



The Fogarty International Center MISMS Newsletter

FALL 2011

Scientists convene at training workshops in Beijing, Kathmandu, and DC

The MISMS research team organized three interdisciplinary training workshops this summer, both in the US and abroad. On June 7-8, the Fogarty International Center hosted the [Second Annual Interdisciplinary Meeting & Workshop on Influenza Virus Evolution, Immunity, and Epidemiology](#) at the NIH campus in Bethesda, Maryland. Participants had the opportunity to discuss in detail the molecular epidemiology, antigenic evolution, and transmission dynamics of influenza viruses in humans and non-human hosts. The phylogenetics workshop that followed the general meeting was designed to build analytical capacity for molecular studies of influenza, identify potential collaborators, and disseminate new scientific findings from participants. Scientists from various divisions of the NIH, other federal institutions, and a number of universities attended both days. The complete agendas of the [general scientific meeting](#) and [training workshop](#) can be found on our website.



MISMS Interdisciplinary Meeting & Workshop on Influenza Virus Evolution, Immunity, and Epidemiology
June, 2011, Bethesda, MD, USA

In August, we conducted two consecutive meetings and training workshops in Asia—one in Beijing, China and the other in Kathmandu, Nepal. In coordination with the China Center for Disease Control and Prevention (China CDC, Beijing), Fogarty co-hosted the [International Forum on Influenza and Other](#)



MISMS International Influenza Technical Training Workshop
August, 2011, Beijing, China

[Respiratory Infections 2011](#) (August 2-4) and the [MISMS Beijing Technical Training Workshop](#) (August 4-6). The international forum focused on the burden, transmission dynamics, virology, and evolution of influenza and respiratory bacterial infections in East Asia. The conference was attended by leading public health officers, academic scientists, and government researchers from China and a number of other countries. As with previous MISMS workshops, the training sessions that followed focused on phylogenetic evolution, reproductive number estimation, and the analysis of time-series and spatial epidemiologic data.

The FIC team spent the following week in Kathmandu, Nepal to host the [MISMS South Asian Influenza Meeting and Training Workshop](#). Marking the milestone tenth MISMS regional influenza meeting, this workshop took place on August 9-13, 2011. Both the general scientific meeting and training workshop were by attended by epidemiologists, physicians, microbiologists, and health policymakers from Nepal, Bangladesh, India, and Pakistan, among a number of other countries. Participant presentations focused on the obstacles and successes of influenza surveillance programs, the disease burden of the 2009 A/H1N1 pandemic, and various issues related to national vaccine and control policies.



Participants also had the opportunity to share information about their datasets, with a primary focus on the disease burden and transmission dynamics of influenza viruses in human and avian populations from this region. The technical workshops helped build analytical capacity for epidemiologic and molecular studies of influenza, identify potential collaborators, and disseminate new scientific findings. Particular emphasis was given to the mathematical and statistical modeling of epidemiologic, vital-statistic, and virologic data, as well as the analysis of phylogenetic and antigenic data.

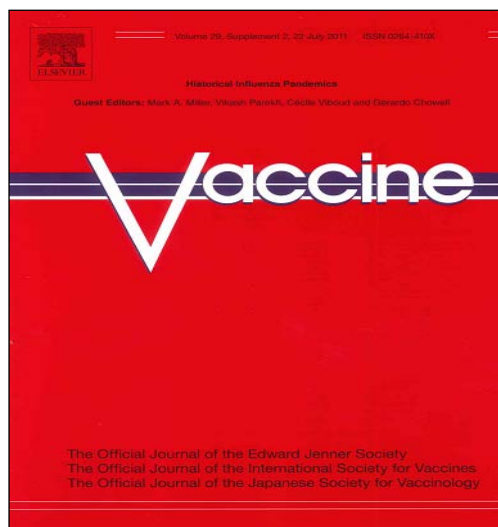


MISMS South Asia Influenza Meeting and Workshop
August, 2011, Kathmandu, Nepal

As with previous MISMS training workshops, many three workshops have helped facilitate future conversations that were initiated during each of these interdisciplinary multinational collaborations.

Special issue on “Historical Influenza Pandemics” published in *Vaccine*

On July 22, 2011, after months of editorial preparation by the MISMS team, the scientific journal *Vaccine* published a special issue focusing on historical influenza pandemics, specifically the methodologies used to analyze data from past pandemics and the relevance of findings to the development of future pandemic preparedness efforts. In addition to an editorial commentary written by MISMS staff, the special issue contains 11 original studies that were presented in May 2010 at the [MISMS “Historical Influenza Pandemics: Lessons Learned” Meeting and Workshop](#) in Copenhagen, Denmark. This multidisciplinary conference was coordinated by the Fogarty International Center, in partnership with the Statens Serum Institute and Roskilde University, both of Denmark, and was comprised of epidemiologists, mathematicians, historians, sociologists, public health officials, virologists, evolutionary biologists, and demographers. This issue of *Vaccine* addresses a broad range of topics related to pandemic influenza data, including early attempts to characterize and control the 1889 pandemic; the transmission and burden patterns of the 1918 pandemic in Peru, Brazil,



the US, Canada, and Italy; the impact of the recent 2009 A/H1N1 pandemic in Denmark; and the implementation of global surveillance systems to monitor the 2009 pandemic. The [full issue](#) of this supplement is available for download on our website. Limited hard copies are available by request at (ficmisms@mail.nih.gov).



Fogarty Collaborator Spotlights

Among its many collaborative mechanisms, the Fogarty International Center supports visiting fellows and scholars who perform research and receive individualized training at the NIH Headquarters in Bethesda, Maryland. Recent visiting researchers have come from France, Italy, Iceland, Taiwan, Brazil, Japan, South Korea, South Africa, Portugal, Denmark, and the US. Here we spotlight Drs. Dan Weinberger, Magnus Gottfredsson, and Aba Mahamat.

Dan Weinberger, PhD

Fogarty International Center, Bethesda, USA

Dan Weinberger, PhD joined the Fogarty International Center in July 2010, shortly after completing his doctoral training in the Biological Science in Public Health (BPH) and Epidemiology of Infectious Diseases programs at Harvard School of Public Health (HSPH). At HSPH, Dan worked with MISMS collaborator Marc Lipsitch, DPhil to identify the underlying biological mechanisms influencing the epidemiological patterns of pneumococcal carriage and disease.

Dan was initially interested in pursuing a career in basic science with a specific focus on host-pathogen interactions and bacterial genetics; however, this interest soon expanded and evolved to include research on microbial population biology and epidemiology. Fortunately, Marc Lipsitch's lab provided him with a unique opportunity to pursue research questions that were relevant to both basic microbiology and to population biology and epidemiology.

At Fogarty, Dan is investigating the interactions between influenza, respiratory syncytial viruses, and pneumococcal disease. He has collaborated with the Statens Serum Institut in Copenhagen, Denmark to examine the associations between influenza viruses and the incidence of specific pneumococcal serotypes. In another project, he has used data from the Agency for Healthcare Research and Quality to estimate the impact of the 2009 A/H1N1 pandemic

on the incidence of hospitalizations for pneumococcal disease in the US, the findings of which will appear in the *Journal of Infectious Diseases*. He is also working with Magnus Gottfredsson, a MISMS collaborator from Iceland, also spotlighted in this issue, to better understand the long-term trends in the timing and seasonality of influenza epidemics in Iceland over the course of the last century.



At Fogarty, Dan has had the opportunity to interact and collaborate with a diverse group of researchers from around the world. Beyond his research responsibilities, he enjoys exploring Washington, DC's various museums and bicycle trails.



Aba Mahamat, MD, PhD

Fogarty International Center, Bethesda, USA; General Hospital, Cayenne, French Guiana

Originally from Cayenne, the capital of the French overseas region of French Guiana, **Aba Mahamat, MD, PhD** was a visiting researcher at Fogarty from November 2010 to March 2011. During his time at the NIH, he studied the epidemiology of influenza in the equatorial regions of the Americas, working closely with Wladimir Alonso, PhD and other MISMS scientists and collaborators. Dr. Mahamat also performed related analyses on the seasonality of influenza in tropical regions and the impact of rainfall and humidity on influenza in French Guiana.



In his primary affiliation with the Infectious Diseases Unit of the General Hospital in Cayenne, his central responsibilities include medical consultations and the development of antibiotic prescription guidelines. In contrast, much of his time at Fogarty was spent using statistical software packages to analyze epidemiologic data. During his time in the US, he enjoyed attending scientific lectures at the NIH and visiting the Smithsonian Museums and national monuments in Washington, DC.

Dr. Mahamat received his MD from the University of Lille in 2001 and his PhD in epidemiology from the University of Montpellier in 2008.

Magnus Gottfredsson, MD, PhD,

Fogarty International Center, Bethesda, USA; Landspítali Hospital, Reykjavik, Iceland

Originally from Iceland, **Magnus Gottfredsson, MD, PhD** has developed a close working relationship with Fogarty over the past few years.

Dr. Gottfredsson received his MD and PhD from the University of Iceland and completed a residency in internal medicine and a fellowship in infectious diseases at Duke University. Now based at Landspítali Hospital in Reykjavik, his busy schedule is split between clinical work, teaching, and research.



Why study population health in Iceland? “Iceland is a fascinating example of a relatively isolated and sparsely-populated island with a long history of carefully recorded demographic, disease, and genealogy data. Therefore, it is an ideal place for the population-level study of a variety of illnesses.”

At the NIH, Magnus initially partnered with Mark Miller, MD and researchers from NICHD on a joint project on the late sequelae of invasive meningococcal disease, the results of which will be published this fall in *Clinical Infectious Diseases*, and then collaborated with Fogarty researchers on the analysis of historical influenza data from Iceland. This work then led to an extended visit at the “Stone House”, during which he continued his collaborations at NICHD and FIC. He is currently completing a paper comparing the seasonality of influenza in Iceland to the US and Northern Europe over the past 100 years. The data from this study has allowed him to study the determinants of global disease spread in the context of changing international travel patterns.

Always adventurous, Magnus spends his free time reading, hiking, mountain-climbing, running, and skiing. During his time in the DC, he particularly enjoyed visiting a number of the Smithsonian museums. “I turned into a curious ten-year-old every time I visited them.”



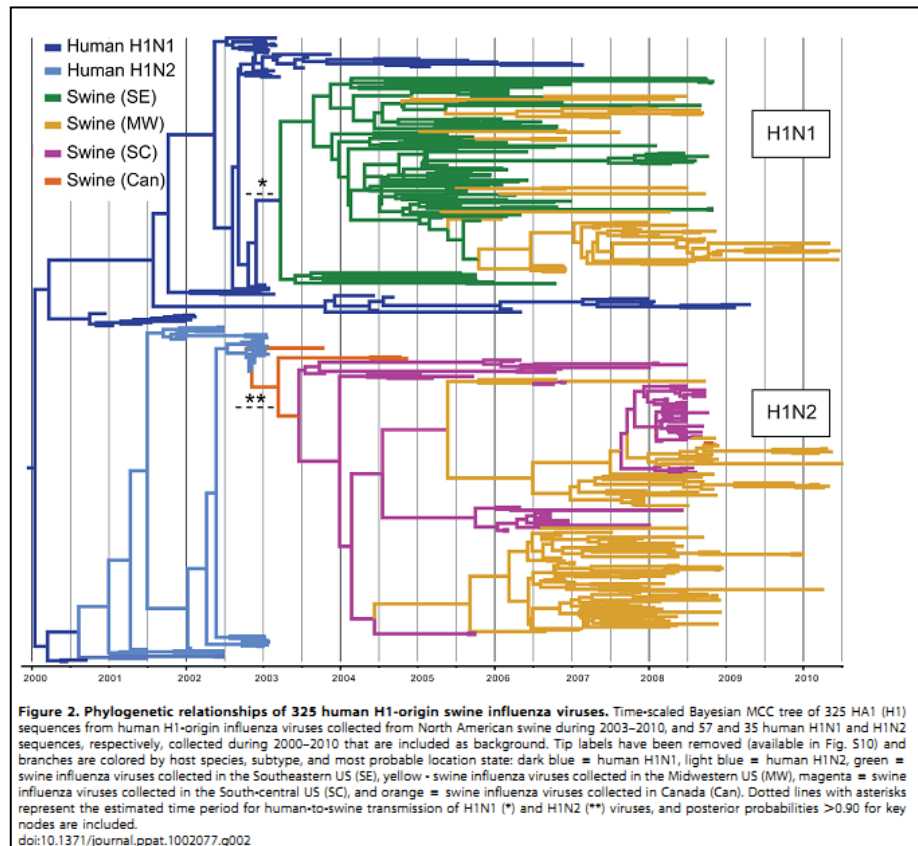
Study Highlights

The MISMS research initiative has published a breadth of articles on influenza viruses over the years. Articles have focused on topics as diverse as influenza evolutionary dynamics, the disease burden and transmission of influenza, and the effectiveness of control strategies. A selection of recent articles is summarized here, and the [full MISMS bibliography](#) can be found on our website.

SPATIAL DYNAMICS OF HUMAN-ORIGIN H1 INFLUENZA A VIRUS IN NORTH AMERICAN SWINE

Nelson MI, Lemey P, Tan Y, Vincent A, Lam TT, Detmer S, Viboud C, Suchard MA, Rambaut A, Holmes EC, Gramer M. *PLoS Pathog.* 2011 Jun; 7(6): e1002077.

The emergence and rapid global spread of the swine-origin H1N1/09 pandemic influenza A virus in humans underscores the importance of swine populations as reservoirs for genetically diverse influenza viruses with the potential to infect humans. However, despite their significance for animal and human health, relatively little is known about the phylogeography of swine influenza viruses in the United States. This study utilizes an expansive data set of hemagglutinin (HA1) sequences (n = 1516) from swine influenza viruses collected in North America during the period 2003-2010. With these data we investigate the spatial dissemination of a novel influenza virus of the H1 subtype that was introduced into the North American swine population via two separate human-to-swine transmission events around 2003. Bayesian phylogeographic analysis reveals that the spatial dissemination of this influenza virus in the US swine population follows long distance swine movements from the Southern US to the Midwest, a corn-rich commercial center that imports millions of swine annually. Hence, multiple genetically diverse influenza viruses are introduced and co-circulate in the Midwest, providing the opportunity for genomic reassortment. Overall, the Midwest serves primarily as an ecological sink for swine influenza in the US, with sources of virus genetic diversity instead located in the Southeast (mainly North Carolina) and South-central (mainly Oklahoma) regions. Understanding the importance of long-distance pig transportation in the evolution and spatial dissemination of the influenza virus in swine may inform future strategies for the surveillance and control of influenza, and perhaps other swine pathogens.



ELEVATED INFLUENZA-RELATED EXCESS MORTALITY IN SOUTH AFRICAN ELDERLY INDIVIDUALS, 1998-2005

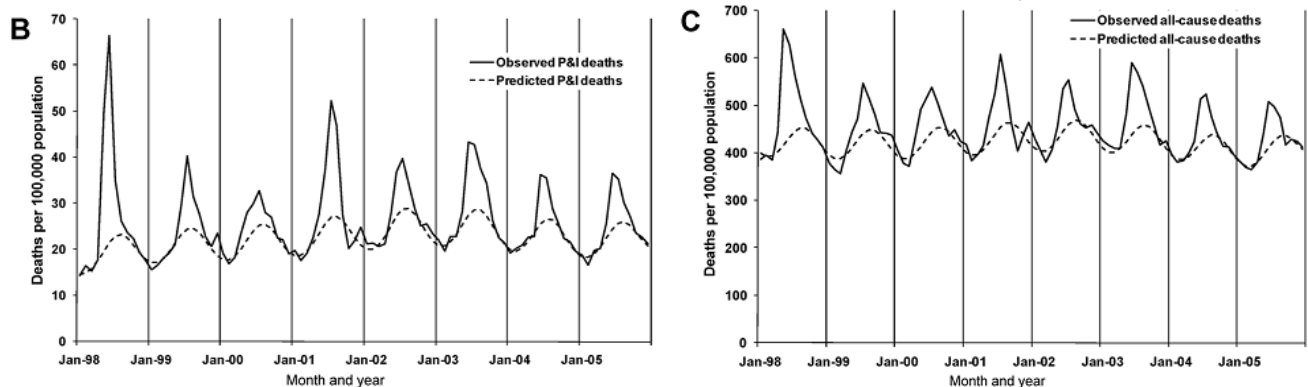
Cohen C, Simonsen L, Kang JW, Miller M, McAnerney J, Blumberg L, Schoub B, Madhi SA, Viboud C. *Clin Infect Dis.* 2010 Dec 15; 51(12): 1362-9.

BACKGROUND: Although essential to guide control measures, published estimates of influenza-related seasonal mortality for low- and middle-income countries are few. We aimed to compare influenza-related mortality among individuals aged ≥ 65 years in South Africa and the United States.

METHODS: We estimated influenza-related excess mortality due to all causes, pneumonia and influenza, and other influenza-associated diagnoses from monthly age-specific mortality data for 1998-2005 using a Serfling regression model. We controlled for between-country differences in population age structure and non-demographic factors (baseline mortality and coding practices) by generating age-standardized estimates and by estimating the percentage excess mortality attributable to influenza.

RESULTS: Age-standardized excess mortality rates were higher in South Africa than in the United States: 545 versus 133 deaths per 100,000 population for all causes ($P < .001$) and 63 vs 21 deaths per 100,000 population for pneumonia and influenza ($P = .03$). Standardization for non-demographic factors decreased but did not eliminate between-country differences; for example, the mean percentage of winter deaths attributable to influenza was 16% in South Africa and 6% in the United States ($P < .001$). For all respiratory causes, cerebrovascular disease, and diabetes, age-standardized excess death rates were 4-8-fold greater in South Africa than in the United States, and the percentage increase in winter deaths attributable to influenza was 2-4-fold higher.

CONCLUSIONS: These data suggest that the impact of seasonal influenza on mortality among elderly individuals may be substantially higher in an African setting, compared with in the United States, and highlight the potential for influenza vaccination programs to decrease mortality.



B, Deaths due to pneumonia and influenza (P&I). C, Deaths due to all causes. Note that the number of deaths predicted is under the assumption that influenza viruses were not circulating.



GLOBAL INFLUENZA SEASONALITY: RECONCILING PATTERNS ACROSS TEMPERATE AND TROPICAL REGIONS

Tamerius J, Nelson MI, Zhou SZ, Viboud C, Miller MA, Alonso WJ. *Environ Health Perspect.* 2011 Apr; 119(4): 439-45.

BACKGROUND: Despite the significant disease burden of the influenza virus in humans, our understanding of the basis for its pronounced seasonality remains incomplete. Past observations that influenza epidemics occur in the winter across temperate climates, combined with insufficient knowledge about the epidemiology of influenza in the tropics, led to the perception that cool and dry conditions were a necessary, and possibly sufficient, driver of influenza epidemics. Recent reports of substantial levels of influenza virus activity and well-defined seasonality in tropical regions, where warm and humid conditions often persist year-round, have rendered previous hypotheses insufficient for explaining global patterns of influenza.

OBJECTIVE: In this review, we examined the scientific evidence for the seasonal mechanisms that potentially explain the complex seasonal patterns of influenza disease activity observed globally.

METHODS: In this review we assessed the strength of a range of hypotheses

that attempt to explain observations of influenza seasonality across different latitudes and how they relate to each other. We reviewed studies describing population-scale observations, mathematical models, and ecological, laboratory, and clinical experiments pertaining to influenza seasonality. The literature review includes studies that directly mention the topic of influenza seasonality, as well as other topics we believed to be relevant. We also developed an analytical framework that highlights the complex interactions among environmental stimuli, mediating mechanisms, and the seasonal timing of influenza epidemics and identify critical areas for further research.

CONCLUSIONS: The central questions in influenza seasonality remain unresolved. Future research is particularly needed in tropical localities, where our understanding of seasonality remains poor, and will require a combination of experimental and observational studies. Further understanding of the environmental factors that drive influenza circulation also may be useful to predict how dynamics will be affected at regional levels by global climate change.

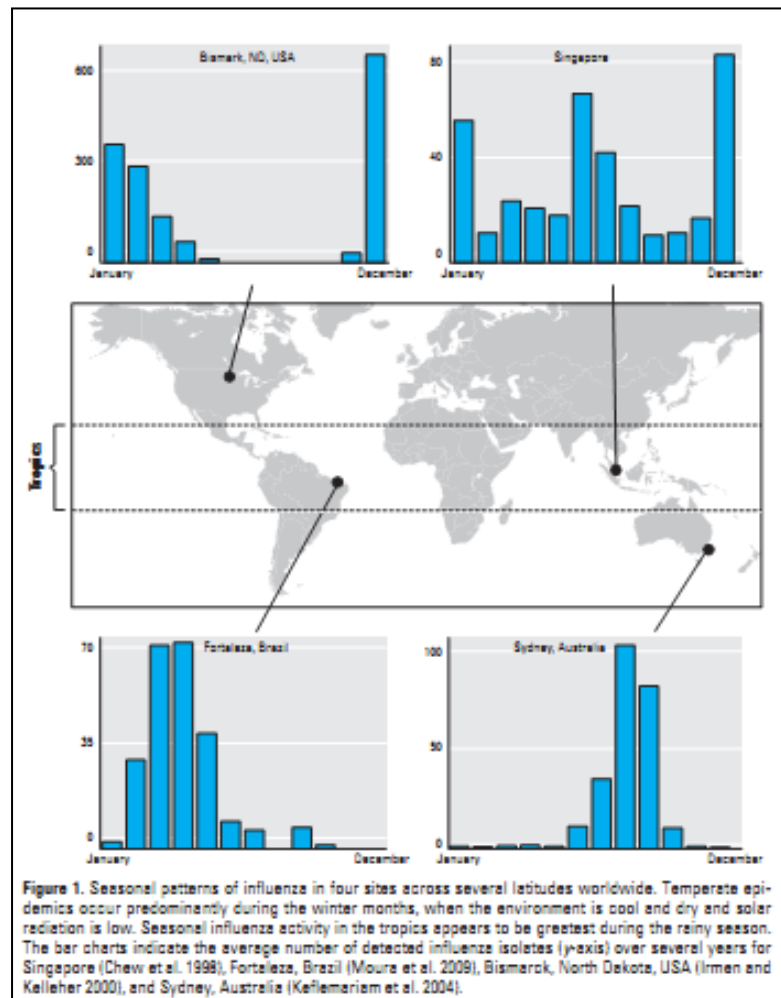


Figure 1. Seasonal patterns of influenza in four sites across several latitudes worldwide. Temperate epidemics occur predominantly during the winter months, when the environment is cool and dry and solar radiation is low. Seasonal influenza activity in the tropics appears to be greatest during the rainy season. The bar charts indicate the average number of detected influenza isolates (y-axis) over several years for Singapore (Chew et al. 1998), Fortaleza, Brazil (Moura et al. 2008), Bismarck, North Dakota, USA (Imren and Kelleher 2000), and Sydney, Australia (Kelleher et al. 2004).



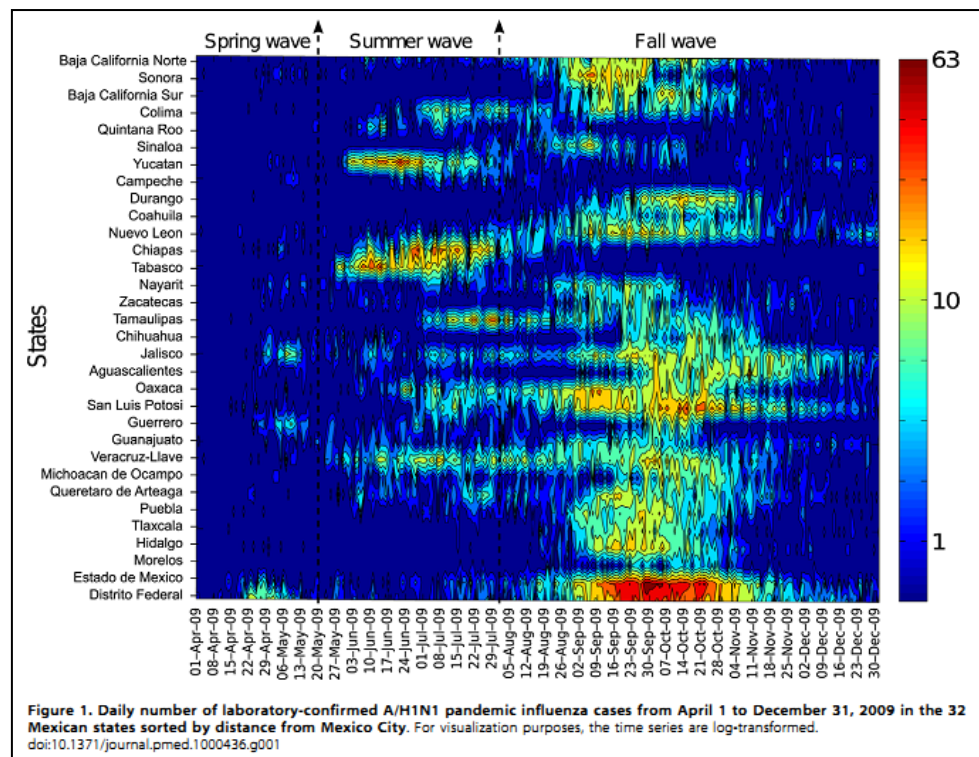
CHARACTERIZING THE EPIDEMIOLOGY OF THE 2009 INFLUENZA A/H1N1 PANDEMIC IN MEXICO

Chowell G, Echevarría-Zuno S, Viboud C, Simonsen L, Tamerius J, Miller MA, Borja-Aburto VH. PLoS Med. 2011 May; 8(5): e1000436.

BACKGROUND: Mexico's local and national authorities initiated an intense public health response during the early stages of the 2009 A/H1N1 pandemic. In this study, we analyzed the epidemiological patterns of the pandemic during April-December 2009 in Mexico and evaluated the impact of nonmedical interventions, school cycles, and demographic factors on influenza transmission.

METHODS AND FINDINGS: We used influenza surveillance data compiled by the Mexican Institute for Social Security, representing 40% of the population, to study patterns in influenza-like illness (ILIs) hospitalizations, deaths, and case-fatality rate by pandemic wave and geographical region. We also estimated the reproduction number (R) on the basis of the growth rate of daily cases and used a transmission model to evaluate the effectiveness of mitigation strategies initiated during the spring pandemic wave. A total of 117,626 ILI cases were identified during April-December 2009, of which 30.6% were tested for influenza and 23.3% were positive for the influenza A/H1N1 pandemic virus. A three-wave pandemic profile was identified, with an initial wave in April-May (Mexico City area), a second wave in June-July (southeastern states), and a geographically widespread third wave in August-December. The median age of laboratory confirmed ILI cases was ~18 years overall and increased to ~31 years during autumn ($p < 0.0001$). The case-fatality ratio among ILI cases was 1.2% overall, and highest (5.5%) among people over 60 years. The regional R estimates were 1.8-2.1, 1.6-1.9, and 1.2-1.3 for the spring, summer, and fall waves, respectively. We estimate that the 18-day period of mandatory school closures and other social distancing measures implemented in the greater Mexico City area were associated with a 29%-37% reduction in influenza transmission in spring 2009. In addition, an increase in R was observed in late May and early June in the southeast states, after mandatory school suspension resumed and before summer vacation started. State-specific fall pandemic waves began 2-5 weeks after school reopened for the fall term, coinciding with an age shift in influenza cases.

CONCLUSIONS: We documented three spatially heterogeneous waves of the 2009 A/H1N1 pandemic virus in Mexico, which were characterized by a relatively young age distribution of cases. Our study highlights the importance of school cycles on the transmission dynamics of this pandemic influenza strain and suggests that school closure and other mitigation measures could be useful to mitigate future influenza pandemics.



MORTALITY BURDEN OF THE A/H1N1 PANDEMIC IN MEXICO: A COMPARISON OF DEATHS AND YEARS OF LIFE LOST TO SEASONAL INFLUENZA

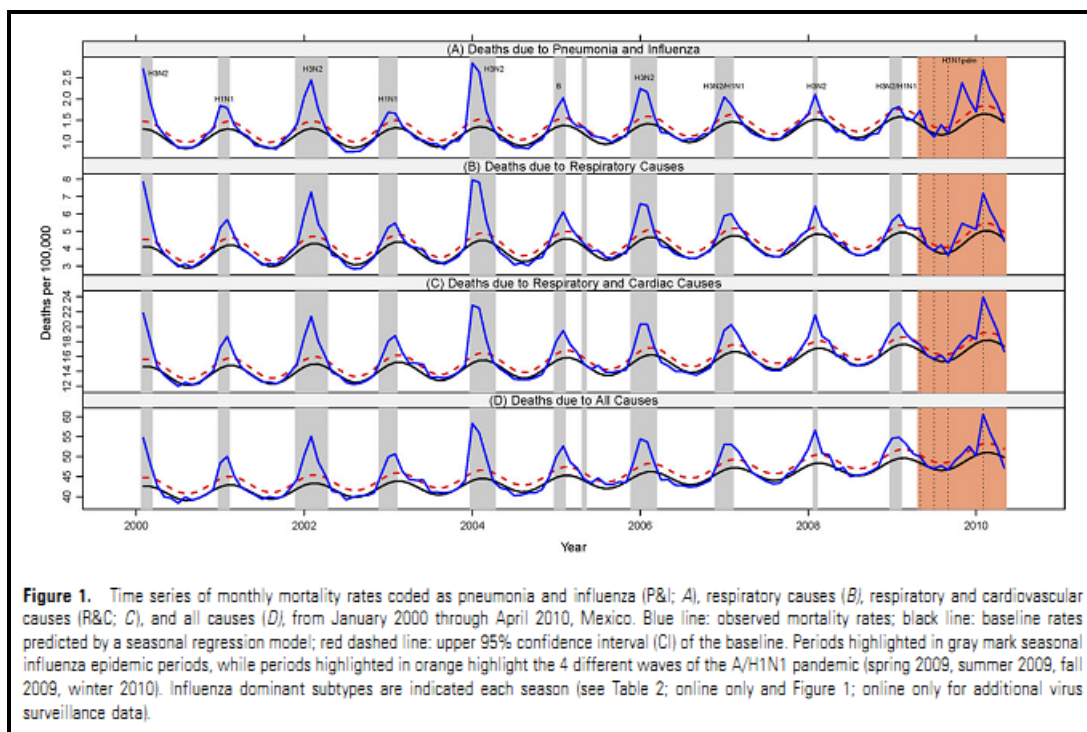
Charu V, Chowell G, Palacio-Mejia LS, Santiago Echevarría-Zuno, Borja-Aburto VH, Simonsen L, Miller MA, Viboud C. *CID*. 2011. In press.

BACKGROUND: The mortality burden of the 2009 A/H1N1 influenza pandemic remains controversial, in part because of delays in reporting of vital statistics that are traditionally used to measure influenza-related excess mortality. Here, we compare excess mortality rates and years of life lost (YLL) for pandemic and seasonal influenza in Mexico and evaluate laboratory-confirmed death reports.

METHODS: Monthly age- and cause-specific death rates from January 2000 through April 2010 and population-based surveillance of influenza virus activity were used to estimate seasonal excess mortality and YLL in Mexico. Age-stratified laboratory-confirmed A/H1N1 death reports were obtained from an active surveillance system covering 40% of the population.

RESULTS: The A/H1N1 pandemic was associated with 11.1 excess all-cause deaths per 100,000 population and 445,000 YLL during the 3 waves of the pandemic during April–December 2009 in Mexico. The mortality burden was 0.6–2.6-fold higher than that during a typical influenza season and lower than that during the severe 2003–2004 influenza epidemic. Individuals aged 5–19 and 20–59 years were disproportionately affected, relative to their experience with seasonal influenza. Laboratory-confirmed deaths captured 1 of 7 pandemic excess deaths overall but only 1 of 41 deaths in persons >60 years of age in 2009. A recrudescence of excess mortality was observed in older persons during winter 2010, in a period when influenza and respiratory syncytial virus cocirculated.

CONCLUSIONS: Mexico experienced higher 2009 A/H1N1 pandemic mortality burden than other countries for which estimates are available. Further analyses of detailed vital statistics are required to assess geographical variation in the mortality patterns of this pandemic.



NATALITY DECLINE AND MISCARRIAGES ASSOCIATED WITH THE 1918 INFLUENZA PANDEMIC: THE SCANDINAVIAN AND UNITED STATES EXPERIENCES

Bloom-Feshbach K, Simonsen L, Viboud C, Mølbak K, Miller MA, Gottfredsson M, Andreasen V. J Infect Dis. 2011 Oct; 204(8): 1157-64.

BACKGROUND: Although pregnancy is a recognized risk factor for severe influenza infection, the effect of influenza on miscarriages and births remains unclear. We examined the relationship between influenza and birth rates during the 1918 pandemic in the United States, Denmark, Sweden, and Norway.

METHODS: We compiled monthly birth rates from 1911 through 1930 in 3 Scandinavian countries and the United States, identified periods of unusually low or high birth rates, and quantified births as "missing" or "in excess" of the normal expectation. Using monthly influenza data, we correlated the timing of peak pandemic exposure and depressions in birth rates, and identified pregnancy stages at risk of influenza-related miscarriage.

RESULTS: Birth rates declined in all study populations in spring 1919 by a mean of 2.2 births per 1000 persons, representing a 5%-15% drop below baseline levels ($P < .05$). The 1919 natality depression reached its trough 6.1-6.8 months after the autumn pandemic peak, suggesting that missing births were attributable to excess first trimester miscarriages in ~ 1 in 10 women who were pregnant during the peak of the pandemic. Pandemic-related mortality was insufficient to explain observed patterns.

CONCLUSION: The observed birth depressions were consistent with pandemic influenza causing first trimester miscarriages in ~ 1 in 10 pregnant women. Causality is suggested by temporal synchrony across geographical areas.

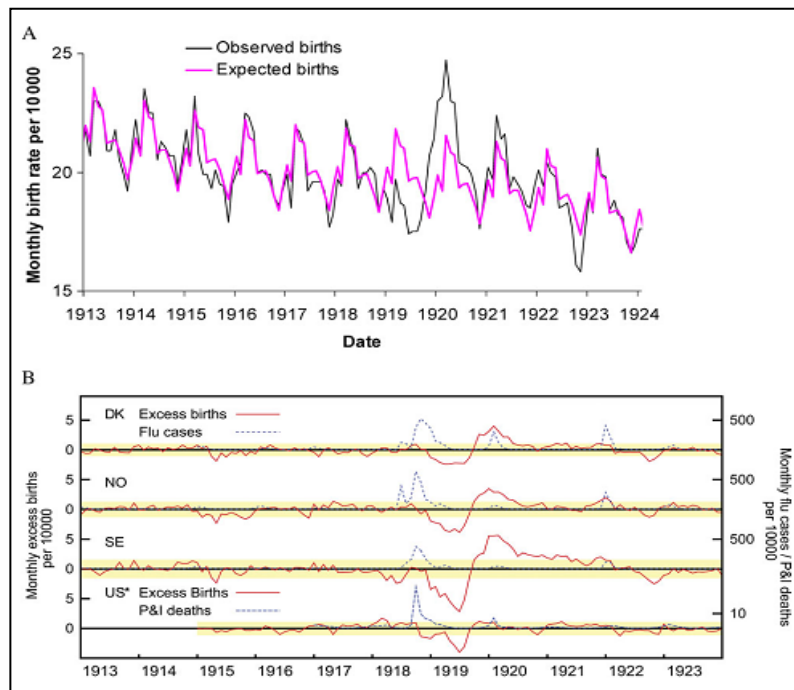


Figure 1. Timing of influenza pandemic and birth rate reduction in Denmark, Norway, Sweden, and the United States. *A*, Time series of monthly natality rates in Denmark during several decades surrounding the 1918 pandemic. It can be seen that an unusual and unseasonal birth rate depression occurred in early 1919, followed by an equally unusual increase (compensation) from late 1919 through early 1920. The natality patterns are typical for natality data from each of the populations studied. *B*, Time series of residual natality rates after subtracting out the expected (modeled) baseline, contrasted with the peak influenza (flu) periods, for Denmark (DK), Norway (NO), Sweden (SE), and the United States (US). For each study population, the severe autumn 1918 peak was followed by a temporary period of compensation 6–9 months later. This decline is attributed to first trimester miscarriages among a subset of all pregnant women who had pandemic influenza. The shaded areas represent the 95% confidence intervals P&I deaths indicate respiratory mortality due to pneumonia and influenza.



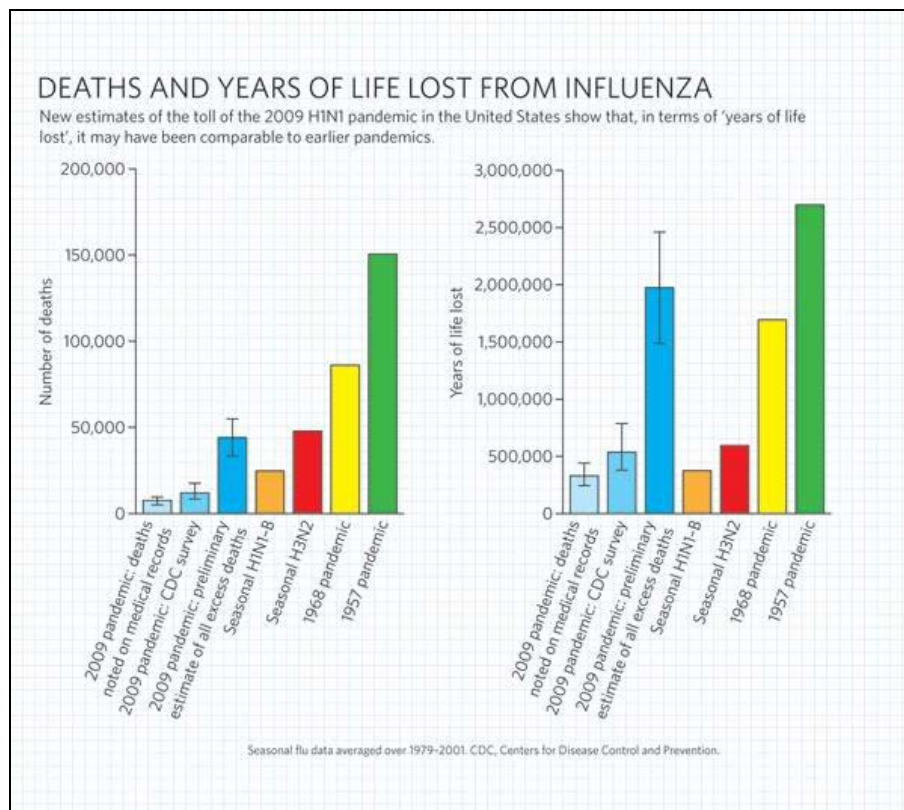
PORTRAIT OF A YEAR-OLD PANDEMIC

Butler D. Nature. 2010 Apr 22; 464(7292): 1112-3. Commentary

“The 2009 pandemic was not the killer of 1918. ‘Most people were less likely to get infected than in previous pandemics, less likely to get sick if they did, and less likely to die if they got sick,’ says Marc Lipsitch, an epidemiologist at Harvard School of Public Health in Boston, Massachusetts. But with the pandemic still playing out, it may be years before we get a reliable estimate of how many deaths it has caused. **Research published last month in the journal *PLoS Currents Influenza*, by Cécile Viboud of the US National Institutes of Health (NIH) in Bethesda, Maryland, and her colleagues, suggests that the first waves may have been more severe than is widely perceived.**

Viboud and her team tested different approaches for estimating flu mortality in the United States, with the most conservative estimates based on medical records that officially reported flu as the cause of death. This is likely to be an underestimate: many flu deaths are not recorded as such, with death often ascribed instead to an underlying condition, such as heart disease or diabetes.

This conservative approach estimated US pandemic flu deaths at around 7,500–12,000: less than half the number caused annually in the United States by seasonal influenza H1N1 and influenza B viruses. But this method also revealed that the number of life years lost was around a quarter more than usual because the 2009 pandemic deaths were skewed towards younger ages than seasonal flu (see '[Deaths and years of life lost from influenza](#)'). Under a less conservative estimate, based on comparing overall mortality during the pandemic with mortality over the same period in previous years, excess deaths numbered 44,100, surpassing those of a typical flu season. Years of life lost were three to four times higher than a virulent H3N2 season and five times higher than years of life lost to seasonal H1N1 and B viruses — of the same order as the 1968 flu pandemic.”



A selection of recent MISMS publications

For a full list of Fogarty International Center publications, visit <http://origem.info/FIC/Bibliography.html>

Influenza virus evolutionary patterns

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Pandemic influenza

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Influenza vaccine benefits and control strategies

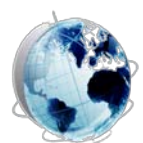
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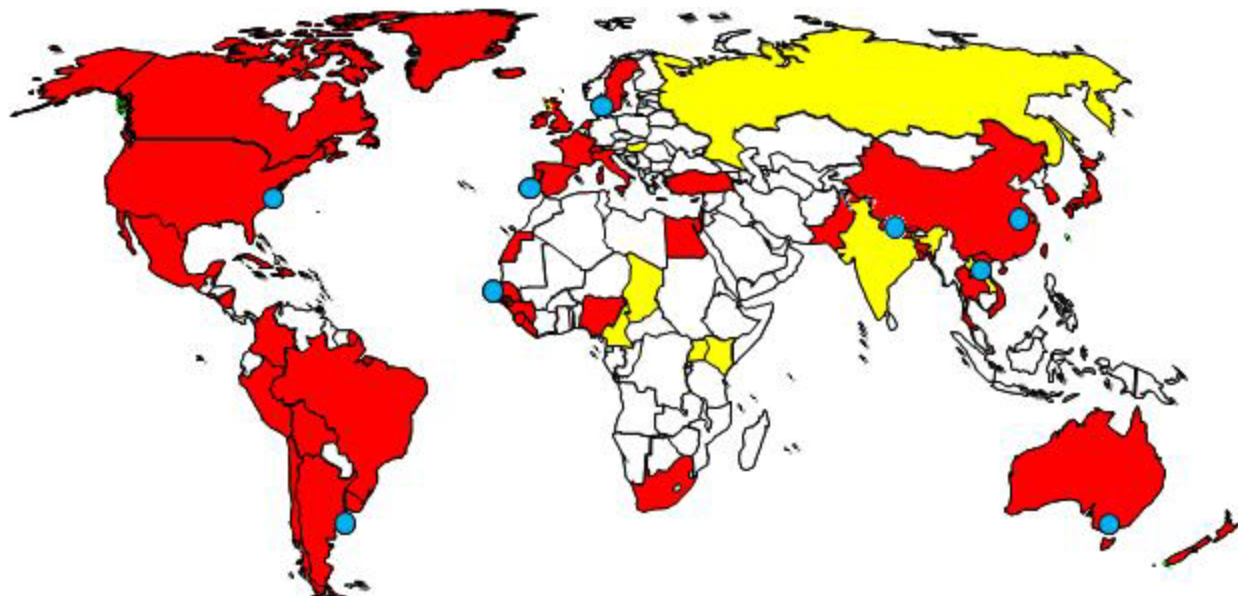
MISMS Overview

Originally called the Multinational Influenza Seasonal Mortality Study, MISMS was initiated in 2001 to analyze national and global mortality patterns associated with influenza virus circulation. The focus of MISMS has since expanded to include evaluating the interaction between the epidemiology, ecology, and evolutionary dynamics of influenza, including natural selection, reassortment, migration, and antigenic change.

MISMS has two specific aims:

1. To analyze the transmission patterns of influenza viruses, quantify time trends and geographical variations in age-specific disease burden, and evaluate control strategies.
2. To understand the interaction between the health impact and the antigenic, genomic, and evolutionary characteristics of influenza viruses in human, avian, and swine populations.

Global map of MISMS research activities and regional meetings:



- MISMS regional workshops
- Genomic or epidemiologic data acquired/analyzed and ongoing data collection
- Interest

Updated September 2011

For more information about MISMS, our publications, and our upcoming meetings, visit our website: <http://origem.info/misms>

