

Prediction of Transcriptional Regulatory Network for Suspension Adaptation of Vero Cells Via Multi-omics Integration

Jiantao Zheng^{1,2}, Derong Zhang^{1,2,*}

¹Biomedical Research Center, Northwest Minzu University, Lanzhou, China

²College of Bioengineering, Northwest Minzu University, Lanzhou, China

Email address:

y252530989@stu.xbmu.edu.cn (Jiantao Zheng), zhangdr@xbmu.edu.cn (Derong Zhang)

*Corresponding author

Abstract

Adherent Vero cells are widely used for viral vaccine production, while suspension culture is the key strategy for large-scale industrial manufacturing. Nevertheless, the transcriptional and translational molecular reprogramming that enables Vero cells to resist anoikis after detachment from extracellular matrix remains poorly characterized by single-omics analysis. This study aims to systematically screen core regulatory genes and transcription factors governing suspension adaptation and construct a reliable bidirectional regulatory model through multi-omics integration and multi-layer cross-verification. RNA-seq transcriptome and TMT quantitative proteomics data from adherent and suspension-adapted Vero cells were collected. Genes with significant synchronous mRNA and protein changes were filtered under unified thresholds of $|\log_2FC| > 1$ and adjusted $P < 0.05$, and an equal-weighted comprehensive scoring model was established to rank top 20 hub genes. GSEA revealed global suppression of ribosome biogenesis, mitochondrial translation and MYC/E2F-mediated G2/M cell cycle pathways in suspension cells. Four-dimensional radar profiling, DepMap CRISPR dependency data and two independent transcription factor activity enrichment pipelines jointly verified two regulatory cascades. Stress-responsive TFs EPAS1, CEBPD, IRF1 and SMAD3 were activated to upregulate MMP1/MMP9 for ECM degradation and anoikis resistance, whereas MYC, E2F and LEF1 were suppressed to inhibit metabolism and cell proliferation and reduce matrix dependence. This multi-computational analysis constructs a predictive molecular network of Vero suspension adaptation and provides a credible candidate library for subsequent wet-lab functional validation and genetic engineering of high-yield suspension cell lines.

Keywords

Vero Cells, Suspension Adaptation, Multi-omics Integration, Transcription Factor, Anoikis Resistance, Bioinformatic Analysis