



Eurosurveillance

Europe's leading journal on infectious disease epidemiology, prevention and control

Vol. 15 | Weekly issue 31 | 05 August 2010

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High prevalence of antibodies to the 2009 pandemic influenza A(H1N1) virus in the Norwegian population following a major epidemic and a large vaccination campaign in autumn 2009

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Citation style for this article:

Waalen K, Kilander A, Dudman SG, Krogh GH, Aune T, Hungnes O. High prevalence of antibodies to the 2009 pandemic influenza A(H1N1) virus in the Norwegian population following a major epidemic and a large vaccination campaign in autumn 2009. *Euro Surveill.* 2010;15(31):pii=19633. Available online: <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19633>

Article published on 5 August 2010

The prevalence of antibodies reactive to the 2009 pandemic influenza A(H1N1) was determined in sera collected before the start of the pandemic, during the early phase, and after the main epidemic wave and nationwide vaccination campaign in Norway. A substantial rise in prevalence of antibodies at protective titres, from 3.2% to 44.9%, was observed between August 2009 and January 2010. The highest prevalence, 65.3%, was seen in the age group of 10-19 year-olds.

Introduction

A new influenza virus in humans emerged in the spring of 2009 in Mexico. The virus was identified to be a triple reassorted A(H1N1) variant of swine origin but with a still unknown reservoir. Due to the wide spread of the virus around the globe the World Health Organization (WHO) declared within a few weeks the first pandemic of the 21st century. In Norway, the first cases of 2009 pandemic influenza A(H1N1) virus infections were recorded in early May. Until mid-summer, cases were scattered and they were almost exclusively travellers from abroad and their contacts. A minor epidemic occurred from late July to early August, with a high but gradually declining proportion of travel-related cases. This was followed by a comparatively calm period leading up to a major influenza epidemic during October and November 2009, surpassing all previous peaks recorded in the current Norwegian clinical influenza surveillance system which monitors influenza-like illness consultation rates and has been in operation since 1998 [1]. This wave culminated in early November and largely subsided by the end of 2009. Subsequent influenza activity from January to May 2010 has been unusually low.

The 2009 pandemic influenza A(H1N1) surveillance and vaccination in Norway

Virological influenza surveillance in Norway is based on reporting from diagnostic laboratories to the

Norwegian Institute for Public Health (NIPH). During the pandemic period, laboratories performed virus detection through reverse transcription–polymerase chain reaction (RT-PCR) in the great majority of cases, with a small minority done through virus isolation or antigen detection. Based on virologically-confirmed cases notified to the NIPH, the highest impact of the epidemic was among the younger age groups (Figure 1).

The recorded incidence declined with increasing age; less than 10% of the confirmed cases were aged 50 years or above, and less than 2% were aged 65 years or above. By week 36 in 2009, after the first small pandemic wave in July–August, the majority of confirmed cases were seen in the age groups of 10–19 year-olds and 20–29 year-olds (34% and 34%, respectively). The age groups under the age of 10 years became more prominent during the main pandemic wave in autumn, increasing from 10% to 27% of all confirmed cases. Similar age patterns were seen when looking at positivity rates within age groups (per cent of specimens testing positive; data not shown), indicating that the patterns were not strongly distorted by testing biases.

As part of the national pandemic preparedness, Norwegian health authorities had entered an advance purchase agreement that secured the country a population-wide supply of monovalent adjuvanted vaccine in case of a pandemic. When deliveries of Pandemrix (GlaxoSmithKline Biologicals s.a.) commenced in mid-October 2009, a large-scale vaccination campaign was launched. Designated priority risk groups and exposed healthcare workers were vaccinated first. Then the general population was offered the vaccine, beginning with the younger age groups, particularly children below school-age, school-age children and adolescents. The great majority of vaccinated individuals received one dose with the exception of immunocompromised persons, and, to some extent, children under ten years of age for whom a two-dose recommendation was given

initially. Vaccinated individuals were recorded in the national vaccination registry, SYSVAK. Preliminary data indicate that around 40% of the Norwegian population (approximately 1.9 million people) have been recorded as vaccinated, varying from 25% for the age group of 20–29 year-olds up to 52% for the age group of six months–two year-olds and 57% for three–nine year-olds. For the other age groups, the vaccination coverage figures are within the range 35%–46%. The majority of recorded vaccinations (>95%) was carried out from October to December 2009. However, the present SYSVAK records are not considered to be complete, and a provisional estimate of 2.2 million people (45% of the population) vaccinated is being used by the Norwegian Health authorities (B Feiring, personal communication June 2010).

Serological survey during the pandemic

Since the late 1970s, an annual serosurvey of antibodies reactive to contemporary influenza viruses has been carried out in Norway [2,3]. The annual serum panel is collected in August each year, consisting of approximately 2,200 age- and geographically representative residual sera from hospital laboratories. The information regarding each serum is limited to patient age and sex, and county of residence. Serum antibody titres were determined using the haemagglutination–inhibition (HI) test [4], testing sera in serial two-fold dilutions starting at dilution 1:20, with turkey red blood cells (RBC) as indicator cells. A HI titre of 40 or higher is considered protective against the test virus strain, while sera with HI titre of 20 or more were counted as seropositive.

The serum panel collected in August 2009 (n=2,116) was analysed for antibodies reactive to the pandemic reference virus A/California/07/2009 (H1N1v) in addition to the preceding winter's seasonal influenza viruses (data not shown). Viral antigen was grown in embryonated chicken eggs and used non-inactivated.

In January 2010, a supplementary serum panel (n=541) was collected from five hospital laboratories across Norway. Like the main panel, these sera were also representative for the various age groups. The January 2010 panel was collected in the wake of a major influenza epidemic, and, in order to avoid over-representation of influenza cases, laboratories were asked to exclude sera which had been submitted due to respiratory illness.

In addition, a subset of the serum panel collected in August 2008 (n=689), representative for all age groups and counties across the country, was tested for HI reactivity to the pandemic influenza virus in order to determine the background level of pre-existing antibodies reactive to this virus.

Results and discussion

The results of the HI analysis for various serum panels are shown in Figure 2 (A–C) and in the Table.

The data for the 2008 serum panel show that there was a low frequency of pre-existing protective antibodies to the 2009 pandemic influenza A(H1N1) virus (1.7%, all ages, HI \geq 40). The highest frequency was seen in people over 80 years of age (4.8%). Interestingly, pre-existing antibodies at titres correlating with protection were also seen in adolescents (10–19 years) and young adults (20–29 years) with frequencies of 1.8% and 3.9%, respectively. The nature of pre-existing antibodies reactive to the pandemic influenza virus in this age segment is unclear since exposure to viruses resembling the pandemic strain is unlikely, and further investigation is warranted. Detectable antibodies (HI \geq 20) were seen in all age groups except for children under the age of ten years (Table). In the elderly, those born before 1950, and in particular those older than 80 years, cross-reactive antibodies might be due to earlier infection with influenza viruses sharing similar antigenic epitopes with the current pandemic influenza virus as suggested in recent reports [5,6]. In these

FIGURE 1

Virologically-confirmed cases of 2009 pandemic influenza A(H1N1) per 100,000 population, by age group, Norway, 2009 and 2010

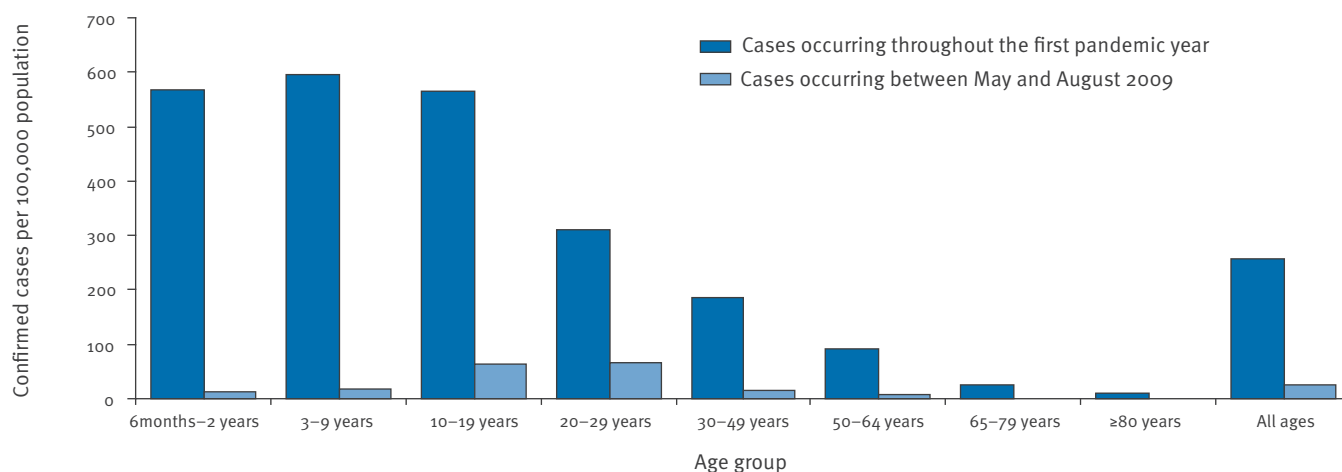
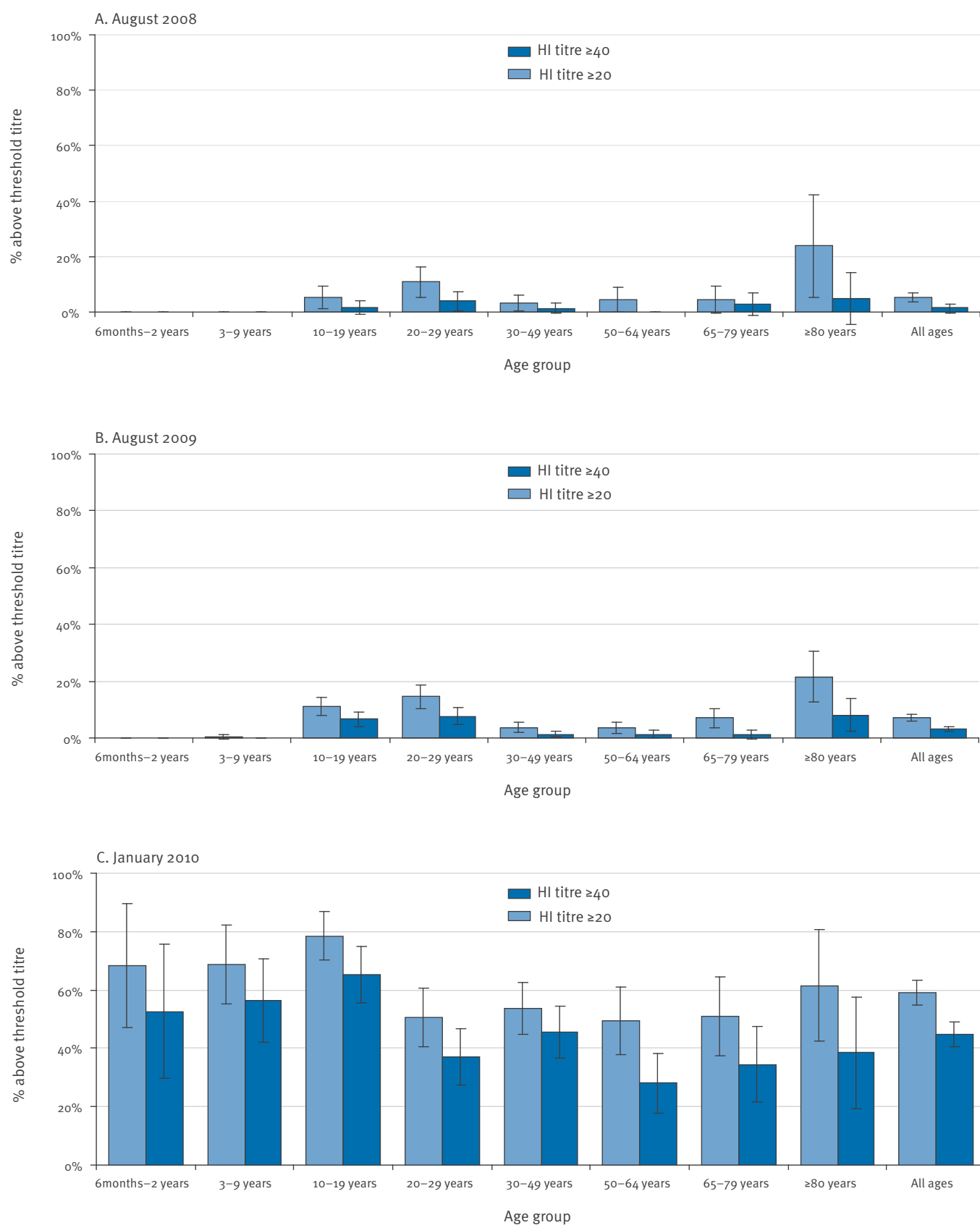


FIGURE 2

Frequency of seropositivity and seroprotection to 2009 pandemic influenza A(H1N1) virus in sera collected in Norway in (A) August 2008, (B) August 2009, and (C) January 2010



HI: haemagglutination-inhibition.

studies, various levels of pre-existing cross-reactive antibodies to the 2009 pandemic influenza A(H1N1) virus were found.

In August 2009 the prevalence of antibodies to the 2009 pandemic influenza A(H1N1) virus shows only minor differences from the pre-pandemic 2008 baseline level (Figure 2B). This may be an indication that the early wave in the summer of 2009 was too small to substantially influence the immunity at population level. However, during May–August, confirmed cases in Norway were mainly in adolescents and young adults (Figure 1), and a slight increase in seropositivity in that age segment (significant only for the group of 10–19

year-olds, $p < 0.05$) may reflect immunity acquired from recent infection. Contrary to the situation in the United Kingdom [7], few cases were seen in children under school age and in school age children at that time, possibly because the school vacation in Norway spans from late June until late August, thus limiting the scope for effective transmission of virus in the age groups below 15–20 years of age during summer. In the August 2009 serum panel, the overall prevalence across age groups of titres 40 or above for the seasonal H1N1 virus A/Brisbane/59/2007 was 13%. The age pattern of seasonal influenza A(H1N1) seroprevalence was somewhat more skewed towards younger persons, and a large percentage (44%) of sera with protective titres to the

TABLE

Prevalence of antibodies to the 2009 pandemic influenza A(H1N1) virus (A/California/07/09) in Norway

Age group (years)	n	HI titre ≥20		HI titre ≥40	
		% positive	95% CI	% positive	95% CI
Serum panel A, August 2008					
≤2	44	0.0	0.0–0.0	0.0	0.0– 0.0
3-9	74	0.0	0.0–0.0	0.0	0.0– 0.0
10-19	114	5.3	1.1– 9.4	1.8	-0.7– 4.2
20-29	129	10.9	5.4– 16.3	3.9	0.5– 7.3
30-49	150	3.3	0.4– 6.3	1.3	-0.5– 3.2
50-64	89	4.5	0.1– 8.9	0.0	0.0– 0.0
65-79	68	4.4	-0.6– 9.4	2.9	-1.2– 7.0
≥80	21	23.8	5.2– 42.4	4.8	-4.5– 14.1
All ages	689	5.4	3.7– 7.1	1.7	-0.4– 2.7
Serum panel B, August 2009					
≤2	113	0.0	0.0– 0.0	0.0	0.0– 0.0
3-9	249	0.4	-0.4– 1.2	0.0	0.0– 0.0
10-19	372	11.0	7.8– 14.3	6.7	4.1– 9.3
20-29	301	14.6	10.5– 18.7	7.6	4.6– 10.7
30-49	456	3.7	2.0– 5.5	1.3	0.2– 2.4
50-64	312	3.5	1.4– 5.6	1.3	0.0– 2.6
65-79	225	7.1	3.7– 10.5	1.3	-0.2– 2.9
≥80	88	21.6	12.8– 30.4	8.0	2.2– 13.7
All ages	2,116	7.0	5.9– 8.2	3.2	2.5– 4.0
Serum panel C, January 2010					
≤2	19	68.4	47.1– 89.7	52.6	29.7– 75.5
3-9	48	68.8	55.4– 82.1	56.3	41.9– 70.6
10-19	98	78.6	70.3– 86.9	65.3	55.7– 74.9
20-29	97	50.5	40.4– 60.7	37.1	27.3– 46.9
30-49	123	53.7	44.7– 62.7	45.5	36.5– 54.5
50-64	75	49.3	37.8– 60.9	28.0	17.6– 38.4
65-79	55	50.9	37.4– 64.4	34.5	21.7– 47.4
≥80	26	61.5	42.5– 80.6	38.5	19.4– 57.5
All ages	541	59.0	54.7– 63.2	44.9	40.6– 49.2

CI: confidence interval; HI: haemagglutination-inhibition.

The data shown are fractions of HI-positive sera (%) determined at the following time points: (A) a pre-pandemic serum panel from August 2008, (B) a serum panel from August 2009 following the first wave during the summer of 2009 and (C) a serum panel from January 2010 following the main wave during the autumn (October–November) of 2009 and the mass vaccination period during October–December of 2009.

The differences between the 2009 and the 2010 serum panels for all the age groups were significant for both fractions with HI titre ≥ 20 and HI titre ≥ 40 (chi square test, $p < 0.001$).

The differences between the 2008 and the 2009 serum panels reached significance only for the 10–19 year-olds ($p = 0.043$) and All ages ($p = 0.044$) in the category of HI titre ≥ 40 .

pandemic virus was not reactive to the current seasonal influenza A(H1N1) vaccine strain (data not shown). This probably indicates that the observed reactivity to pandemic influenza A(H1N1) prior to the pandemic cannot be explained solely as cross-reactivity of antibodies raised in response to recent seasonal viruses.

A substantial and significant increase in overall prevalence of protective antibodies (HI titre ≥ 40) to the pandemic 2009 A(H1N1) influenza virus was observed from August 2009 to January 2010, from 3.2% to 44.9% ($p < 0.001$) (Figure 2, Table). Similarly, all age groups showed a significant increase in the prevalence of detectable as well as protective antibodies. The frequency of protective antibodies was particularly high in persons under 20 years of age (61.2%, 95% confidence interval (CI): 53.6%–68.8%), while 74.5% (95% CI: 67.8%–81.3%) had detectable antibodies (titre ≥ 20). In people aged 20 years and older the figures were substantially lower, 37.8% (95% CI: 32.8%–42.8%) and 52.1% (95% CI: 47.0%–57.3%), respectively. In particular, the 50–64 year-olds age group had the lowest prevalence of protective antibody in January 2010 (28.0%) despite recorded vaccination coverage of about 43%. A higher proportion (49.3%) had detectable antibodies. The incidence of laboratory-confirmed infections was comparatively low in this age group (Figure 1). Conceivably, the immune response to vaccination or infection in this age group resulted in antibodies that were only partially directed against the pandemic strain, possibly due to the phenomenon of original antigenic sin [8]. A similar pattern was also seen in the age group 65–79 year-olds, but to a somewhat lesser extent.

Our sera from January 2010 were collected approximately four to six weeks after the main pandemic wave had subsided, and also after the main drive of a nationwide vaccination campaign with a population vaccine uptake probably well exceeding 40%. The vaccination status of the serum donors is not known, therefore our analysis cannot differentiate between seropositivity resulting from infection, from immunisation, or from a combination of the two.

Our data are thus less suitable for estimating the extent of infection than corresponding studies performed in populations with a lower vaccination coverage [9,10]. In light of age patterns of infection and vaccination, infection is likely to have contributed most to the rise in immunity in the 20–29-year-olds who had the lowest recorded vaccine uptake. Conversely, vaccination might have contributed most to the rise in the elderly who appear to have been spared of widespread infection. Our data furthermore indicate that immunity in the population against the pandemic virus has risen substantially. Approximately 45% of the population has antibodies at a level corresponding to protection and an additional 15% of the population has detectable antibodies at lower titres which may also offer some protection. This observed level of population immunity

may prove to be sufficient to prevent a new pandemic wave of high magnitude. However, lesser outbreaks cannot be excluded, and antigenic drift of the virus might impair the protective effect. Furthermore, it is not known how well the observed immunity to the pandemic virus will be sustained.

Conclusions

A substantial increase in antibodies against pandemic 2009 A(H1N1) influenza virus was observed in population representative serum panels in Norway between August 2009 and January 2010. This is consistent with recorded high incidence of infection and a high rate of vaccine uptake, both taking place during October–December 2009. Provided that this level of immunity does not wane substantially, and that the antigenic properties of the virus do not change significantly, the high population immunity may prove sufficient to prevent large-scale epidemics of the pandemic influenza virus in Norway in the upcoming influenza season.

Acknowledgements

We would like to thank laboratories in the following hospitals for their invaluable contribution in providing the sera used in the present study: Østfold Hospital/Fredrikstad; Akershus University Hospital; Oslo University Hospital, Innlandet Hospital/Lillehammer; Buskerud Hospital/Drammen; Vestfold Hospital/Tønsberg; Unilabs Telelab AS/Skien; Sørlandet Hospital/Kristiansand; Stavanger University Hospital, Haukeland University Hospital/Bergen; Førde Central Hospital; Molde Hospital; St.Olav Hospital, Trondheim; Levanger Hospital; Nordlandssykehuset/Bodø; University Hospital of North Norway/Tromsø, Hammerfest Hospital. The WHO Collaborating Centre at the National Institute for Medical Research, London, UK, is gratefully acknowledged for providing virus and ferret control serum used in the HI test. The Department for Infectious Disease Epidemiology and Department of Vaccinology at NIPH are gratefully acknowledged for contributing incidence and vaccination data, respectively. We further thank the staff of the influenza laboratory, Department of Virology, NIPH; Valentina Johansen, Anne Marie Lund, Marianne Morken, and Remilyn Ramos-Ocao for excellent technical assistance.

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Toxigenic *Corynebacterium ulcerans* infection in a veterinary student in London, United Kingdom, May 2010

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Citation style for this article:

Taylor J, Saavedra-Campos M, Harwood D, Pritchard G, Raphaely N, Kapadia S, Efstratiou A, White J, Balasegaram S. Toxigenic *Corynebacterium ulcerans* infection in a veterinary student in London, United Kingdom, May 2010. Euro Surveill. 2010;15(31):pii=19634. Available online: <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19634>

Article published on 5 August 2010

We report on a case of toxigenic *Corynebacterium ulcerans* infection in a fully immunised veterinary student, investigated in London, United Kingdom, in May 2010. There was no ongoing transmission in human contacts. Possible animal sources were identified.

Introduction

Diphtheria can result in an acute infection of the upper respiratory tract or a cutaneous lesion. It is caused by three toxin-producing *Corynebacterium* species: *C. diphtheriae* responsible for epidemic disease, *C. ulcerans* and, more rarely, *C. pseudotuberculosis*, the last two being zoonotic infectious agents [1,2].

In the United Kingdom (UK) between 2000 and 2009, 43 isolates of toxigenic corynebacteria were identified in England and Wales, 27 of which were *C. ulcerans*. Three unvaccinated individuals presented with clinical symptoms typical of classic diphtheria, but most had milder respiratory infections (sore throat or tonsillitis) and had been either partially or fully immunised [3,4].

Cattle are a documented reservoir for *C. ulcerans* and risk factors for human infection with this species include contact with these and other farm animals [5]. Less commonly, *C. ulcerans* can also be spread through consumption of unpasteurised milk and unpasteurised milk products [6]. More recently, contact with dogs and other companion animals has also been proposed as a source of infection [7-9]. Despite limited evidence of person-to-person spread of *C. ulcerans*, this is a potential route of transmission [6,10]. It is therefore recommended that the public health response following isolation of toxigenic *C. ulcerans* from a human case be the same as that for toxigenic *C. diphtheriae* [6].

A primary course of diphtheria-containing vaccine is included in the UK's vaccination schedule and is given

at the age of two, three and four months, plus a pre-school booster between the age of three years four months and five years. This is followed by a booster between the age of 13 and 18 years [11].

Case report

A 20-year-old veterinary student in London, United Kingdom, with no significant medical history, experienced four to five weeks of recurrent sore throat and tonsillitis unresponsive to a full course of penicillin towards the end of March 2010. As symptoms remained, the case was reviewed by the family doctor and a throat swab was taken from white tonsillar lesions on 10 May 2010.

The local Health Protection Unit (HPU) was notified by a hospital microbiology registrar on 17 May 2010 that the throat swab had grown *C. ulcerans*. A second throat swab, taken on 18 May, when the case was still symptomatic was then sent to the Streptococcus and Diphtheria Reference Unit for primary culture and toxigenicity testing. The case was clinically assessed by the family doctor and, in consultation with the HPU and microbiology registrar, a course of erythromycin was started on 18 May 2010. The sample was confirmed as toxigenic on 21 May 2010.

The case had received a full recommended UK course of immunisation with diphtheria toxoid, plus a booster at 14 years. The family doctor was advised by the HPU to offer a convalescent diphtheria booster vaccination as part of the routine management of the case.

In-depth discussions with the case confirmed that there was no exposure to unpasteurised milk and no recent overseas travel.

As part of a veterinary medicine undergraduate course, the case had been in recent contact with animals on two separate farming placements. The date of symptom onset was determined to be during a lambing placement at a farm in the last two weeks of March 2010.

Risk assessment of human contacts

All close contacts were followed up as indicated by national guidelines [6].

The risk assessment identified four household contacts sharing college accommodation, two close contacts and a partner. One household contact had mild symptoms (sore throat). Four of these seven contacts had records of a full course of immunisation for diphtheria, while the others had no record of past immunisations against diphtheria (including the contact with mild symptoms).

Three family members were also identified as contacts, as the case had stayed with family during the farm placements. One family member had developed a sore throat after the case's onset of symptoms. A complete immunisation record was found for two of these family contacts, including the one who developed a sore throat.

Throat swabs were taken from all of these contacts, who were also provided with prophylaxis and advised on signs and symptoms of the infection by their family doctor. Family doctors were advised by the HPU to offer a booster vaccination if none had been received in the previous 12 months. All swabs were found to be negative for *C. ulcerans*.

One further asymptomatic contact who accompanied the case during the lambing placement (and was therefore subject to the same potential exposure) was also identified. As all samples of contacts had been negative for *C. ulcerans*, a throat swab was taken, but no prophylaxis or vaccination given. This throat swab was also negative.

Risk assessment of animal contacts

A detailed risk assessment of the two farming placements was undertaken by the local HPU, in close collaboration with the Veterinary Laboratories Agency, to determine if a likely source of infection could be identified and if there was any ongoing risk to the public or farm owners and workers.

The second placement commenced after symptom onset and was therefore disregarded as a possible source of infection. The first was a lambing placement on a farm with 800 sheep. However, enquiries to the farm's veterinarian established that the usual standard of animal health and hygiene on the farm was high, there were no reported health problems in the sheep flock during lambing and there were no dogs (working or pets) on the farm. The farm owners and workers were

all reported to be fit and well and their contact with the sheep and lambs was determined to be minimal outside lambing season, which had ended some weeks before the case was notified to the HPU. Moreover, this farm is not open to the public. Consequently, the ongoing risk to human health was assessed to be very low and no further investigations were deemed to be necessary.

The case had been in close contact with a number of domestic animals (dogs, cat, rabbit and chickens) during the same period as the lambing placement. However, none of these were reported to have exhibited any clinical signs suggestive of *C. ulcerans* infection and, in view of the time lapse and large number of potential exposures, it was not feasible to undertake any animal sampling [7].

Discussion

Infection with a toxigenic strain of *C. diphtheriae* or *C. ulcerans* can cause serious illness in unvaccinated individuals: five deaths from diphtheria have been recorded in the UK since 1986, three of them due to *C. ulcerans* infection [10]. The number of clinical cases is small and there have been no previous toxigenic corynebacterial isolates from veterinarians. There is no booster vaccination for the general adult population, and the severity of the infection can be especially serious in elderly people in contact with pets [12,13].

While the source of infection for this case was not proven, the lambing farm or domestic animals were considered to be the most likely sources. Domesticated animals have been implicated as potential reservoirs of *C. ulcerans* and the organism is a recognised commensal in several animal species, usually without overt clinical signs, although it has been associated with nasal discharge in cats [5-8]. Furthermore, the antibiotics licensed to eliminate the pathogen in humans are often not licensed for animals. As discussed previously by other authors, a number of difficult issues arise in attempting to eliminate subclinical zoonotic infections from healthy animals for perceived public health reasons [7]. It may be more appropriate to ensure that occupationally exposed groups, such as veterinary students, are appropriately immunised.

The case presented here had been fully immunised against diphtheria. This probably explains the relatively mild presentation of symptoms, as the vaccine provides protection against the effects of toxin produced by the bacteria. Most UK laboratories will only screen for corynebacteria if there is a clinical indication of diphtheria and/or contact with a known case, which suggests that other mild diphtheria cases may be missed. Indeed, the delay in initial diagnosis of this case was due to the low level of clinical suspicion.

Conclusions

Toxigenic *C. ulcerans* infection remains rare, but it can be fatal, especially among those who are not

immunised. As animal sources can be difficult to identify and control, maintenance of high vaccination coverage among the child and adult populations is essential.

Acknowledgements

We would like to acknowledge the primary care doctors of the case and all contacts, as well as staff at University College London Hospital, the Streptococcus and Diphtheria Reference Unit and Health Protection Agency (HPA) local and regional services who supported contact tracing. Finally, we would like to thank the case who kindly consented to this article being written.

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The impact of the pandemic influenza A(H1N1) 2009 virus on seasonal influenza A viruses in the southern hemisphere, 2009

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Citation style for this article:

Blyth CC, Kelso A, McPhie KA, Ratnamohan VM, Catton M, Druce JD, Smith DW, Williams SH, Huang QS, Lopez L, Schoub BD, Venter M, Dwyer DE. The impact of the pandemic influenza A(H1N1) 2009 virus on seasonal influenza A viruses in the southern hemisphere, 2009. *Euro Surveill.* 2010;15(31):pii=19631. Available online: <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19631>

Article published on 5 August 2010

Data collected over winter 2009 by five World Health Organisation National Influenza Centres in the southern hemisphere were used to examine the circulation of pandemic and seasonal influenza A strains during the first pandemic wave in the southern hemisphere. There is compelling evidence that the pandemic influenza A(H1N1) 2009 virus significantly displaced seasonal influenza A(H1N1) and, to a lesser extent, A(H3N2) viruses circulating in the southern hemisphere. Complete replacement of seasonal influenza A strains, however, was not observed during the first pandemic wave.

Introduction

Historically influenza pandemics have been associated with replacement of the previously circulating influenza A subtype, as was observed in 1957 when influenza A(H2N2) replaced A(H1N1), and in 1968 when influenza A(H3N2) subsequently replaced A(H2N2). As global viral surveillance was limited during the pandemics of 1957 and 1968, the proportion of disease attributable to seasonal influenza viruses during the early pandemic periods and the rate of subtype replacement are uncertain. It is postulated that cross-protective immunity following infection with a pandemic influenza virus results in protection against circulating seasonal influenza subtypes. This protection results in displacement and replacement of seasonal influenza subtypes by pandemic viruses [1-3]. Co-existence of different subtypes is possible when the introduction of a virus does not generate a pandemic. The reintroduction of an influenza virus in a context of considerable residual herd immunity, as was observed with

influenza A(H1N1) in 1977, can result in co-circulation of more than one influenza subtype [1,3]. We cannot be certain whether emerging pandemic influenza strains will replace or co-exist with the previously circulating subtypes or strains, and if replacement is observed, how quickly this will occur. As this outcome has implications on the selection of viruses to be included in influenza vaccines, improved surveillance and rapid influenza A subtyping methods have important roles to play in monitoring the circulation dynamics of influenza strains during modern epidemics and pandemics.

The pandemic influenza A(H1N1) 2009 virus was first identified in April 2009 [4-6]. As its detection in the northern hemisphere coincided with declining seasonal influenza activity, the impact on the circulation of seasonal influenza viruses could not be fully assessed [7]. In contrast, the first wave of the pandemic influenza virus in the southern hemisphere coincided with the onset of the winter influenza and respiratory virus season. Thus, data obtained from the 2009 southern hemisphere winter provide an opportunity to examine the circulation dynamics of pandemic and seasonal viruses during the early pandemic period.

This report presents data obtained by five World Health Organization (WHO) National Influenza Centres in the southern hemisphere for the winter of 2009. The pattern of circulating pandemic and seasonal influenza A strains in the southern hemisphere provides important information that can contribute to decision making regarding vaccine strain selection, and preventative and therapeutic strategies.

Methods

Influenza A subtyping data from all diagnostic respiratory tract specimens submitted in winter 2009 to five WHO National Influenza Centres (NICs) in Australia, New Zealand and South Africa were collated and analysed. NICs in Melbourne, Sydney and Perth receive samples from the Australian states of Victoria, New South Wales and Western Australia, respectively, whereas NICs in Wellington and Johannesburg receive the samples from across New Zealand and South Africa, respectively.

Influenza detection and subtyping was performed within each laboratory by nucleic acid testing using polymerase chain reaction (PCR) of type-specific targets within the matrix gene and subtype-specific targets within the haemagglutinin gene regions of the influenza virus genome. To assist with interpretation of the raw data, samples that tested positive for influenza A yet were not subtyped were removed prior to analysis. Where available, the PCR-positive detection rates from respiratory samples received during previous seasons (examined in similar populations using similar surveillance methods) were compared with those from the 2009 season.

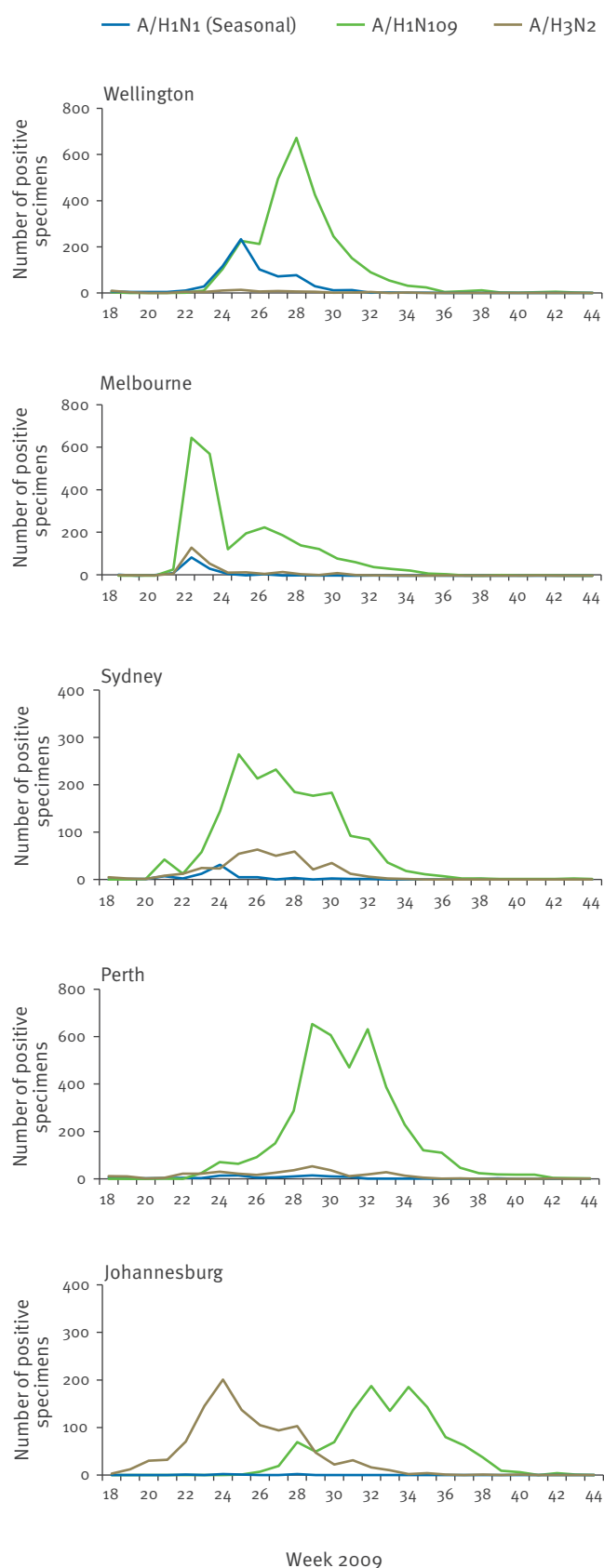
Results

Influenza A was detected by PCR in 17,328 respiratory tract specimens collected at the five NICs from May to October 2009 (week 18 to week 44). Influenza A subtyping was available for 90% of influenza A positive specimens (Wellington: 73%; Melbourne: 95%, Sydney: 89%, Perth: 100%, Johannesburg: 97%). The number of typed and untyped specimens as a proportion of total positive tests remained consistent in all centres across the study period. Epidemic curves from the five NICs were constructed (Figure 1). Data were expressed as a proportion of total tests positive for influenza by PCR (Figure 2) and as a proportion of total tests performed (Figure 3).

Pandemic influenza A(H1N1) 2009 activity in the southern hemisphere was first detected in New Zealand in week 18 (peak activity in week 28), followed by Melbourne, Sydney and Perth in week 21 (peak activity in weeks 22, 25 and 29 respectively) and then South Africa in week 25 (peak activity in week 32) (Figure 1). Significant pandemic influenza activity was detected in all locations: The overall proportion of influenza A-positive specimens from May to October 2009 subtyped as pandemic influenza A(H1N1) 2009 was 78% in Wellington, 85% in Melbourne, 80% in Sydney, 89% in Perth and 53% in Johannesburg (Figures 2 and 3). The proportion of influenza viruses typed as pandemic influenza A(H1N1) 2009 following first identification of the pandemic virus was 78% in Wellington, 85% in Melbourne, 80% in Sydney, 90% in Perth and 68% in Johannesburg. These proportions increased to 93%, 95%, 92%, 96% and 94%, respectively, if only those specimens received during the second half of the pan-

FIGURE 1

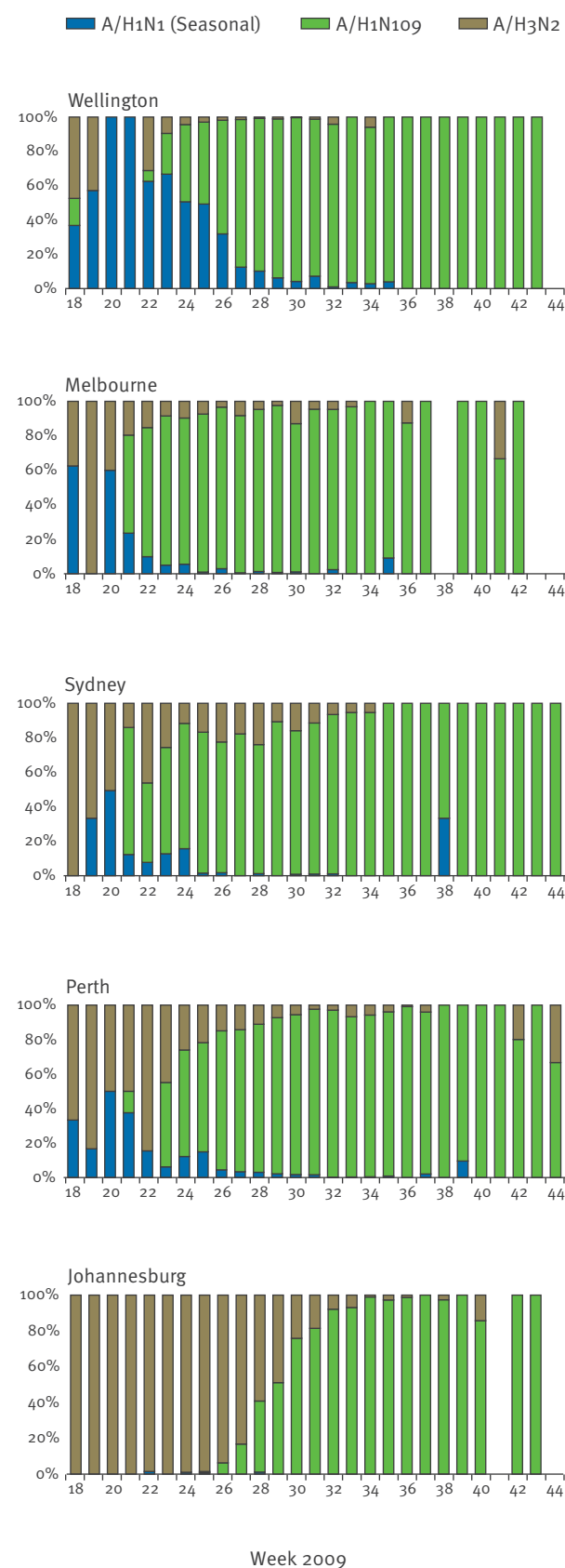
Number of positive influenza specimens per week, by subtype, southern hemisphere, weeks 18-44, 2009



Note: untyped specimens have been excluded from graphs and analysis.

FIGURE 2

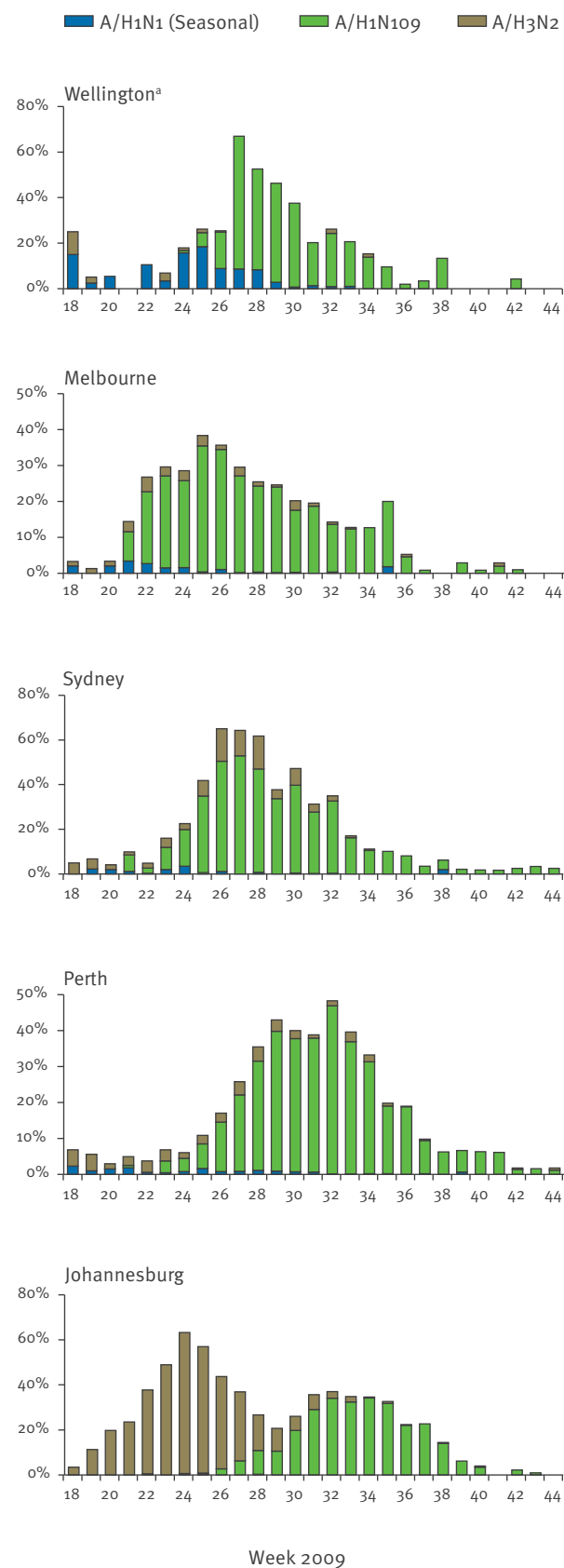
Proportion of positive influenza tests, by subtype, southern hemisphere, weeks 18-44, 2009



Note: untyped specimens have been excluded from graphs and analysis.

FIGURE 3

Positive influenza specimens as a proportion of all tests, by subtype, southern hemisphere, weeks 18-44 2009



Note: untyped specimens have been excluded from graphs and analysis.

^a Wellington data obtained from sentinel surveillance only.

demic from August to October 2009 (week 31 to week 44) were examined independently.

Seasonal influenza A activity coincided with pandemic influenza activity in New Zealand, and preceded it in Australia and South Africa. Total seasonal influenza virus activity was generally modest. Twenty per cent of PCR-positive specimens were subtyped as seasonal influenza A(H1N1) in Wellington, 5% in Melbourne, 3% in Sydney, 2% in Perth and less than 1% in Johannesburg. The corresponding figures for influenza A(H3N2) were 2% in Wellington, 10% in Melbourne, 17% in Sydney, 8% in Perth and 47% in Johannesburg (Figure 3). Despite the low levels in most catchment areas, both seasonal influenza A(H1N1) and A(H3N2) activity were detected in all three countries throughout the winter 2009.

Samples from sentinel general practitioner surveillance systems provide the best estimate of community influenza activity. The 2009 influenza season was compared with previous seasons using sentinel data from the NICs in Wellington, Melbourne and Perth, each of which receives samples from country-wide (Wellington) or state-wide (Melbourne, Perth) surveillance systems operating during the winter influenza season. In 2009, 27-35% of surveillance specimens were influenza A-positive compared to 20-39% in 2007 and 13-27% in 2008 (Figure 4). Pandemic influenza A(H1N1) 2009 virus was identified in 71-98% of influenza PCR-positive samples in 2009. The absolute number and proportion of samples positive for seasonal influenza viruses (Figure 4; dark blue) in all three locations was lower in 2009 compared with the previous two seasons.

Discussion and conclusions

The impact of the pandemic influenza A(H1N1) 2009 virus on circulating seasonal influenza strains was demonstrated using data obtained by five WHO National Influenza Centres in the southern hemisphere in the winter of 2009. Examination of influenza strains as a proportion of the subtyped influenza A positive

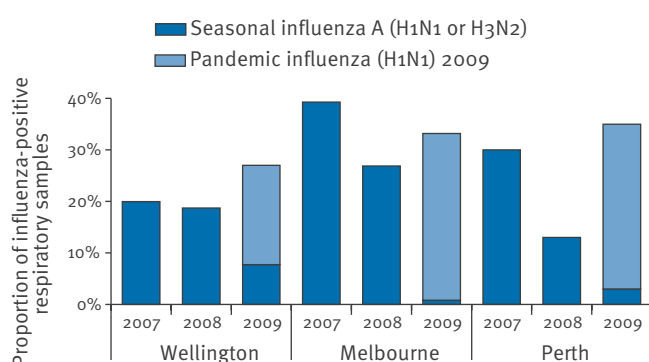
specimens in 2009 (Figure 2), total test specimens in 2009 (Figure 3) and 2007-2009 sentinel surveillance specimens (3 sites only, Figure 4) provides compelling evidence that the pandemic virus significantly displaced seasonal influenza viruses. Consistently across Australia, New Zealand and South Africa, the replacement was rapid and progressive with seasonal strains comprising a low and declining proportion of influenza A detections from the peak of the pandemic wave through to the end of the season. Complete seasonal influenza A strain replacement, however, was not observed. These data are consistent with data presented by Tang *et al.* when examining 2009 influenza activity in Singapore [2]. Raw data and the shape of epidemic curves need to be interpreted with caution given the impact of testing behaviour (particularly elevated testing at the beginning of the pandemic) and modifications of testing algorithms through the course of the season (e.g. Figure 1, Melbourne).

The reduction in seasonal influenza A(H1N1) activity was the most obvious effect of the 2009 pandemic. Significant early activity of seasonal influenza A(H1N1) was observed in New Zealand and, to a lesser extent, Australia. Following the entry of the pandemic virus, detection of seasonal A(H1N1) viruses quickly decreased and remained at low levels throughout the winter. The majority of tested seasonal influenza A(H1N1) viruses were resistant to oseltamivir (A Kelso, unpublished data), as observed in the previous northern hemisphere winter. Seasonal influenza A(H3N2) activity also declined as the pandemic progressed, but the effect was less obvious and activity continued at higher levels than those of seasonal influenza A(H1N1) throughout the season.

A similar observation was made in North America in 2009. While the absolute numbers of detected seasonal influenza viruses increased in the United States (US) from April to May 2009, the proportion of specimens positive for seasonal influenza strains continued to decrease during this time [7]. This increase in absolute numbers yet decrease in the proportion of positive specimens is likely to reflect an increase in the number of influenza tests performed [7]. The 2009-2010 winter data from the US WHO and National Respiratory and Enteric Virus Surveillance System (NREVSS) Collaborating Laboratories demonstrated that, although more than 99% of reported influenza A-positive tests were subtyped as pandemic influenza A(H1N1) 2009, ongoing transmission of seasonal strains was detected [8].

Given the high mutation rate and continual emergence of novel genetic lineages of influenza virus, it remains uncertain why pandemic influenza viruses replace existing seasonal influenza A subtypes and strains. Transient heterosubtypic immunity – short-lived immunity which is cross-protective against different subtypes and declines rapidly over time – has been shown to inhibit re-infection by any new strain in animal

FIGURE 4
Proportion of submitted respiratory samples PCR-positive for influenza, by year and influenza subtype, sentinel general practitioner surveillance data (Wellington, Melbourne, Perth), 2007-2009



models [1,9,10]. It is postulated that, during pandemics, a substantial fraction of the global population is infected with the new virus and is then transiently immune to infection with the previously circulating subtypes [3]. This leaves a critically low number of susceptible individuals, leading to the extinction of seasonal influenza strains. It is important to note that the effect is specific for influenza A viruses as the replacement of circulating influenza B virus lineages is not observed.

Data from both the 2009 southern hemisphere and 2009-2010 northern hemisphere influenza season [7,8] suggest that pandemic influenza A(H1N1) 2009 will be the predominant influenza A strain in the 2010 influenza season in the southern hemisphere. Whether complete subtype replacement will be observed in 2010 remains uncertain. These data support the recommendation that seasonal influenza vaccines for the southern hemisphere in 2010 and the northern hemisphere in 2010-2011 contain representative pandemic influenza A(H1N1) and seasonal influenza A(H3N2) viruses (as well as an influenza B virus) [11], but not the previously circulating seasonal influenza A(H1N1) virus. Given the evidence of ongoing, albeit sporadic, transmission of seasonal influenza A viruses eleven months after pandemic influenza was first detected, it is likely that influenza A(H3N2) and perhaps also seasonal influenza A(H1N1) infections will be observed during the coming season. Whether ongoing suppression of seasonal viruses will lead to complete replacement remains to be determined.

Acknowledgements

The authors would like to thank the Melbourne WHO Collaborating Centre for Reference and Research on Influenza for their assistance with influenza subtyping and analyses. The Melbourne WHO Collaborating Centre for Reference and Research on Influenza is supported by the Australian Government Department of Health and Ageing.

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General practice out-of-hours service in Ireland provides a new source of syndromic surveillance data on influenza

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Citation style for this article:

Brabazon ED, Carton MW, Murray C, Hederman L, Bedford D. General practice out-of-hours service in Ireland provides a new source of syndromic surveillance data on influenza. *Euro Surveill.* 2010;15(31):pii=19632. Available online: <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19632>

Article published on 5 August 2010

The use of routinely available electronic sources of healthcare data on the spread of influenza has the potential to enhance current surveillance activities. This study aimed to develop a method for identifying influenza-related records from general practitioner (GP) out-of-hours (OOH) services in Ireland. Data from one such service were interrogated for keywords relating to influenza-like illness (ILI) and a proxy measure of influenza activity in the community setting was developed. Comparison of this syndromic surveillance measure with national data on ILI consultation rates demonstrated a statistically significant temporal correlation. In five out of six influenza seasons investigated, peaks in the GP OOH influenza-related calls appeared at least one week ahead of peaks in the national ILI consultation rates. The method described in this paper has been extended to nine OOH services in Ireland (covering 70% of the Irish population) to provide weekly figures on self-reported illness for influenza in the community and its data have been incorporated into the national weekly influenza reports produced by the Health Protection Surveillance Centre. These data should provide early warnings of both seasonal and pandemic influenza in Ireland.

Introduction

The recent influenza pandemic reemphasised the need to ensure that a reliable, comprehensive system is in place for influenza surveillance. It is worthwhile assessing all available data sources for their potential for detecting influenza. Indicators of influenza activity in the community warrant particular attention. Data that are gathered electronically and maintained as part of routine community medical care might be expected to provide a timely and readily available source of information on the transmission of influenza and influenza-like illness (ILI).

Telehealth data in Ireland

Data from healthcare call centres or 'telehealth' data, which log direct interactions of patients with a

healthcare service and maintain records of patients' symptoms at particular points in time, have in recent years become a source of information for syndromic surveillance. Systems such as NHS Direct in the United Kingdom [1-5], the Ontario Telehealth System in Canada [6,7] and Melbourne Medical Deputising Service in Australia [8] have been used successfully to monitor trends in ILI.

In Ireland, one such telehealth system is the out-of-hours (OOH) or 'doctor-on-call' service, which provides general practitioner (GP) care at times when doctors' surgeries are closed. Since 1998, nine OOH cooperative organisations (coops) have been developed, which cover about 70% of the Irish population [9]. These services operate from 18:00 to 08:00 on weekdays and 24 hours a day during weekends and bank holidays. The mean contact rate is 221 contacts per 1,000 population per year [10]. These cooperatives aim to provide an urgent OOH GP service to their patients and to facilitate continuity of care. The services provide access to a doctor through a call centre telephone number. Clerical personnel answer calls and record details in a computerised system. The information is triaged by either a nurse or a doctor (depending on the OOH service) and a clinician calls the patient back promptly. The doctor may offer advice on the telephone or arrange for the patient to be seen at the local doctor-on-call centre or visited at home if necessary. Details of the consultation are recorded in the computer system and the information is faxed to the patient's own GP before surgery reopens, ensuring that follow-up can be carried out if required.

Large data repositories, which contain records of self-reported illness (syndromes) in the community and clinicians' subsequent diagnoses, are therefore maintained by the GP OOH service. The potential exists to utilise this valuable data source as an early warning or alert system for community illness in Ireland.

National sentinel GP influenza surveillance system

The Irish sentinel GP influenza surveillance system gathers data electronically from sentinel GPs throughout the country to provide clinical data on all cases of ILI diagnosed in their practices each week. These data form the basis for the main national influenza indicator, the GP ILI consultation rates, and provide internationally comparable figures. During the 2008–9 influenza season, 54 GPs took part in the surveillance programme, which covered about 5% of the Irish population. Sentinel GPs are also required to send nasal and throat swabs – for at least one patient per week presenting with ILI – to the National Virus Reference Laboratory for virological type confirmation. Other sentinel data from hospitals and schools around the country are also monitored nationally during the influenza season (further information on routine national influenza surveillance can be found at <http://www.hpsc.ie/hpsc/A-Z/Respiratory/Influenza/>).

The aim of this work was to identify a feasible and practical means for identifying ILI-related records from OOH services in Ireland and to evaluate the results by comparing this syndromic surveillance data with national indicators and standards for influenza. To the best of our knowledge, this is the first time in Ireland that GP OOH services have been investigated as a potential source of syndromic surveillance data.

Methods

Strategy

Calls to GP OOH services in Ireland are not currently recorded using clinical codes, so a strategy to identify influenza-related calls had to be developed. We searched for specific key words, using Microsoft (MS) Access [11] to interrogate the data. The aim of this process was to design and validate a query that would act as a proxy measure for influenza activity in the community.

Quantitative data analysis

Anonymised data on all calls for six influenza seasons between 2003 and 2009 were obtained from one call centre that covers two OOH GP services (North East Doctor on Call and Midlands Doctor on Call). Data were extracted from the Adastra software system [12] into plain text or comma separated values (CSV) files. The fields in the datasets consisted of call number, date of call, patient age, patient sex, patient's reported condition, and doctor's diagnosis/outcome. Records that contained 'test call' in the reported condition field were deleted from the file – these referred to information technology maintenance records. Data were imported into MS Access to enable us to examine free-text fields. Data were aggregated weekly (Monday to Sunday inclusive) to coincide with the weekly influenza season calendar, which runs from week 40 (mid-September) to week 20 (mid-May).

Design of queries

Comparing total calls per week with the national ILI consultation rates for the corresponding periods showed no particular synchronisation (Spearman's rank correlation coefficient ranged from -0.02 to 0.42 over the six years investigated). Therefore, in an attempt to identify specific influenza/ILI-related records in the dataset, keyword queries were designed in MS Access to extract records based on information from the 'patient's reported condition' field as this field contained a large amount of information for each record. Three queries were initially designed. The first was based on the Irish national definition for ILI used by the Health Protection Surveillance Centre (HPSC) [13], the second on an American definition for ILI used by the United States Centers for Disease Control and Prevention (CDC) [14] and the third on a self-reported illness query for flu/influenza. The query for the national ILI standard definition was designed to extract records with the terms 'fever' or 'high temperature' and two or more of the following – 'headache', 'sore throat', 'cough' and 'aches and pains' ('aches and pains' was chosen instead of 'myalgia' in the national ILI definition as it represents the lay term for the medical phrase). The query for CDC's ILI definition was designed to extract records with the terms 'fever' or 'high temperature' and 'cough' or 'sore throat'. The final query, based on patients' self-reported illness, was designed to extract the keywords 'flu' or 'influenza'.

Choice of proxy measure for influenza activity

In order to ensure that the queries extracted appropriate records from the free-text fields – in other words to test, refine and validate these specific queries – a subset of data (5,732 records from a period of high influenza activity during the 2005–6 season) were manually categorised using a binary system. For all 5,732 records, the value of 1 or 0 was allocated for each of a range of influenza-related keywords recorded in the patient's reported condition field (i.e. headache, cough, sore throat, high temperature, aches and pains, fever, flu, influenza). Specific binary codes represented the national ILI definition, the CDC definition, or the self-reported illness definition for influenza and each

TABLE 1

Sensitivity, specificity and positive predictive values for three query methods, Ireland, 2005–6 influenza season (n=5,732)

Query	Sensitivity (%)	Specificity (%)	Positive predictive value (%)
Irish national ILI definition	97.7	99.9	93.6
CDC ILI definition	98.6	100	100
Flu/influenza self-reported illness definition	100	99.9	98.6

CDC: United States Centers for Disease Control and Prevention; ILI: influenza-like illness.

record was classified accordingly. Thus it was possible to compare the manually categorised subset of data with the results of the MS Access queries. For each query, true positives, true negatives, false positives and false negatives were identified, and sensitivity, specificity and positive predictive values were calculated for each individual query. All queries had high sensitivity, specificity, and positive predictive values (>93%; Table 1), but these values were lowest for the query for the national definition for ILI. The complex nature of the national ILI case definition means that inevitably a slightly higher level of false positives will be extracted from a free-text system.

Comparison of the data extracted for the three queries over the six influenza seasons showed that the numbers of records extracted overall for the national definition query were much lower than for the other queries (overall only 0.37% of all calls were extracted with this query) and therefore the data were quite 'noisy' and uninformative (Figure 1 as an example). For the query representing the American ILI definition during the six influenza seasons, peaks occurred during the periods of increased national consultation rates for ILI and more records were extracted than for the national ILI definition. The highest numbers of records, however, were extracted with the self-reported illness query for flu/influenza (overall 3.2% of all calls were extracted with this query). This trend was seen consistently in all the influenza seasons we investigated and substantial peaks were obtained throughout the six-year period for the self-reported illness query. The self-reported

illness query was used, therefore, as our proxy measure of influenza activity in the community.

Source of data on routine influenza surveillance indicators

National data on routine influenza surveillance indicators, including GP ILI consultation rates, were obtained upon request from the HPSC.

Statistical analysis

Data were analysed using the statistics package JMP [15]. We used Spearman's rank correlation coefficient to compare temporal trends in the extracted OOH data and national influenza indicators. This tool has been used previously [7,16,17] to assess the relationship between syndromic influenza surveillance datasets and corresponding influenza indicators.

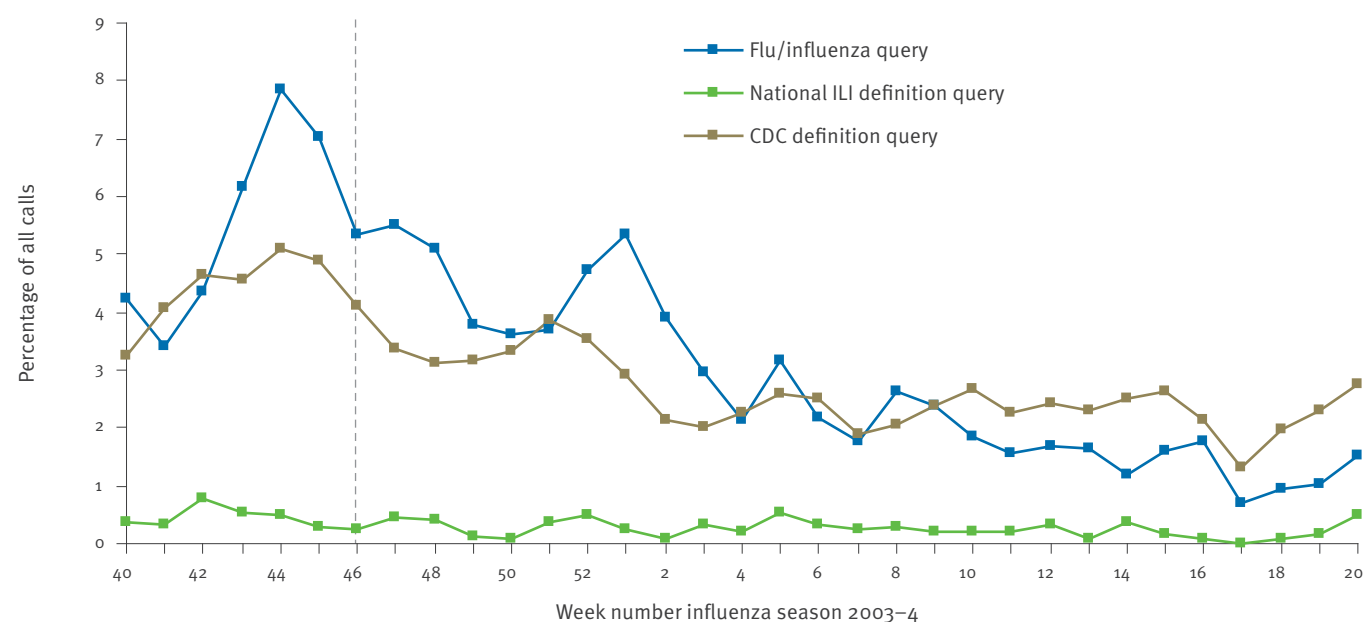
Results

All calls data

In total, during the six influenza seasons between 2003–4 and 2008–9, there were 539,732 calls to the two GP OOH services studied (Table 2), a mean of 2,712 calls per week. These calls included 210,932 calls (39%) for paediatric patients (<15 years of age), 253,703 calls (47%) for patients aged 15 to 69 years, and 73,648 calls (14%) for patients aged 70 years of age and over. More calls were received for female patients than for male patients (male to female ratio 1:1.2). Calls to the services increased year by year, as more doctors joined the scheme (199 GPs in 2003,

FIGURE 1

Ascertainment of apparent influenza using three query methods, Ireland, 2003–4 influenza season



CDC: United States Centers for Disease Control and Prevention; ILI: influenza-like illness.

General practice out-of-office hours extracted data are plotted as a weekly proportion of all calls. The vertical dashed line highlights the week of peak national ILI consultations.

269 GPs in 2009). The population coverage grew from 298,500 to 403,500 between 2003 and 2009 (see [10] for calculation of population coverage estimates for Irish GP OOH coops). Between 2003 and 2009 these GP coops provided OOH care for between 7% and 9.5% of the national population.

Ascertainment of influenza-like illness from general practitioner out-of-office hours records

Over the six influenza seasons, 17,062 records (3.2% of all records) were extracted using the self-reported illness query for flu/influenza (Table 2). The commonest age group for these calls varied with the influenza season. Calls were commonest among those aged 70 years and over for the first four seasons (2003–4 to 2006–7), in the 30–34 years group in 2007–8, and in children aged four years and under in 2008–9. Female patients accounted for more calls for flu or influenza symptoms than male patients.

Seasonal comparison with national indicators

The extracted records and national ILI consultation rates were compared for each influenza season over the six-year period by time series plot (Figure 2). The relationship between the datasets followed a similar pattern each year. National rates for ILI consultations peaked at various points in the season and peaks in extracted call data occurred at much the same time – early in the 2003–4 influenza season; over the Christmas period in the 2004–5, 2007–8, and 2008–9 seasons; and late in the season in 2005–6 and 2006–7 (Table 2 and Figure 2). The most notable difference between the datasets was that the peak in extracted call data occurred before the peak in national ILI consultation rates in five out of the six influenza seasons studied and was on average 1.5 weeks earlier over the six-year period (Table 2). It is worth noting that late

in the 2007–8 season, a second peak was observed in the regional ILI rates that was not reflected in the national data. A corresponding second peak was also observed in the call data (Figure 2). This demonstrates the ability of the call data to identify regional trends in influenza activity.

Spearman's rank correlation coefficient demonstrated a statistically significant temporal correlation between extracted call data and national ILI rates for all six seasons (Table 2). The highest correlation (0.909) was seen for the 2003–4 season, when two distinct peaks in activity early in the season were evident in both datasets. The lowest correlation (although still statistically significant) was observed in 2005–6.

Discussion

The GP OOH services in Ireland account for substantial healthcare interactions with patients in the community, and details of its activity are routinely recorded on computer. We have validated a method for extracting influenza-related call data from one such service using a commonly available database software package. Specific keyword queries were designed, based on widely accepted definitions for ILI. This was necessary as the service maintains records of the patients self-reported symptoms or illness in free text, rather than a clinical coding system.

We have shown from the six-year period examined in this study that extracted influenza-related call data closely matched patterns in national ILI rates (our gold standard) and this temporal association was shown to be statistically significant. For five out of the six seasons analysed, the week with the highest number of influenza-related calls for each season was at least one week ahead of the peaks in national ILI rates,

TABLE 2

Influenza-related calls extracted from general practitioner out-of-office hours data using influenza proxy measure, 2003–4 to 2008–9 influenza seasons

Item	Influenza season					
	2003–4	2004–5	2005–6	2006–7	2007–8	2008–9
Total number of call records for season	71,703	83,269	84,764	94,638	103,191	102,167
Number of call records extracted (%)	2,376 (3.3)	3,004 (3.6)	2,308 (2.7)	2,629 (2.8)	3,275 (3.2)	3,470 (3.4)
Male:female ratio for patients, from extracted records	1:1.4	1:1.2	1:1.3	1:1.3	1:1.2	1:1.4
Modal age group of patients (number of extracted records)	≥70 years (295)	≥70 years (292)	≥70 years (238)	≥70 years (283)	30–34 years (343)	0–4 years (363)
Week of highest number of extracted records/total (percentage of total)	W44 (7.85)	W53 (11.1)	W6 (4.9)	W6 (6)	W1 (7.8)	W52 (19)
Week of peak national ILI consultations	W46	W1	W10	W7	W1	W2
Number of weeks call-data peak leads ILI-data peak	2	1	4	1	0	2
Spearman's rank correlation coefficient ^a	0.901	0.709	0.679	0.888	0.858	0.759

ILI: influenza-like illness; W: week.

^a Spearman's rank correlation coefficient was calculated between the extracted calls as a proportion of total calls and the national ILI consultation rates compared weekly during the corresponding influenza season.

thus offering the potential for our self-reported illness query to be a useful syndromic surveillance measure, an early warning system.

The OOH service may provide an earlier indication of ILI activity partly because of the long periods for which it is operational. During an average week, the OOH service is in operation for over two thirds of the week (118 of 168 hours) and therefore patients with acute illnesses that need urgent attention may contact the OOH service rather than wait to make a daytime appointment to see their GP.

GP coops that provide OOH healthcare have become widely used by the Irish population in recent years [9,10]. The large scale of this interaction with the population and electronic availability of their records are not the only advantages that OOH datasets can provide. Data are entered into computer systems in real time while a patient calls the service, which means that information about the patient's reported condition, and often the doctor's diagnosis, is potentially available immediately for analysis. This may have important implications during a pandemic, when trends in influenza transmission may need to be analysed daily. Other than the information technology requirement to extract information daily or weekly, depending on the surveillance protocol, the service would bear no additional costs or workload, as the data would be collected routinely in any case.

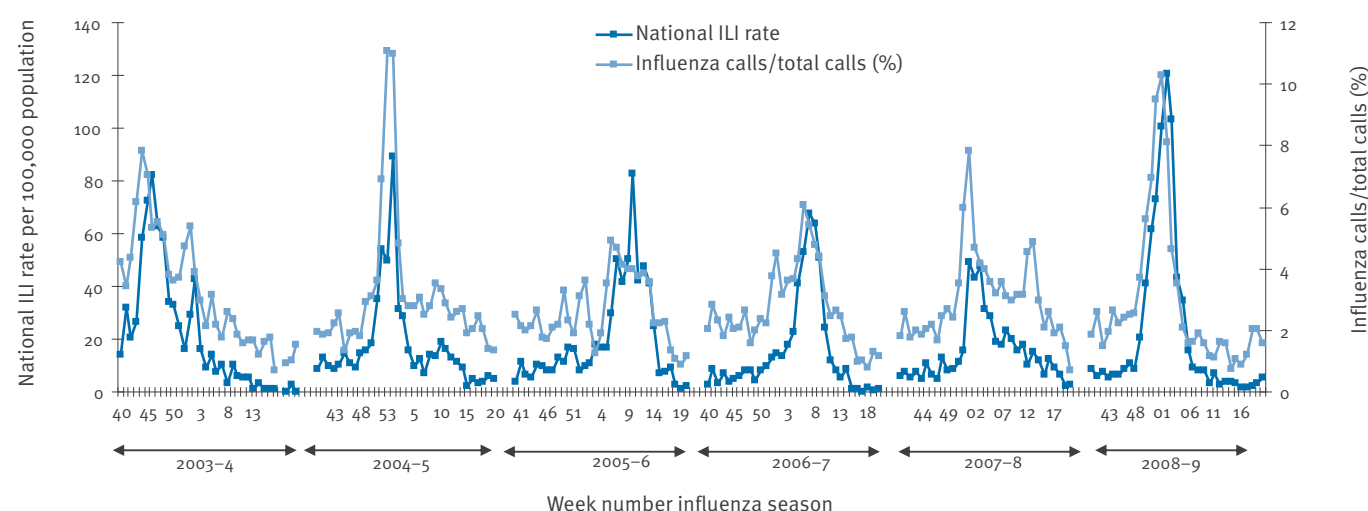
Another aspect of the dataset which could be utilised is the linkage of patient demographic data to the call record. Although this information was not collected for analysis in this study due to data protection issues,

it may be possible in the future to map demographic data for influenza-related calls by time and location. This type of analysis has the potential to identify local influenza outbreaks and their points of origin, thereby providing valuable insights on the geographical dissemination of new influenza viruses. Analysis of this type has already been employed with influenza military emergency and primary care surveillance data in the United States [16] and fever and vomiting calls to NHS Direct in the United Kingdom [3] to generate a 'moving picture' or tracking of cases through location and time.

There are, of course, some caveats to using data from the OOH services as an indicator of influenza activity. In the first instance, these services operate outside normal GP working hours (i.e. 18:00 to 08:00 for Monday to Friday and 24 hours for weekends and bank holidays). This means that some patients with ILI who present at GP surgeries during the day are being lost to this surveillance process. In addition, although most GPs in Ireland do participate in these OOH coops, the service is not ubiquitous. As the scheme is voluntary among GPs and GP practices are independent businesses, the services may never reach 100% coverage of the Irish population. The most important limitation of the data from the OOH services is the recording of the patient's reported condition in a free-text format. Clearly, analysis of free-text fields to identify trends and patterns in data over time can be a time-consuming and difficult task. Other analyses of influenza-related healthcare syndromic surveillance data have used software systems that map symptoms to syndromes [18-22] or used a decision support system or natural language processing tool to categorise all calls [1,2,17,23,24].

FIGURE 2

National data on influenza-like illness consultation rate^a and extracted influenza calls^b, 2003-4 to 2008-9 influenza seasons



ILI: influenza-like illness.

^a Per 100,000 population per week.

^b As a percentage of all weekly calls to the general practitioner out-of-office hours services under study.

Currently, there is no facility for mapping of patient symptoms to syndromes or clinical coding – e.g. International Classification of Diseases (ICD) – of the data by the majority of Irish OOH services, although the Adastra software system could be upgraded to allow for this. The benefits of such an upgrade would include uniform classification of calls, the ability to easily review and analyse trends over time and the possibility of integration into a syndromic surveillance system that could provide an early warning system for outbreaks and other conditions of public health importance. However, additional time on each call and a change in work practice by the services would be needed in order to implement coding/mapping on the service and this is not envisaged at present.

On completion of this study, the nine OOH services in Ireland were approached and asked to provide a weekly extract for analysis of influenza-related calls using the methodology described in this paper. All of these OOH services now provide data regularly for analysis, covering about 70% (three million) of the Irish population. Results of this weekly analysis have been available since week 19 of the 2008–9 influenza season and are included in the national weekly influenza report produced by the HPSC [13]. Increases in influenza-related calls to these OOH services observed since week 29 of the season coincided with increases seen in national ILI consultation rates, reflecting the spread of the pandemic influenza A(H1N1) virus in Ireland.

Most significantly, the weekly analysis of the GP OOH influenza-related call data was used by the National Crisis Management Team in combination with other influenza indicators to shape the response to the 2009 influenza pandemic in Ireland. These data may also provide information for action at local level. It has been observed anecdotally that increases in calls for influenza in younger age groups to the OOH service may herald an increase in presentations to hospital emergency departments. Advance notice of such increases in the community, particularly during a pandemic, can give hospitals valuable time to prepare separate waiting areas, obtain adequate stocks of antiviral drugs and diagnostic swabs, and ensure that an action plan for rapid admission to isolation of suspected cases is in place. Furthermore, analysis of past trends in influenza-related calls can allow individual OOH services to review their own personnel arrangements for peak influenza and indeed pandemic periods.

Conclusions

This study has shown that it is possible to extract influenza-related patient contact records from an urgent OOH GP service in Ireland and that the data have the potential to be utilised as an early alert system for seasonal and pandemic influenza. Collection of data from all OOH services to obtain a national overview can provide valuable epidemiological information at a relatively low resource and infrastructure cost. This meth-

odology could be applied to other important areas of public health surveillance.

Acknowledgements

The authors would like to thank the GP OOH services for their continuing participation in this study and also the HPSC for providing the national influenza indicator data.

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