

Control of Influenza: Individual and Population Immunity

Clustering and superspreading potential of SARS-CoV-2 infections in Hong Kong

Using contact tracing data from SARS-CoV-2 cases in Hong Kong, researchers found that a small percentage of cases (19%) led to the majority of local transmission through superspreading events (SSEs). Transmission in social settings was more impactful than in households. Rapid contact tracing and quarantine measures are crucial in controlling SSEs and reducing transmission.

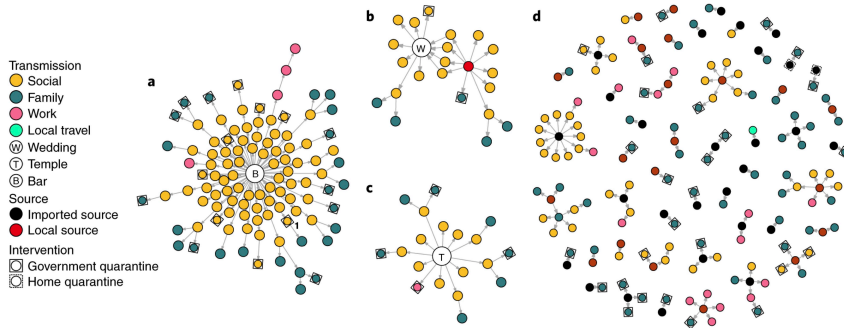


Figure 1. Transmission networks of the (a) 'bar and band' cluster, (b) a wedding cluster, (c) a temple cluster and (d) other clusters where the source and transmission chain could be determined

Integrated immune dynamics define correlates of COVID-19 severity and antibody responses

In a study of 85 SARS-CoV-2-infected individuals, acute COVID-19 exhibited high levels of IL-6, IL-18, and IL-10, with broad immune activation marked by CD38 upregulation. Activated CXCR3+cTFH1 cells in acute phase correlated with antibody levels in convalescence. Severe cases showed hyperactivation of immune compartments, suggesting potential biomarkers and immunotherapeutic targets.

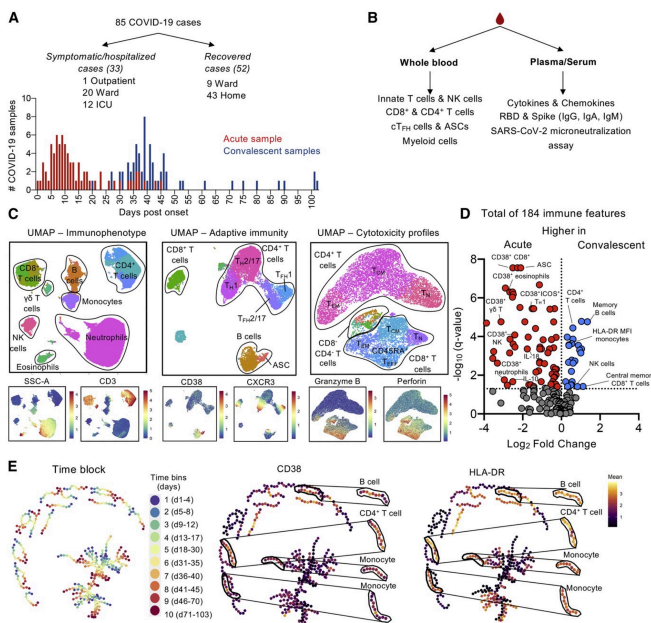


Figure 2. Broad immune activation in longitudinal COVID-19 samples.

Preliminary Findings From the Dynamics of the Immune Responses to Repeat Influenza Vaccination Exposures (DRIVE I) Study: A Randomized Controlled Trial

A 5-year randomized placebo-controlled trial examined the impact of repeated annual influenza vaccination on vaccine effectiveness. Participants aged 18-45 received either vaccine or placebo for two years. Antibody titers increased for all vaccine strains in repeat vaccinees, with significant differences observed in antibody responses for certain strains. Results suggest similar protection levels for both repeat and first-time vaccinees.

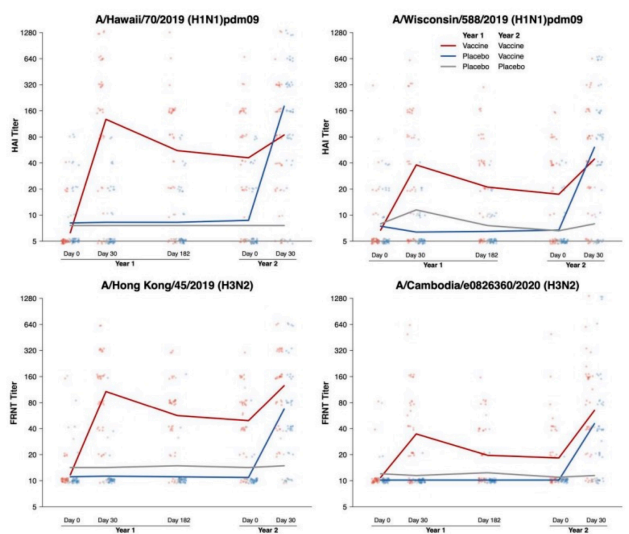


Figure 3. Antibody titers at various time points by haemagglutination inhibition (HAI) assay for influenza A(H1N1) and by focus reduction neutralization test (FRNT₅₀) for influenza A(H3N2).

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Reconstructing household transmission dynamics to estimate the infectiousness of asymptomatic influenza virus infections

During the 2009 pandemic influenza A(H1N1) outbreak in Hong Kong, a Bayesian methodology was developed to analyze household transmission dynamics. Results suggest that asymptomatic influenza cases may be less infectious than symptomatic cases, with an estimated relative infectiousness of 0.57. Further research is needed to better understand the role of asymptomatic cases in influenza transmission.

HLA-A*11:01-restricted CD8⁺ T cell immunity against influenza A and influenza B viruses in Indigenous and non-Indigenous people

This study focused on identifying novel CD8⁺ T cell epitopes for influenza A and B viruses (IAV and IBV) in HLA-A*11:01-expressing individuals, especially Indigenous populations at high risk for severe influenza. Mass spectrometry revealed immunogenic IAV and IBV peptides, paving the way for universal vaccine design to enhance protective immunity in high-risk populations.

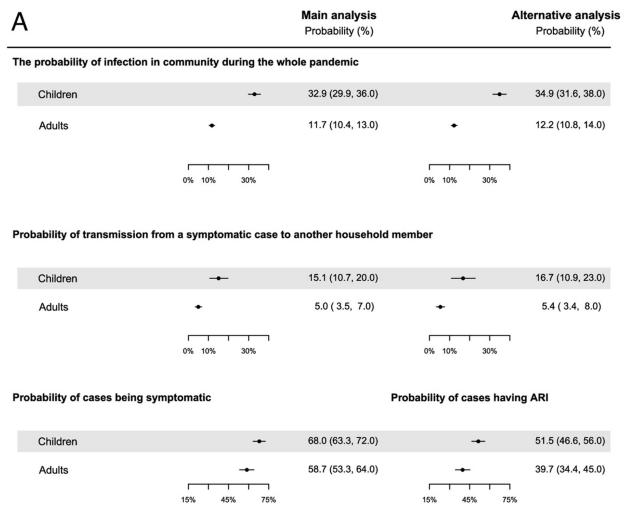


Figure 4. Summary of estimates derived from the models fitted in main and alternative analyses.

Ancestral sequence reconstruction pinpoints adaptations that enable avian influenza virus transmission in pigs

Ancestral sequence reconstruction was used to study the evolution of European avian-like (EA) H1N1 swine influenza viruses from avian to swine hosts since 1979. Changes in haemagglutinin receptor-binding specificity and adaptations in viral polymerase and nucleoprotein enabled efficient transmission in piglets. Understanding these adaptations could aid in detecting zoonotic viruses with pandemic potential.

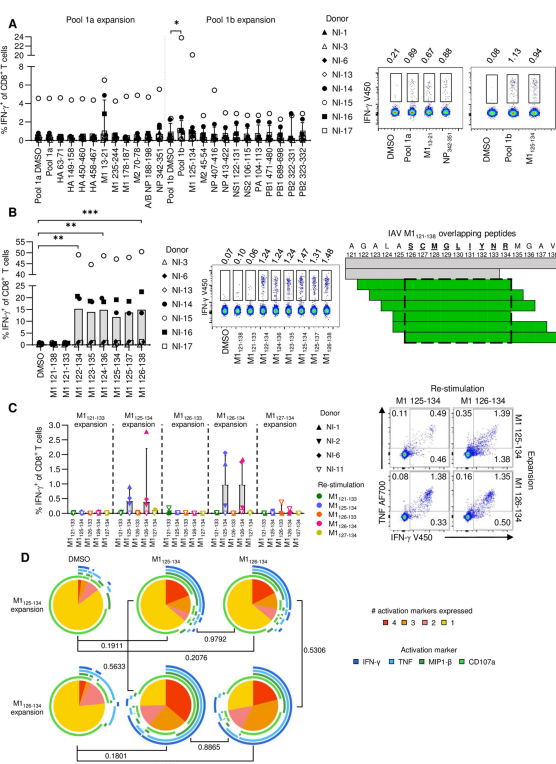


Figure 5. CD8⁺ T cell responses targeting established HLA-A*11:01-restricted IAV epitopes.

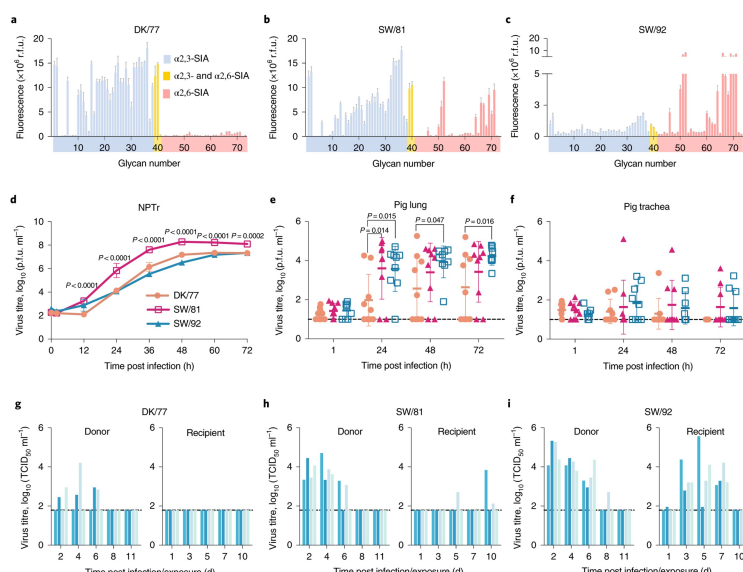


Figure 6. Avian and EA swine influenza viruses exhibited variances in receptor binding characteristics, replication efficiencies in vitro and ex vivo, and contact transmissibility in pigs.