The within-host evolutionary dynamics of seasonal and pandemic human influenza A viruses in young children

Alvin X. Han[1,*], Zandra C. Felix Garza[1,*], Matthijs R. A. Welkers[1,*], René M. Vigeveno[1], Tran Nhu Duong[2], Le Thi Quynh Mai[2], Pham Quang Thai[2], Tran Thi Ngoc Anh[3], Ha Manh Tuan[3], Nguyen Thanh Hung[4], Le Quoc Thinh[4], Le Thanh Hai[5], Hoang Thi Bich Ngoc[5], Kulkanya Chokephaibulkit[6], Pilaipan Puthavathana[6], Nguyen Van Vinh Chau[7], Nghiem My Ngoc[7], Tran Tinh Hien[7,8], Heiman F. L. Wertheim[8,9,10], Peter Horby[10,11], Annette Fox[11, 12, 13], H. Rogier van Doorn[10,11], Dirk Eggink[1,14,†], Menno D. de Jong[1,†], Colin A. Russell[1,†]

*Contributed equally, †Contributed equally

[1]Laboratory of Applied Evolutionary Biology, Department of Medical Microbiology & Infection Prevention, Amsterdam University Medical Center, Amsterdam, The Netherlands

[2]National Institute of Hygiene and Epidemiology, Hanoi, Vietnam

[3]Children's Hospital 2, Ho Chi Minh city, Vietnam

[4]Children's Hospital 1, Ho Chi Minh city, Vietnam

[5]Vietnam National Children's Hospital, Hanoi, Vietnam

[6]Siriraj Hospital, Mahidol University, Bangkok, Thailand

[7]Hospital for Tropical Diseases, Ho Chi Minh city, Vietnam

[8]Oxford University Clinical Research Unit, Ho Chi Minh city, Vietnam

[9]Radboud Medical Centre, Radboud University, Nijmegen, The Netherlands

[10]Nuffield Department of Medicine, University of Oxford, Oxford, UK

[11]Oxford University Clinical Research Unit, Hanoi, Vietnam

[12]Peter Doherty Institute for Infection and Immunity, University of Melbourne, Melbourne, Australia

[13]WHO Collaborating Centre for Reference and Research on Influenza, Melbourne, Australia

[14]Centre for Infectious Disease Control, National Institute for Public Health and the Environment, Bilthoven, The Netherlands

Correspondence to A.X.H. (x.han@amsterdamumc.nl) & C.A.R. (c.a.russell@amsterdamumc.nl)

Abstract (148/150 words)

The evolution of influenza viruses is fundamentally shaped by within-host processes. However, the within-host evolutionary dynamics of influenza viruses remain incompletely understood, in part because most studies have focused on within-host virus diversity of infections in otherwise healthy adults based on single timepoint data. Here, we analysed the within-host evolution of 82 longitudinally sampled individuals, mostly young children, infected with A/H3N2 or A/H1N1pdm09 viruses between 2007 and 2009. For A/H1N1pdm09 infections during the 2009 pandemic, nonsynonymous changes were common early in infection but decreased or remained constant throughout infection. For A/H3N2 viruses, early infection was dominated by purifying selection. However, as the A/H3N2 infections progressed for longer-than-average duration (up to 2 weeks) in relatively young or influenza naive individuals, nonsynonymous variants increased in frequencies even though within-host virus titres decreased, leading to the maintenance of virus diversity via mutation-selection balance and provide important opportunities for within-host virus evolution.

Main text (4,958/5,000 words excluding Methods)

Introduction

Influenza A viruses (IAV) are some of the most prevalent human respiratory pathogens, infecting hundreds of millions of people worldwide each year. Because of the high error rates of the viral RNA polymerase complex, *de novo* mutants are generated as the viruses replicate within infected hosts[1]. However, the emergence of these variants within host does not mean that they will become the majority variant within the infected host or be transmitted between hosts. The evolution of IAVs is the product of a complex mosaic of evolutionary processes that include genetic drift, positive selection[2] , transmission bottleneck effects[3,4] and global migration patterns[5,6]. Importantly, the resulting evolutionary dynamics can differ at the individual and population levels[7].

For seasonal IAVs at the global population level, antibody-mediated immune selection pressure from natural infection or vaccination positively selects for novel antigenic variants that facilitate immune escape resulting in antigenic drift[2]. However, at the within-host level, the role of positive selection exerted by immunity is less obvious. Several next generation sequencing studies of typical, short-lived seasonal IAV infections in adult humans showed that intra-host genetic diversity of influenza viruses is low and dominated by purifying selection[4,8–11]. Additionally, large scale comparative analyses of IAV haemagglutinin (HA) consensus sequences found limited evidence of positive selection on HA at the individual level regardless of the person's expected influenza virus infection history[12]. Importantly, these studies focused on virus samples from only one or two time points, mostly early in infection, limiting the opportunities to study how virus populations evolved over the course of infection.

Separate from seasonal IAVs, zoonotic IAVs constantly pose new pandemic threats. Prior to becoming human-adapted seasonal strains, IAVs are introduced into the human population from an animal reservoir through the acquisition of host adaptive mutations, sometimes via reassortment, resulting in global pandemics such as the 2009 swine influenza pandemic[13]. In the 2009 pandemic, global virus genetic diversity increased rapidly during the early phases of the pandemic as a result of rapid transmissions in the predominantly naïve human population[14]. Over subsequent waves of the pandemic, host adapting mutations that incrementally improved viral fitness and transmissibility in humans of A/H1N1pdm09 viruses emerged[15], eventually reaching fixation in the global virus population[16].

At the individual level, the within-host evolutionary dynamics of the pandemic A/H1N1pdm09 virus, particularly in the early stages of the 2009 pandemic, have been

84 relatively underexplored. To date, the only within-host genetic diversity analysis of
85 A/H1N1pdm09 viruses during the initial phase of the pandemic was based on mostly single-
86 timepoint samples collected within ~7 days post-symptom onset[17]. Despite initial findings of
87 high within-host diversity and loose transmission bottlenecks[17], these results were later
88 disputed due to technical anomalies and subsequent reanalyses of a smaller subset of the
89 original data found that intra-host genetic diversity of the pandemic virus was low and
90 comparable to levels observed in seasonal IAVs[18,19]. It remains unclear how frequently host
91 adaptive mutations appear within hosts infected by a pandemic IAV and if these mutants are
92 readily transmitted between individuals.

93

94 Here, we deep sequenced 275 longitudinal clinical specimens sampled from 82 individuals
95 residing in Southeast Asia between 2007 and 2009 that were either infected with seasonal
96 A/H3N2 or pandemic A/H1N1pdm09 viruses. By analysing minority variants found across
97 the whole IAV genome, we characterised the evolutionary dynamics of within-host virus
98 populations in these samples collected up to two weeks post-symptom onset.

99

100 Results

101 *Study participants*

102 The A/H3N2 virus samples were collected from 51 unlinked individuals as part of an
103 oseltamivir dosage trial[20,21]. 48 of the 51 A/H3N2 virus infected individuals were young
104 children (median age=2 years; interquartile range (IQR)=2-3 years) at the time of sampling
105 and most had low or no detectable anti-influenza virus antibody titers on day 0 and 10 post-
106 symptom onset[21]. Given that young children are substantial contributors to influenza virus
107 transmission[22,23], the samples analysed here offer a valuable opportunity to investigate the
108 within-host IAV evolutionary dynamics in this key population. The A/H1N1pdm09 virus
109 specimens were collected from 32 individuals up to 12 days post-symptom onset. These
110 individuals include both children and adults (median age=10 years; IQR=4-20 years) infected
111 during the first wave of the pandemic in Vietnam (July-December 2009). 15 of the 32
112 individuals (including 6 index patients) were sampled in a household-based influenza cohort
113 study[24]. The remaining 16 unlinked individuals were hospitalised patients that were involved
114 in two different oseltamivir treatment studies[20,25] Details of all study participants are
115 described in the respective cited studies and Table S4.

116

117 *Genetic diversity of within-host virus populations*

118 We used the number of minority intra-host single nucleotide variants (iSNVs; ≥ 2% in
119 frequencies) to measure the levels of genetic diversity of within-host IAV populations.
120 Similar to previous studies[4,8,9,11], within-host genetic diversity of human A/H3N2 virus

populations was low (median = 11 iSNVs, interquartile-range (IQR) = 7-16; Figure 1A). Within-host genetic diversity of pandemic A/H1N1pdm09 virus populations was also low, with a median number of 21 iSNVs (IQR = 13.5-30.0; Figure 1B) identified. Cycle threshold (Ct) values, and thus likely virus shedding, correlated with the number of days post-symptom onset for both IAV subtypes (A/H3N2: Spearman's $\rho = 0.468$, $p = 1.38 \times 10^{-10}$; A/H1N1pdm09: $\rho = 0.341$, $p = 0.048$; Figure 1C and D). The number of iSNVs observed in within-host A/H3N2 virus populations weakly correlated with days since onset of symptoms in patients ($\rho = 0.463$, $p = 2.22 \times 10^{-10}$) and Ct values ($\rho = 0.508$, $p = 1.20 \times 10^{-12}$), suggesting that as infection progresses, genetic variants accumulate within-host even as virus population size decreases (Figure 1A). On the other hand, there was no significant correlation between the number of iSNVs observed in within-host A/H1N1pdm09 virus populations and Ct values ($\rho = 0.198$, $p = 0.21$) or days post-symptom onset ($\rho = -0.021$, $p = 0.91$) (Figure 1B).

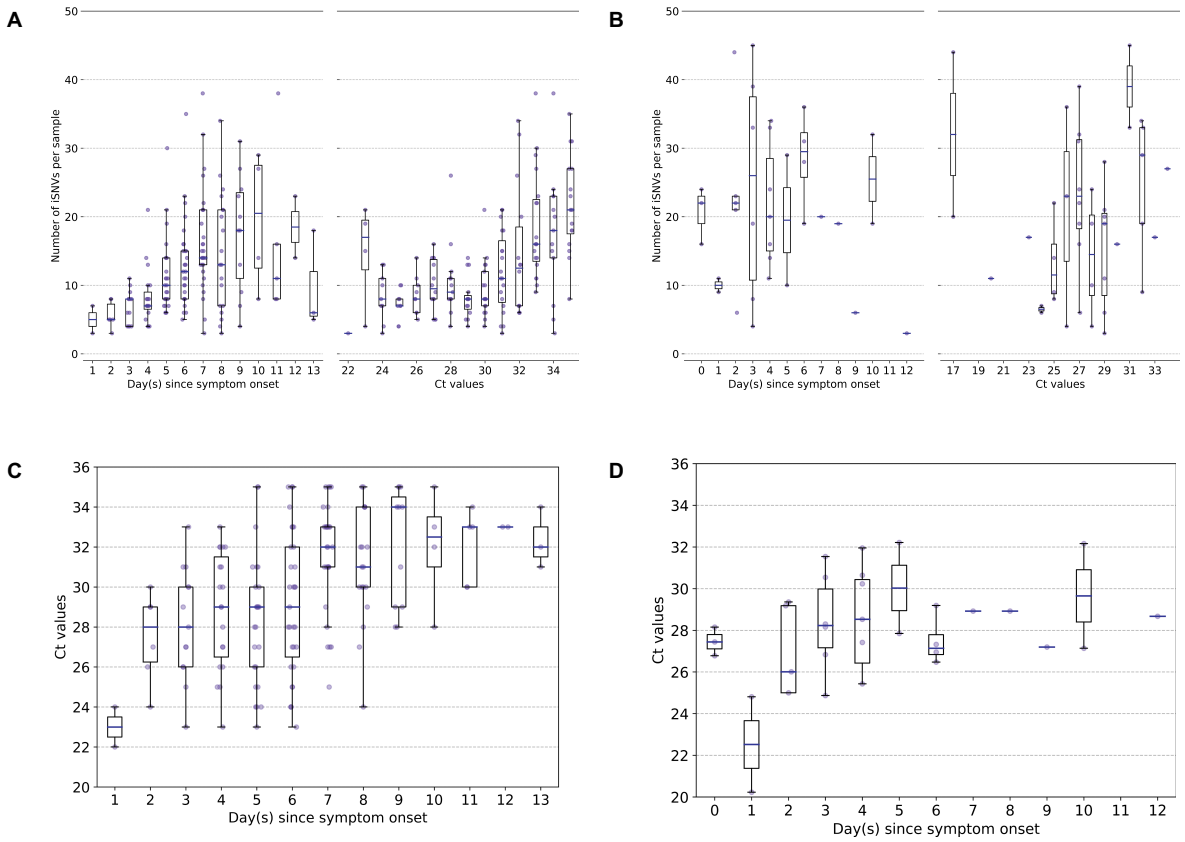


Figure 1: Genetic diversity of within-host influenza A virus populations. Box plots summarizing the number of intra-host single nucleotide variants (iSNVs; median, interquartile range (IQR), and whiskers extending within median $\pm 1.5 \times$ IQR) identified in samples with adequate breadth of coverage across the whole influenza virus genome in (**A**) seasonal A/H3N2 and (**B**) pandemic A/H1N1pdm09 virus samples, stratified by day(s) since symptom onset or qPCR cycle threshold (Ct) values. (**C**, **D**) Ct values as a function of day(s) since symptom onset for A/H3N2 viruses (**C**) and A/H1N1pdm09 viruses (**D**).

143 *Within-host evolutionary rates of influenza A viruses*

144 To investigate within-host evolutionary dynamics, empirical rates of synonymous, non-
145 synonymous, and premature stop-codon (i.e. nonsense) iSNVs were calculated by
146 normalizing the summation of observed iSNV frequencies with the number of available sites
147 and time since symptom onset (see Methods). The overall within-host evolutionary rates of
148 A/H3N2 viruses observed here are in the same order of magnitude ($<\sim 10^{-5}$ divergence per
149 site per day) as those reported in previous within-host seasonal influenza virus evolution
150 studies (Figure 2A)[26]. Synonymous evolutionary rates were significantly higher than
151 nonsynonymous rates during the initial phase of A/H3N2 virus infections (Figure 2A),
152 primarily in the polymerase complex and HA genes (Figure 2A and S1-2). Importantly,
153 nonsynonymous variants gradually accumulated, increasing in rates around four days post-
154 symptom onset to similar levels relative to synonymous rates. Aggregating over all samples,
155 most nonsynonymous variants were found in the nucleoprotein (NP) and neuraminidase (NA)
156 gene segments (nonsynonymous to synonymous variant (NS/S) ratios = 1.69 (NP) and 1.32
157 (NA) whereas NS/S ratios were ≤ 1 for all other gene segments; Figure S1 and Table S1).
158 While nonsynonymous NA mutations associated with oseltamivir resistance were positively
159 selected for a subset of individuals in response to the antiviral treatment[21], nonsynonymous
160 changes to NP were likely mediated by protein stability, T-cell immune response and/or host
161 cellular factors (see next section).

162

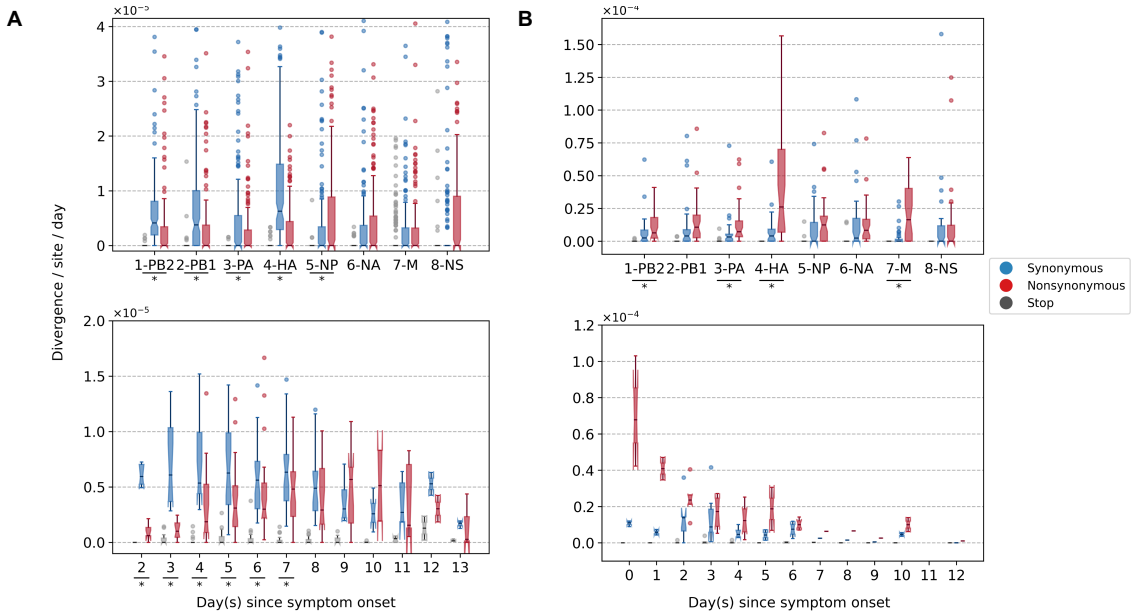
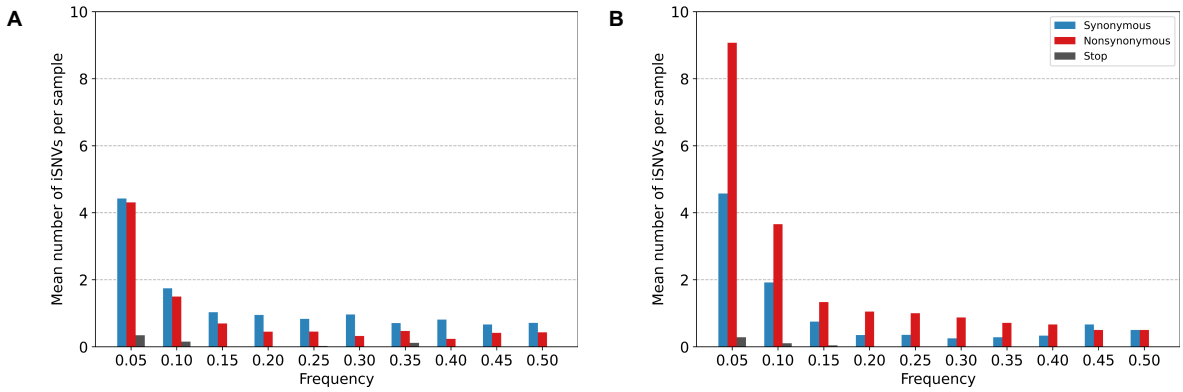


Figure 2: Box plots (median, interquartile range (IQR), and whiskers extending within median $\pm 1.5 \times$ IQR) summarizing the empirical within-host evolutionary rates of (**A**) seasonal A/H3N2 viruses and (**B**) pandemic A/H1N1pdm09 viruses. Top panel shows the evolutionary rate of individual gene segments over all timepoints (r_g) while the bottom panel depicts the genome-wide evolutionary rate (r_t) for each day since symptom onset. All rates are stratified by substitution type (synonymous – blue; nonsynonymous – red; grey – stop-codon). Wilcoxon signed-rank tests were performed to assess if the paired synonymous and nonsynonymous evolutionary rates are significantly distinct per individual gene segment or timepoint (annotated with "$*$" if $p < 0.05$). This was done for all sets of nonsynonymous and synonymous rate pairs except for those computed per day since symptom onset for A/H1N1pdm09 viruses due to the low number of data points available (median number of A/H1N1pdm09 virus samples collected per day since symptom onset = 2). Note that the scales of the y axes differ between A and B to better show rate trends.

For A/H1N1pdm09 viruses during the first wave of the pandemic, the overall within-host evolutionary rate was as high as $\sim 10^{-4}$ divergence per site per day in some samples on day 0 post-symptom onset (Figure 2B). Nonsynonymous evolutionary rates were higher than synonymous rates from the start of symptom onset when overall evolutionary rates were also the highest. However, we were unable to determine if the per-day post-symptom onset nonsynonymous and synonymous rates were significantly different from each other due to the low number of samples (i.e. median = 2 samples per day post-symptom onset). Nonetheless, consolidating over all samples across all time points, the polymerase basic 2 (PB2), polymerase acidic (PA), HA and matrix (M) gene segments were the main contributors to the observed rate disparity (Figure 2B and S3-4) with nonsynonymous variants emerging at significantly higher rates relative to synonymous ones. All gene segments also yielded NS/S ratios > 1 (Table S1).

190 *Intra-host minority variants*

191



192 **Figure 3**. Histogram of the mean number of minority iSNVs identified per sample across all (**A**) A/H3N2 and
193 (**B**) A/H1N1pdm09 virus specimens, sorted by frequency bins of 5% and substitution type (synonymous – blue;
194 nonsynonymous – red; stop-codon – grey).

195

196 Most of the iSNVs identified for both virus subtypes were observed at low frequencies (2-
197 5%; Figure 3), and appear to be stochastically introduced across the virus genome (Figure 4).
198 Purifying selection dominated within-host seasonal A/H3N2 virus populations as the ratio of
199 nonsynonymous to synonymous variants was 0.72 across all samples and variant frequencies
200 (Figures 3A and S2). Of note, the canonical antigenic sites of the HA gene segment[27] of the
201 A/H3N2 virus populations experienced strong negative selection as evidenced by the
202 occurrence of synonymous variants (median frequency = 0.14, IQR range = 0.09-0.27) at far
203 greater frequencies relative to those at non-antigenic sites of HA (median frequency = 0.03,
204 IQR range = 0.03-0.05; Mann-Whitney U test $p = 1.18 \times 10^{-24}$; Figure 4C). There were no
205 significant differences in the frequencies of nonsynonymous iSNVs between the antigenic
206 sites of H3 (median frequency = 0.04, IQR range = 0.03-0.06) and the rest of the HA gene
207 segment (median frequency = 0.03, IQR range = 0.02-0.06; Mann-Whitney U test $p = 0.29$;
208 Figure 4C). In contrast, there was 1.94 times as many nonsynonymous minority iSNVs
209 relative to synonymous ones identified in the pandemic A/H1N1pdm09 virus samples
210 (Figures 3B and S4). Variant frequencies of nonsynonymous iSNVs found in the antigenic
211 epitopes of H1[28] (median frequency = 0.04, IQR range = 0.04-0.05) were, however, not
212 significantly different from those of non-antigenic sites (median frequency = 0.05, IQR range
213 = 0.03-0.16; Mann-Whitney U test $p = 0.34$; Figure 4D).

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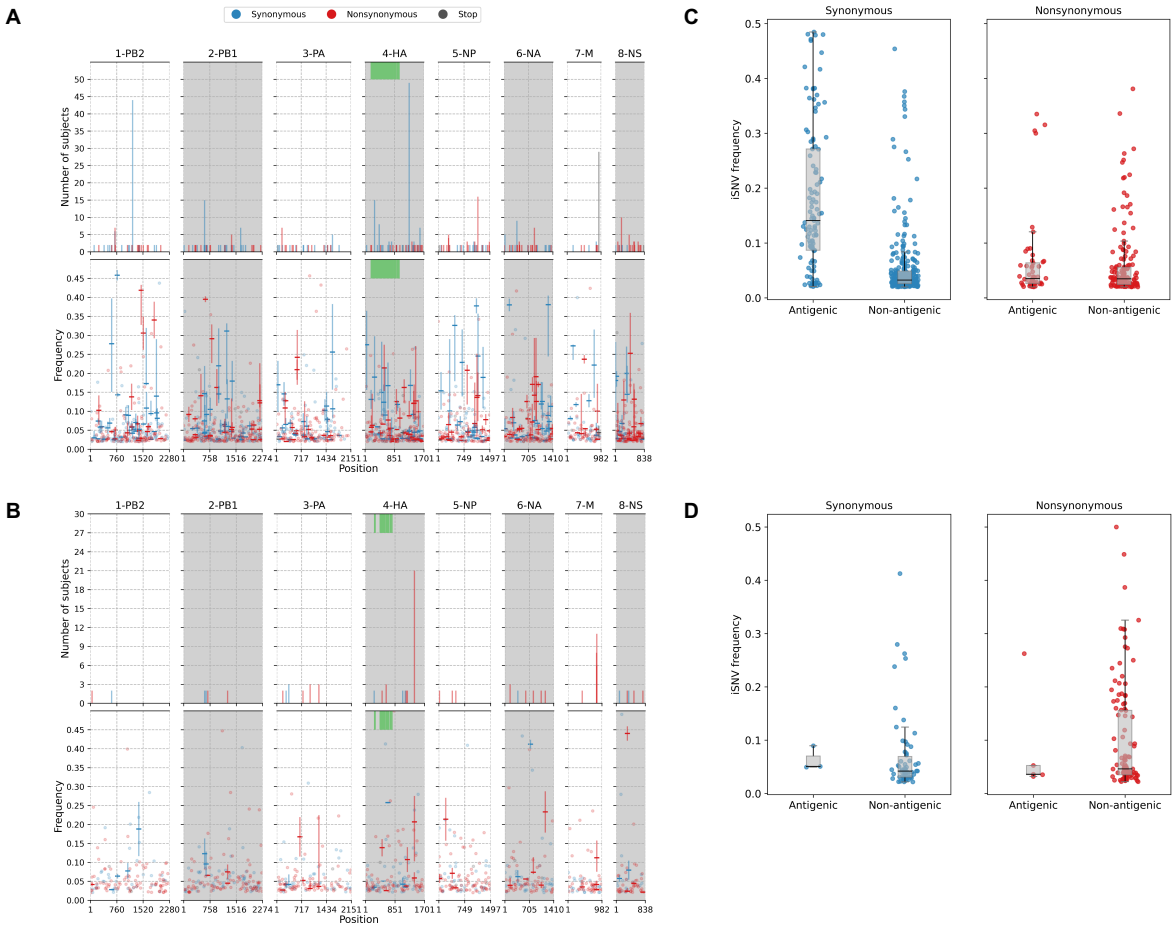

Figure 4: (**A**) Breakdown of iSNVs identified in seasonal A/H3N2 virus samples. The top panels plot the nucleotide positions where iSNVs were found in at least two subjects. The bottom panels shows the frequencies at which iSNVs were identified. For sites with iSNVs that were found in two or more subjects, the interquartile ranges of variant frequencies are plotted as vertical lines and the median frequencies are marked with a dash. If the iSNV was only found in one subject, its corresponding frequency is plotted as a circle. All iSNVs are stratified to either synonymous (blue), nonsynonymous (red) or stop-codon (grey) variants. Only the nonsynonymous variants are plotted if both types of variants are found in a site. Positions of antigenic sites of the haemagglutinin gene segment[29] are marked in green on the top panels. (**B**) Similar plots to (A) for iSNVs found in pandemic A/H1N1pdm09 virus samples. (**C**) Box plots of the frequencies of synonymous and nonsynonymous variants between antigenic and non-antigenic sites of seasonal A/H3N2 haemagglutinin gene segment. (**D**) Similar plots to (C) for HA iSNVs identified in the pandemic A/H1N1pdm09 virus samples.

As observed in a previous study using different data[26], premature stop-codon (nonsense) mutations accumulated within-host, though only at low rates. Here, we observed similarly low median nonsense rates, ranging between 0 and 1.29×10^{-6} divergence per site per day across the entire A/H3N2 virus genome over the course of infection (IQR limits range between 0 and at most, 1.82×10^{-6} divergence per site per day; Figure 2A). Premature stop-codons accumulated in the matrix (M) genes predominantly but also appeared in all other influenza gene segments within various individuals (Figures 2A and 4A). Nonsense mutations also accumulated within the A/H1N1pdm09 virus samples (Figure 2B). Similar to

236 A/H3N2 viruses, nonsense mutation rates were much lower compared to the synonymous and
237 nonsynonymous counterparts (median genome-wide rate across all samples between 0 and
238 1.43×10^{-6} divergence per site per day; IQR limits between 0 and 2.18×10^{-6} divergence
239 per site per day).

240

241 The premature stop-codon mutations were mostly found at low frequencies for both influenza
242 subtypes (<10%; Figure 3). The exception lies with one of the A/H3N2 virus samples where
243 a premature stop codon was found in position 77 of the M2 ion channel with variant
244 frequency as high as 34.6% (Patient 1843, day 6 since symptom onset; Figures 3A and S5D).
245 The premature stop codon in M2-77 was also found in 27 other individuals across multiple
246 timepoints, albeit at a much lower frequency that never amounted more than 10% (Figures
247 4A and S5D). This was unlikely to be a sequencing artefact resulting from a mistaken
248 incorporation of the primer sequence as its carboxyl terminal falls outside the coding region
249 of the M gene segment (Table S3) and the variant frequencies would have been much higher
250 in all samples if this was the case.

251

252 Despite the dominance of purifying selection in seasonal A/H3N2 intra-host viral
253 populations, we detected several nonsynonymous variants of interest. Amino acid variants
254 emerging in the HA and NA proteins were discussed in a previous work[21] (see
255 Supplementary Materials). In the nucleoprotein, there were two notable nonsynonymous
256 variants, D101N/G and G384R, that appeared in multiple individuals who were sampled
257 independently between 2007 and 2009 (Figure 4A and S5C). D101N/G was found in 7
258 different patients and at least for D101G, the mutation was previously linked to facilitating
259 escape from MxA, a key human antiviral protein[30]. However, the nonsynonymous mutation
260 was only found in low frequencies and remained invariant during the respective courses of
261 infection for all seven patients (median variant frequency across all samples = 0.03; IQR =
262 0.02-0.07).

263

264 NP-G384R emerged in sixteen unlinked patients infected by A/H3N2 virus. Even though
265 G384R did not become the majority variant in any of these individuals (median variant
266 frequency across all samples = 0.14; IQR = 0.07-0.20), the variant emerged around day 4-5
267 post-symptom onset and mostly persisted within each individual for the rest of sampled
268 timepoints. G384R is a stabilizing mutation in the A/Brisbane/10/2007 A/H3N2 virus NP
269 background[31] that is similar to the viruses investigated here. Interestingly, position 384 is an
270 anchor residue for several NP-specific epitopes recognised by specific cytotoxic T
271 lymphocytes (CTLs) that are under continual selective pressure for CTL escape[32,33]. The
272 wild-type glycine residue is known to be highly deleterious even though it was shown to
273 confer CTL escape among HLA-B*2705-positive individuals[34–36].

Using a maximum likelihood approach to reconstruct and estimate the frequencies of the most parsimonious haplotypes of each gene segment, we computed linkage disequilibrium and found evidence of potential epistatic co-variants to NP-G384R in the A/H3N2 virus populations of multiple individuals (Figure 5 and Table S2). When analysing how these variants could alter protein stability using FoldX, the stabilizing effects of G384R (mean $\Delta\Delta G = -3.84$ kcal/mol (SD = 0.06 kcal/mol)) was found to alleviate the likely destabilizing phenotype of a functionally relevant linked variant in two of the three co-mutation pairs identified in separate individuals (i.e. G384R/M426I and G384R/G102R; Table S2). In the first individual (subject 1224), M426I was inferred to have emerged among the viral haplotypes encoding NP-G384R on the 10th day post-symptom onset (D10). M426I may be compensating for T-cell escape that was previously conferred by 384G even though the two amino acid sites are anchor residues of different NP-specific CTL epitopes[32]. M426I was found to be highly destabilizing (mean $\Delta\Delta G = 2.61$ kcal/mol (standard deviation (SD) = 0.05 kcal/mol); Table 1) but when co-mutated with G384R, stability changes to NP was predicted to be neutral (mean $\Delta\Delta G = -0.42$ kcal/mol (SD = 0.06 kcal/mol)). In the second individual (subject 1686), G102R was likely linked to G384R in the within-host virus populations found in the D10 sample. As a single mutant, G102R is also destabilizing to NP (mean $\Delta\Delta G = 4.87$ kcal/mol (SD = 0.00 kcal/mol)). However, when combined with G384R, NP protein stability was only weakly destabilizing (mean $\Delta\Delta G = 0.76$ kcal/mol (SD = 0.09 kcal/mol)). G102R was previously found to bypass the need for cellular factor importin-α7 which is crucial for viral replication and pathogenicity of IAVs in humans[37–39].

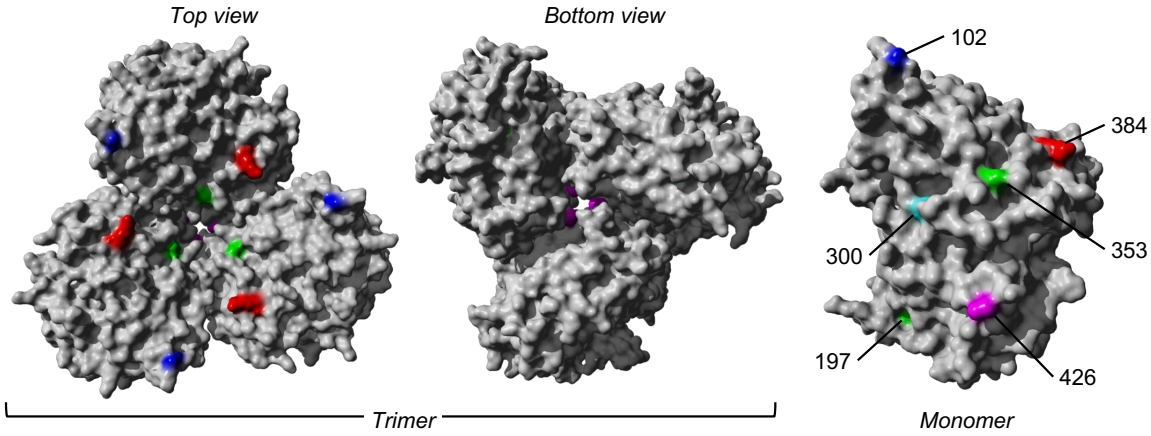

Figure 5: The trimeric and monomeric crystal structures of nucleoprotein (PDB: 3ZDP)[40] of influenza A viruses. Amino acid sites with potentially linked epistatic amino acid variants as tabulated in Table 1 are separately coloured, with their corresponding positions annotated on the monomeric structure.

Variants	$\Delta\Delta G$ (kcal/mol) Mean	S.D.
G384R	-3.84	0.06
M426I	2.61	0.05
G384R,M426I	-0.42	0.06
G102R	4.87	0.00
G384R,G102R	0.76	0.09
A493T	11.96	0.30
G384R,A493T	5.56	0.19
V197I	-3.11	0.02
S353Y	-1.97	0.68
V197I,S353Y	-4.48	0.14

Table 1: FoldX stability predictions of likely linked nonsynonymous minority variants found in A/H3N2 nucleoprotein. The mean $\Delta\Delta G$ and standard deviation (S.D.) values reported are based on the results of five distinct simulations. Variants with mean $\Delta\Delta G < -0.46$ kcal/mol are deemed to be stabilizing while destabilizing mutants were estimated to yield $\Delta\Delta G > 0.46$ kcal/mol.

For the pandemic A/H1N1pdm09 viruses, most of the nonsynonymous variants were found singularly in individual patients (Figure 4B). Putative HA antigenic minority variants were found in four individuals in distinct amino acid sites (G143E, N159K, N197K and G225D; H3 numbering without signal peptide; Figure S5E). All of these variants were found at frequencies $\leq 5\%$ and the wild-type residues have been conserved in the corresponding positions globally to date, with the exception of position 225. Here, HA-225G was the majority variant (76%) in a hospitalised individual (subject 11-1022; Table S4) and D225G is linked to infections with severe disease outcomes[41]. Furthermore, one of the few nonsynonymous iSNVs that co-emerged in multiple unlinked patients was found in the usually conserved stem of the HA protein, L455F/I (H3 numbering without signal peptide), appearing in 17 separate individuals (Figures 4B and S5E). The amino acid variant was found in patients from different time periods and geographical locations (Table S4), thus it is unlikely this was a unique variant shared among individuals in the same transmission cluster. It was observed as early as day 0 post-symptom onset for some patients and seemed to persist during the infection but only as a minority variant at varying frequencies (median frequency across all samples with mutation = 0.20; IQR = 0.08-0.28). However, this position has also been conserved with the wild-type Leucine residue in the global virus population to date. Hence, it is unclear if HA-L455F/I actually confers any selective benefit even though it was independently found in multiple patients.

329 We also found oseltamivir resistance mutation H275Y[42] in the NA proteins in two unlinked
330 individuals who were infected with the A/H1N1pdm09 virus and treated with oseltamivir
331 (Figure S5F and Table S4). 275Y quickly became the majority variant in both patients within
332 3-4 days after the antiviral drug was first administered. Finally, there were two other amino
333 acid variants in the M2 ion channel that appeared within multiple subjects in parallel across
334 different geographical locations – L46P and F48S were identified in 8 and 16 patients
335 respectively in a range of frequencies (L46P: median frequency = 0.04, IQR = 0.04-0.05;
336 F48S: median frequency = 0.08, IQR = 0.03-0.13) but similarly, never becoming a majority
337 variant in any of them (Figures 4B and S5G). Again, the wild-type residues were mostly
338 conserved in the global virus population since the pandemic.

339

340 *Within-host simulations*

341 To investigate the evolutionary pressures that likely underpin the observed patterns of
342 synonymous and nonsynonymous substitutions (Figure 2), we performed forward-time
343 Monte Carlo simulations. Given that the median age of the children infected by A/H3N2
344 virus at the time of sample collection was 2 years of age (IQR=2-3 years), most of them were
345 likely experiencing one of their first influenza virus infections. Furthermore, influenza
346 vaccination for children is not part of the national vaccination programme in Vietnam. As
347 such, most of the children analysed here lacked influenza virus specific antibodies based on
348 haemagglutination inhibition assays[21]. For individuals infected by the pandemic
349 A/H1N1pdm09 virus, all but one patient was under 60 years of age and thus lacked immunity
350 to the virus as well. Furthermore, patients infected by either viruses mount little-to-no
351 humoral immune selection pressure during the first 7-10 days of infection[43]. As such, the
352 contrasting evolutionary dynamics between these viruses (Figure 2) are unlikely to have been
353 driven by antibody-mediated selection pressure.

354

355 Seasonal A/H3N2 viruses, having circulated within the human population since 1968, are
356 expected to be well adapted to human hosts at this point such that most nonsynonymous
357 mutations are likely highly deleterious and would not reach detectable frequencies. Those
358 that were detected are mostly expected to be weakly deleterious, and thus not purged fast
359 enough by selection such that mutation-selection balance was observed. In contrast, there was
360 evolutionary space for A/H1N1pdm09 virus to further adapt to its new found human hosts
361 during the initial waves of the pandemic. Since no mutation selected by rapid directed
362 positive selection was observed, most of the detected nonsynonymous mutations were
363 expected to be neutral and a small but non-trivial fraction are likely to be weakly beneficial.

364

365 Our simulations used a simple within-host evolution model represented by a binary genome
366 that distinguishes between synonymous and nonsynonymous loci. Given that the estimated

transmission bottleneck sizes for pandemic A/H1N1pdm09 (see Supplementary Materials) and seasonal A/H3N2 viruses[4,44] are narrow at 1-2 genomes, we modelled an expanding virus population size during the initial timepoints of the infection that started with one virion. If within-host virus populations were to evolve neutrally, we would observe similar synonymous and nonsynonymous evolutionary rates throughout the infection (Figure 6C). On the other hand, if selection is sufficiently strong, accumulation of beneficial (or deleterious) nonsynonymous variants will increase (or decrease) substantially with time (Figure 6B and 6E). Clearly, these patterns were not observed for both IAVs (Figure 2).

However, if most *de novo* nonsynonymous mutations are only weakly deleterious, we would observe larger synonymous evolutionary rates initially before nonsynonymous variants accumulate to similar levels (Figure 6A). By then, virion population size (N) would also be large enough relative to the virus mutation rate (μ) (i.e. $N\mu \gg 1$; see Supplementary Materials) such that mutation-selection balance is expected and evolutionary rates remain fairly constant, similar to the patterns empirically observed for within-host A/H3N2 virus populations (Figure 2A). Contrastingly, if the majority of nonsynonymous variants are neutral and only a small subset confers weakly beneficial effects, nonsynonymous evolutionary rates would consistently be larger than their synonymous counterpart but never accumulate to levels akin to those observed for strong positive selection (Figure 6D). Although the simulation results here does not entirely reflect the evolutionary dynamics observed for A/H1N1pdm09 viruses in Figure 2B, we hypothesised that there was substantial virus replication prior to symptom onset and that our samples better reflect the virus populations present midway or nearing the end of the infection when compared to our simulation results. This is further evidenced by the relatively large number of iSNVs detected at the time of symptom onset (Figure 1B) and the tight transmission bottleneck sizes we estimated for the pandemic virus (see Supplementary Materials).

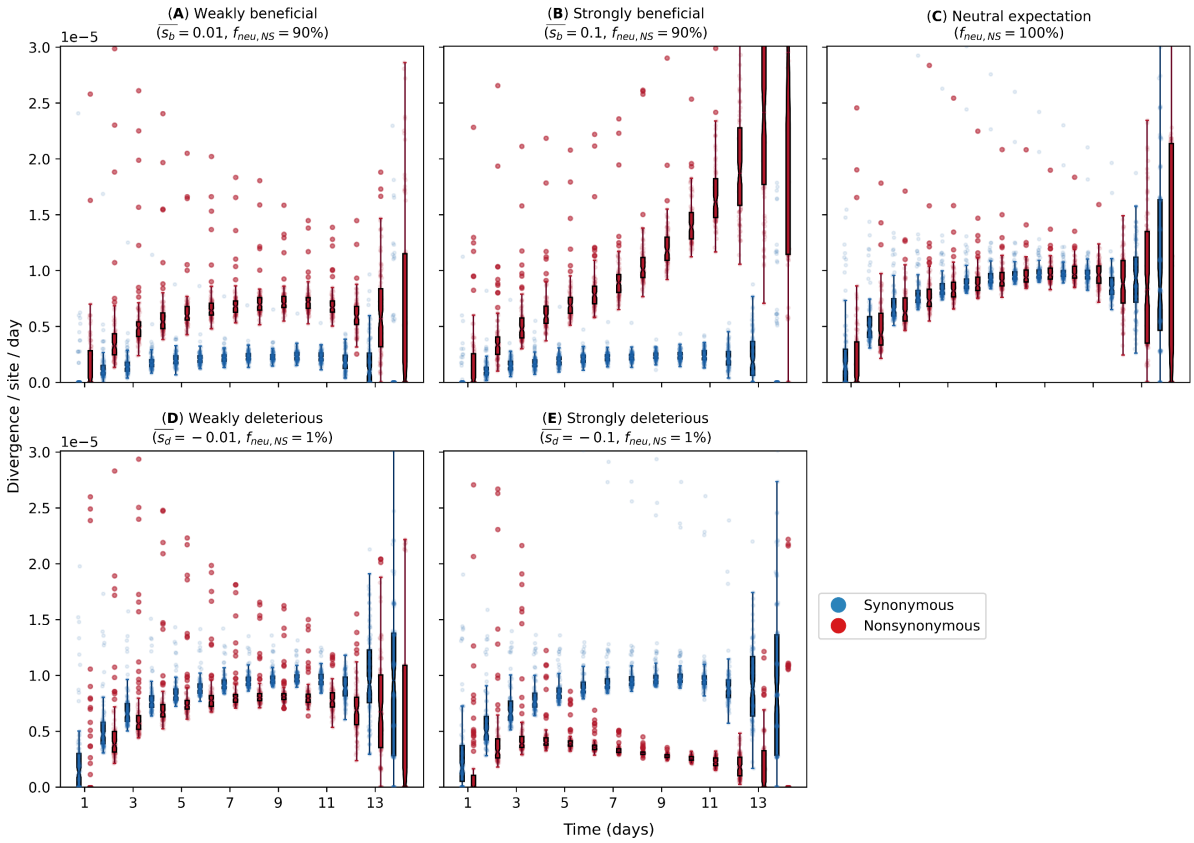

Figure 6: Evolutionary rates computed from forward-time Monte Carlo within-host simulations for different fitness effects of nonsynonymous mutations ($\overline{s_b}$ and $\overline{s_d}$ denote mean beneficial and deleterious effects respectively) and fraction of neutral nonsynonymous mutations ($f_{neu,NS}$). We assumed that synonymous mutations are neutral for all simulations. For A/H1N1pdm09 viruses, we assumed that only a small fraction of nonsynonymous mutations is neutral ($f_{neu,NS} = 1\%$) and performed simulations where the remaining nonsynonymous mutations are either (**A**) weakly ($\overline{s_b} = 0.01$) or (**B**) strongly ($\overline{s_b} = 0.1$) beneficial. For A/H3N2 viruses, we tested the hypotheses where majority of nonsynonymous mutations are neutral ($f_{neu,NS} = 90\%$) while the remaining ones are either (**D**) weakly ($\overline{s_d} = -0.01$) or (**E**) strongly ($\overline{s_d} = -0.1$) deleterious. (**C**) Neutral expectation where all nonsynonymous mutations are neutral ($f_{neu,NS} = 100\%$).

Discussion

Multiple next-generation sequencing studies have found little evidence of positive selection in seasonal influenza virus populations of acutely infected individuals[4,8–11,45]. Recent modelling work showed that the time required to initiate new antibody production and asynchrony with virus exponential growth limits the selection of *de novo* antigenic variants within host in acute seasonal influenza virus infections[46]. In contrast, phenotypically relevant variants that were positively selected in within-host virus populations of severely immunocompromised patients coincided with those selected by the global seasonal IAV population[47,48]. This implies that within-host evolutionary dynamics of seasonal IAVs in immunocompromised individuals are likely to be substantially different owing to the increased time for virus diversity to accumulate and for selection to act[49]. In other words, the

416 duration of infection is likely to be critical for positive evolutionary selection to be effective
417 within host.

418

419 Viral shedding duration is often longer in young children infected with seasonal influenza
420 virus compared to otherwise healthy adults[50]. Children also play a critical role in "driving"
421 influenza epidemics due to their higher contact and transmission rates[22,23]. As such, our
422 seasonal A/H3N2 virus results fill an important gap in the current literature of within-host
423 evolutionary studies of seasonal IAVs as most of the samples analysed were collected from
424 children under the age of six years up to two weeks post-symptom onset. Importantly, the
425 absence of antibody-mediated immunity in young unvaccinated children, which would
426 otherwise reduce the extended duration of infection, has the potential to facilitate other routes
427 of virus evolution.

428

429 Similar to the aforementioned within-host studies, the A/H3N2 virus population within these
430 children was characterised by low genetic diversity and dominated by purifying selection
431 early in the infection. Due to a lack of antibody response against the antigenic regions of
432 HA[21], it is unsurprising that we observed a lack of adaptive changes to the HA antigenic
433 regions, similar to adults in previous studies[4]. We also found that the polymerase genes were
434 subjected to purifying selection, indicating their critical role in virus replication as negative
435 selection purges deleterious variation. However, while purifying selection is detectable, it is
436 incomplete[26]. We observed that most nonsynonymous variants began to accumulate around
437 3-4 days post-symptom onset, with incrementally higher empirical rates as the infection
438 progressed.

439

440 Through simulations of a within-host evolution model, we hypothesised that the
441 accumulation of nonsynonymous iSNVs was a result of their weakly deleterious effects and
442 expanding virion population size such that mutation-selection balance was reached. The
443 maintenance of genetic diversity through mutation-selection balance within these children
444 may provide opportunities for the emergence of phenotypically relevant mutations which
445 deleterious effects could be alleviated by the accumulation of a secondary compensatory
446 mutations. For example, in one individual NP-G384R was accompanied by NP-M426I which
447 is an anchor residue of a CTL epitope of NP, abrogating recognition by HLA-B*3501-
448 positive CTLs[32] but is likely to be deleterious based on our computational protein stability
449 predictions. G384R, which is located in a CTL epitope distinct from M426I[32], was previously
450 shown to be a stabilizing substitution[31].

451

452 Interestingly, we also observed G384R in the minority virus population of 15 other unlinked
453 individuals. Besides improving NP protein stability, G384R restores recognition by HLA-
454 B*2705-positive NP-specific CTLs[36]. The NP gene segment in the global A/H3N2 virus
455 population has an evolutionary history of fixating destabilizing amino acid mutations that
456 promote CTL immune escape alongside stabilizing substitutions that compensate for the
457 deleterious effects of the former[34]. The reversal R384G mutation confers CTL escape but is
458 known to be highly deleterious. This substitution was fixed in the global A/H3N2 virus
459 population during the early 1990s as other substitutions such as S259L and E375G
460 epistatically alleviated its destabilizing effects[34]. One possible explanation for the emergence
461 of G384R as a minority variant within these unlinked individuals is that they are all HLA-
462 B*2705 negative. However, we did not collect the necessary blood samples to investigate this
463 possibility.

464

465 In contrast, we found a substantially higher fraction of nonsynonymous variants in the
466 within-host virus populations of individuals infected A/H1N1pdm09 virus during the
467 pandemic. Owing to the different next-generation sequencing platforms used to sequence
468 samples of the two virus subtypes and consequently differences in base calling error rates and
469 depth of coverage (Figure S6), we did not directly compare the observed levels of within-host
470 genetic diversity between the two influenza subtypes here. However, given that only iSNVs
471 with frequencies ≥ 2% were called, low-frequency minority variants arising from technical-
472 related errors should be minimised[51]. Importantly, the relative number of nonsynonymous
473 iSNVs identified were far greater than synonymous ones early in the pandemic
474 A/H1N1pdm09 virus infections, suggesting that there was room for further human host
475 adaptation, particularly in the HA but also in the polymerase gene segments similar to those
476 observed in other zoonotic influenza virus infections[52].

477

478 Given the tight estimated transmission bottleneck size (see Supplementary Materials), the
479 relatively large number of iSNVs identified at the start of symptom onset and simulations of
480 within-host evolution (see Supplementary Materials, Figure 1B, 2B and 6D), it is unlikely
481 that the initial within-host A/H1N1pdm09 virus populations sampled were the inoculating
482 population that founded the infection. Instead, the inoculating viral population had already
483 undergone substantial within-host replication during the incubation period before symptom-
484 onset. In fact, four of the individuals analysed were asymptomatic (i.e. H058/S02, H089/S04,
485 H186/S05 and H296/S04; Table S4). Additionally, pre-symptomatic virus shedding was
486 observed in some of the secondary household cases[53] and presymptomatic transmission has
487 been documented in other settings[54]. Nonetheless, this would not meaningfully impact our
488 conclusions as most of the within-host viral populations sampled at the start of symptom
489 onset should still constitute those found early in infection and the contrasting feature where

490 nonsynonymous iSNVs outnumbered synonymous ones were not observed in the seasonal
491 A/H3N2 virus samples.

492

493 For both A/H3N2 and A/H1N1pdm09 virus samples, nonsense iSNVs resulting in premature
494 stop codons were found to accumulate within host, even though only at low proportions. The
495 accumulation of premature stop-codon mutations further suggest that while purifying
496 selection dominates within-host influenza virus populations, it may not be acting strongly
497 enough to completely purge these lethal nonsense mutations[26]. Additionally, it has been
498 recently found that incomplete influenza virus genomes frequently occur at the cellular level
499 and that efficient infection depends on the complementation between different incomplete
500 genomes[55]. As such, nonsense mutations may not be as uncommon as previously thought. In
501 particular, nonsense mutations in position 77 of the M2 ion channel were independently
502 found in 27 unlinked individuals infected by A/H3N2 virus. While these nonsense mutations
503 are generally considered to be lethal, ion channel activity is retained even if the M2 protein
504 was prematurely truncated up to position 70 at its cytoplasmic tail[56].

505

506 Our study has several limitations. The number of iSNVs identified can potentially be biased
507 by variations in sequencing coverage[57]. As such, the number of iSNVs observed in one intra-
508 host virus populations may not be directly comparable to another with a distinct coverage
509 profile (Figure S6). As an alternative, the nucleotide diversity π statistic[58] may be a more
510 robust measure of within-host diversity as it solely depends on the underlying variant
511 frequencies[57]. Computing the corresponding π statistics for our data, we observed trends in
512 genetic diversity that were similar to those inferred using iSNV counts (see Supplementary
513 Materials and Figure S7).

514

515 To ensure accurate measurements of virus diversity in intra-host populations, we would also
516 need to be certain that the estimated variant frequencies precisely reflect the distributions of
517 variants that comprise the sampled virus populations. The inferred variant frequencies can be
518 significantly distorted if virus load is low[59,60]. As such, we limited our analyses for both virus
519 subtypes to samples with Ct-values $\leq$35 which likely afford sufficient virus material for
520 sequencing[60]. We were unable to estimate the amount of frequency estimation errors for the
521 A/H1N1pdm09 virus samples as only one sequencing replicate was performed using the
522 universal 8-segment PCR method[61]. However, for the A/H3N2 virus samples, independent
523 PCR reactions were performed using three partly overlapping amplicons for all gene
524 segments other than the non-structural and matrix genes. We compared the variant
525 frequencies estimated for any overlapping sites generated by reads derived from distinct
526 amplicons with sufficient coverage (>100x). Variant frequencies computed from independent
527 amplicons agreed well with each other across the range of Ct values of the samples from

528 which variants were identified (Figure S8), affirming the precision of our iSNV frequency
529 estimates for the A/H3N2 virus samples, including those with higher Ct values.

530

531 Finally, most study participants received oseltamivir during the course of their infections
532 (Table S4). Although we were unable to identify any potential effects of enhanced viral
533 clearance or any other evolutionary effects due to the treatment, besides oseltamivir-
534 resistance associated mutations, it is unlikely that the antiviral treatment had a substantial
535 impact on our results. First, the median timepoint in which the antiviral was initially
536 administered was 4 days post-symptom onset (IQR = 3-6 days; Table S4). Previous studies
537 showed that enhanced viral clearance of IAVs was mostly observed among patients who were
538 treated with oseltamivir within 3 days of symptom onset[20,62,63]. Of note, late timepoint
539 samples in this study (≥ 8 days since symptom onset) mostly came from individuals who
540 started oseltamivir treatments ≥ 4 days post-symptom onset (Figure S12). Second, at least *in*
541 *vitro*, there were no differences in the levels of genetic diversity observed in influenza virus
542 populations after multiple serial passages whether they were treated with oseltamivir or not[64].

543

544 To conclude, we presented how intra-host populations of seasonal and pandemic influenza
545 viruses are subjected to contrasting evolutionary selection pressures. In particular, we showed
546 that the evolutionary dynamics and ensuing genetic variation of these within-host virus
547 populations changes during the course of infection, highlighting the importance for sequential
548 sampling, particularly for longer-than-average infections such as those in the young children
549 studied here.

550

551 **Methods (2,840/3,000 words)**

552 *Sample collection and viral sequencing*

553 The A/H3N2 virus samples were collected from 52 patients between August 2007 and
554 September 2009 as part of an oseltamivir dosage trial conducted by the South East Asia
555 Infectious Disease Clinical Research Network (SEAICRN), which is detailed in a previous
556 work[20]. Briefly, patients with laboratory confirmed influenza virus infection and duration of
557 symptoms ≤ 10 days were swabbed for nose and throat samples daily between 0 and 10 days
558 as well as day 14 upon enrolment for the study (Table S4). All PCR-confirmed A/H3N2 virus
559 samples with cycle threshold (Ct) values ≤ 35 were included for sequencing.

560

561 Library preparation and viral sequencing protocols performed on these A/H3N2 virus
562 samples are elaborated in detail in [21]. Here, we highlight key aspects of our preparation and
563 sequencing procedures. Using segment specific primers (Table S3), we performed six

564 independent PCR reactions, resulting in three partly-overlapping amplicons for each
565 influenza virus gene segment other than the matrix (M) and non-structural (NS) genes where
566 a single amplicon was produced to cover the entirety of the relatively shorter M and NS
567 genes. The use of shorter but overlapping amplicons in the longer gene segments improve
568 amplification efficiency, ensuring that these longer segments are sufficiently covered should
569 there be any RNA degradation in the clinical specimen. These overlapping PCR products
570 were pooled in equimolar concentrations for each sample and purified for subsequent library
571 preparation. Sequencing libraries were prepared using the Nextera XT DNA Library
572 Preparation kit (Illumina, FC-131-1096) as described in [21]. Library pools were sequenced
573 using the Illumina MiSeq 600-cycle MiSeq Reagent Kit v3 (Illumina, MS-102-3003).

574

575 The A/H1N1pdm09 virus samples were obtained as part of a household-based influenza virus
576 cohort study that was also performed by SEAICRN. The study was conducted between July
577 and December 2009, involving a total of 270 households in Ha Nam province, Vietnam[24].
578 Similarly, combined nose and throat swabs were collected daily for 10-15 days from
579 individuals with influenza-like-illness (i.e. presenting symptoms of fever >38°C and cough,
580 or sore throat) and their household members, including asymptomatic individuals (Table S4).
581 We also analysed additional samples collected from unlinked hospitalised patients who were
582 infected by the A/H1N1pdm09 virus from two major Vietnamese cities (Hanoi and Ho Chih
583 Minh) during the first wave of the pandemic[20,25]. A total of 32 PCR-confirmed
584 A/H1N1pdm09-infected individuals originating from both households and hospitalised cases
585 were selected for sequencing based on availability and Ct-values ≤ 33 (Table S4).

586

587 For the A/H1N1pdm09 virus samples, RNA extraction was performed manually using the
588 High Pure RNA isolation kit (Roche) with an on-column DNase treatment according to the
589 manufacturer's protocol. Total RNA was eluted in a volume of 50 µl. Universal influenza
590 virus full-genome amplification was performed using a universal 8-segment PCR method as
591 described previously[51,65,66]. In short, two separate RT-PCRs were performed for each sample,
592 using primers common-uni12R (5'-GCCGGAGCTCTGCAGAT ATCAGCRAAAGCAGG-
593 3'), common-uni12G (5'-GCCGGAGCTCTG CAGATATCAGCGAAAGCAGG-3'), and
594 common-uni13 (5'-CAGGAA ACAGCTATGACAGTAGAAACAAGG-3'). The first RT-
595 PCR mixture contained the primers common-uni12R and common-uni13. The second RT-
596 PCR mixture contained the primers common-uni12G and common-uni13, which greatly
597 improved the amplification of the PB2, PB1, and PA segments. Reactions were performed
598 using the One-Step RT-PCR kit High Fidelity (Invitrogen) in a volume of 50 µl containing
599 5.0 µl eluted RNA with final concentrations of 1xSuperScript III One-Step RT-PCR buffer,
600 0.2 µM of each primer, and 1.0 µl SuperScript III RT/Platinum Taq High Fidelity Enzyme
601 Mix (Invitrogen). Thermal cycling conditions were as follows: reverse transcription at 42°C
602 for 15 min, 55°C for 15 min, and 60°C for 5 min; initial denaturation/enzyme activation of

603 94°C for 2 min; 5 cycles of 94°C for 30 s, 45°C for 30 s, slow ramp (0.5°C/s) to 68°C, and
604 68°C for 3 min; 30 cycles of 94°C for 30 s, 57°C for 30 s, and 68°C for 3 min; and a final
605 extension of 68°C for 5 min. After the PCR, equal volumes of the two reaction mixtures were
606 combined to produce a well-distributed mixture of all 8 influenza virus segments. All RT-
607 PCRs were performed in duplicate. Samples were diluted to a DNA concentration of 50 ng/µl
608 followed by ligation of 454 sequencing adaptors and molecular identifier (MID) tags using
609 the SPRIworks Fragment Library System II for Roche GS FLX+ DNA Sequencer (Beckman
610 Coulter), excluding fragments smaller than 350 base pairs, according to the manufacturers
611 protocol to allow for multiplex sequencing per region. The quantity of properly ligated
612 fragments was determined based on the incorporation efficiency of the fluorescent primers
613 using FLUOstar OPTIMA (BMG Labtech). Emulsion PCR, bead recovery and enrichment
614 were performed manually according to the manufacturers protocol (Roche) and samples were
615 sequenced in Roche FLX+ 454. Sequencing was performed at the Sanger Institute, Hinxton,
616 Cambridge, England as part of the FP7 program EMPERIE. Standard flowgram format (sff)
617 files containing the filter passed reads were demultiplexed based on the molecular identifier
618 (MID) sequences using QUASR package version 7.0[51].

619

620 *Read mapping*

621 Trimmomatic (v0.39; Bolger et al. 2014) was used to discard reads with length <30 bases
622 while trimming the ends of reads where base quality scores fall below 20. The MAXINFO
623 option was used to perform adaptive quality trimming, balancing the trade-off between longer
624 read length and tolerance of base calling errors (target length=40, strictness=0.4). For the
625 A/H3N2 virus samples, the trimmed paired reads were merged using FLASH (v1.2.11)[68]. All
626 remaining reads were then locally aligned to A/Brisbane/10/2007 genome (GISAID
627 accession: EPI_ISL_103644) for A/H3N2 virus samples and A/California/4/2009 genome
628 (EPI_ISL_376192) for A/H1N1pdm09 virus samples using Bowtie2 (v2.3.5.1)[69]. Aligned
629 reads with mapping scores falling below 20 alongside bases with quality score (*Q-score*)
630 below 20 were discarded.

631

632 *Variant calling and quality filters*

633 Minority variants of each nucleotide site with a frequency of at least 2% were called if the
634 nucleotide position was covered at least 50x (H1N1pdm09) or 100x (H3N2) and the
635 probability that the variant was called as a result of base calling errors (p_{Err}) was less than
636 1%. p_{Err} was modelled by binomial trials[70]:

637 $$p_{Err} = \sum_{i=n}^{N} \binom{N}{i} p_e^i (1 - p_e)^{N-i}$$

638 where $p_e = -10^{-\frac{Q-score}{10}}$, N is the coverage of the nucleotide site in question and n is the
639 absolute count of the variant base tallied.

640

641 While lower coverage at both ends of individual gene segments was expected, there were also
642 variable coverage results across gene segments for some samples that were mapped to
643 A/H3N2 virus (Figure S6). In order to retain as many samples deemed to have adequate
644 coverage across whole genome, a list of polymorphic nucleotide sites found to have >2%
645 minority variants in more than 1 sample was compiled. Each gene segment of a sample was
646 determined to achieve satisfactory coverage if >70% of these polymorphic sites were covered
647 at least 100x. For A/H1N1pdm09, the gene segment of a sample was deemed to be
648 adequately covered if 80% of the gene was covered at least 50x.

649

650 The number of iSNVs observed in A/H3N2 virus samples collected from subject 1673 (39-94
651 iSNVs in three samples collected from three (D3) to five (D5) days post-symptom onset) and
652 the D8 sample for subject 1878 (73 iSNVs) were substantially greater than numbers in all
653 other samples. The putative majority and minority segment-concatenated sequences of these
654 samples did not cluster as a monophyletic clade among themselves phylogenetically (Figure
655 S9), suggesting that these samples might be the product of mixed infections or cross-
656 contamination. These samples were consequently excluded from further analyses.

657

658 *Empirical within-host evolutionary rate*

659 The empirical within-host evolutionary rate ($r_{g,t}$) of each gene segment (g) in a sample
660 collected on t day(s) since symptom onset were estimated by:

661 $$r_{g,t} = \frac{\sum_i^{n_{g,t}} f_{g,t,i}}{n_{g,t} \cdot t}$$

662 where $f_{g,t,i}$ is the frequency of minority variants present in nucleotide site i for gene segment
663 g and $n_{g,t}$ is the number of all available sites[26]. Distinct rates were calculated for
664 synonymous and non-synonymous iSNVs. The corresponding whole-genome evolutionary
665 rate (r_t) on day t is computed by summing the rates across all gene segments:

666 $$r_t = \sum_g r_{g,t}$$

667

668 *Within-host simulations*

669 We implemented forward-time Monte Carlo simulations with varying population size using a
670 simplified within-host evolution model to test if our hypotheses could explain the different
671 evolutionary dynamics observed between A/H3N2 and A/H1N1 viral populations. We
672 assumed that a single virion leads to a productive influenza virus infection within an
673 individual and computed changes in the virus population size (N) using a target cell-limited
674 model. New virions are produced upon infection by existing virions at a rate of βCN where C
675 is the existing number of target cells while β is the rate of per-cell per-virion infectious
676 contact. Upon infection, a cell will produce r number of virions before it is rendered
677 unproductive. We assume that infected individuals did not mount any antibody-mediated
678 immune response, setting the virus' natural per-capita decay rate (d) such that virions
679 continue to be present within host for 14 days (Figure S11 and Table 2). β is then computed
680 by fixing the within-host basic reproduction number (R_0):

681 $$R_0 = \frac{\beta C_0 r}{d}$$

682 where C_0 is the initial (maximum) target cell population size. We solve the following system
683 of ordinary differential equations numerically to compute the number of virions per viral
684 replicative generation ($N(t)$):

685 $$\frac{dC}{dt} = -\beta CN$$

686 $$\frac{dN}{dt} = \beta CN - dN$$

687

688 We assume a binary genome of length L, distinguishing between synonymous and
689 nonsynonymous loci. For A/H3N2 viruses, we hypothesised that most *de novo* mutations are
690 either weakly deleterious or neutral. To estimate the number of such sites, we aligned
691 A/H3N2 virus sequences that were collected between 2007 and 2012 and identified all
692 polymorphic sites with variants that did not fixate over time (i.e. <95% frequency over one-
693 month intervals). We estimated $L = 1050$ with 838 and 212 synonymous and
694 nonsynonymous loci respectively. On the other hand, for A/H1N1pdm09 viruses, we
695 assumed that any variants that emerged are likely neutral or weakly beneficial. In the absence
696 of strong purifying selection, ~75% of mutations are expected to be nonsynonymous[26]. Here,
697 we assumed $L = 1000$ sites of which 750 of them are synonymous and the rest are
698 nonsynonymous.

699

700 We tracked the frequency distribution of genotypes present for every generation t. We
701 assumed that mutations occur at per-locus, per-generation rate μ. During each generation t,
702 the number of virions incurring a single-locus mutation followed a Poisson distribution with
703 mean $N(t)\mu L$. For each virion, the mutant locus was randomly selected across all loci. We

704 assumed that all synonymous and a fraction of nonsynonymous sites ($f_{neu,NS}$) are neutral (i.e.
705 (log) fitness effect $s = 0$). The remaining nonsynonymous sites either had an additive
706 deleterious (s_d) or beneficial (s_b) fitness effect when mutated. The magnitude of s_d/s_b follow
707 an exponential distribution with mean effect $|\bar{s}|$. Epistasis was neglected throughout. The
708 distribution of genotypes in the next generation $t + 1$ was achieved by resampling
709 individuals according to Poisson distribution with mean $N(t + 1)P_f(g, t)$ where $P_f(g, t)$ is
710 the relative fitness distribution of genotype g during generation t.

711

712 To decrease the computational costs of the simulations, specifically when $N(t)$ reaches
713 orders of $10^{10} - 10^{11}$ virions (Figure S11), we implemented an upper population size limit
714 of 10^7 virions. Given the mutation rate assumed (Table 2), $N(t)\mu \gg 1$ for $N(t) \geq 10^7$
715 virions, mutation-selection balance is theoretically expected for a single-locus (deleterious)
716 mutant model (see Supplementary Materials). We ran 500 simulations for each variable set of
717 $f_{neu,NS}$ and s_d/s_b values. All parameter values used in the model are given in Table 2.

718

719 **Table 2**: Parameter values used in within-host model

Parameter	Meaning	Value (units)	Source
-	Number of hours per replicative generation	6 hours	Assumption
r	Average number of virions produced by an infected cell	100 virions	[71]
C_0	Initial target cell population size	4×10^8 virions	[72]
d	Per-capita decay rate	2 per-generation	Assumption
R_0	Within-host basic reproduction number	5	[72]
μ	Per-site, per-generation mutation rate	3×10^{-5} per-site, per-generation	[45]

720

721 *Haplotype reconstruction*

722 The most parsimonious viral haplotypes of each gene segment were reconstructed by fitting
723 the observed nucleotide variant count data to a Dirichlet multinomial model using a
724 previously developed maximum likelihood approach to infer haplotype frequencies[44].
725 Assuming that the viral population is made up of a set of K haplotypes with frequencies $\boldsymbol{q_k}$,
726 the observed partial haplotype frequencies $\boldsymbol{q_l}$ for a polymorphic site l can be computed by
727 multiplying a projection matrix $\boldsymbol{T_l}$. For instance, if the set of hypothetical full haplotypes is
728 assumed to be $\{AA, GA, AG\}$, the observed partial haplotype frequencies for site $l = 1$, q_{A-}
729 and q_{G-} are computed as:

$$\boldsymbol{q_l} = \boldsymbol{T_l q_k} \Rightarrow \begin{bmatrix} q_{A-} \\ q_{G-} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{bmatrix} \times \begin{bmatrix} q_{AA} \\ q_{GA} \\ q_{AG} \end{bmatrix}$$

A list of potential full haplotypes was generated from all combinations of nucleotide variants observed in all polymorphic sites of the gene segment. Starting from $K = 1$ full haplotype, the optimal full haplotype frequency q_k is inferred by maximizing the likelihood function:

$$LL = \sum_{l} \log \mathcal{L}(\boldsymbol{x_l} | \boldsymbol{T_l q_k}, \varphi)$$

where $\mathcal{L}$ is Dirichlet multinomial likelihood, $\boldsymbol{x_l}$ is the observed variant count data for read type l and φ is the overdispersion parameter, assumed to be 1×10^{-3}. Simulated annealing was used to optimise the haplotype frequencies by running two independent searches for at least 5000 states (iterations) until convergence was reached. In each state, the distribution of $\boldsymbol{q_k}$ was drawn from a Gaussian distribution centered at the frequency distribution of the previous state with a standard deviation of 0.05. One additional haplotype was added to the set of K full haplotypes during each round of optimization.

The resulting K haplotypes reconstructed depend on the order in which the list of potential full haplotypes is considered. As mentioned above, paired-end reads were merged to produce longer reads (up to ~500-600 base pairs) for mapping in the case of the seasonal A/H3N2 virus samples. Additionally, the single-stranded A/H1N1pdm09 viral reads generated from 454 sequencing can be as long as ~500 base pairs. Consequently, there was a non-trivial number of reads where co-mutations were observed in multiple polymorphic sites. Since iSNV frequencies are generally low, haplotypes with co-mutating sites would inevitably be relegated to end of the list order if ranked by their expected joint probabilities. As such, the list of full potential haplotypes was ordered in descending order based on the score of each full haplotype set k (s_k):

$$s_k = f_{ss,k} \times f_{ms,k}$$

where $f_{ss,k}$ and $f_{ms,k}$ are both joint probabilities of the full haplotype k computed in different ways. $f_{ss,k}$ is the expected joint probability frequency calculated from the observed independent frequencies of each variant for each polymorphic site found in the full haplotype k. $f_{ms,k}$ is based on the observed frequencies of variants spanning across the sets of highest hierarchal combination of polymorphic sites ($f_{ms,k}$).

For example, given a segment where iSNVs were found in three sites, the following reads were mapped: (A, A, C), (T, A, C), (A, T, C), (A, C, –), (–, A, C) and (–, T, C). We can immediately see that the top hierarchal combination of polymorphic sites (i.e. possible

764 haploptes) are (A, A, C), (T, A, C) and (A, T, C) (i.e. we would compute $f_{ms,(A,A,C)}$,
765 $f_{ms,(T,A,C)}$ and $f_{ms,(A,T,C)}$ respectively). The observed number of reads with (–, A, C) will
766 counted towards the computation of both $f_{ms,(A,A,C)}$ and $f_{ms,(T,A,C)}$ since they could be
767 attributed to either haplotype. Similarly, reads with (–, T, C) will be absorbed towards the
768 counts to compute $f_{ms,(A,T,C)}$. Finally, we see that reads with (A, C, –) are not a subset of any
769 of the top hierarchal haplotypes considered. As such, they form the 4th possible top hierarchal
770 haplotype on its own. As such, if we were to compute the ranking for haplotype (A, A, C):

771 $$s_{(A,A,C)} = f_{ss,(A,A,C)} \times f_{ms,(A,A,C)}$$
772 $$= \{f_{(A,-,-)} \times f_{(-,A,-)} \times f_{(-,-,C)}\} \times f_{ms,(A,A,C)}$$

773

774 If any nucleotide variants in the observed partial haplotypes were unaccounted for in the
775 current round of full haplotypes considered, they were assumed to be generated from a cloud
776 of "noise" haplotypes that were present in no more than 1%. Bayesian information criterion
777 (BIC) was computed for each set of full haplotypes considered and the most parsimonious set
778 of K haplotypes was determined by the lowest BIC value.

779

780 *Linkage disequilibrium*

781 Using the estimated frequencies of the most parsimonious reconstructed haplotypes,
782 conventional Lewontin's metrics of linkage disequilibrium were computed to detect for
783 potential epistatic pairs of nonsynonymous variants:

784 $$LD_{ij} = \hat{q}_{ij} - \hat{q}_i\hat{q}_j$$

785 where $\hat{q}_i$ and $\hat{q}_j$ are the estimated site-independent iSNV frequencies of sites i and j
786 respective while $\hat{q}_{ij}$ is the frequency estimate of variants encoding co-variants in both i and j.
787 Dividing LD by its theoretical maximum normalises the linkage disequilibrium measure:

788 $$LD' = \frac{LD}{LD_{max}}$$

789 $$LD_{max} = \begin{cases} \max\{-\hat{q}_i\hat{q}_j, -(1-\hat{q}_i)(1-\hat{q}_j)\} & if\ LD > 0 \\ \min\{\hat{q}_i(1-\hat{q}_j), (1-\hat{q}_i)\hat{q}_j\} & if\ LD < 0 \end{cases}$$

790

791

792 *FoldX analyses*

793 FoldX (https://foldxsuite.crg.eu/) was used to estimate structural stability effects of likely
794 linked nonsynonymous minority variants found in the nucleoprotein (NP) of within-host
795 A/H3N2 virus populations. At the time of writing of this paper, there was no A/H3N2-NP

796 structure available. Although the eventual NP structure (PDB: 3ZDP) adopted for stability
797 analyses was originally derived from H1N1 virus (A/WSN/33)[40], it was the most well
798 resolved (2.69Å) crystal structure available, with 78.5% amino acid identity relative to the NP
799 protein of A/Brisbane/10/2007. Previous work has shown that mutational effects predicted by
800 FoldX using a NP structure belonging to A/WSN/33 (H1N1) was similar to those
801 experimentally determined on a A/Brisbane/10/2007 nucleoprotein[31]. FoldX first removed
802 any potential steric clashes to repair the NP structure. It then estimated differences in free
803 energy changes as a result of the input amino acid mutation (i.e. $\Delta\Delta G = \Delta G_{mutant} -$
804 $\Delta G_{wild-type}$) under default settings (298K, 0.05M ionic strength and pH 7.0). Five distinct
805 simulations were made to estimate the mean and standard deviation $\Delta\Delta G$ values.

806

807 *Phylogenetic inference*

808 All maximum likelihood phylogenetic trees were reconstructed with IQTREE (v. 1.6.10)[73],
809 using the GTR+I+G4 nucleotide substitution model.

810

811 **References**

812 1. Andino, R. & Domingo, E. Viral quasispecies. *Virology* **479–480**, 46–51 (2015).
813 2. Smith, D. J. *et al.* Mapping the Antigenic and Genetic Evolution of Influenza Virus.
814 *Science (80-.).* **305**, 371–376 (2004).
815 3. Varble, A. *et al.* Influenza A Virus Transmission Bottlenecks Are Defined by Infection
816 Route and Recipient Host. *Cell Host Microbe* **16**, 691–700 (2014).
817 4. McCrone, J. T. *et al.* Stochastic processes constrain the within and between host
818 evolution of influenza virus. *Elife* **7**, e35962 (2018).
819 5. Russell, C. A. *et al.* The global circulation of seasonal influenza A (H3N2) viruses.
820 *Science* **320**, 340–6 (2008).
821 6. Rambaut, A. *et al.* The genomic and epidemiological dynamics of human influenza A
822 virus. *Nature* **453**, 615–619 (2008).
823 7. Nelson, M. I. & Holmes, E. C. The evolution of epidemic influenza. *Nat. Rev. Genet.*
824 **8**, 196–205 (2007).
825 8. Dinis, J. M. *et al.* Deep Sequencing Reveals Potential Antigenic Variants at Low
826 Frequencies in Influenza A Virus-Infected Humans. *J. Virol.* **90**, 3355–65 (2016).
827 9. Debbink, K. *et al.* Vaccination has minimal impact on the intrahost diversity of H3N2
828 influenza viruses. *PLOS Pathog.* **13**, e1006194 (2017).
829 10. Valesano, A. L. *et al.* Influenza B Viruses Exhibit Lower Within-Host Diversity than
830 Influenza A Viruses in Human Hosts. *J. Virol.* **94**, e01710-19 (2020).
831 11. Sobel Leonard, A. *et al.* Deep Sequencing of Influenza A Virus from a Human
832 Challenge Study Reveals a Selective Bottleneck and Only Limited Intrahost Genetic
833 Diversification. *J. Virol.* **90**, 11247–11258 (2016).
834 12. Han, A. X., Maurer-Stroh, S. & Russell, C. A. Individual immune selection pressure
835 has limited impact on seasonal influenza virus evolution. *Nat. Ecol. Evol.* 1 (2018).
836 doi:10.1038/s41559-018-0741-x
837 13. Smith, G. J. D. *et al.* Origins and evolutionary genomics of the 2009 swine-origin
838 H1N1 influenza A epidemic. *Nature* **459**, 1122–1125 (2009).
839 14. Su, Y. C. F. *et al.* Phylodynamics of H1N1/2009 influenza reveals the transition from
840 host adaptation to immune-driven selection. *Nat. Commun.* **6**, 7952 (2015).
841 15. Elderfield, R. A. *et al.* Accumulation of Human-Adapting Mutations during
842 Circulation of A(H1N1)pdm09 Influenza Virus in Humans in the United Kingdom. *J.*
843 *Virol.* **88**, 13269 LP – 13283 (2014).
844 16. Nogales, A., Martinez-Sobrido, L., Chiem, K., Topham, D. J. & DeDiego, M. L.
845 Functional Evolution of the 2009 Pandemic H1N1 Influenza Virus NS1 and PA in
846 Humans. *J. Virol.* **92**, e01206-18 (2018).
847 17. Poon, L. L. M. *et al.* Quantifying influenza virus diversity and transmission in humans.
848 *Nat. Genet.* **48**, 195–200 (2016).
849 18. Xue, K. S. & Bloom, J. D. Reconciling disparate estimates of viral genetic diversity
850 during human influenza infections. *Nat. Genet.* **51**, 1298–1301 (2019).
851 19. Poon, L. L. M. *et al.* Reply to 'Reconciling disparate estimates of viral genetic
852 diversity during human influenza infections'. *Nat. Genet.* **51**, 1301–1303 (2019).
853 20. South East Asia Infectious Disease Clinical Research Network. Effect of double dose
854 oseltamivir on clinical and virological outcomes in children and adults admitted to
855 hospital with severe influenza: Double blind randomised controlled trial. *BMJ* **346**,
856 f3039 (2013).
857 21. Koel, B. F. *et al.* Longitudinal sampling is required to maximize detection of intrahost
858 A/H3N2 virus variants. *Virus Evol.* **6**, veaa088 (2020).
859 22. Worby, C. J. *et al.* On the relative role of different age groups in influenza epidemics.

Epidemics **13**, 10–16 (2015).
23. Viboud, C. *et al.* Risk factors of influenza transmission in households. *Int. Congr. Ser.* **1263**, 291–294 (2004).
24. Horby, P. *et al.* The epidemiology of interpandemic and pandemic influenza in Vietnam, 2007-2010. *Am. J. Epidemiol.* **175**, 1062–1074 (2012).
25. Hien, T. T. *et al.* Early Pandemic Influenza (2009 H1N1) in Ho Chi Minh City, Vietnam: A Clinical Virological and Epidemiological Analysis. *PLOS Med.* **7**, e1000277 (2010).
26. Xue, K. S. & Bloom, J. D. Linking influenza virus evolution within and between human hosts. *Virus Evol.* **6**, 812016 (2020).
27. Wiley, D. C. C., Wilson, I. A. A. & Skehel, J. J. J. Structural identification of the antibody-binding sites of Hong Kong influenza haemagglutinin and their involvement in antigenic variation. *Nature* **289**, 373–378 (1981).
28. Caton, A. J., Brownlee, G. G., Yewdell, J. W. & Gerhard, W. The antigenic structure of the influenza virus A/PR/8/34 hemagglutinin (H1 subtype). *Cell* **31**, 417–27 (1982).
29. Igarashi, M. *et al.* Predicting the Antigenic Structure of the Pandemic (H1N1) 2009 Influenza Virus Hemagglutinin. *PLoS One* **5**, e8553 (2010).
30. Mänz, B. *et al.* Pandemic Influenza A Viruses Escape from Restriction by Human MxA through Adaptive Mutations in the Nucleoprotein. *PLOS Pathog.* **9**, e1003279 (2013).
31. Ashenberg, O., Gong, L. I. & Bloom, J. D. Mutational effects on stability are largely conserved during protein evolution. *Proc. Natl. Acad. Sci. U. S. A.* **110**, 21071–6 (2013).
32. Berkhoff, E. G. M. *et al.* Functional Constraints of Influenza A Virus Epitopes Limit Escape from Cytotoxic T Lymphocytes. *J. Virol.* **79**, 11239 LP – 11246 (2005).
33. Gog, J. R., Rimmelzwaan, G. F., Osterhaus, A. D. M. E. & Grenfell, B. T. Population dynamics of rapid fixation in cytotoxic T lymphocyte escape mutants of influenza A. *Proc. Natl. Acad. Sci.* **100**, 11143 LP – 11147 (2003).
34. Gong, L. I., Suchard, M. A. & Bloom, J. D. Stability-mediated epistasis constrains the evolution of an influenza protein. *Elife* **2**, e00631 (2013).
35. Rimmelzwaan, G. F., Berkhoff, E. G. M., Nieuwkoop, N. J., Fouchier, R. A. M. & Osterhaus, A. D. M. E. Functional Compensation of a Detrimental Amino Acid Substitution in a Cytotoxic-T-Lymphocyte Epitope of Influenza A Viruses by Comutations. *J. Virol.* **78**, 8946 LP – 8949 (2004).
36. Berkhoff, E. G. M. *et al.* A Mutation in the HLA-B*2705-Restricted NP383-391 Epitope Affects the Human Influenza A Virus-Specific Cytotoxic T-Lymphocyte Response In Vitro. *J. Virol.* **78**, 5216 LP – 5222 (2004).
37. Resa-Infante, P. *et al.* Targeting Importin-α7 as a Therapeutic Approach against Pandemic Influenza Viruses. *J. Virol.* **89**, 9010 LP – 9020 (2015).
38. Resa-Infante, P. *et al.* Alternative interaction sites in the influenza A virus nucleoprotein mediate viral escape from the importin-α7 mediated nuclear import pathway. *FEBS J.* **286**, 3374–3388 (2019).
39. Gabriel, G. *et al.* Differential use of importin-α isoforms governs cell tropism and host adaptation of influenza virus. *Nat. Commun.* **2**, 156 (2011).
40. Chenavas, S. *et al.* Monomeric Nucleoprotein of Influenza A Virus. *PLOS Pathog.* **9**, e1003275 (2013).
41. Mak, G. C. *et al.* Association of D222G substitution in haemagglutinin of 2009 pandemic influenza A (H1N1) with severe disease. *Eurosurveillance* **15**, (2010).
42. Mai, L. Q. *et al.* A Community Cluster of Oseltamivir-Resistant Cases of 2009 H1N1 Influenza. *N. Engl. J. Med.* **362**, 86–87 (2010).

43. Lam, J. H. & Baumgarth, N. The Multifaceted B Cell Response to Influenza Virus. *J. Immunol.* **202**, 351 LP – 359 (2019).
44. Ghafari, M., Lumby, C. K., Weissman, D. B. & Illingworth, C. J. R. Inferring Transmission Bottleneck Size from Viral Sequence Data Using a Novel Haplotype Reconstruction Method. *J. Virol.* **94**, (2020).
45. McCrone, J. T., Woods, R. J., Monto, A. S., Martin, E. T. & Lauring, A. S. The effective population size and mutation rate of influenza A virus in acutely infected individuals. *bioRxiv* 2020.10.24.353748 (2020). doi:10.1101/2020.10.24.353748
46. Morris, D. H. *et al.* Asynchrony between virus diversity and antibody selection limits influenza virus evolution. *Elife* **9**, 1–62 (2020).
47. Xue, K. S. *et al.* Parallel evolution of influenza across multiple spatiotemporal scales. *Elife* **6**, e26875 (2017).
48. Lumby, C. K., Zhao, L., Breuer, J. & Illingworth, C. J. R. A large effective population size for established within-host influenza virus infection. *Elife* **9**, e56915 (2020).
49. Petrova, V. N. & Russell, C. A. The evolution of seasonal influenza viruses. *Nat. Rev. Microbiol.* **16**, 47–60 (2017).
50. Ng, S. *et al.* The Timeline of Influenza Virus Shedding in Children and Adults in a Household Transmission Study of Influenza in Managua, Nicaragua. *Pediatr. Infect. Dis. J.* **35**, 583–586 (2016).
51. Watson, S. J. *et al.* Viral population analysis and minority-variant detection using short read next-generation sequencing. *Philos. Trans. R. Soc. Lond. B. Biol. Sci.* **368**, 20120205 (2013).
52. Welkers, M. R. A. *et al.* Genetic diversity and host adaptation of avian H5N1 influenza viruses during human infection. *Emerg. Microbes Infect.* **8**, 262–271 (2019).
53. Thai, P. Q. *et al.* Pandemic H1N1 virus transmission and shedding dynamics in index case households of a prospective Vietnamese cohort. *J. Infect.* **68**, 581–590 (2014).
54. Suess, T. *et al.* Comparison of Shedding Characteristics of Seasonal Influenza Virus (Sub)Types and Influenza A(H1N1)pdm09; Germany, 2007–2011. *PLoS One* **7**, e51653 (2012).
55. Jacobs, N. T. *et al.* Incomplete influenza A virus genomes occur frequently but are readily complemented during localized viral spread. *Nat. Commun.* **10**, 3526 (2019).
56. McCown, M. F. & Pekosz, A. The Influenza A Virus M₂ Cytoplasmic Tail Is Required for Infectious Virus Production and Efficient Genome Packaging. *J. Virol.* **79**, 3595 LP – 3605 (2005).
57. Zhao, L. & Illingworth, C. J. R. Measurements of intrahost viral diversity require an unbiased diversity metric. *Virus Evol.* **5**, (2019).
58. Nei, M. & Li, W. H. Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proc. Natl. Acad. Sci.* **76**, 5269 LP – 5273 (1979).
59. Illingworth, C. J. R. *et al.* On the effective depth of viral sequence data. *Virus Evol.* **3**, (2017).
60. Xue, K. S., Moncla, L. H., Bedford, T. & Bloom, J. D. Within-Host Evolution of Human Influenza Virus. *Trends Microbiol.* **26**, 781–793 (2018).
61. Hoffmann, E., Stech, J., Guan, Y., Webster, R. G. & Perez, D. R. Universal primer set for the full-length amplification of all influenza A viruses. *Arch. Virol.* **146**, 2275–2289 (2001).
62. Lee, N. *et al.* Viral Loads and Duration of Viral Shedding in Adult Patients Hospitalized with Influenza. *J. Infect. Dis.* **200**, 492–500 (2009).
63. Ling, L. M. *et al.* Effects of early oseltamivir therapy on viral shedding in 2009 pandemic influenza A (H1N1) virus infection. *Clin Infect Dis* **50**, 963–969 (2010).
64. Renzette, N. *et al.* Evolution of the Influenza A Virus Genome during Development of

Oseltamivir Resistance In Vitro *J. Virol.* **88**, 272 LP – 281 (2014).
65. Zhou, B. *et al.* Single-reaction genomic amplification accelerates sequencing and vaccine production for classical and Swine origin human influenza a viruses. *J. Virol.* **83**, 10309–13 (2009).
66. Jonges, M. *et al.* Emergence of the Virulence-Associated PB2 E627K Substitution in a Fatal Human Case of Highly Pathogenic Avian Influenza Virus A(H7N7) Infection as Determined by Illumina Ultra-Deep Sequencing. *J. Virol.* **88**, 1694–702 (2014).
67. Bolger, A. M., Lohse, M. & Usadel, B. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* **30**, 2114–2120 (2014).
68. Magoč, T., Magoč, M. & Salzberg, S. L. FLASH: fast length adjustment of short reads to improve genome assemblies. **27**, 2957–2963 (2011).
69. Langmead, B. & Salzberg, S. L. Fast gapped-read alignment with Bowtie 2. *Nat. Methods* **9**, 357–359 (2012).
70. Illingworth, C. J. R. SAMFIRE: multi-locus variant calling for time-resolved sequence data. *Bioinformatics* **32**, 2208–2209 (2016).
71. Frensing, T. *et al.* Influenza virus intracellular replication dynamics, release kinetics, and particle morphology during propagation in MDCK cells. *Appl. Microbiol. Biotechnol.* **100**, 7181–7192 (2016).
72. Hadjichrysanthou, C. *et al.* Understanding the within-host dynamics of influenza A virus: from theory to clinical implications. *J. R. Soc. Interface* **13**, 20160289 (2016).
73. Nguyen, L.-T., Schmidt, H. A., von Haeseler, A. & Minh, B. Q. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol. Biol. Evol.* **32**, 268–74 (2015).

Data availability

All raw sequence data have been deposited at NCBI sequence read archive under BioProject Accession number PRJNAXXXXXX. All custom Python code and Jupyter notebooks to reproduce the analyses in this paper are available online: https://github.com/AMC-LAEB/Within_Host_H3vH1.

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Competing interests

The authors declare no competing interests.

Author contributions

A.X.H., Z.C.F.G., M.R.A.W., D.E., M.D.d.J., and C.A.R. designed the research; A.X.H., Z.C.F.G. and M.R.A.W. performed the data analyses; M.R.A.W., R.M.V., T.N.D, L.T.Q.M., P.Q.T., T.T.N.A., H.M.T., N.T.H., L.Q.T., L.T.H., H.T.B.N., K.C., P.P., N.V.V.C., N.M.N., T.T.H., H.F.L.W., P.H., A.F., H.R.V.D., D.E. and M.D.d.J. collected the clinical samples and generated the sequencing data; A.X.H., Z.C.F.G. and C.A.R. wrote the first draft of the paper. All authors contributed to the critical review and revision of the paper.