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Multi-omics investigation of L-sorbose metabolism in high-risk Escherichia coli lineages linking fitness and virulence

Tuesday, October 14, 2025 2:30 PM (15 minutes)

Certain sequence types (STs) of *Escherichia coli*, such as ST131 and ST648, belong to high-risk clonal lineages that pose serious public health threats by combining antimicrobial resistance (AMR), fitness, and virulence. In contrast, other subtypes e.g., ST10 are typically harmless and beneficial colonizers. To identify characteristics beyond AMR, we analyzed over 22,000 *E. coli* genomes and discovered the L-sorbose (sor) phosphotransferase system (PTS) as a marker enriched in high-risk lineages but nearly absent in commensals. Multi-omics analyses revealed sor-dependent induction of the sor PTS and activation of associated pathways including motility, capsule biosynthesis, and purine and tryptophan metabolism. Functional validation via knockout mutants confirmed a fitness advantage linked to the sor-operon. Notably, introducing the operon into a commensal strain increased virulence in the Galleria mellonella model. The widespread presence and induction of the sor-PTS in high-risk clones highlight its potential role in linking metabolism, fitness, and virulence. Further studies, including in vivo models, are planned to elucidate its potential as a pathogen-specific target for alternative therapies. Such targeted strategies may reduce antimicrobial use and thereby resistance selection, supporting One Health goals by limiting AMR emergence and spread across human, animal, and environmental sectors.

Keywords

Antimicrobial resistance; E. coli; Multi-omics investigation; Sorbose and associated fitness

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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