

Phylogenetic and Prevalence Analysis of Avian Influenza in Marine Mammals

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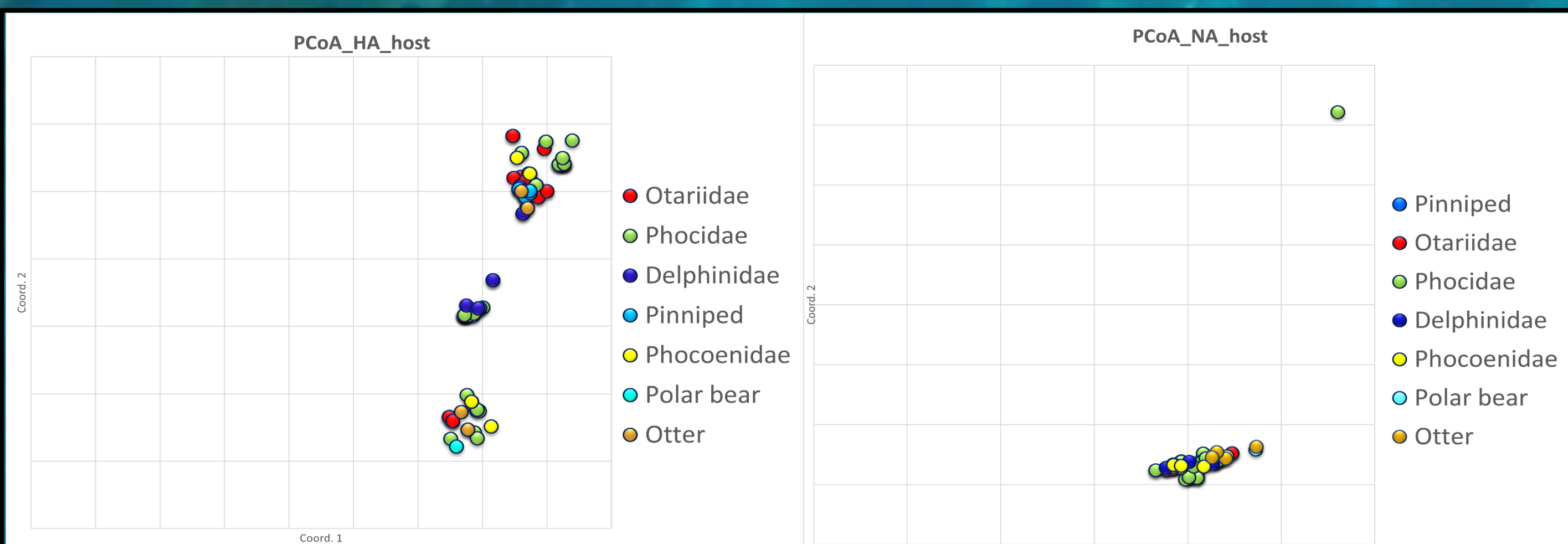
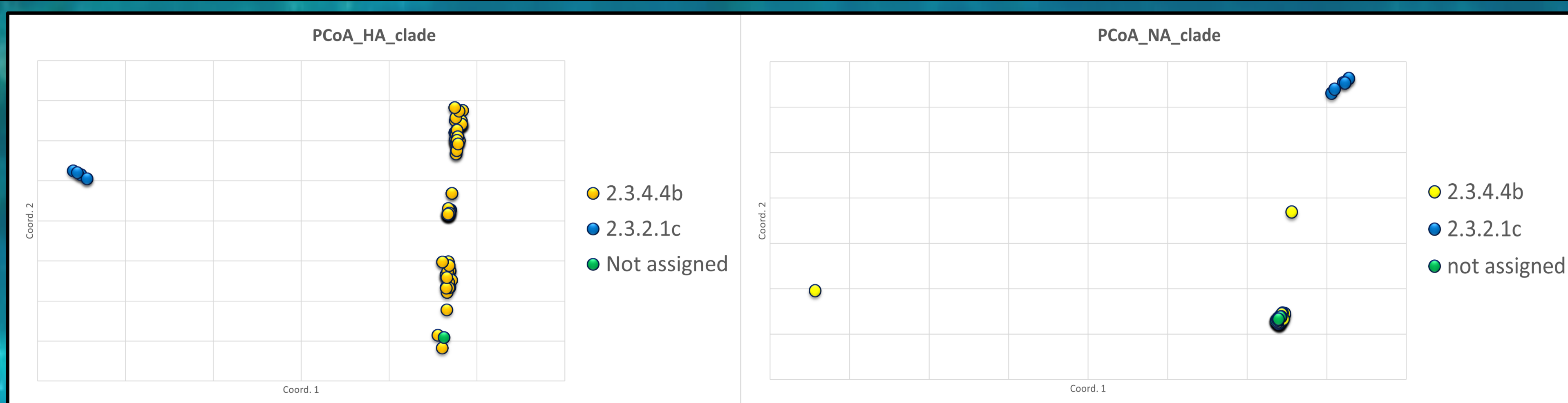
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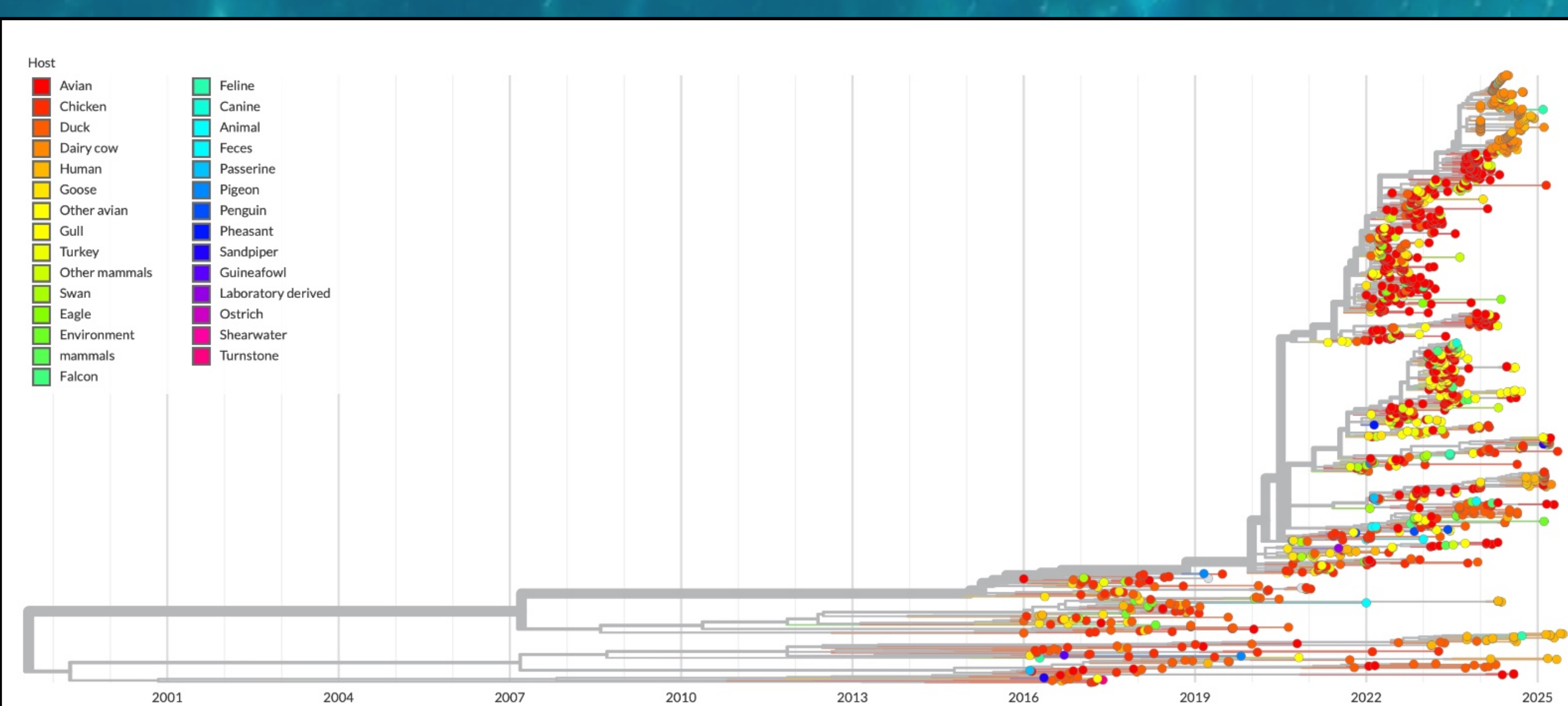
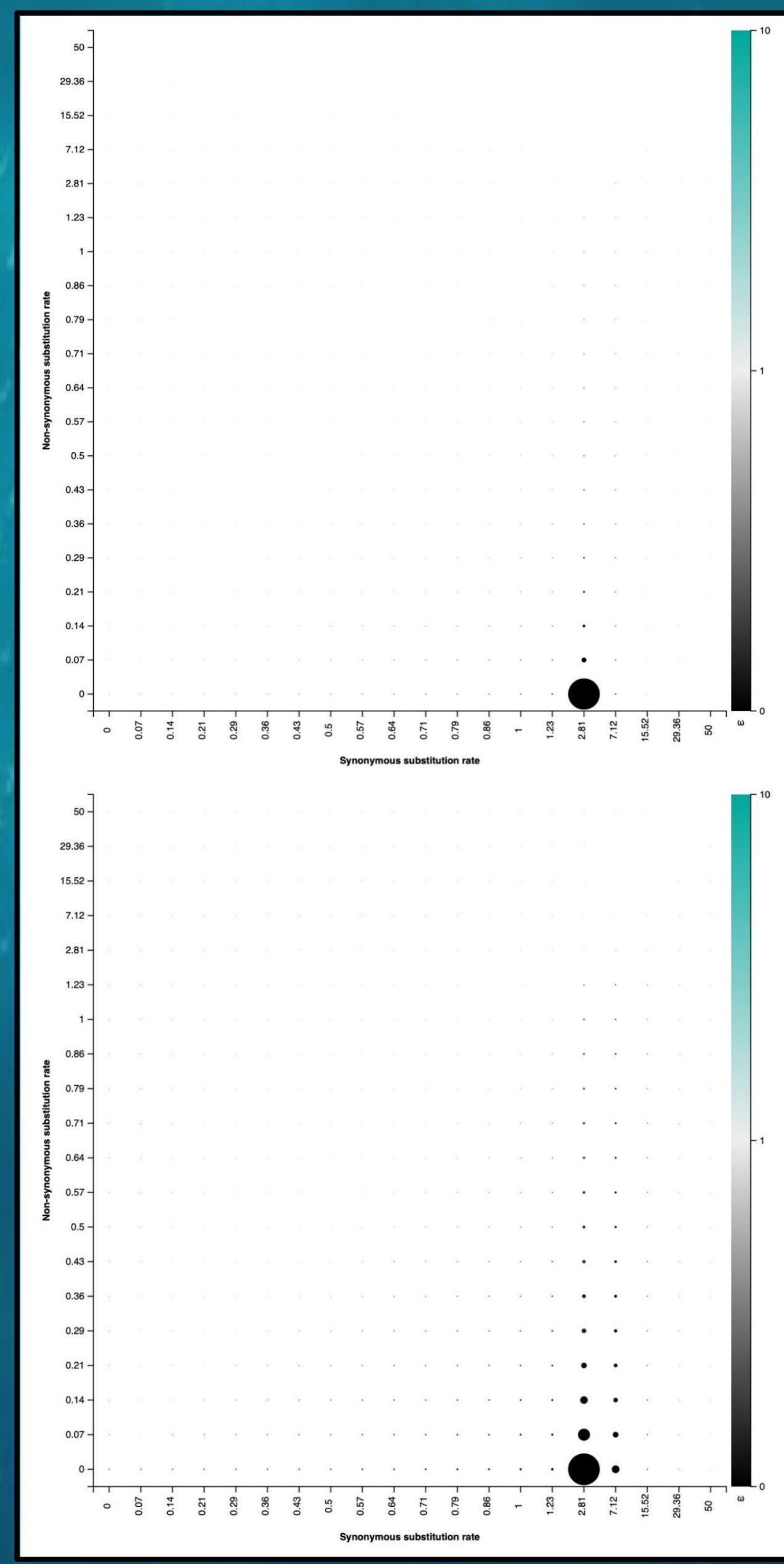
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H5N1 avian influenza is becoming a worldwide concern, with numerous marine mammal fatalities recorded in recent years. The virus has shown a remarkable ability to jump between species, underscoring its adaptive potential. In this research, we reconstructed the phylodynamics of all strains found in marine mammals to assess how different viral lineages spread and how quickly they transmit between hosts. We also analyzed the prevalence of all available isolates in public databases to explore whether host-specific prevalence varies by viral clade. Furthermore, we examined selective pressures to identify signs of adaptive evolution in viral genomes from marine mammal samples.

The results of our investigation show that the viral strains are not randomly distributed, but instead exhibit a **clear structuring by clade**



No notable host-associated genetic structure was detected



Marine mammals notably display a transmission pattern that differs significantly from that of non-marine mammals. The observation that their pattern aligns more closely with avian species than with dairy cattle suggests that the virus has **not undergone substantial adaptation to this new host**.

Using the FUBAR method to analyze selection pressure, **no positively selected sites** were detected in the HA gene. In contrast, only two sites within the NA gene showed signs of weak positive selection.

The study highlights that currently the virus shows a limited capacity for molecular adaptation, consistent with the observation that birds remain its primary hosts. Although some genetic variation was detected—likely influenced by farming practices and environmental conditions—there is **no strong evidence of host-specific evolutionary change**. These findings help clarify the mechanisms of cross-species transmission and reveal how spillover events can affect animal populations and disrupt ecological interactions, offering valuable insights into current wildlife health and their conservation.