

Figure 1. Sampling maps of H5N1 clades in the Mekong region. Crosses and dots refer to sampling locations of H5N1 sequences assigned to an admin-1 or admin-2 polygon, respectively.

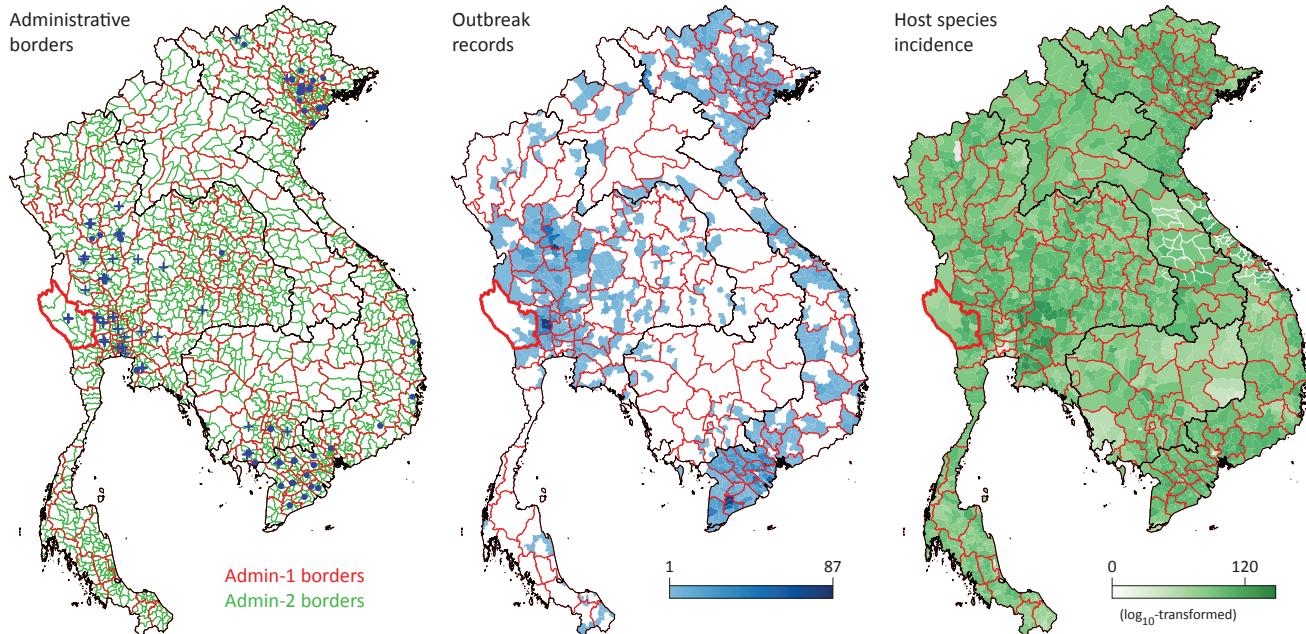


Figure 2. External data used to assign sampling probabilities to admin-2 polygons. The map of outbreak records gathers data cumulated from 2004 to 2012 for admin-2 polygons (see also Figure S1 for annual maps), and the host species incidence map displays log-transformed occurrences for both host species (poultry, ducks) per admin-2 polygon. For illustrative purpose, the admin-1 area highlighted by the red contour is displayed in a bigger size in Figure 3. The first map also displays the sampling locations of H5N1 clade 1 sequences considered in this study. As in Figure 1, crosses and dots refer to sampling locations of H5N1 sequences assigned to an admin-1 or admin-2 polygon, respectively.

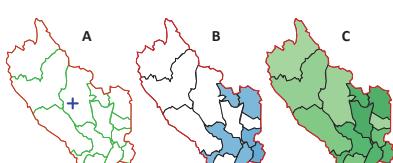


Figure 3. Zoom on a given admin-1 polygon for which a sampled sequence is assigned. Admin-2 polygons are delimited by green borders (A) and further coloured by outbreak records (B) and log-transformed host species occurrences (C). In this example, only 6 out of 13 admin-2 polygons are associated with a non-null number of outbreak records. If none of these admin-2 were associated with outbreak records, the host incidence data would have been used to assign a sampling probability to each admin-2 polygon.

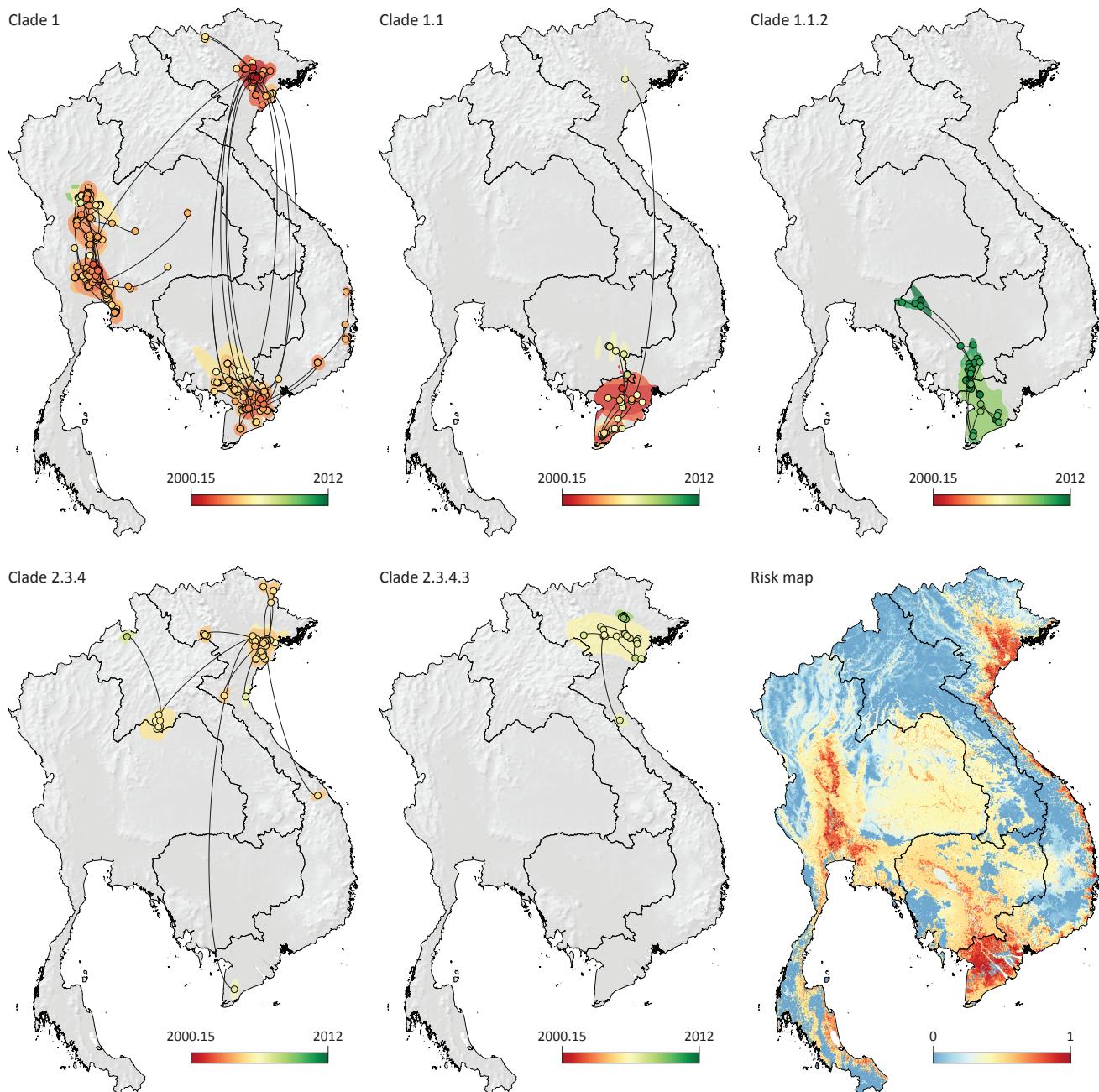


Figure 4. Risk map and reconstructed spatiotemporal diffusion for each H5N1 clade considered in the present study: mapped consensus trees and 95% HPD regions. Consensus trees and 95% HPD regions are based on 100 trees subsampled from each post burn-in posterior distribution. Nodes of consensus trees are coloured according to their time of occurrence. 95% HPD regions were computed for successive time layers and then superimposed using the same colour scale reflecting time.