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► **COVER:** 'Light work' by Patrick Morgan, inspired by the Review on p217



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**A**vian flu has hardly left the news since 2004 when the first infections with H1N5 influenza virus were reported in south-east Asian birds. Since then, domestic and wild birds have been affected in several European countries. Most recently, several hundred thousand British turkeys had to be destroyed following a large outbreak of the virus in East Anglia. Although no human cases of bird flu have been reported in the European Union to date, earlier this year four people died in Turkey having contracted the avian H1N5 virus from their poultry flocks. The first H1N5-caused human deaths have now been reported in Africa. In the United States, the Department of Health and Human Services is preparing a Critical Pandemic Planning Communications Campaign.

Although H1N5 has shown only limited ability to infect humans, history teaches us that influenza pandemics can have devastating effects. The pandemic of 1918–1919 might have been the single most devastating disease outbreak in human history, having potentially caused up to 50 million deaths worldwide. But even on the epidemic scale, influenza remains one of the most important human infectious diseases, which makes it all the more important for us to understand the evolutionary dynamics of the virus.

On page 196 of this issue, Martha Nelson and Eddie Holmes review how the recent developments in complete-genome sequencing, antigenic mapping and epidemiological modelling are improving our knowledge of the evolution of the human influenza virus. Their focus is on the patterns and processes of influenza virus evolution at the level of recurrent human epidemics. Nelson and Holmes argue that a genomic view of the virus's genetic diversity, including the acquisition of polymorphism data from within individual hosts and hitherto poorly surveyed regions, is a prerequisite for a complete understanding of this pathogen's evolutionary biology.

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