Combined Transcriptomic and Proteomic Profiling of *E. coli* under Microaerobic versus Aerobic Conditions: The Multifaceted Roles of Noncoding Small RNAs and Oxygen-Dependent Sensing in Global Gene Expression Control

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Abstract

This study compared gene and protein expression of *E.coli* under aerobic vs. microaerobic conditions. Under micro aerobiosis, genes related to acid stress, biofilm formation, electron transport, peptide uptake, and anaerobic respiration were upregulated, while those for iron transport, Fe–S cluster assembly, aerobic respiration, and nucleotide synthesis were downregulated. Proteomic data confirmed these trends. Key small RNAs (CsrC, RyhB, RprA, GcvB) were also identified as regulators. Overall, the results highlight transcriptional and post-transcriptional adjustments enabling *E. coli* survival in low-oxygen environments.

Winpact Parallel Fermentation System

Introduction

This study examined how *Escherichia coli* adapts to low oxygen. Adaptation is mediated by ArcA- and FNR-driven gene reprogramming that regulates metabolism, energy production, and iron homeostasis, yet previous work lacked an integrated transcriptional and post-transcriptional view. By comparing transcriptomes and proteomes of aerobic and microaerobic cultures, we identified major gene clusters required for microaerobic growth and showed their regulation by small RNAs (RyhB, RprA, GcvB, CsrB, CsrC).

Materials and Methods

The Winpact Parallel Fermentation System FS-05-220 (Major Science, Saratoga, CA, USA) was used to culture E. coli MG1655 under both aerobic and microaerobic conditions. Each 1 L vessel contained 750 mL of M9 medium, inoculated to an initial OD_{460} = 0.04–0.05, and maintained at 37 °C, 200 rpm, and pH 7.0.

Aerobic condition: continuous air supply at 0.4 L/min.

Microaerobic condition: nitrogen gas supplied at 0.4 L/min until dissolved oxygen reached zero, continued for 30 min, then stopped and the vessel was sealed.

The system automatically controlled agitation and pH, ensuring a stable environment for transcriptomic and proteomic analyses. Samples were harvested at OD_{460} = 0.5–0.6, with five biological replicates for aerobic and ten for microaerobic conditions to ensure reproducibility..

Results

High reproducibility across biological replicates (correlation coefficients > 0.97 and 0.91).

High RNA-seq mapping coverage (94.6% for aerobic, 88.8% for microaerobic).

PCA results showed distinct clustering between aerobic and microaerobic samples, confirming the system's stability and precise environmental control.

References

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