

FluPrep: Identifying novel risk markers for emerging zoonotic influenza A viruses

Inhalt

The FluPrep consortium aims to establish a reliable, multipronged risk assessment pipeline to evaluate the health risk and pandemic potential of emerging influenza A viruses (IAVs) for humans. This is critical as avian H5Nx IAVs of clade 2.3.4.4b have caused widespread outbreaks and spillover events in wild birds and mammals, facilitating genetic reassortment and stepwise adaptations to mammalian hosts. Consequently, zoonotic H5Nx strains have emerged with poorly defined risk profiles for humans.

This project seeks to characterize the immunopathological signatures of these emerging IAVs to define new risk criteria for integration into the FluPrep risk assessment. By employing human lung epithelial cells and *ex vivo* human lung explants, we will examine strain-specific phosphorylation of host immune regulatory kinases, specifically focusing on the TRIM28 pathway to identify patterns in immune signalling activation of emerging IAVs. To evaluate the intensity of the immune response, we will further analyse the transcription and secretion profiles of pro-inflammatory cytokines. Additionally, we will investigate the immune regulatory functions of the viral non-structural protein 1 (NS1) and the impact of specific mutations on the host immune response.

Ultimately, we aim to identify novel risk markers for emerging zoonotic IAVs by using native human lung tissue, thereby improving the predictions of disease severity and pandemic risk within FluPrep.

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Professional status of the speaker

PhD student

Junior scientist status

Yes, I am a junior scientist.

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