

Unravelling H9N2 and H5N1 avian influenza virus dispersal along Bangladeshi poultry trading networks

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Avian influenza viruses (AIVs) in Bangladesh

- Endemic low-pathogenic H9N2 and high-pathogenic H5N1

(Parvin et al. 2020)

- Pose threat to poultry industry and human health

(Rimi et al. 2019)

- Trading practices vary between major cities, live bird markets (95% of poultry sales), chicken types

(Moyen et al. 2018)

Aim of Study: Explore how complexity within the system affects local patterns of AIV dispersal

Method

Data: Haemagglutinin (HA) H9N2 and H5NX Bangladeshi sequences obtained from GISAID, IRD, and collaborators (most sequences are from two largest cities (Fig. 1))

1. Generated molecular clock phylogenies for both subtypes (n > 200) using BEAST v1.10.4.

2. Downsample H9N2 tree to 70 sequences from a cross-sectional study:

A. Determine if sequences cluster by city and/or chicken type (BaTS v1.0)

B. Discrete trait analyses with generalised linear models (DTA-GLMs) - predictors of viral movement between pairwise combinations of city and chicken type

C. Identify phylogenetic clades using genetic threshold (ClusterPicker v1.2.5):

i) Adjusted Rand index; explore if clade diversity between and within markets in a city differs from random viral movement (null distribution, n = 1000 permutations)

ii) Network density; investigate if distribution of clades across a city's markets differs from random viral movement (null distribution, n = 1000 permutations)

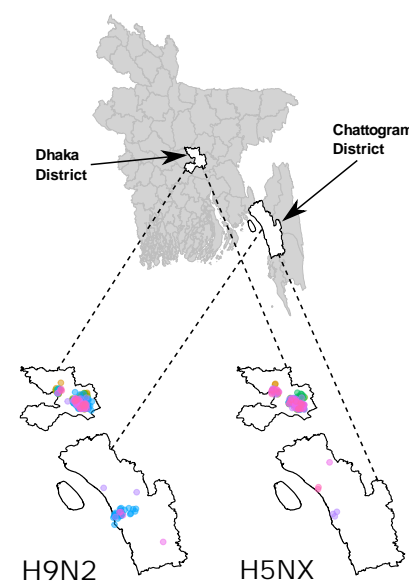


Figure 1. AIV Genomic sampling: Dhaka & Chattogram

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1. Molecular Clock Phylogenies

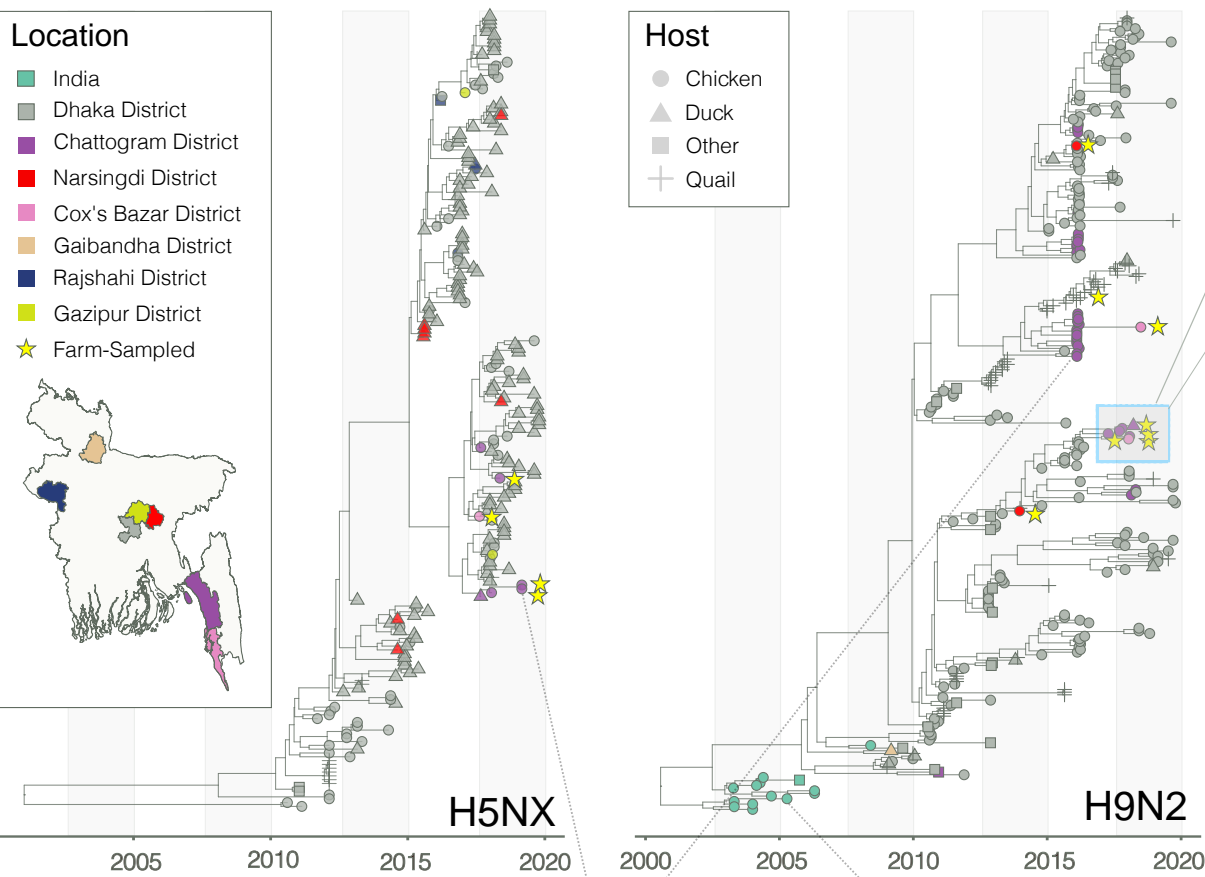


Figure 2. H5NX (left) and H9N2 (right) Maximum clade credibility trees

Multiple instances where sequences from Dhaka and Chattogram intermix - although very few Chattogram sequences in H5 tree, so pattern is less clear.

Basal Indian clade

Results

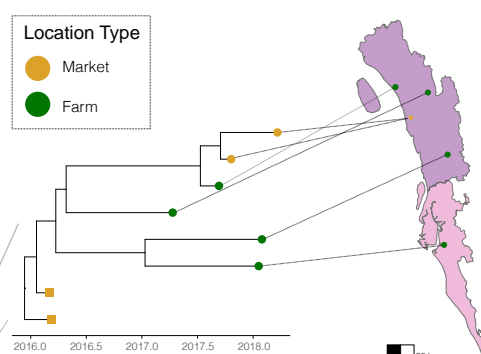


Figure 3. Virus movement between farms and markets

2B. DTA-GLMs

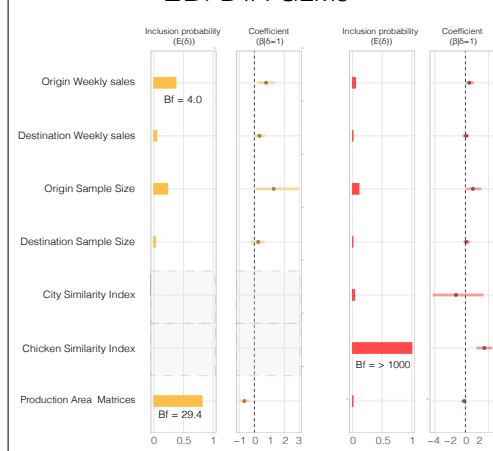


Figure 4. DTA-GLM results. Inclusion probability; probability of inclusion within model. Coefficient: log contribution of predictor when included in model

2A. Trait-clustering analyses

Table 1. Clustering by city

	PS	AI
City (statistic observed)	4	0.30
City (median statistic permutation)	22 (19-25)	3.76 (2.80-4.70)
City (p value)	<0.001	<0.001

Table 2. Clustering by chicken type in Dhaka and Chattogram

	PS	AI
Dhaka (statistic observed)	19	3.04
Dhaka (median statistic permutation)	20 (17-23)	3.29 (2.5-4)
Dhaka (p value)	0.363	0.307
Chattogram (statistic observed)	10	1.26
Chattogram (median statistic permutation)	12 (10-14)	1.9 (1.31 - 2.44)
Chattogram (p value)	0.076	0.038*

2C. Clade dispersal between markets

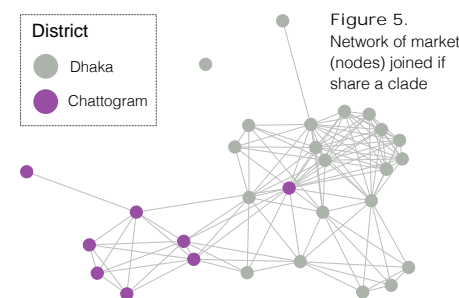


Table 3. Observed and permuted adjusted rand index values

	Adjusted Rand Index
Both Cities (statistic observed)	0.100
Both Cities (median statistic permutation)	0.050
Both Cities (p value)	0.981

Table 4. Observed and permuted network density values

	Density
Both Cities (statistic observed)	0.300
Both Cities (median statistic permutation)	0.340
Both Cities (p value)	0.942

Discussion

Result 1. Most movement between birds sold in same city (Table 1), but some lineages are shared between cities (Fig. 2)

Unclear if shared lineage imports from production areas OR actual direct/indirect viral movement between cities

Result 2. Possible evidence for rapid viral movement between farm and market (Fig. 3)

Hard to infer direction or frequency of viral dispersal due to lack of sequencing at farms

Result 3. Sequences cluster significantly by chicken type for Chattogram but not Dhaka (Tables 2-3)

May reflect different transaction patterns between cities (e.g. more inter-market trade in Dhaka)

Result 4. DTA-GLM - Only weak evidence for degree of overlap between chicken production area matrices (Fig. 4)

Result not robust to inclusion of matrices of whether a bird was sold in same city

Result 5. Virus clades may be randomly distributed across a city's markets (Tables 3-4, Fig. 5)

Surveillance at a few markets in a city could capture viral diversity? (No need testing hundreds of Dhaka markets?)
*Some markets only had one sequence - reduce statistical power.

Recommendations

Surveillance should address genomic sampling biased towards Dhaka (and to lesser extent Chattogram). Increase sampling at farms.

References

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