ECDC RISK ASSESSMENT

Human cases of influenza A(H1N1)

20 May 2009

Source and date of request

ECDC internal decision, 18 May 2009

Public health issue

Implication for Europe of the new influenza A(H1N1) virus

Disease background information

A new influenza A(H1N1) virus was first identified by US CDC on 17 April 2009 in samples from two Californian children. It was reported in MMWR on 21 April [1]. The basic genetic structure of the virus which was first described in Eurosurveillance on 30 April [2], demonstrated that the virus had many genetic elements from porcine (swine) influenza. The new virus was thus initially called 'swine flu' even though its pig origin later came into question, and it is now clearly evident that it can spread from human to human.

There are now well over 8 000 cases confirmed from at least four continents, of which almost 300 from Europe.

The virus has genetic components from swine influenza (two different types), avian influenza and human influenza viruses. This is thus a 'quadruple' recombinant virus. Triple recombinant swine influenza viruses with avian, human and swine genes have previously been circulating in pigs in the US, and have been transmitted to humans [3, 4]. There are several recent examples where influenza viruses of animal origin have been transmitted not only from the animal to humans but also from human to human – the most obvious example being the avian H5N1 influenza which has been circulating in Southeast Asia for more than a decade, and which still causes deaths in the region (even if human-to-human transmission has been very limited for this virus).

The current outbreak of H1N1 influenza is well established in North America, and new cases are continuously being reported from Europe, Oceania and Asia. Recent reports from Japan may indicate community spread there, which would mean that we now are very close to the definition of a pandemic.

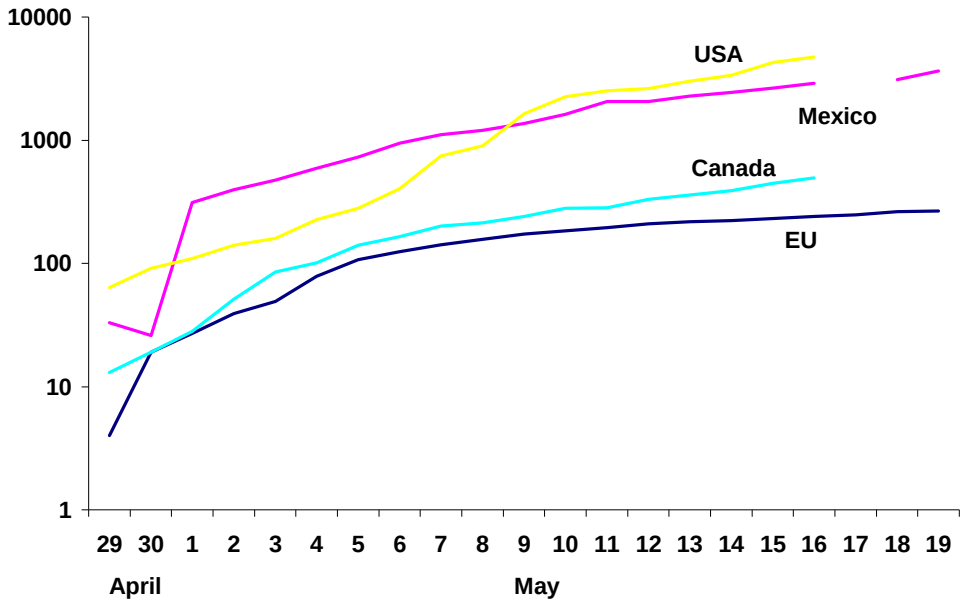
Stockholm, May 2009

ECDC threat assessment for the EU

The previous threat assessment from 8 May listed a number of unknown parameters needed for proper risk assessment. Many of these are still unknown, but for some we are getting more data:

Cumulative epidemic curve: The figure below shows that – after having followed the Mexican rate of increase for the first 10 days of May – the rate of increase of new cases in the EU may now follow a slower pace than in the three countries of North America.

Figure 1. Cumulative reported incidence (logarithmic) in EU/EFTA compared to Mexico, Canada and the US (some gaps in the North American data from the weekend)



Infectivity: There is now more evidence that the virus transmits in the same way and with the same ease as seasonal influenza, judging from the widespread transmission in the US. There have already been several estimates of the basic reproductive rate (Ro), which all lie between 1 and 2 (with some outliers); the range 1.4 to 1.6 being most probable. This is higher than the value observed for seasonal influenza but in line with previous pandemics. At present, about one third of the cases in Europe have acquired the infection in their own country (mainly in Spain and the UK). Almost all these endogenous cases are secondary to someone who has travelled to North America, but there have also been a few reports of tertiary transmission.

Immunity: Laboratory studies are being undertaken and they are showing some cross-reactivity in sera from older people. Epidemiological data from the US also indicate that older age groups may be less affected. Virus of the same subtype, A(H1N1), has been responsible for seasonal influenza during several years, but that subtype is quite different from the current one. Most of the genes of the novel virus are similar to genes that have developed in pigs – independently of human H1N1 viruses – probably since 1918.

Virulence and risk groups: We still do not know what proportion of infected people develop disease. That will have to be assessed from future serological studies. There are no reports of known genetic markers associated with severe disease, and even if animal challenges show that the virus does cause disease, the results are less severe than, for instance, for the highly pathogenic influenza A(H5N1). So far, the disease seems to have been generally mild in Europe. It should be noted, however, that the majority of cases so far have been young adults who returned from travel to the Americas, and who do not constitute a representative cross-section of the population.

Spectrum of disease: This is beginning to be described. The only notable features are preliminary reports that the incubation period may have a longer tail than observed previously (up to 8 days). There are also reports of more gastro-enteric symptoms than are common for seasonal influenza. There will probably be many mild cases that will be difficult to differentiate from other respiratory tract infections until serological studies are undertaken.

Case fatality rate: This is unknown at present but there are certainly some cases of severe disease and deaths reported from Mexico and the US. The present reported case fatality rate from Mexico of some 2% is probably biased by more severe cases being diagnosed more readily. The figure for the US of about one death per 1 000 lies close to what is observed for seasonal influenza.

Age distribution: The present age distribution is skewed towards younger age groups: returning travellers in the age group of 20-29 year-olds, and secondary spread in a number of schools in the age group of teenagers. There are some indications from epidemiology and serology that older people may be less affected perhaps due to some enduring immunological memory of an earlier influenza A(H1N1) infection.

Susceptibility to antivirals: Based on genetic evidence, all the indications are that the neuraminidase inhibitors oseltamivir and zanamivir will be effective treatment, but that the virus will be resistant to adamantenes (amantadine). There is some concern that genetic recombination could take place with circulating oseltamivir-resistant viruses.

Community spread: Since the present case definition is mainly directed at identifying cases who have travelled to North America, there could be a risk that community spread in the Europe is not detected quickly. However, the EU influenza sentinel surveillance system is quite sensitive in detecting the start of an influenza season, and one could already last week see an increase in the number of laboratory samples submitted by the sentinel doctors. Usually at this time of the year, there are almost no influenza tests taken. Also, the fact that no transmission chain followed from a diagnosed case has been longer than two further cases, speaks against a wide community spread.

In addition to close surveillance of cases in the EU, ECDC will continue to closely monitor the situation in Mexico and the US. It is mainly from these two countries that further information for the parameters listed above will have to come. We will continuously provide information through our website and update this risk assessment as needed. For rapid updates, please see the Situation Reports published on our website (www.ecdc.europa.eu) every morning.

The current ECDC assessment is that the new influenza A(H1N1) virus will continue to spread. Though it seems mild in the US and in Europe, this picture is still unclear as there has not been enough transmission to judge the effects, especially in those more at risk. Also pandemic viruses are unpredictable, and can change their characteristics as they evolve. Even pandemics usually slow down in summer, only to pick up in autumn, and the virus may then come back, perhaps in a more aggressive form as happened in 1919.

References

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