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## Influencing influenza

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The emergence of lethal, [virulent variants](#) of the influenza A virus, such as the one that caused the 1918 'flu pandemic that killed 50 million people, presumably arise from specific mutations. In the Early Edition of [Proceedings of the National Academy of Sciences](#), Brown *et al.* describe studies designed to investigate the molecular basis of [viral virulence](#). They performed serial passaging in mouse lungs to select for highly virulent strains. The adaptation of the H3N2 prototype clinical isolate, A/HK/1/68, resulted in a virulent variant which is caused by a group of 11 mutations. The virulence mutations involve nuclear localization signals and sites of protein and RNA interactions. Three mutations are also found in the virulent human H5N1 isolate A/HK/156/97. Thus, viral adaptation experiments give insights into viral virulence mechanisms and convergent viral evolution.

## References

1. Avian-to-human transmission of H9N2 subtype influenza A viruses: relationship between H9N2 and H5N1 human isolates.
2. Perspectives on pandemics: a research agenda.
3. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]
4. Pattern of mutation in the genome of influenza A virus on adaptation to increased virulence in the mouse lung: Identification of functional themes, [<http://www.pnas.org/cgi/doi/10.1073/pnas.111165798>]