

**Supplemental Figures 1a-c.** Bayesian maximum clade credibility (MCC) phylogenetic trees based on tMRCA analysis of influenza A(H5) HA genes of viruses belonging to clade 1.1.2 (S. Figure 1a), 2.3.2.1c (S. Figure 1b) and 2.3.4.4 (S. Figure 1c) in Vietnam, 2012-2015. The x-axis on the tree is the estimated timeline of genetic divergence among viruses in each clade. The estimated tMRCA in years is shown to the right of each node on the tree. Viruses sequenced for this study are shown in color.

**Supplemental Figures 2a-h.** Bayesian maximum clade credibility (MCC) phylogenetic trees based on tMRCA analysis of influenza A(H5) virus gene segments included in this study (S. Figure 2a, all virus clade HA genes; S. Figure 2b, PB2; S. Figure 2c, PB1; S. Figure 2d, PA; S. Figure 2e, NP; S. Figure 2f, NA; S. Figure 2g, M; S. Figure 2h, NS). The x-axis on the tree is the estimated timeline of genetic divergence among viruses in each clade. The estimated tMRCA in years is shown to the right of each node on the tree. The gene segments of each virus are color-coded based on the origin of the HA gene. Tree branches for clade 1.1.2 viruses are shown in red, 2.3.2.1a in light green, 2.3.4.4 A(H5N6) in brown (except for the N1 NA gene tree), 2.3.2.1c in purple, 2.3.4 in blue, and 7.2 in dark green.

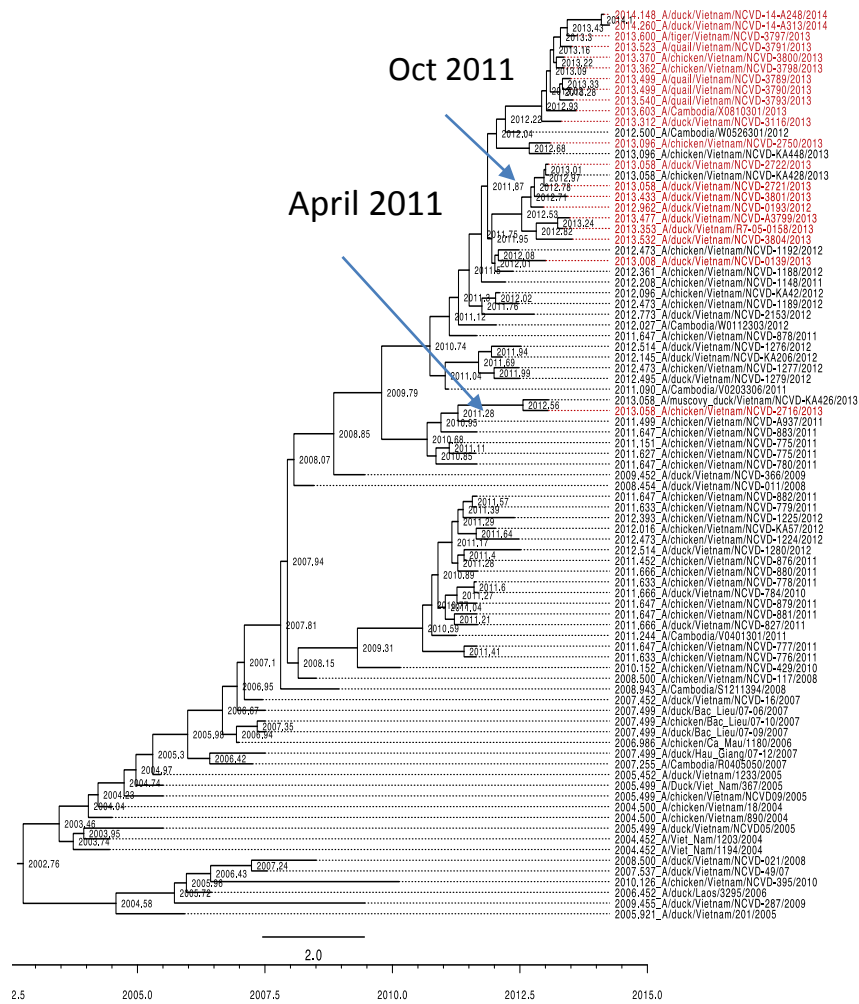
**Supplemental Table 1.** Annual passive and active sample collection by province, region and A(H5) HA clade from September 2012 to August 2015.

**Supplemental Table 2.** Strain names, collection information, genotypes and GISAID accession numbers associated with whole genome sequences created for this study.

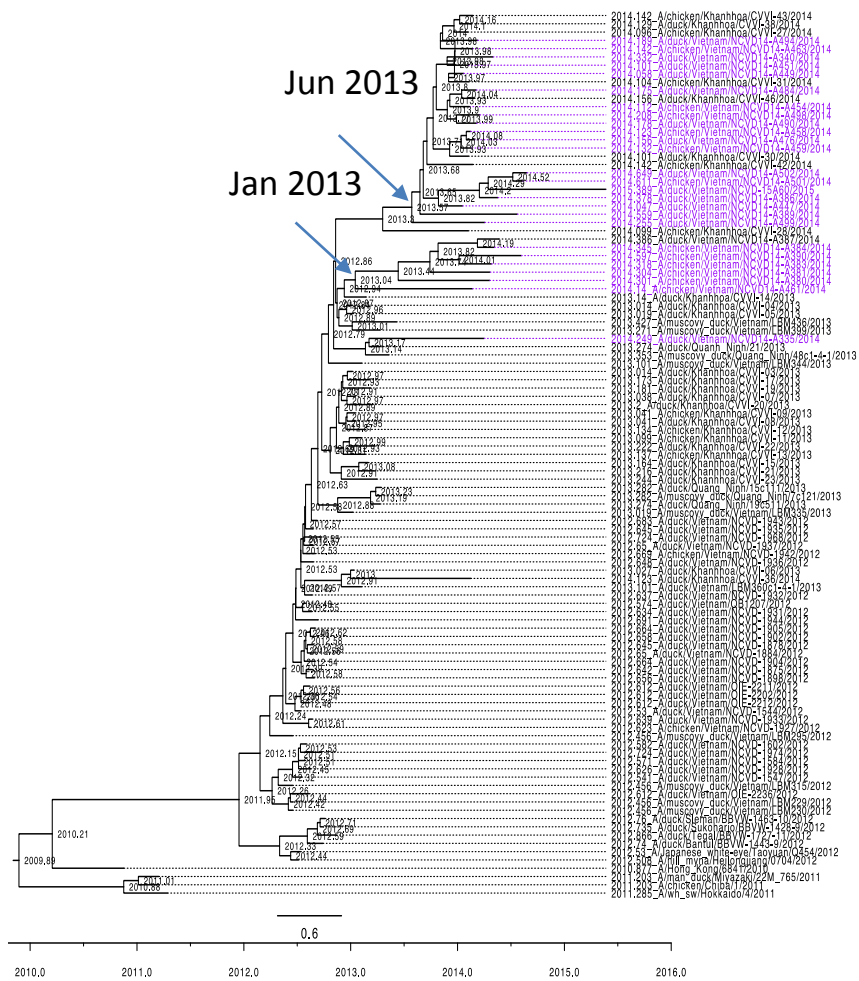
**Supplemental Table 3-8.** Amino acid differences identified in each virus compared to the nearest vaccine strain for clades 1.1.2 (S. Table 3), 2.3.2.1a (S. Table 4), 2.3.2.1b (S. Table 5), 2.3.2.1c (S. Table

6), 2.3.4.4 (S. Table 7), 7.2 (S. Table 8). Amino acid differences at putative antigenic sites are annotated on the right side of the table to indicate the antigenic site of the residue or other molecular marker.

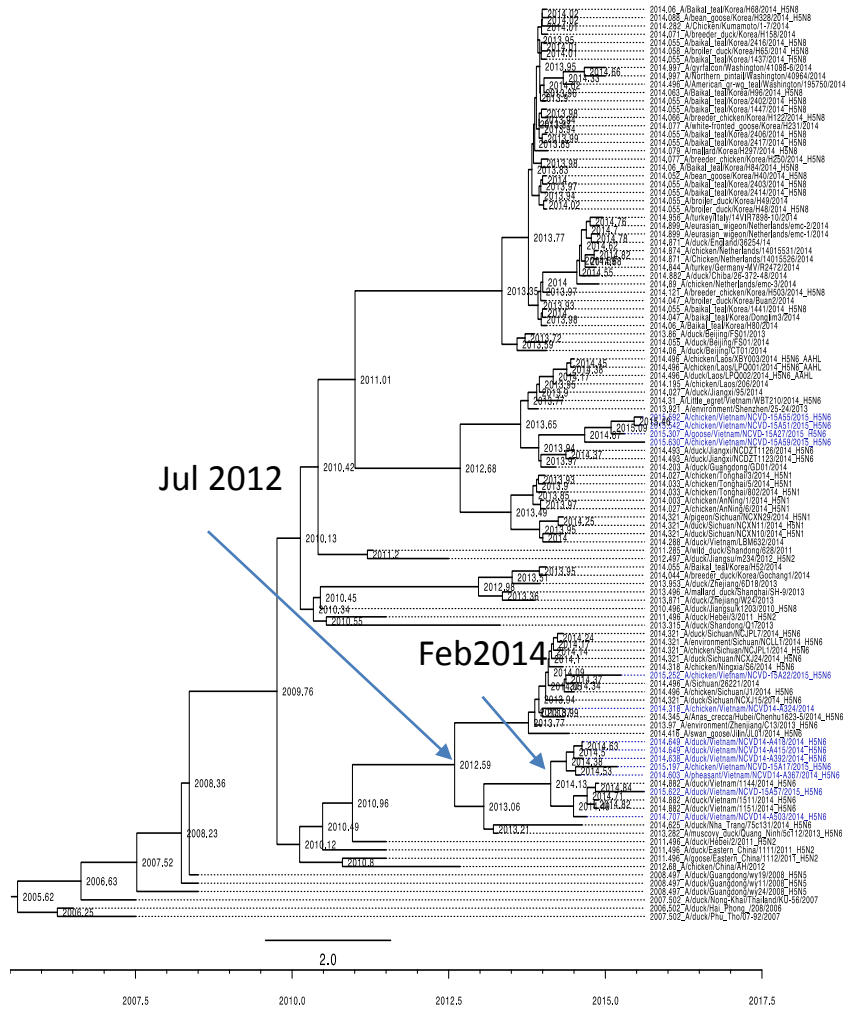
# Supplemental Figure 1a: Evolution of the HA gene of clade 1.1.2 Vietnamese H5N1 viruses, 2012-2015



# Supplemental Figure 1b: Evolution of the HA gene of clade 2.3.2.1c Vietnamese H5N1 viruses, 2012-2015

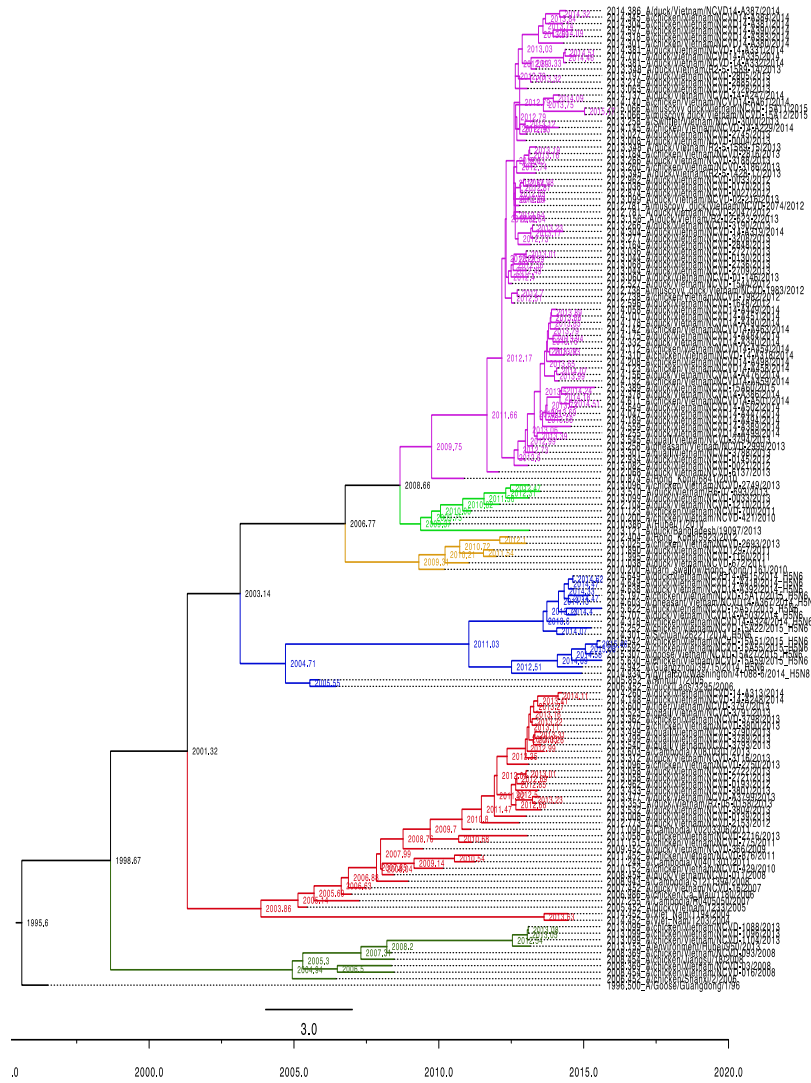


# Supplemental Figure 1c: Evolution of the HA gene of clade 2.3.4.4 Vietnamese H5N6 viruses, 2014-2015



# Supplemental Figure 2a: Evolution of the HA gene of recent Vietnamese H5Nx viruses

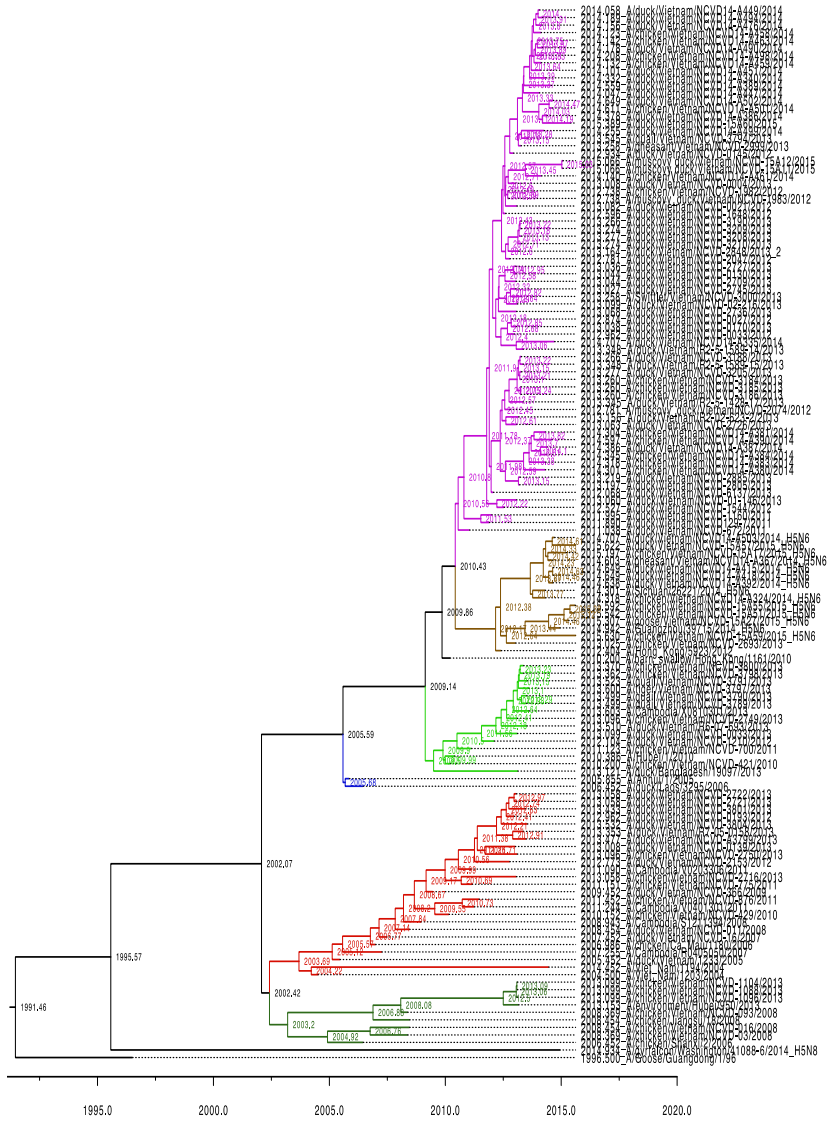
- Clade 1.1.2
- Clade 2.3.2.1a
- Clade 2.3.2.1b
- Clade 2.3.2.1c
- Clade 2.3.4.4
- Clade 7.2





# Supplemental Figure 2c: Evolution of the PB1 gene of recent Vietnamese H5 viruses

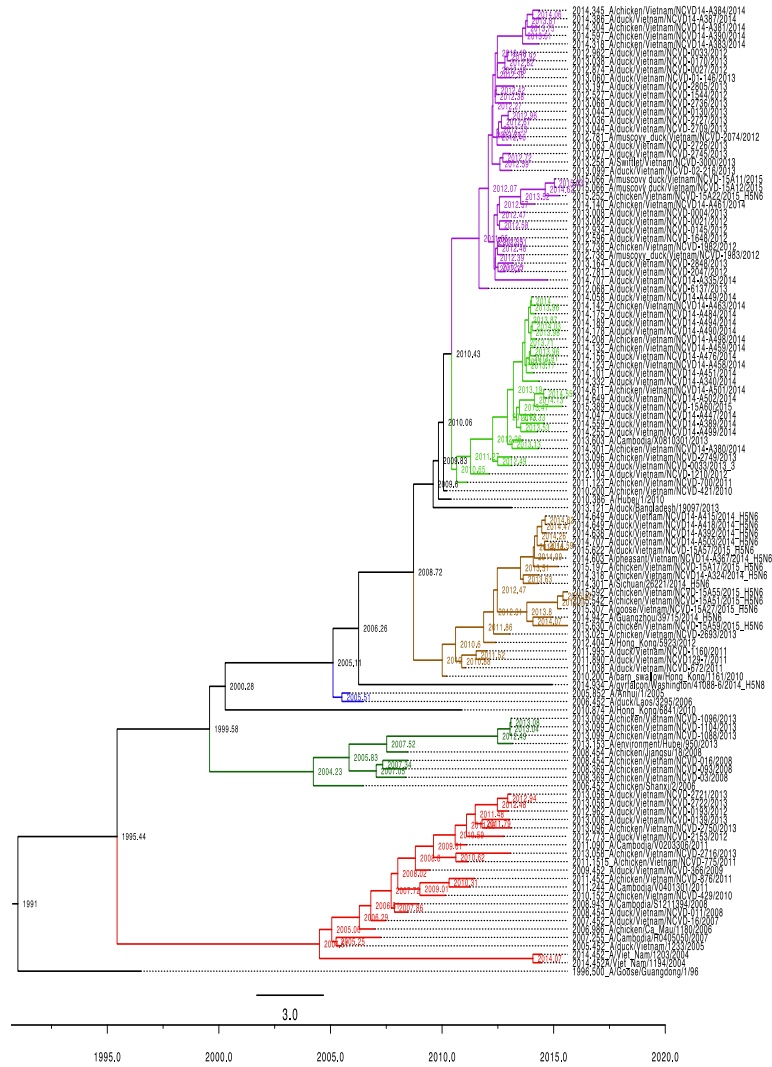
- Clade 1.1.2
- Clade 2.3.2.1a
- Clade 2.3.2.1b
- Clade 2.3.2.1c
- Clade 2.3.4.4
- Clade 7.2





# Supplemental Figure 2d: Evolution of the PA gene of recent Vietnamese H5Nx viruses

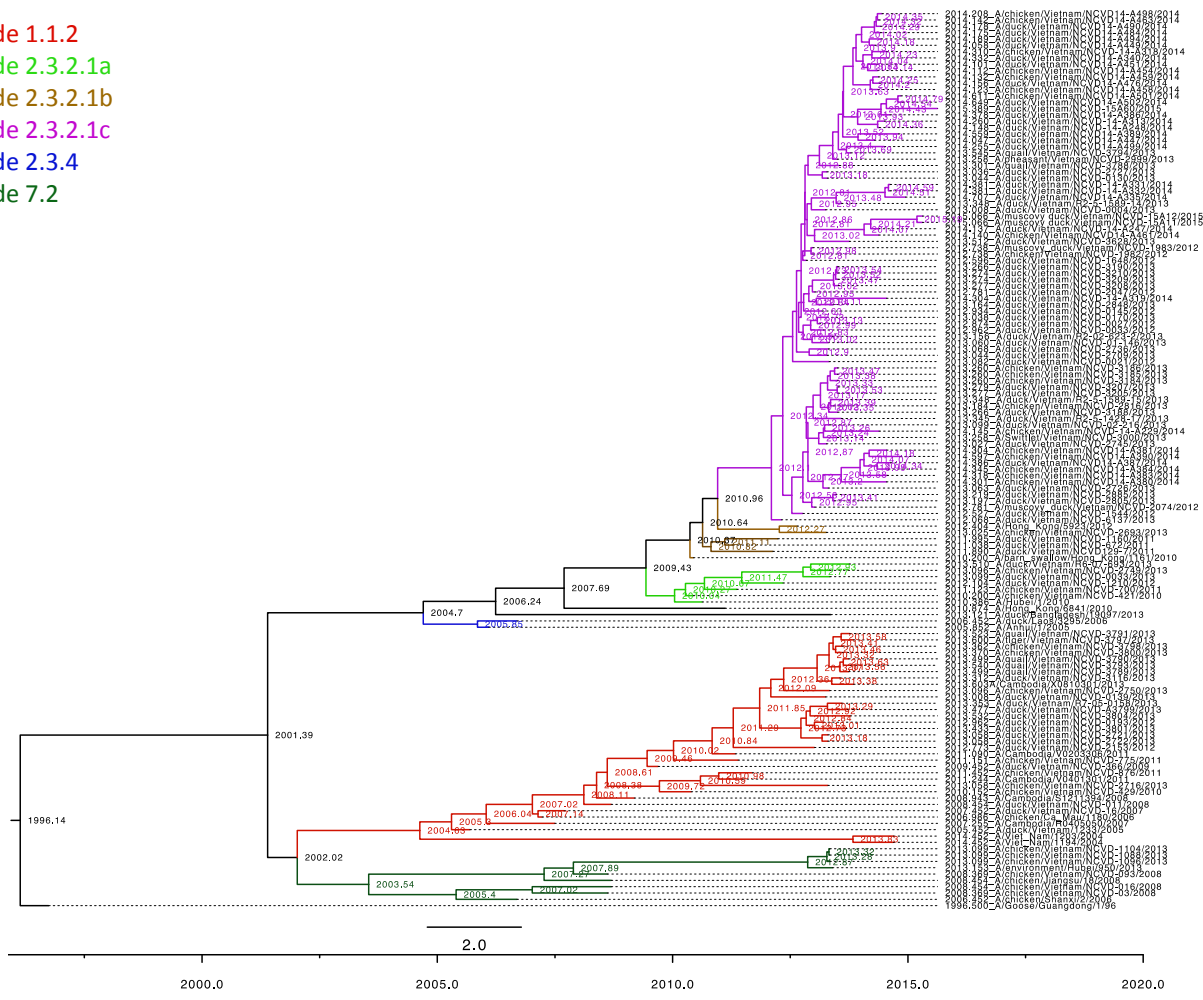
- Clade 1.1.2
- Clade 2.3.2.1a
- Clade 2.3.2.1b
- Clade 2.3.2.1c
- Clade 2.3.4.4
- Clade 7.2





# Supplemental Figure 2f: Evolution of the NA gene of recent Vietnamese H5Nx viruses

- Clade 1.1.2
- Clade 2.3.2.1a
- Clade 2.3.2.1b
- Clade 2.3.2.1c
- Clade 2.3.4
- Clade 7.2



# Supplemental Figure 2g: Evolution of the MP gene of recent Vietnamese H5 viruses

- Clade 1.1.2
- Clade 2.3.2.1a
- Clade 2.3.2.1b
- Clade 2.3.2.1c
- Clade 2.3.4.4
- Clade 7.2



# Supplemental Figure 2h: Evolution of the NS gene of recent Vietnamese H5 viruses

- Clade 1.1.2
- Clade 2.3.2.1a
- Clade 2.3.2.1b
- Clade 2.3.2.1c
- Clade 2.3.4.4
- Clade 7.2

