

Comparative Genomic Assessment of Thermotolerant Fungi from Geothermal Habitats and Their Evolutionary Responses to Elevated Temperatures

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DESCRIPTION

Fungi occupy environments that range from frozen polar soils to geothermal terrains where temperatures remain consistently high. Among these organisms, thermotolerant fungi have attracted increasing scientific attention because of their capacity to survive and reproduce under conditions that would severely limit the growth of many other eukaryotic microorganisms. Geothermal habitats, including hot springs, volcanic sediments, and thermally influenced soils, provide valuable opportunities to investigate how fungal genomes respond to long-term thermal stress. Comparative genomic studies have revealed that adaptation to elevated temperatures involves a complex combination of genetic variation, gene expansion, protein modification, and cellular regulation that collectively contribute to persistence in these demanding environments.

The genomes of thermotolerant fungi often display characteristics that distinguish them from relatives inhabiting moderate climates. One recurring observation is the enrichment of genes associated with protein stability and cellular maintenance. Elevated temperatures increase the probability of protein misfolding, aggregation, and degradation. As a result, fungi living in geothermal habitats frequently possess expanded families of molecular chaperones and heat-responsive proteins. These genetic elements assist in preserving protein structure during periods of thermal exposure and contribute to cellular survival when environmental temperatures fluctuate.

Thermotolerant fungi also exhibit distinctive patterns in membrane-associated genes. Cellular membranes are particularly vulnerable to high temperatures because excessive heat can alter membrane fluidity and compromise cellular integrity. Genomic investigations have identified genes involved in lipid metabolism that differ substantially from those observed in fungi adapted to cooler habitats. Alterations affecting fatty acid synthesis and membrane composition contribute to the maintenance of stable cellular structures despite elevated environmental temperatures. These genetic characteristics represent important components of thermal adaptation and demonstrate how genomic variation influences fundamental biological processes.

Another notable feature of geothermal fungi involves Deoxyribonucleic Acid (DNA) repair systems. Increased temperatures can elevate mutation rates by promoting chemical reactions that damage nucleic acids. Comparative genomic assessments frequently reveal expanded repertoires of repair-associated genes in thermotolerant species. Efficient repair mechanisms reduce the accumulation of harmful mutations and contribute to long-term genomic stability. In some cases, sequence comparisons indicate positive selection acting on proteins associated with DNA maintenance, suggesting that these functions have undergone evolutionary modification in response to persistent thermal stress.

The study of regulatory sequences has provided additional insight into fungal adaptation. Changes in promoter regions, transcription factor binding sites, and regulatory networks can influence gene expression patterns without altering protein-coding sequences. Thermotolerant fungi often display distinct transcriptional responses when exposed to elevated temperatures. Comparative genomics combined with transcriptomic analyses has demonstrated that certain stress-response genes are activated more rapidly and maintained for longer periods than in related species from temperate environments. These differences indicate that adaptation involves both structural genomic changes and alterations in regulatory architecture.

Geothermal ecosystems frequently contain diverse chemical compounds derived from volcanic activity. Consequently, fungi inhabiting these environments encounter not only heat but also exposure to metals and mineral-rich substrates. Genomic surveys have identified genes associated with metal transport, detoxification, and cellular protection that appear enriched in some thermotolerant species. The coexistence of thermal and chemical stressors may contribute to the evolution of multifunctional genetic systems capable of addressing multiple environmental challenges simultaneously. Such findings illustrate the interconnected nature of adaptation in complex ecosystems.

Comparative studies involving phylogenetic reconstruction have enhanced understanding of the evolutionary origins of

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Received: 01-Jun-2026, Manuscript No. FGB-26-42486; **Editor assigned:** 03-Jun-2026, PreQC No. FGB-26-42486 (PQ); **Reviewed:** 17-Jun-2026, QC No. FGB-26-42486; **Revised:** 24-Jun-2026, Manuscript No. FGB-26-42486 (R); **Published:** 01-Jul-2026, DOI: 10.35248/2165-8056.26.16.312

Citation: Voss E (2026). Comparative Genomic Assessment of Thermotolerant Fungi from Geothermal Habitats and Their Evolutionary Responses to Elevated Temperatures. *Fung Genom Biol.* 16:312.

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thermotolerance. Evidence suggests that adaptation to elevated temperatures has emerged independently in multiple fungal lineages rather than arising from a single ancestral source. Similar environmental conditions have therefore produced comparable genetic outcomes through separate evolutionary pathways. This phenomenon demonstrates how natural selection can shape unrelated organisms toward analogous solutions when they experience comparable ecological pressures.

Horizontal gene transfer has also been proposed as a contributing factor in certain fungal groups. Although traditionally associated with prokaryotes, gene transfer events have been documented among fungi and other microorganisms. In geothermal habitats where microbial communities exist in close proximity, transferred genetic material may occasionally provide traits advantageous for survival under thermal stress. Genomic comparisons have identified candidate genes with unusual evolutionary histories, suggesting possible acquisition from distantly related organisms. Continued investigation is required to determine the frequency and significance of such events in thermotolerant fungal populations.

The ecological significance of thermotolerant fungi extends beyond their immediate habitats. These organisms participate in nutrient cycling, organic matter decomposition, and interactions with other microorganisms. Their activities influence the

movement of carbon and other elements through geothermal ecosystems. Understanding the genomic basis of their survival therefore contributes not only to evolutionary biology but also to broader ecological research. Furthermore, enzymes derived from thermotolerant fungi often remain functional at temperatures that inactivate many conventional biological catalysts. Such properties have generated interest in industrial applications involving biofuel production, waste processing, and biochemical manufacturing.

CONCLUSION

Thermotolerant fungi provide an exceptional model for examining how eukaryotic microorganisms adapt to challenging environmental conditions. Their genomes contain evidence of long-term evolutionary responses that support survival in habitats characterized by elevated temperatures and complex chemical landscapes. Through comparative genomic assessment, scientists are gaining deeper insight into the mechanisms that shape fungal diversity and ecological specialization. These investigations continue to expand understanding of microbial evolution while revealing the remarkable capacity of fungi to persist in environments that test the limits of biological endurance.