Birth year, immune history and differences in risk from seasonal influenza H1N1 and H3N2

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# Abstract

Across decades of co-circulation in humans, seasonal influenza A subtypes H1N1 and H3N2 have consistently caused different age distributions of infection and mortality. H3N2 typically causes the majority of cases in high-risk elderly cohorts, and the majority of overall deaths, whereas H1N1 has a greater impact in young and middle-aged adults. We re-examine possible drivers of these patterns, motivated by the recent discovery of broadly-protective immunity arising from flu viruses encountered in childhood. Using two large, epidemiological data sets, we tested the possibility that immune imprinting shapes seasonal flu epidemiology via narrow immune memory to a particular subtype, or via broader immune memory that acts across subtypes. We also explore a separate hypothesis about evolutionary rate. Likelihood-based model comparison showed that within-subtype imprinting is the strongest driver of cohort-specific seasonal influenza risk. The data did not support a strong effect of evolutionary rate, or of broadly protective imprinting. However, our separate analysis of 2009 pandemic data showed support for broadly protective imprinting during the first pandemic wave, but not during the second pandemic wave. Altogether, these population-level patterns mirror within-host immunological outcomes, where broadly protective antibody responses are reliably deployed against novel flu variants, but not against familiar seasonal strains. Our findings emphasize that childhood exposures can imprint a lifelong immunological bias toward particular influenza subtypes, and that this imprinting shapes epidemic age distributions. These results illuminate the epidemiological impacts of antigenic seniority, indicating that less “senior” antibody responses acquired later in life do not provide the same strength of protection as responses imprinted in childhood. Finally, these results imply that H1N1’s mortality burden (currently low) may increase in the coming decades, as cohorts that lack H1N1-specific imprinting eventually become elderly.

# Introduction

Childhood exposures to influenza leave an immunological imprint, which has reverberating, lifelong impacts on immune memory. Foundational work on original antigenic sin (1) and antigenic seniority (2), showed that individuals maintain the highest titers against influenza strains encountered in childhood. But how these serological patterns translate to functional immune protection, and shape cohort-specific risk, remains an active research frontier [CITE]. Since 1977, two distinct subtypes of influenza A, H1N1 and H3N2, have circulated seasonally in humans, and these subtypes show consistent differences in age distribution (17–20). H3N2 causes the vast majority of cases in older adults, while H1N1 causes a greater proportion of cases in younger and middle-aged adults. These differences in age distribution are qualitatively consistent with childhood imprinting patterns, in that older cohorts (i.e. those born before 1957 when H2N2 replaced H1N1) were almost certainly exposed to historical variants of H1N1 in childhood, and may now be preferentially protected against modern, seasonal H1N1 (18–20). Likewise, younger cohorts (born after 1968) have the highest probabilities of childhood imprinting to H3N2, and may now be preferentially protected against modern H3N2 variants.

One key point of debate is whether preferential immune memory of strains encountered in childhood interferes with effective *de novo* responses, and immune protection, against drifted or shifted strains encountered later in life. Classical studies by Francis (1), and later Lessler et al. (2), observed (uncontroversially) that adults maintain the ability to mount new antibody titers against drifted influenza strains, and that these *de novo* responses are almost always accompanied by back-boosting of cross reactive memory primed earlier in life [CITE]. Repeated back-boosting of responses primed in childhood could give rise to serological antigenic seniority, even in the absence of any antigenic interference between existing immune memory and *de novo* responses. On the other hand, immunological studies have demonstrated the potential for antigenic interference, where upon infection by a drifted influenza strain, cross-reactive memory B cells (MBCs) can exclude *de novo* clones from the naïve B cell pool, leading immune memory to focus on the few epitopes held in common between current and past strains. Antigenic interference has been shown to negatively impact immune protection in a few special cases [CITE], and may contribute to decreased efficacy of repeated influenza vaccination [CITE]. But so far, the epidemiological impacts of antigenic interference remain poorly understood, and have not been directly linked to childhood immune imprinting. If antigenic interference has widespread impacts on immune memory, then

A new wave of studies has instead focused on potential benefits of immune imprinting. Childhood imprinting is thought to have shaped population immunity against every pandemic in the modern epidemiological record (5–11). We also now know that immune imprinting can provide broad, cross-subtype protection against novel, emerging avian influenza viruses (12). As avian and pandemic influenza viruses were historically considered too novel to encounter substantial population immunity as they emerged into humans, the existence of any protection from imprinting is a welcome discovery.

Recent studies have also highlighted the ability of imprinting to shape multiple layers of influenza immune memory, both broad and narrow. Influenza’s immunodominant epitopes, the primary targets of most antibody responses, show considerable structural diversity and drift antigenically over time. As a result, most seasonal influenza immunity provides only narrow, ephemeral, protection. Until recently, broader cross-subtype (heterologous) responses were considered rare or anomalous, and so research on immune imprinting focused primarily on narrow within-subtype (homologous) responses.

More recently, the 2009 H1N1 pandemic, and subsequent efforts to develop a universal influenza vaccine, have drawn attention to antibody responses that can indeed provide broad, heterologous protection (13–15). Broadly protective antibodies that target conserved epitopes on the HA stalk have been particularly well studied, and are common in existing human antibody repertoires (13–16). These broadly protective antibodies typically provide cross protection at the HA group-level, i.e. across all subtypes in genetic group 1, or group 2 of the HA tree (14). Recently, we showed that childhood imprinting strongly shapes the population-level impacts of these broadly protective, HA group-level responses against avian influenza. Individuals show strong, lifelong protection against novel avian influenza viruses from the same HA group as the seasonal strains that circulated shortly after their birth year (12).

Similar imprinting effects may also shape birth year-specific risk from familiar, seasonal influenza viruses.

Here, we aim to test whether birth year-specific risk from seasonal influenza is primarily driven by broad imprinting to a specific HA group, or by narrower imprinting to a specific HA or NA subtype. If HA subtype-level imprinting is the key driver, then childhood imprinting to H1 or to H3 would provide lifelong protection against seasonal variants of the same HA subtype. Similarly, childhood imprinting might act strongly at the NA subtype level, providing lifelong protection specific to N1 or to N2 (Fig. ***1***). Alternatively, broad HA group-level imprinting might drive seasonal influenza cohort effects. Although the antibodies involved in group-level protection usually play a minimal role in immunity against familiar, seasonal influenza viruses, these antibodies can rise in frequency and play a strong role in immunity if the host lacks immune memory of more variable, immunodominant epitopes (13–15,21). Thus, in theory, HA group-level immune memory may serve as a second line of defense against drifted seasonal strains, called in as backup to target conserved epitopes when narrow, first-line memory B cells are unable to recognize their drifted, variable targets. If HA group-level imprinting strongly shapes cohort effects, then cohorts imprinted to H1 or H2 (both group 1) should be protected against modern, seasonal H1N1, while only cohorts imprinted to H3 (group 2) would be protected against modern, seasonal H3N2 (Fig. 1). Furthermore, because broadly protective influenza immunity is most often deployed against antigenically novel strains, whose conserved epitopes may provide the only recognizable immune targets, we predict that broad, group-level imprinting will show stronger impacts during the 2009 H1N1 pandemic than during normal, seasonal H1N1 circulation.

In addition to cohort effects from childhood imprinting, differences in H1N1 and H3N2’s rates of antigenic drift may also contribute to differences in subtype-specific age distribution. Subtype H1N1 drifts more slowly than H3N2, and as a result, H3N2 may be more able to cause infections in older, immunologically experienced cohorts, whereas H1N1 may be relatively restricted to incidence in immunologically naïve children (22).

Using two large data sets on seasonal influenza incidence, which together represent 22,041 confirmed influenza A cases across 18 years and 15 countries, we tested whether observed differences in age distribution of H1N1 and H3N2 cases are primarily driven by cohort effects from childhood imprinting, or by other factors. To test whether HA group-level imprinting, HA subtype-level imprinting, NA subtype-level imprinting or no effect of imprinting was most consistent with observed patterns, we developed a suite of models, fitted models to data using maximum likelihood, and performed model selection using AIC. Additionally, to test whether differences in H1N1 and H3N2’s rates of antigenic advance were a dominant driver of observed subtype-specific differences in age distribution, we analyzed the relationships between the annual magnitude of antigenic advance, and season-specific age distributions of infection.

# The Data

We analyzed two large epidemiological data sets. The first was provided by the Arizona Dept. of Health Services (AZDHS), and contained 18,812 H1N1 and H3N2 cases, confirmed using a combination of rapid tests, serology and PCR, per established department protocols (23). Cases were observed across 22 years of influenza surveillance, from the 1993-1994 influenza season through the 2014-2015 season, but within-season sample sizes increased dramatically during and after the 2009 pandemic, which precipitated increases in sampling efficiency (Table 1). Per epidemiological standards, the Arizona influenza season was defined as beginning in epidemiological week 40 (around early October) and ending in week 39 of the following year.

A second data set provided by the INSIGHT outpatient study (http://insight.ccbr.umn.edu/) contained 3,612 PCR-confirmed H1N1 and H3N2 cases, observed across 16 countries between 2009 and 2016 (Table 2). The INSIGHT data contained information not available in the AZDHS data, including the age distribution of cases that tested negative for influenza, and three binary medical history variables: antiviral treatment used, presence of any underlying conditions, and recent influenza vaccination. Note that we use the non-specific term “recent influenza vaccination” because some study sites recorded whether patients had been vaccinated in the past 6 months, and others recorded whether patients had been vaccinated in the past 12 months. To facilitate comparison between data sets, we defined INSIGHT cases enrolled from Oct-May as part of the Northern Hemisphere influenza season, and cases enrolled from June-Sept as part of the Southern Hemisphere season. These definitions were used to facilitate comparison between data sets. October 1 roughly aligns with the week 40 Northern Hemisphere season start date used in the Arizona data set.

### Differences between datasets

The INSIGHT dataset was smaller, and sampled across a shorter period of time than the AZDHS data. The INSIGHT data also excluded children under age 18, and enrolled relatively few elderly and young adult subjects, whereas the AZDHS data contained cases large numbers of cases at the extremes of age, including in children (Fig. S1). The INSIGHT data sampled a greater geographic range, contained denominator data on the age distribution of all tested cases, and contained details on patient medical history that were not available in the AZDHS data.

# The Model

## Reconstructed imprinting patterns

Reconstructed, birth year-specific probabilities of imprinting mirror the timeline of influenza circulation in humans (Fig. 1A). Older cohorts born between pandemics in 1918 and 1957 imprinted to H1N1, and middle-aged cohorts born between pandemics in 1957 and 1968 imprinted to H2N2. Ever since its emergence in 1968, H3N2 has dominated seasonal circulation in humans, and caused the majority of imprinting in younger cohorts. However, H1N1 has also caused some seasonal circulation since 1977, and thus a fraction of post-1977 cohorts are imprinted to H1N1.

We reconstructed birth year-specific probabilities of imprinting to H1N1, H2N2 and H3N2 using methods described previously (12). We repeated reconstructions for every country and year of case observation in the data. Country-specific reconstructions differed only in the virological surveillance data used to estimate the fraction of seasonal influenza cases caused by H1N1 or H3N2 in recent decades, and year-specific reconstructions differed only in the birth years that remained young enough (ages 0-12) to have a non-negligible probability of not yet having imprinted. Code to perform reconstructions is available at %%DOI HERE%%.

## Expected age distributions under alternate imprinting models

All tested models assumed childhood imprinting to H1N1 would protect against modern, seasonal H1N1, and that childhood imprinting to H3N2 would protect against modern, seasonal H3N2 (Fig. 1B). Collinearities between the predictions of different imprinting models (Fig. 1G-I) were inevitable, given the limited diversity of influenza circulation in humans over the past century. However, differences in the shape of predicted risk in middle-aged, H2N2 imprinted cohorts provided leverage to differentiate between imprinting at the HA subtype, HA group or NA subtype level (Fig. 1).

To tease apart age-specific risk factors from birth year-specific imprinting effects, we noted that age-specific risk factors for influenza infection are largely subtype-independent. Specifically, age-specific risk, or age-specific probabilities of case ascertainment could be influenced by medical factors like age-specific vaccine coverage, age-specific risk of severe disease, and immunosenescence, or by behavioral factors like age-assorted social mixing, and age-specific healthcare seeking behavior. All these factors should have similar impacts on any influenza subtype.

Thus, we fit a single step function to characterize the shape of age-specific risk of any confirmed influenza infection. Then, we modeled residual, subtype-specific differences in risk as a function of birth year, which enabled us to focus on the possible role of imprinting status. Note that for a given birth cohort, age-specific risk changed over time, and depended specifically on the individual’s age in the year of case observation, whereas birth year-specific risk was fixed for all years of case observation. Finally, each tested model used a linear combination of age-specific risk (Fig. 1C) and birth year-specific risk (Fig. 1D-F) to generate an expected distribution of H1N1 or H3N2 incidence (Fig. 1G-I).

To test quantitatively whether observed, subtype-specific differences in age distribution were most consistent with imprinting at the HA subtype, NA subtype or HA group level, or with no contribution of imprinting, we fitted a suite of models to each data set using a multinomial likelihood and then performed model selection using AIC. Technical details and a link to all relevant code are provided in the Methods.

### AZDHS Models

We fit a set of four models to the AZDHS data set. The simplest model contained only age-specific risk (A), and more complex models added effects from imprinting at the HA subtype level (S), at the HA group level (G), or at the NA subtype level (N). The age-specific risk curve took the form of a step function, in which relative risk was fixed to 1 in age bin 0-4, and one free parameter was fit to relative risk in each of the following 12 age bins: {5-10, 11-17, 18-24, 25-31, 32-38, 39-45, 46-52, 53-59, 60-66, 67-73, 74-80, 81+}. Within models that contained imprinting effects, two additional free parameters estimated the relative risk of confirmed H1N1 or H3N2 infection given imprinting protection.

### INSIGHT Models

When fitting to the INSIGHT data, which contained additional medical details, the suite of tested models included three additional risk factors: vaccination (V), antiviral treatment (T), and presence of underlying conditions (U). Factors T and U each added one free parameter, which characterized the relative risk of any influenza infection, given antiviral treatment or given the presence of underlying conditions. Factor V added two free parameters which characterized the relative risk of H1N1 or of H3N2 infection, given recent influenza vaccination. We tested all possible combinations of V, T, and U, in and each of the three imprinting hypotheses (S, N and G), for a total of 32 tested INSIGHT models. All tested models contained age-specific risk (A).

### Interpretation of the age-specific risk curve

The INSIGHT study collected denominator data on the age distribution of all tested cases (including cases that tested negative for influenza), whereas the AZDHS data contained only information on confirmed cases, with no age-specific denominators. When fitting to INSIGHT data, we input the age distribution of all tested cases as the null, expected age distribution in each country and season. Because these denominator data were not available in the AZDHS dataset, the age-specific risk curves fit to each data set must be interpreted differently. Age-specific risk curves fitted to INSIGHT data only represented, age-specific differences in the rate of testing positive for influenza, residual to observed denominators. On the other hand, age-specific risk curves fitted to the AZDHS data captured all aspects of the infection and case observation process. Thus, curves fitted to INSIGHT data showed much less variation between age groups than curves fitted to AZDHS data.

# Results

### Subtype-specific differences in age distribution

In both AZDHS and INSIGHT data, H3N2 consistently caused more cases in older cohorts, while H1N1 caused more cases in younger cohorts (Figs. 2-3, S2-S7). These patterns are qualitatively consistent with the predicted effects of cohort-specific imprinting (Fig 1), and with previously reported differences in age distribution (17–20). Overall, differences between H1N1 and H3N2’s age distributions were more pronounced in the Arizona data than in the INSIGHT data. But despite some variation between countries, seasons and data sets, observed patterns never contradicted the expected effects of imprinting. Whenever subtype-specific differences in age distribution were apparent, H3N2 always caused greater impacts in the oldest cohorts, while H1N1 caused greater impacts in young and middle-aged adults (Figs. 2-3).

To facilitate comparison between subtypes, and across data sets, Figs. 2-3 only included data from countries and seasons in which H1N1 and H3N2 both circulated (≥50 confirmed cases of each subtype). Figures S2-S7 show similar plots for all countries and seasons represented in the data, and plots showing alternate smoothing parameters.

## Imprinting model selection

Model selection on seasonal influenza data supported effects from narrow, within-subtype imprinting to NA or HA. Whether we fit to INSIGHT or to AZDHS data, models containing NA subtype-level imprinting received the most statistical support, and models containing HA subtype-level imprinting were the second most preferred in terms of AIC (Fig. 4, Table 3). The AZDHS data showed a preference for NA subtype-level imprinting over HA subtype-level imprinting (ΔAIC=23.42), and effectively no statistical support for broad, HA group-level imprinting (ΔAIC=245.18), or for an absence of imprinting effects (ΔAIC=380.47). Visual assessment of model fits (Fig. 4F,G) confirmed that models containing imprinting effects at the narrow, NA or HA subtype levels provided the best fits to data. As expected (see Fig. 1), predictions from the two best models were highly collinear, except in their risk predictions among middle-aged, H2N2-imprinted cohorts (birth years 1957-1968). Predictions of two best models (HA and NA subtype-level imprinting) were much more similar to each other than to predictions from models with much worse AIC (HA group-level imprinting and no imprinting).

Model selection on AZDHS data showed much greater differences in AIC, and much stronger effects of all tested factors than model selection on INSIGHT data (Fig. 4, Table 3). This was unsurprising due smaller sample sizes, increased noise from geographic variation, and smaller apparent differences in subtype-specific impact in the INSIGHT data. Although no single model fit to INSIGHT data was definitively preferred (six had ΔAIC<4, and differences between fits were negligible (Fig. 4, Table 3)), results of model selection on INSIGHT data aligned qualitatively with model selection on AZDHS data, in that none of the six best models contained HA group-level imprinting effects (Table 3), and overall, NA subtype-level imprinting or HA subtype-level imprinting received the most statistical support. Akaike weights can be interpreted as the proportional support for a given model, out of all models tested (24). The total Akaike weight for INSIGHT models including NA subtype level imprinting was 0.38, and for models including HA subtype-level imprinting was 0.34. Models including HA group-level imprinting or no imprinting received much less support, with Akaike weights of 0.04 and 0.23 respectively (Fig. 4E).

## Fitted risk patterns

When fitted to AZDHS data, age-specific risk curves took similar forms in all models, with risk decreasing rapidly from birth through adolescence, and then decreasing much more slowly until the end of life (Fig. 4A). When fitted to INSIGHT data, age-specific risk effects always took values close to 1, indicating that the age distribution of confirmed influenza cases was roughly proportional to denominator data on the age distribution of all tested cases (Fig. 4C, Fig. S1).

Tables S1-S3 show parameter estimates and 95% profile confidence intervals from all models fitted to AZDHS And INSIGHT data. Fits to AZDHS data estimated moderate reductions in risk due to imprinting protection, and fits to INSIGHT data estimated weak reductions in risk (Fig. 4B,D, Table S2-S3). Overall, risk parameters fitted to the INSIGHT data took values closer to 1 and had wider confidence intervals than risk parameters fitted to the Arizona data (Fig. 4, Tables S1-S3). As fitted to INSIGHT data, the estimated relative risk of infection given antiviral treatment was usually greater than one, which may reflect that antiviral treatment is often prescribed in response to a positive influenza test. Vaccination was consistently associated with small reductions in risk, although confidence intervals often overlapped the null value of one. The presence of underlying conditions did not strongly impact relative risk and was not included in preferred models (Table 3, Tables S1-S3).

## Strength and specificity of imprinting protection against 2009 pandemic H1N1

The AZDHS data contained large numbers of H1N1 cases confirmed during the 2009 pandemic (Table 1). We repeated model selection on these pandemic H1N1 cases to assess the strength and breadth of imprinting protection against the pandemic strain during the first pandemic wave (2008-2009 influenza season), and during the second pandemic wave (2009-2010 season). Minimal H3N2 circulation during the pandemic prevented us from re-fitting the age-specific risk curve to pandemic data. Instead, we input the age-specific risk curve fitted to seasonal AZDHS data, and then re-fit models assuming HA group, HA subtype and NA subtype-level imprinting to H1N1 data from the first and second pandemic wave.

Results showed that, under any imprinting model, the estimated strength of imprinting protection was strongest during the first pandemic wave, intermediate during the second wave, and weakest during seasonal influenza circulation (Fig. 5A). Model selection on first-wave pandemic data (2008-2009 influenza season) showed the strongest support for HA group-level imprinting (Fig. 5B). However, model selection on second wave data agreed with model selection on seasonal influenza data, where narrower, NA and HA subtype-level imprinting received the most statistical support (Fig. 5C).

## Effect of evolutionary rate

To test the impact of antigenic evolutionary rate on epidemic age distribution, we used publicly available data from *Nextstrain* (25,26), and from one previously published study (27), to calculate annual antigenic advance, which we defined as the antigenic distance between strains of a given lineage (pre-2009 H1N1, post-2009 H1N1 or H3N2) that circulated in consecutive seasons (Methods).

If the rate of antigenic drift is a strong driver of age-specific influenza risk, then the fraction of influenza cases observed in children should be negatively related to antigenic advance (22). In other words, strains that have not changed much antigenically since the previous season should be unable to escape pre-existing immunity in immunologically experienced adults, and more restricted to causing cases in immunologically naïve children. Consistent with this expectation, the AZDHS data showed a slight negative association between annual advance and the fraction of H3N2 cases observed in children, but the Pearson correlation was not strong enough to reach significance in any age group (Fig. 6A). The data contained too few influenza seasons with >100 confirmed H1N1 cases to support meaningful Pearson correlation coefficients specific to pre-2009 or post-2009 H1N1 lineages.

Furthermore, if evolutionary rate has a strong impact on epidemic age distribution, then outbreaks caused by H1N1 and H3N2 should converge in age distribution when annual antigenic advance is similar.However, the data showed that differences in H1N1 and H3N2’s age-specific impacts persisted, even when lineages showed similar annual advance (Fig. 6A). When comparing the fraction of cases observed in specific age classes, H1N1 data consistently clustered separately from H3N2, with H1N1 consistently causing fewer cases in children (0-10), and elderly adults (71-85), and more cases in adults than H3N2 strains with similar rates of antigenic advance. Smoothed density plots showed no clear relationship between annual antigenic advance and age distribution (Fig. 6B). Overall, the data did not show a strong signal that epidemic age distribution varies with the magnitude of antigenic drift.

# Discussion

Altogether, results showed that childhood imprinting to a particular NA or HA subtype is the most likely tested driver of observed differences in the age-specific impacts of seasonal H1N1 and H3N2. The data did not support strong effects from broader HA group-level imprinting, as recently detected for novel zoonotic subtypes, or from differences in each subtype’s rates of antigenic advance. Model comparison on both data sets independently provided the strongest support for effects from childhood imprinting to NA. Although NA is not as intensively studied as HA, these results emphasize the importance of both antigens as drivers of protection against seasonal influenza.

Based on widely used rules of thumb for the interpretation of ΔAIC values, the model based on HA subtype-level imprinting effects (AZDHS ΔAIC=23.42) would be ruled definitively inferior to NA subtype-level imprinting. However, predictions from models containing HA and NA-subtype level imprinting were very similar, but because the dataset was very large, small differences the fit of models containing NA and HA subtype-level imprinting produced substantial differences in likelihood and hence in AIC. It is likely that some combination of effects from both HA and NA subtype-level imprinting shapes seasonal influenza risk, but given extensive collinearities between predictions of the simplest models containing HA and NA subtype-level effects, we could neither directly test, nor definitively rule out the possibility of combined effects.

The low diversity of influenza circulation in the past century, and unbalanced sampling across time, space and age groups limited the scope of inference supported by this study, or any study relying exclusively on cross-sectional population data. Deeper insights into the relative impacts of HA-specific or NA-specific childhood imprinting will most likely need to come from immunological data. The recent NIH initiative to fund large cohort studies (28), is a promising development, but these studies may not yield results for over a decade. Development of an assay to diagnose imprinting status in cross-sectional data from individuals, or from banked blood and serum samples would be a major step forward.

Our finding that narrow, within-subtype imprinting has much stronger impacts than broader, HA group-level imprinting on seasonal influenza is consistent with decades of research on seasonal influenza immunity, where narrow, homologous immune memory is known to drive well-documented epidemiological and phylodynamic patterns, permitting repeated influenza infections and demanding frequent vaccine updates (22,29). Still, given that narrow, within-subtype immunity is known to decay rapidly in the face of antigenic drift, it is somewhat surprising that signatures of narrow, within-subtype imprinting protection persist across an entire human lifetime, and remain evident even in the oldest cohorts in the data. On average, H1N1 and H3N2 viruses drift by 0.62 and 1.01 antigenic units per year, respectively (27), which roughly corresponds to a two-fold drop in titer for every 1.61, or 0.99 years of antigenic evolution between strains. Strains that circulated more than 14 years apart do not show measurable cross-protective titers (27). In this context, it is puzzling that narrow, homologous influenza immunity primed in childhood provides any meaningful protection after adolescence, let alone decades later in old age. However we note that standard serologic assays used to assess cross-reactivity are focused on variable epitopes, and do not capture effects of T cell help and other cellular immunity [refs].

One possible explanation for the evident longevity of homologous childhood imprinting protection is that imprinting to a particular HA or NA subtype builds strong memory of epitopes conserved among homologous variants of the same subtype, but not across subtypes. Another possible explanation is that the memory B cell clones developed during the first childhood influenza exposure later adapt via somatic hypermutation to “follow” homologous antigenic targets as they drift over time. Thus, childhood imprinting may provide preferential, lifelong protection against a particular HA or NA subtype by filling a child's memory B cell repertoire with clones that will serve in the future, not as final products but as prototypes that can be rapidly and effectively tailored to recognize drifted influenza strains of the same subtype. A third possibility is that signals of imprinting protection are anomalously strong in the current cohort of elderly adults. For nearly four decades, from 1918-1957, H1N1 persisted as the only strain circulating in humans. The oldest subjects in our data were born slightly after its emergence in 1918, and would not have encountered an influenza virus of any subtype but H1N1 until after age 30. Decades of early-life exposures to H1N1 variants may have reinforced and expanded the breadth of H1N1-specific immune memory in these oldest cohorts. Furthermore, despite the passage of decades the oldest cohorts have encountered strains quite similar to modern H1N1 lineages, as the lineages that emerged in 1977 and in 2009 both had similar antigenic properties to strains that circulated earlier in the 20th century (5,6,30,31). Given that younger cohorts, especially those born before 1977, have had much more varied early life exposures to both H1N1 and H3N2, it is unclear whether equally strong, subtype-specific biases in imprinting protection will be evident when the next generation becomes elderly.

Although the data did not support effects from broad HA group-level imprinting against familiar, seasonal influenza viruses, or during the second wave of the 2009 H1N1 pandemic, broad HA group-level imprinting was the preferred model for protection during the first pandemic wave. The cleanest interpretation is that population-level impacts of broadly protective, HA group-level immunity occurred transiently at the beginning of the 2009 pandemic, but decayed rapidly as the novel, pandemic strain established in humans and became familiar to our immune systems. Recent immunological findings show similar patterns at the within-host scale, and highlight that narrow immunity is not an intrinsic property of the influenza virus, but an emergent property of within-host competition between broadly and narrowly neutralizing B cell clones. Due to structural properties of the hemagglutinin antigen, whose variable epitopes are exposed and highly immunogenic, narrowly neutralizing antibodies can exclude their less-fit, broadly neutralizing competitors in most cases. But primary exposure to novel avian or pandemic strains, whose immunodominant variable regions are unfamiliar, can release broadly protective antibodies from competition and facilitate transient, broadly protective responses (13). These immunodominance patterns, which now form the conceptual basis for stalk-based universal influenza vaccines (14), were first observed during the 2009 pandemic. Individuals who lacked pre-existing titers against the 2009 pandemic strain initially mounted broadly protective antibody responses, targeting conserved epitopes on the HA stalk (initially the only recognizable immune targets), but on secondary exposure to the pandemic strain, the same individuals had developed some immune memory of more variable epitopes, and reverted to expressing immunodominant, narrowly protective antibodies (13).

It is tempting to interpret our results as a population-level manifestation of well-documented within-host patterns, where the pandemic strain was initially novel enough to elicit a signal of broadly protective immunity, and where that signal of broadly protective immunity quickly disappeared as the pandemic strain became established in humans. But for now, other explanations cannot be definitively ruled out. During the first pandemic wave, the model containing broad, group-level imprinting performed best primarily because it predicted few cases in cohorts born between 1957 and 1968. But the model still failed to fit the data well in cohorts born between 1968 and 1977, and during the 1990s (Fig. 5B). These residual patterns suggest our set of tested hypotheses may not have contained all influential factors. Visually, the low number of first-wave cases in cohorts born before c.1976 (Fig. 5B) is consistent with the hypothesis that widespread vaccination against 1976 strain of swine influenza provided cross-protection against the 2009 pandemic strain.

Overall, differences between age distributions of infection caused by H1N1 or H3N2 were much more pronounced in the AZDHS data than in the INSIGHT data. Differences between the datasets may arise due to geographic variation in influenza’s epidemiology; the INSIGHT data were collected across five continents, whereas all the AZDHS data came from a single US state. Climatic or demographic characteristics, or high rates of influenza vaccination (32,33), may magnify subtype-specific differences in age distribution within the United States. It is noteworthy that within the INSIGHT data, the subset of cases observed in the United States showed more dramatic differences in age distribution than data collected in many other countries (Fig. 3). Similarly, apparent differences between H1N1 and H3N2’s age distributions were greater in the United States than in Europe in one previous study (17).

On the other hand, the United States was not the only country in the INSIGHT data to show relatively strong differences in age distribution (Fig. 3), and study-specific differences in sampling almost certainly were another contributing factor to apparent differences between the datasets. The INSIGHT study did not enroll children, and a dearth of enrolled cases in the youngest and oldest included age groups may have dampened the signal of subtype-specific differences in risk (Fig. S1). To illustrate the impact of uneven sampling across age groups, we subset the AZDHS data to match the sample size and age distribution of all confirmed cases from the INSIGHT study. Filtering the AZDHS data in this way made differences in age-specific risk from H1N1 and H3N2 appear much smaller (Fig. S1D).

The potential for age-specific sampling biases to erode or magnify the signal of imprinting effects highlights some limitations of existing epidemiological surveillance data, which in turn limited this study’s scope of inference. The largest, long-term epidemiological data sets on influenza come from massive, global surveillance efforts. But due to practical and economic constraints, these data are often collected opportunistically, meaning that sampling effort is uneven over time, and across age groups, and denominator data are rarely documented or shared. Furthermore, while some aspects of surveillance data are already shared publicly by WHO (34), and by the US CDC (35), data on patient ages is not currently reported, or is obscured by aggregation into broad age categories.

As we enter the era of big data, one of the next great challenges for influenza epidemiology will be to understand how measurable genetic and antigenic properties of the circulating viruses impact population-level outcomes, like age-specific risk, birth year-specific risk, vaccine effectiveness and season-specific attack rates. Thanks to ambitious and well-funded open science initiatives like the GISAID genetic database (36), and the *Nextstrain* project (25,37), the genetic and antigenic history of influenza circulation in humans is already well-documented and freely available to scientists. The difficulty of accessing corresponding antigenic and epidemiological data remains a key stumbling block. The expense and difficulty of maintaining large, public databases should not be taken for granted, and those responsible for collecting and curating high-quality data deserve more professional credit for their work. We emphatically echo earlier calls (38) for more systematic sharing of single year-of-age in influenza surveillance data, standardization of sampling effort, and reporting of age-specific denominators, which could represent a turning point in the scientific community’s ability to link influenza's genetic and antigenic properties with epidemiological outcomes.

From an epidemiological standpoint, our results imply that the incidence and mortality impacts of H1N1 may increase in the future as the imprinting status of elderly cohorts shifts. Currently, H3N2 causes the vast majority of influenza-related deaths, whereas H1N1 causes relatively little mortality (20,39). These patterns may reflect intrinsic differences in virulence, but we speculate that population-level imprinting patterns may also shape H3N2’s greater mortality impact. The vast majority of influenza-related deaths occur in adults over age 65, cohorts whose imprinting protection currently limits the incidence of clinically-attended H1N1 infection. In the future, H2N2 imprinted cohorts (born c. 1950-1968) will become elderly, and their imprinting protection will act against seasonal H3N2 (via NA subtype-level imprinting), or against no seasonal strains (via HA subtype-level imprinting). In this scenario, the mortality burden of H1N1 is predicted to increase, while the mortality burden of H3N2 may decrease due to generational shifts in imprinted immunity.

On one hand, this study’s failure to detect any signal of broadly protective imprinting in seasonal influenza surveillance data is unsurprising. Narrow, homologous immunity is a hallmark of seasonal influenza’s evolutionary and epidemic dynamics. But on the other hand, these results raise new questions about the longevity of apparent protection from narrow, homologous immune responses primed in childhood, and about the underlying within-host dynamics of B cell repertoire development. With implications for universal influenza vaccine development, these results also highlight the difficulty of inducing broadly protective antibody responses against immunologically familiar, seasonal influenza strains.

# Methods

## Data inclusion criteria

From the AZDHS data, we excluded 58 cases with birth years before 1918 (whose imprinting status could not be inferred unambiguously), and one case whose year of birth was recorded in error and had not yet occurred. In the INSIGHT data, we excluded 94 cases with missing information in any of five key categories: age, date of enrollment, vaccination, underlying conditions and antiviral treatment. We excluded an additional 7 cases that fell outside the focal age range of 18-90, and 3 cases whose infecting subtype could not be unambiguously identified due to coinfection.

## Classification of pandemic cases

The AZDHS data contained a large number of H1N1 cases observed during the 2009 pandemic. Because the data did not explicitly differentiate between pre-2009 and post-2009 H1N1 lineages, we used the best available information on season of circulation to separate pandemic cases form normal, seasonal H1N1 cases. In the United States, the first wave of the 2009 H1N1 pandemic occurred during the spring and summer of 2009, falling within the 2008-2009 AZDHS influenza season, and the second pandemic wave occurred during the fall and early winter of the 2009-2010 AZDHS season (40), so we assumed that all H1N1 cases observed in these two seasons were part of the first or second pandemic waves, respectively. It is possible that some pre-pandemic H1N1 cases occurring early in the 2008-2009 season were mis-classified as pandemic cases. But due to the dramatic increase in the number of recorded H1N1 cases during the first pandemic wave (Table 1), and due to the distinct age distribution of H1N1 incidence shown in the data during the 2008-2009 season (Fig. 5B), we are confident that the majority of 2008-2009 season H1N1 cases were indeed part of the first pandemic wave.

The INSIGHT study began collecting data in response to the 2009 pandemic, and did not capture the first pandemic wave. Few H1N1 cases were recorded during the second pandemic wave in the Northern and Southern Hemispheres (Table 2, 2009-2010 Northern Hemisphere season, 2010 Southern Hemisphere season), and signals in the INSIGHT data were inherently weak, so we did not analyze these pandemic data.

## Estimation of age from birth year from age in AZDHS data

The AZDHS data contained three variables, influenza season, birth year and confirmed subtype. For most cases, birth year was extracted directly from the reported date of birth in patient medical records. To fit age-specific risk curves to the AZDHS data, we estimated patient age at the time case observation using the formula [year of observation]-[birth year]. To ensure that the minimum estimated age was 0, the second year in the influenza season of case observation was considered the calendar year of observation (e.g. 2013 for the 2012-2013 season).

## Estimation of birth year from age in the INSIGHT data

The INSIGHT data contained patient age, and the exact date of case enrollment, but not birth year. We estimated birth year using a method that took advantage of precise dates of case enrollment available in the INSIGHT data. The simplest approximation of birth year would have been (observation year)-(age), but this approximation is slightly biased, as cases observed earlier in the year (e.g. in January) are less likely to have passed a birthday in the current calendar year. As shown in Fig. S8, we determined the possible birth dates of an individual observed during each month of the year. We then determined that on average, cases observed during months in the Northern Hemisphere season (Oct.-May) had the following probabilities of birth in each of three possible years, relative to the year of case observation:

**1**

Cases observed during months of the Southern Hemisphere had different probabilities:

**2**

Using these probabilities, we took a weighted average of birth year-specific imprinting probabilities for cases observed in the Northern Hemisphere or Southern Hemisphere influenza seasons.

## Splines

In Figures 2-3, smoothing splines were fit to aid visual interpretation of noisy data. We fit splines using the command *smooth.spline(x = AGE, y = FRACTIONS, spar = 0.8)* in R version 3.5.0. Variables *AGE* and *FRACTIONS* were vectors whose entries represented single years of age, and the fraction of cases observed in the corresponding age group. The smoothing parameter 0.8 was chosen to provide a visually smooth fit. Alternative smoothing parameter choices (0.6 & 1.0) are shown in Figs. S3, S6-S7. Although the exact shape of fitted splines changed was sensitive to our choice of smoothing parameter, qualitative differences between H1N1 and H3N2’s age distributions were robust.

## Model formulation

For each unique country and season in which cases were observed, define *p* as a vector whose entriesrepresent the expected probability that a randomly drawn H1N1 or a randomly drawn H3N2 case was observed in an individual of age *a*. Each model defined, *p* as a linear combination of age-specific risk, birth year-specific risk (i.e. imprinting effects), and other medical history variables, and *p* took slightly different shapes for expected H1N1 and H3N2 case age distributions. All tested models were nested within the equation:

**3**

To include risk factors that only modulated risk from one subtype, we included indicator functions ***1H1N1*** and ***1H3N2***, which took value 1 if *p* described the expected age distribution of H1N1 or H3N2 cases, respectively, and 0 otherwise.

### Denominator data (D)

When fitting to INSIGHT data, *D* was a vector whose entries were proportional to the age distribution of all tested cases within a given country and year. As noted above, corresponding denominator data were not available in the AZDHS dataset, and so factor D was not included in models fit to AZDHS data.

### Age-specific risk (A)

Age-specific risk was defined as a step function, in which relative risk was fixed to value 1 in an arbitrarily chosen age bin, and then *z*-1 free parameters, denoted *r*2 to *rz*, were fit to describe relative risk in all other age bins. Below, ***1i*** are indicator functions specifying whether each vector entry is a member of age bin *i.* To obtain the predicted fraction of cases observed in each single year of age, we normalized the risk distribution given by equation 2 so that predicted risk across all age groups summed to 1.

**4**

### Antiviral treatment (T) and underlying conditions (U)

Within each country and season, *fT* defined a vector whose entries describe the fraction of tested cases of a given age that had received antiviral treatment. Free parameter *rT* defines the relative risk of any confirmed influenza infection, given antiviral treatment. Then, risk factor *T* was defined as:

**5**

And risk factor *U* was described similarly:

**6**

### Imprinting (I) and vaccination (V)

Factors describing risk from vaccination and imprinting took forms similar to risk factors *T* and *U*, but with subtype-specific impacts. An indicator function defined whether a given prediction vector described risk of confirmed H1N1 or H3N2 infection. Let *fV* and *fI* be vectors describing the fraction of cases of each age that were vaccinated against influenza, or that were protected against strain *HxNy* by their childhood imprinting

**7**

**8**

## Model fitting and model comparison

We simultaneously estimated all free parameter values using the optim() function in R. We calculated likelihood profiles and 95% profile confidence intervals for each free parameter. Confidence intervals were defined using the method of likelihood ratios (41).

## Antigenic advance

We obtained antigenic distance estimates from *Nextstrain (nextstrain.org) (25,37),* and from source data associated with Figure 3 in Bedford et al. (27). *Nextstrain* calculates antigenic distance using genetic data from GISAID (36), and using methods described by Neher et al. (26). We analyzed “CTiter” estimates from *Nextstrain*, which correspond to Neher et al.’s “tree model” method. Datasets from *Nextstrain* and Bedford et al. both contained redundant antigenic distance estimates for the H3N2 lineage, but only Bedford et al. analyzed the pre-2009 H1N1 lineage, and only *Nextstrain* data analyzed the post-2009 H1N1 lineage. The antigenic distance estimates reported by Bedford et al. were roughly proportional to those reported on *Nextstrain*, but greater in absolute magnitude (26). We analyzed each lineage separately, so enable direct comparison among all three lineages within a single plot, we rescaled pre-2009 H1N1 estimates from Bedford et al. using the formula *dNexsttrain* = 0.47*dBedford*. The scaling factor was chosen so that directly-comparable H3N2 distance estimates obtained using each method were well-aligned (Fig. S9). The *Nextstrain* data files used in this analysis are archived at ###//CODE\_LINK//####.

## Code and data availability

Code to perform all reported analyses and construct all plots is available \#\#HERE\#\#. AZDHS data is available as a supplementary data file. Data from the INSIGHT study are available by application, pending approval from the study's scientific review committee (<http://insight.ccbr.umn.edu/index.php>). Because we are not free to share the INSIGHT data, the posted code contains a dummy INSIGHT data file with scrambled column entries. In other words, the data files are formatted properly, and the code will run, but the actual data entries have no biological meaning.

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