Trends in Microbiology | Microbe of the Month

Influenza Virus

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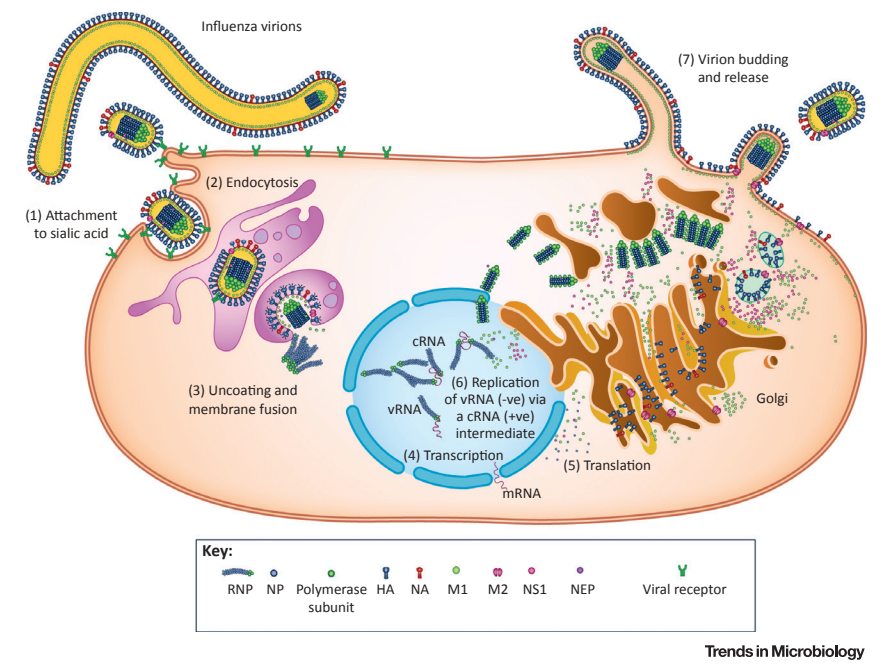
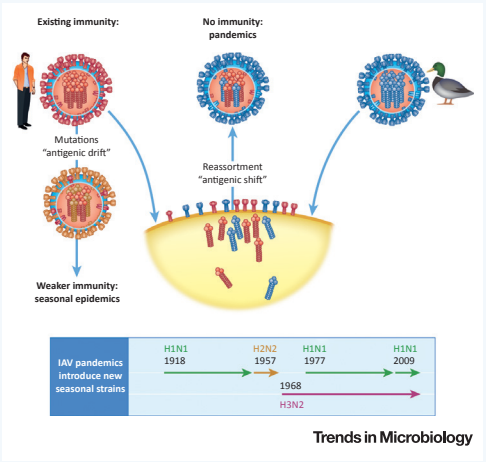


This infographic briefly summarises the natural history, replication cycle, and pathogenesis of influenza viruses, the cause of seasonal influenza and of influenza pandemics.

Influenza viruses infect many vertebrates, with *Influenza A, B* and *C viruses* (IAV, IBV, and ICV) infecting humans. High mutation rates allow the evasion of immunity. IAV from different host species can 'reassort' their segmented genomes, producing pandemic strains that are antigenically novel but otherwise well adapted to humans.

The 'Great Influenza' pandemic of 1918 remains the worst outbreak of infectious disease in history. There is concern that highly pathogenic avian influenza viruses of the H5 and H7 subtypes may evolve to cause similar pandemics.

In humans, influenza viruses infect the respiratory epithelium. The haemagglutinin (HA) proteins of IAV and IBV, or the haemagglutinin-esterase-fusion (HEF) proteins of ICV, bind sialic acid, causing endocytosis. Unusually among RNA viruses, the viral genome replicates in the nucleus. New viruses assemble at the cell surface and are released by the receptor-cleaving neuraminidase (NA) proteins of IAV and IBV or the ICV HEF protein.



TAXONOMY AND CLASSIFICATION:

ORDER: Unassigned

FAMILY: Orthomyxoviridae

GENERA (SPECIES): *Alphainfluenzavirus* (*Influenza A virus*), *Betainfluenzavirus* (*Influenza B virus*), *Gammainfluenzavirus* (*Influenza C virus*) and *Deltainfluenzavirus* (*Influenza D virus*) can all infect mammals. Distinct influenza viruses of fish and amphibians have been reported

SUBTYPES AND LINEAGES: based on the major surface antigens, there are 18 HA (H1–H18) and 11 NA (N1–N11) subtypes of *Influenza A virus* and two recent lineages, 'Victoria' and 'Yamagata,' of *Influenza B virus*

GENOME: segmented, negative-sense RNA

STRUCTURE: enveloped, pleomorphic (ranging from spheres to extremely long filaments) with a helical capsid

KEY FACTS:

Virus with an unusual ability to adapt to new vertebrate host species.

Negative-sense RNA genome, 12–14 kb, in eight (IAV, IBV) or seven (ICV, IDV) segments.

IAV, IBV, and ICV are highly transmissible human respiratory pathogens.

Global distribution. In temperate climates, peaks in winter months.

Adaptation of new IAV strains to humans causes pandemics.

Diverse IAV strains circulate in waterfowl, often as asymptomatic gastrointestinal infections.

DISEASE FACTS:

An acute infection. In humans, viral shedding begins after around 1 day and peaks before the onset of symptoms.

Typical symptoms include sudden onset of fever, muscle pain, headaches and exhaustion, peaking 2–3 days after infection and resolving within 1–2 weeks.

Serious illness occurs in a minority of cases, often due to secondary bacterial infections or exacerbation of cardiovascular and respiratory illness.

At-risk groups include infants, older adults, pregnant women, and the immunocompromised.

The large total number of cases means that seasonal influenza, mainly caused by IAV and IBV, typically kills 290 000–650 000 a year globally.

IAV pandemics can be more serious. The 'Great Influenza' of 1918 killed around 1 in 30 of the global population in 18 months.

IAV also causes serious illness in poultry.

Seasonal influenza vaccines are available but must be regularly updated.

NA inhibitors can be used for treatment.

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