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The [Spanish influenza virus](#) pandemic of 1918 killed more than 20 million people worldwide. In the September 7 [Science](#), Mark Gibbs and colleagues from the [Australian National University](#) in Canberra propose that the pandemic was the result of a recombination between swine-lineage and human-lineage viral strains (*Science* 2001, **293**:1842-1845). They analysed sequences of the hemagglutinin (HA) gene from 30 H1-subtype influenza isolates, using the [sister-scanning method](#) and a [maximum likelihood method](#). They suggest that recombination replaced a central region of the human-lineage HA gene with sequences from the swine-lineage virus. Gibbs *et al.* propose that the recombination event occurred just before outbreak of the pandemic and that HA recombination affected antigenicity and viral virulence. In the same issue of *Science*, Masato Hatta and colleagues from the [University of Wisconsin-Madison](#) describe the molecular basis for virulence of the [H5N1 influenza strain](#) that caused the 'flu outbreak in Hong Kong in 1997 (*Science* 2001, **293**:1840-1842). They show that a glutamate-to-lysine substitution at residue 627 of the PB2 polymerase influences viral virulence in mice.

References

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