

FINE MOLECULAR STRUCTURE OF GLYCOGEN PARTICLES IN ESCHERICHIA COLI

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Glycogen in *Escherichia coli* exhibits dynamic structural alterations, switching between fragile and stable states, yet the molecular mechanisms underlying these changes remain unclear. Recent studies suggest that glycogen degradation enzymes may play a crucial role in the structural regulation of glycogen particles. However, the specific contributions of glycogen phosphorylase (GlgP) and glycogen debranching enzyme (GlgX) have not been thoroughly investigated. This study aims to explore the roles of GlgP and GlgX in glycogen structural stability and fragility. In particular, the fine molecular structure of glycogen particles in E. coli wild-type and three mutant strains, $\Delta g l g P$, $\Delta g l g X$, and $\Delta g l g P / \Delta g l g X$, were explored. Using a combination of biochemical assays and advanced imaging techniques, glycogen particle fragility and stability across these strains were compared. Our findings reveal that glycogen in *E.* coli $\Delta g lg P$ and $\Delta g lg P / \Delta g lg X$ mutants was consistently in a fragile state, whereas glycogen in the $\Delta q l q X$ mutant exhibited a stable conformation. These observations suggest that GlqP plays a dominant role in maintaining glycogen structural stability. The absence of glgP leads to a significant disruption in the structural stability of glycogen particles, while glgX deletion alone does not appear to affect glycogen stability. In sum, this study highlights the essential role of glycogen phosphorylase in regulating glycogen structural stability in *E. coli*. Our findings provide important molecular insights into the mechanisms governing glycogen structural stability, offering a deeper understanding of glycogen metabolism and its regulation in prokaryotic systems.



Figure 1. Schematic illustration of the influences of key genes on glycogen structural stability and fragility in *Escherichia coli* [1].

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References:

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