

# Exploring the dynamics of influenza virus evolution, selection, and host adaptive immunity

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**Abstract:** Advances in high-throughput sequencing and phylogenetic approaches have improved our ability to investigate genetic and antigenic variation of influenza viruses and adaptability of host immunity. I will describe studies characterising the genotypic diversity of swine influenza A viruses circulating in Europe, and the global antigenic diversity of swine influenza A viruses using advances in antigenic cartographic models. In addition, to better understand the molecular evolution and epidemiology of influenza B virus on a global scale, we analysed the most comprehensive dataset of whole influenza B virus genomes to date, identifying distinct patterns of antigenic evolution and genome-wide diversity between the two lineages and in different parts of the world. Finally, as part of on-going work to explore how antigenically-variable pathogens shape B cell selection, we isolated naïve and germinal center (GC) B cells from mice challenged with distinct influenza B viruses. By sequencing and analysing B cell receptor repertoires of the GC response to influenza exposure, we can investigate characteristics of B cell selection and affinity maturation to different strains, furthering our potential to study immune adaptability in more detail.

