence surface weathering and

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nutrient cycling. Genomic studies reveal genes associated with interspecies communication and competitive interactions. These interactions shape community structure and influence colonization dynamics.

Pigmentation is commonly observed in fungi inhabiting concrete surfaces. Darkly pigmented fungi are often more resistant to environmental stress, including ultraviolet radiation and desiccation. Genomic analyses show biosynthetic pathways responsible for melanin production. These pigments provide protective functions by absorbing radiation and reducing cellular damage. Mineral interaction is another important feature of concrete-associated fungi. Some species contribute to bioweathering processes by producing organic acids that dissolve mineral components of concrete. Genomic studies identify genes involved in acid production and mineral transformation. These processes can gradually alter the structural integrity of concrete surfaces over time.

Horizontal gene transfer has been detected in some urban fungal genomes, likely facilitated by close proximity to diverse microbial communities. Genetic exchange with bacteria may contribute to metabolic innovation, particularly in pollutant degradation and stress tolerance pathways. Although not widespread, such events may enhance adaptive potential in chemically complex environments.

CONCLUSION

Overall, fungi inhabiting urban concrete microhabitats demonstrate extensive genomic adaptations that enable survival in alkaline, nutrient-poor, and chemically variable conditions. Their genetic systems reflect evolutionary responses to artificial substrates shaped by human infrastructure. Continued genomic research will further expand understanding of how fungi colonize and persist in built environments and their ecological roles within urban ecosystems.