

Swine flu genes dissimilar to past pandemics

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Some genetic markers of influenza infection severity have been identified from past outbreaks. Researchers have failed to find most of these markers, described in the open access journal *BMC Microbiology*, in samples of the current swine-flu strain.

Jonathan Allen and Tom Slezak from Lawrence Livermore National Laboratory, America, published their analysis identifying 34 conserved amino acid markers from past [pandemic flu](#) strains two weeks ago. They have since studied sequences from the new [virus](#) and found that only about half of their 34 markers are present. Slezak said, "This lack of similarity does not necessarily mean that the current H1N1 virus is not going to be a major problem, but it does suggest that it lacks many of the attributes that have made previous outbreaks deadly".

The researchers stress that, although their work appears to suggest that the current virus may not be as dangerous as feared, more studies are required before any firm conclusions can be drawn.

More information: Conserved amino acid markers from past influenza pandemic strains, Jonathan E Allen, Shea N Gardner, Elizabeth A Vitalis and Tom R Slezak, *BMC Microbiology* 2009, 9:77, doi:10.1186/1471-2180-9-77, www.biomedcentral.com/1471-2180/9/77/

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