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Short Communication

Transposable Elements as Catalysts of Genome Evolution in Fungi

Yuki Takamori*

Department of Applied Microbial Genomics, University of Tokyo, Tokyo, Japan

DESCRIPTION

Transposable Elements (TEs) are mobile Deoxyribonucleic Acid (DNA) sequences capable of relocating within genomes, profoundly influencing structure, regulation, and evolution. In fungi, TEs serve as both sources of genetic diversity and catalysts of genome plasticity. While uncontrolled TE activity can threaten genome integrity, regulated transposition provides raw material for evolutionary innovation, affecting gene expression, chromosomal rearrangements, and the emergence of novel traits. Historically considered "selfish DNA," TEs are now recognized as essential drivers of adaptation, particularly in organisms like fungi that face rapidly changing environments [1].

Fungal genomes harbor a wide variety of TEs, which can constitute from a few percent to over fifty percent of total genomic content depending on the species. These elements are typically classified into two major groups. Class I elements, or retrotransposons, move *via* an Ribonucleic Acid (RNA) intermediate using a copy-and-paste mechanism, which includes Long Terminal Repeat (LTR) retrotransposons and non-LTR retroelements. Class II elements, or DNA transposons, move directly as DNA through a cut-and-paste mechanism mediated by transposase enzymes. Both classes contribute uniquely to genome evolution and adaptive potential [2-4].

TEs influence fungal genomes through several mechanisms. Insertional mutagenesis occurs when TEs integrate near or within genes, altering transcription, splicing, or coding sequences and generating phenotypic diversity [5]. Gene duplication and exon shuffling can result from TE-mediated mobilization, leading to expansion of gene families or creation of novel gene variants. Additionally, TEs facilitate chromosomal rearrangements, including inversions, translocations, and deletions, promoting rapid restructuring of the genome. Collectively, these processes enhance adaptability, especially in TE-rich accessory chromosomes and subtelomeric regions where adaptive genes often reside [6].

Given the potentially deleterious effects of uncontrolled transposition, fungi have evolved sophisticated regulatory mechanisms to maintain genomic stability. Epigenetic silencing through histone modifications, DNA methylation, and heterochromatin formation suppresses TE transcription. RNA interference pathways further control TEs by degrading TE-derived transcripts *via* small RNAs. Despite these safeguards, controlled activation of TEs can occur in response to environmental stressors such as nutrient limitation, oxidative stress, or host interactions [7]. Such transient activation allows fungi to generate genetic variation in a directed manner, enhancing their ability to adapt to fluctuating conditions.

TEs also play significant roles in fungal pathogenicity and ecological adaptation. They frequently integrate near effector genes, secondary metabolite clusters, and other adaptive loci, influencing both gene expression and diversification. In plant-pathogenic fungi, TE activity can produce strain-specific effectors that circumvent host immune responses [8]. In saprotrophic fungi, TEs may promote expansion of genes involved in nutrient acquisition or stress tolerance, enabling survival in complex or competitive environments. This supports the "two-speed genome" model, where TE-rich regions evolve rapidly, creating reservoirs of adaptive potential, while core genomic regions remain conserved.

The evolutionary impact of TEs operates on both short and long timescales. On a rapid timescale, transposition generates immediate genetic variability that can be selected for or against within populations [9]. Over longer evolutionary periods, TE accumulation reshapes genome size, structure, and regulatory networks. Comparative genomics reveals dramatic differences in TE content even among closely related species, reflecting lineage-specific expansion, contraction, and occasional horizontal transfer events. These dynamics make TEs valuable markers for studying fungal evolution and population diversity.

Beyond their evolutionary importance, TEs have practical applications in biotechnology. Their capacity to modulate gene expression has been harnessed to activate silent biosynthetic clusters or modify metabolic pathways in industrial fungi [10]. TE-based vectors also provide tools for functional genomics, enabling targeted mutagenesis, gene tagging, and exploration of gene regulatory networks. Controlled mobilization of TEs offers a potential method for directed evolution experiments, allowing researchers to generate genetic diversity in a structured manner to explore novel metabolic or phenotypic traits.

Correspondence to: Yuki Takamori, Department of Applied Microbial Genomics, University of Tokyo, Tokyo, Japan, E-mail: y.takamori.myco@utokyo-genome.jp

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CONCLUSION

Transposable elements are powerful agents of fungal genome evolution, shaping structure, regulation, and adaptive potential. By maintaining a balance between repression and controlled activity, fungi preserve genome stability while exploiting TEs as a source of innovation. Their influence extends to ecological adaptation, pathogenicity, and biotechnological applications. Continued investigation into fungal TE biology promises to deepen understanding of genome dynamics, rapid adaptation mechanisms, and the evolutionary forces that shape fungal diversity, while also providing novel tools for industrial and medical biotechnology.

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