

Global migration dynamics underlie evolution and persistence of human influenza A (H3N2)

Supporting Information

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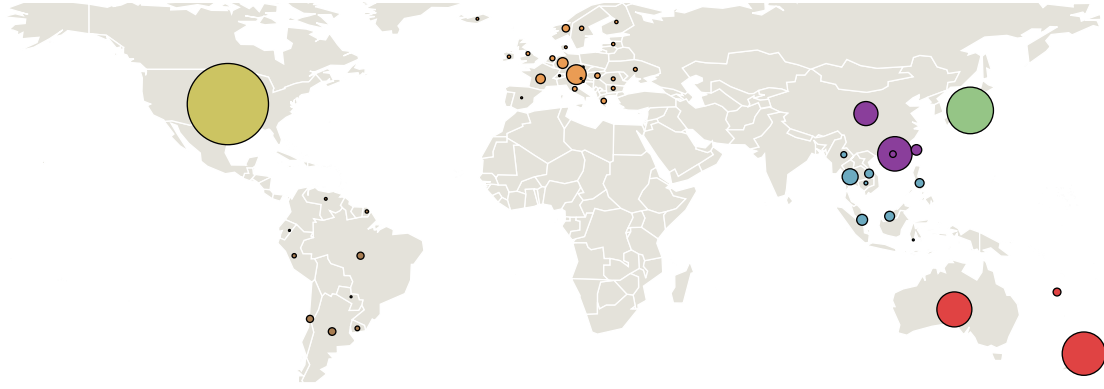


Figure S1. Distribution of 4355 influenza A (H3N2) samples across countries of origin. Circles are colored according to our regional partitioning. Circle areas are proportional to sample count of the full dataset before any resampling took place.

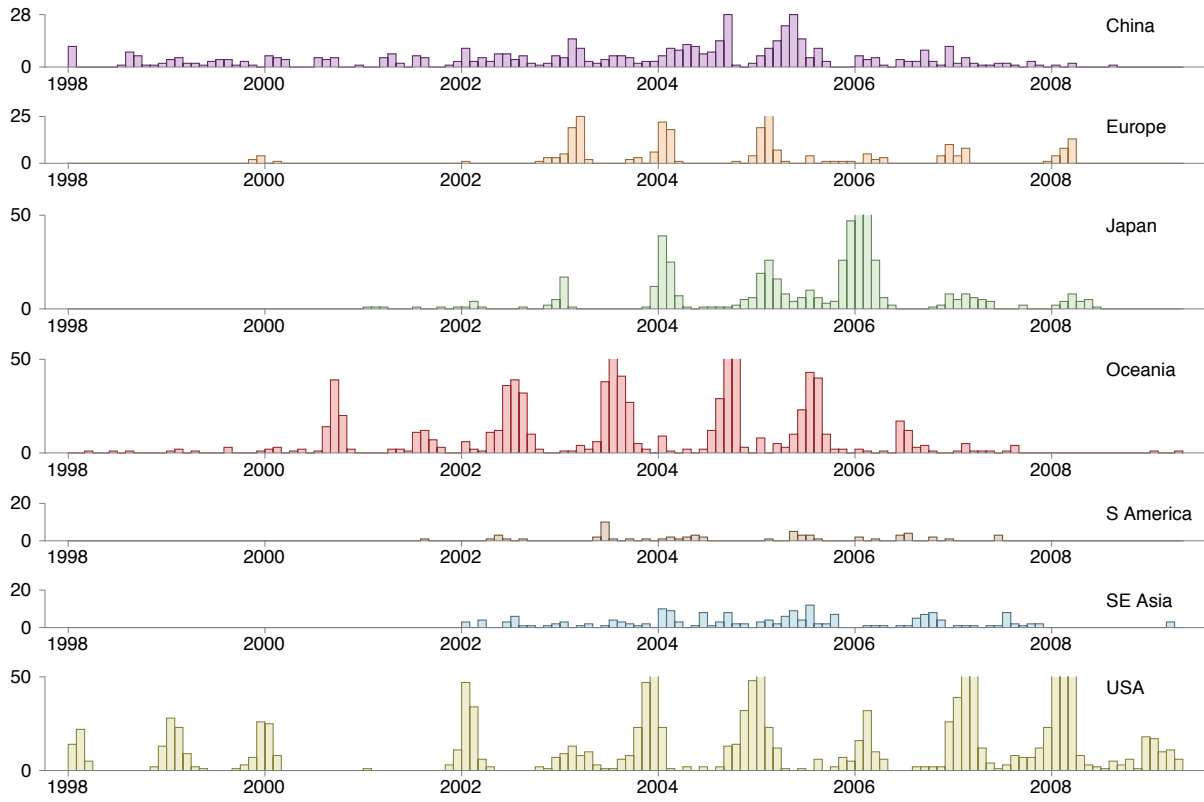


Figure S2. Distribution of 4355 influenza A (H3N2) samples over time across regions. Each bin represents a single month. Sample counts are of the full dataset before any resampling took place.

Table S1. Number of sequences used from each geographic region in different stages of the analysis.

	Diversity estimates	Equal sampling	Proportional sampling	Genealogical estimates
China	534	61	206	463
Europe	248	61	94	174
Japan	603	61	20	280
Oceania	881	61	6	394
South America	62	61	61	62
Southeast Asia	190	61	90	188
USA	1837	61	49	604
Total	4355	427	526	2165

Table S2. Regional genetic diversity π arrayed below the diagonal, measured in terms of 10^{-3} substitutions per site, and regional F_{ST} arrayed above diagonal, with 95% confidence intervals determined by 1000 bootstrap replicates.

	China	Europe	Japan	Oceania	S America	SE Asia	USA
China	6.1 (5.8, 6.5)	0.50 (0.46, 0.54)	0.08 (0.04, 0.12)	0.50 (0.47, 0.52)	0.26 (0.05, 0.43)	0.24 (0.16, 0.30)	0.46 (0.43, 0.48)
Europe	16.5 (15.6, 17.6)	10.3 (9.4, 11.2)	0.07 (0.02, 0.12)	0.34 (0.26, 0.41)	-0.28 (-0.73, 0.05)	0.17 (0.07, 0.25)	-0.02 (-0.10, 0.05)
Japan	8.9 (8.5, 9.2)	11.0 (10.6, 11.4)	10.1 (9.9, 10.3)	0.22 (0.18, 0.26)	-0.20 (-0.48, 0.03)	-0.05 (-0.15, 0.04)	0.16 (0.14, 0.17)
Oceania	11.8 (11.5, 12.1)	12.1 (11.1, 13.2)	10.2 (9.8, 10.6)	5.7 (5.5, 5.9)	0.37 (0.21, 0.51)	0.38 (0.33, 0.43)	0.32 (0.29, 0.35)
S America	15.0 (13.6, 16.2)	9.9 (8.1, 12.1)	10.9 (10.1, 11.7)	17.4 (16.1, 18.7)	16.0 (11.1, 21.2)	0.13 (-0.10, 0.33)	-0.06 (-0.43, 0.23)
SE Asia	9.6 (9.1, 10.0)	11.3 (10.5, 12.2)	8.5 (8.0, 9.0)	11.4 (10.9, 11.9)	14.1 (12.5, 15.8)	8.5 (7.6, 9.4)	0.36 (0.31, 0.41)
USA	10.5 (10.1, 10.8)	7.6 (7.3, 7.9)	9.1 (9.0, 9.3)	8.1 (7.8, 8.4)	10.1 (8.3, 12.1)	10.8 (10.3, 11.3)	5.3 (5.2, 5.3)

Table S3. Estimates for immigration (columns) and emigration (rows) rates between each pair of regions measured in terms of migration events per lineage per year.

	China	Europe	Japan	Oceania	S America	SE Asia	USA
China	—	.07 (.03, .15)	.29 (.14, .42)	.15 (.07, .30)	.06 (.03, .10)	.30 (.11, .51)	.19 (.06, .34)
Europe	.06 (.03, .13)	—	.06 (.02, .12)	.16 (.07, .34)	.08 (.04, .13)	.11 (.05, .23)	.12 (.04, .29)
Japan	.10 (.04, .30)	.07 (.03, .15)	—	.13 (.07, .23)	.04 (.02, .08)	.10 (.04, .21)	.06 (.03, .15)
Oceania	.06 (.03, .13)	.13 (.06, .22)	.07 (.03, .14)	—	.03 (.02, .06)	.10 (.04, .25)	.16 (.05, .41)
S America	.04 (.02, .08)	.05 (.03, .10)	.04 (.02, .07)	.08 (.04, .14)	—	.04 (.02, .06)	.05 (.02, .10)
SE Asia	.27 (.11, .49)	.14 (.06, .25)	.13 (.05, .28)	.23 (.11, .42)	.03 (.02, .07)	—	.11 (.05, .26)
USA	.25 (.10, .47)	.25 (.13, .35)	.19 (.06, .34)	.51 (.20, .89)	.22 (.17, .27)	.20 (.08, .41)	—

Estimates represent means and 95% confidence intervals across 100 resampled replicates.

Sampling was constrained to 61 sequences per deme taken between the years 2002 and 2008.

Migration rates were given an exponential prior with a mean of 0.1 substitutions per site.

Table S4. Estimates for the timescale of coalescence (in years) and the effective population size (in number of individuals) of each region, assuming overlapping generations and an infectious period (generation time) of 5 days.

	Timescale of coalescence	Effective population size
China	0.72 (0.50, 1.01)	105.7 (72.8, 147.4)
Europe	1.62 (1.06, 2.23)	236.2 (154.9, 325.1)
Japan	1.69 (0.93, 2.67)	246.4 (136.4, 389.9)
Oceania	0.50 (0.29, 0.78)	72.6 (42.9, 113.4)
South America	2.68 (2.43, 2.97)	391.3 (354.5, 433.3)
Southeast Asia	1.16 (0.74, 1.72)	168.9 (107.5, 251.1)
USA	0.88 (0.62, 1.15)	128.5 (90.8, 167.4)

Estimates represent means and 95% confidence intervals across 100 resampled replicates.

Sampling was constrained to 61 sequences per deme taken between the years 2002 and 2008.

Migration rates were given an exponential prior with a mean of 0.1 substitutions per site.

Table S5. Estimates using proportional sampling for immigration (columns) and emigration (rows) rates between each pair of regions measured in terms of migration events per lineage per year.

	China	Europe	Japan	Oceania	S America	SE Asia	USA
China	–	0.11	0.43	0.13	0.09	0.38	0.25
Europe	0.06	–	0.05	0.18	0.11	0.17	0.31
Japan	0.10	0.04	–	0.12	0.02	0.05	0.05
Oceania	0.04	0.08	0.05	–	0.05	0.07	0.09
S America	0.03	0.06	0.03	0.07	–	0.04	0.09
SE Asia	0.16	0.15	0.15	0.18	0.04	–	0.13
USA	0.14	0.15	0.08	0.24	0.20	0.13	–

Estimates represent means across 100 resampled replicates.

Sampling was constrained to be proportional to the human population size of each deme, giving 206 samples for China, 94 samples for Europe, 20 samples for Japan, 6 samples for Oceania, 61 samples for Oceania, 90 samples for Southeast Asia and 49 samples for the USA. All samples were taken between the years 2002 and 2008.

Migration rates were given an exponential prior with a mean of 0.1 substitutions per site.

Table S6. Estimates using a 1000-fold larger prior for immigration (columns) and emigration (rows) rates between each pair of regions measured in terms of migration events per lineage per year.

	China	Europe	Japan	Oceania	S America	SE Asia	USA
China	–	0.32	1.83	0.39	0.24	1.93	0.45
Europe	0.10	–	0.31	0.29	0.38	0.32	0.21
Japan	0.23	0.46	–	0.28	0.28	0.68	0.17
Oceania	0.14	0.69	0.40	–	0.28	0.39	0.34
S America	0.08	0.47	0.29	0.19	–	0.27	0.18
SE Asia	0.35	0.45	0.91	0.38	0.28	–	0.21
USA	0.22	0.67	0.46	0.77	1.40	0.55	–

Estimates represent means across 100 resampled replicates.

Sampling was constrained to 61 sequences per deme taken between the years 2002 and 2008.

Migration rates were given an exponential prior with a mean of 100 substitutions per site.

Table S7. Estimates using an alternative geographical grouping for immigration (columns) and emigration (rows) rates between each pair of regions measured in terms of migration events per lineage per year.

	China	Europe	Hong Kong	Japan	Oceania	SE Asia	USA
China	–	0.03	0.57	0.34	0.06	0.10	0.13
Europe	0.03	–	0.09	0.11	0.20	0.17	0.15
Hong Kong	0.12	0.04	–	0.17	0.07	0.23	0.07
Japan	0.07	0.08	0.16	–	0.14	0.12	0.08
Oceania	0.04	0.15	0.04	0.10	–	0.13	0.15
SE Asia	0.11	0.11	0.31	0.16	0.20	–	0.06
USA	0.11	0.18	0.07	0.24	0.30	0.17	–

Estimates represent means across 100 resampled replicates.

Sampling was constrained to 175 sequences per deme taken between the years 2002 and 2008.

Migration rates were given an exponential prior with a mean of 0.1 substitutions per site.

Table S8. Mean estimates and 95% credible intervals for effective population size N_e , rate of migration m and trunk proportion for each region in simulated data sets based on 500 samples from the North, 500 samples from the South and 100 samples from the Tropics over a 10 year period.

		Source-sink model	Equal contact model
Population size	N	116.1 (92.4, 152.2)	126.3 (99.6, 164.6)
	T	165.9 (126.8, 223.2)	222.8 (188.2, 278.8)
	S	169.6 (139.6, 210.2)	158.2 (130.8, 201.6)
Migration rate	$N \rightarrow T$	0.14 (0.01, 0.41)	0.28 (0.10, 0.48)
	$N \rightarrow S$	0.02 (0.00, 0.08)	0.57 (0.31, 0.93)
	$T \rightarrow N$	0.44 (0.23, 0.72)	0.35 (0.19, 0.55)
	$T \rightarrow S$	0.43 (0.23, 0.70)	0.33 (0.17, 0.53)
	$S \rightarrow N$	0.03 (0.00, 0.09)	0.25 (0.06, 0.56)
	$S \rightarrow T$	0.10 (0.00, 0.29)	0.34 (0.19, 0.53)
Trunk proportion	N	0.01 (0.00, 0.13)	0.27 (0.16, 0.39)
	T	0.98 (0.84, 1.00)	0.55 (0.42, 0.67)
	S	0.01 (0.00, 0.08)	0.18 (0.06, 0.31)