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The Ty1 retrotransposon integrase harbors a amyloidogenic region

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В интегразе ретротранспозона Ty1 выявлен амилоидогенный домен

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Retrotransposons are mobile genetic elements that replicate via reverse transcription and constitute substantial fractions of eukaryotic genomes; they are also considered evolutionary precursors of retroviruses, and can affect host fitness. Intriguingly, some retrotransposon proteins share motifs with amyloids – fibrous protein aggregates with cross-β architecture that readily self-assemble into polymeric structures and can, in some cases, self-propagate in an infectious manner (prions). Here, using the ArchCandy algorithm [1], we screened the yeast *Saccharomyces cerevisiae* Ty1 retrotransposon polyprotein and identified a putative intrinsically disordered amyloid-forming domain within the integrase – the enzyme that mediates integration of newly synthesized transposon DNA into the host genome. We validated the domain's amyloidogenic propensity in *S. cerevisiae* using a yeast prion assay [2]. We also showed that, when fused to YFP, the Ty1 fragment formed detergent-resistant aggregates characteristic of amyloids. Confocal fluorescence microscopy of yeast cells producing the truncated integrase fragment revealed aggregates that colocalized with full-length Ty1 integrase, suggesting recruitment of the native protein into these assemblies. In a bacterial C-DAG system [3], the Ty1 fragment assembled into fibrils that were visualized by transmission electron microscopy, providing direct ultrastructural evidence of fibrillization.

Together, these results reveal a previously unrecognized amyloidogenic region in Ty1 integrase and suggest that prion-like aggregation may modulate retrotransposon biology. Because transposons and retrotransposons form the basis of vectors for insertional mutagenesis, gene delivery, and selectable‑marker excision, integrase aggregation may shift transposition kinetics, compromise vector stability, reduce the efficiency of mutagenesis or marker excision, and affect host fitness — with potential implications for GMO performance and biosafety.

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