



Gene expression profiling of high-producer insect cells during Influenza VLPs expression via RNA-sequencing

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Background _____

Adaptive laboratory evolution (ALE) has been used to modulate the phenotype of insect cells during Virus-Like Particles (VLPs) production^{1,2}. However, little is known on the underlying biological mechanisms essential for improved production of Influenza VLPs. This study is focused on identifying gene expression differences between adapted and non-adapted cells during HA-VLPs production using transcriptome analysis (RNA-seq), paving the way for rational cell and/or bioprocess engineering.

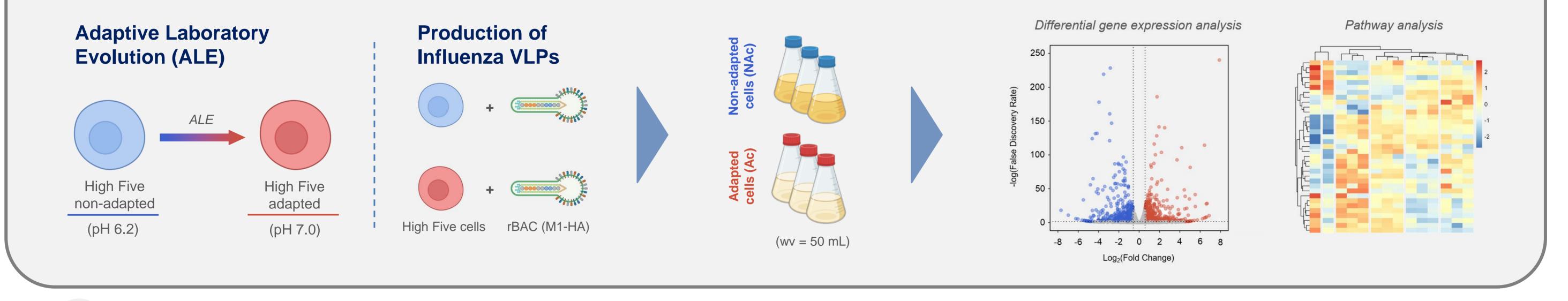


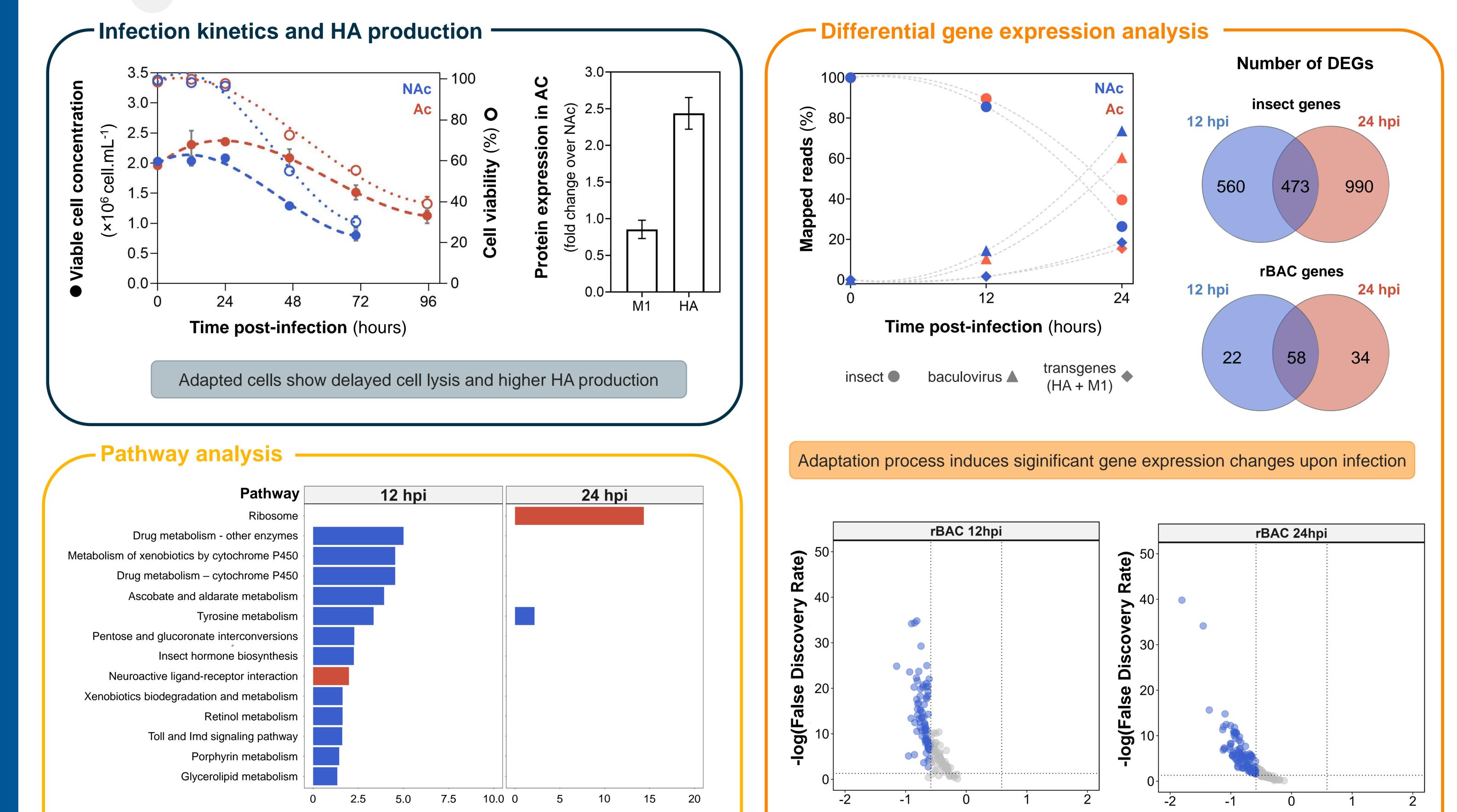
Understand the impact of adaptation process on insect cell phenotype via RNA-seq



RNA extraction (12 and 24hpi)

Whole Transcriptome Analysis





-log(False Discovery Rate) -log(False Discovery Rate)

Down-regulated (in Ac)
Up-regulated (in Ac)

Enriched pathways are mostly down-regulated and associated to rBAC infection

References: 1. Fernandes B et al. Adaptive laboratory evolution of stable insect cell lines for improved HIV-Gag VLPs production. Journal of Biotechnology 307, 139-147 (2020), https://doi.org/10.1016/j.jbiotec.2019.10.004; 2. Correia R et al. Improving Influenza HA-Vlps Production in Insect High Five Cells via Adaptive Laboratory Evolution. Vaccines. 2020 Oct 7;8(4):589. doi: 10.3390/vaccines8040589.

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log₂(Fold Change)

log₂(Fold Change)

27th ESACT Meeting

Significantly downregulated in Ac vs. NAc

Down-regulation of rBAC genes in infected adapted cells



- Infection of Ac and NAc results in significant gene expression changes
- Pathways associated with rBAC infection are down-regulated in

adapted cells

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