

Genetic variability of the Influenza A H5N1 virus

Maria Perra*¹, Ilaria Deplano¹, Ilenia Azzena², Chiara Locci^{1,2}, Noemi Pascale^{1,2,3}, Daria Sanna¹, Marco Casu², Fabio Scarpa¹

¹ Department of Biomedical Sciences, University of Sassari, Viale San Pietro 43b, 07100 Sassari, Italy

² Department of Veterinary Medicine, University of Sassari, Via Vienna 2, 07100 Sassari, Italy

³ Department of Chemical, Physical, Mathematical, and Natural Sciences, Via Vienna 2, 07100 Sassari, Italy

The highly pathogenic avian influenza virus H5N1 has emerged as a pressing global issue due to its rapid dissemination among both wild and domestic bird populations, as well as its occasional spillover into mammals, including humans. Its capacity for cross-species transmission and ongoing genetic changes highlight the need for continuous genomic monitoring and risk evaluation, since avian influenza poses major health and economic challenges worldwide.

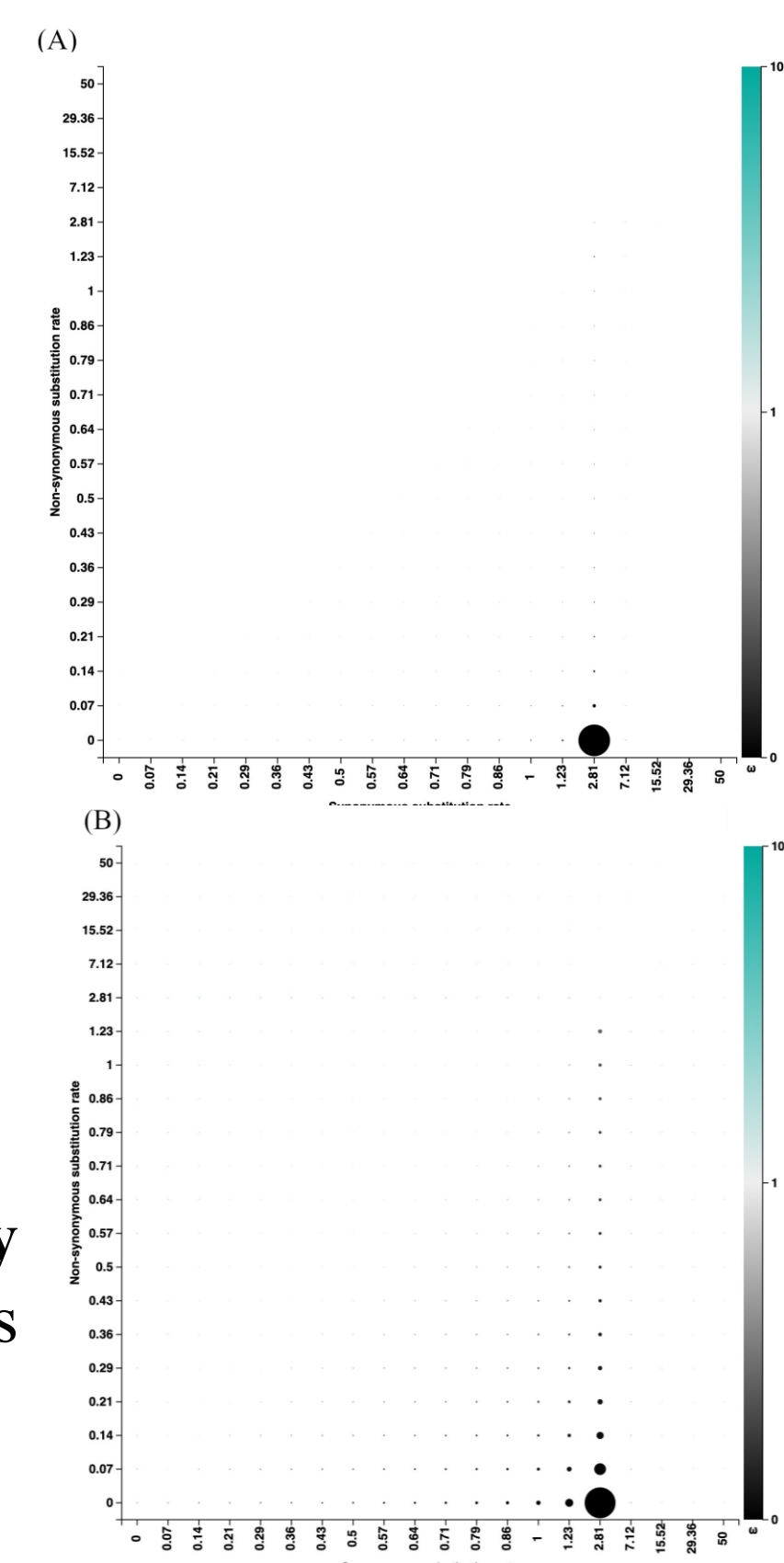
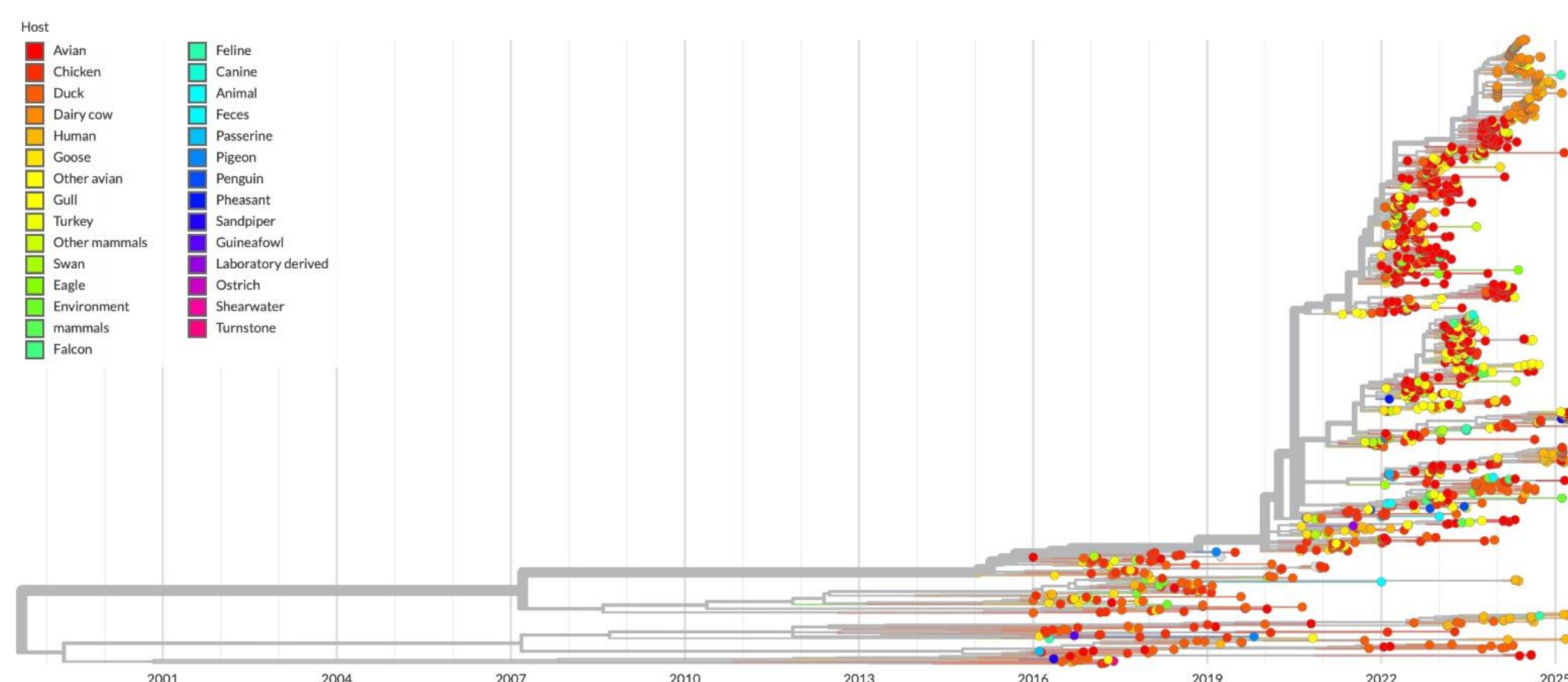
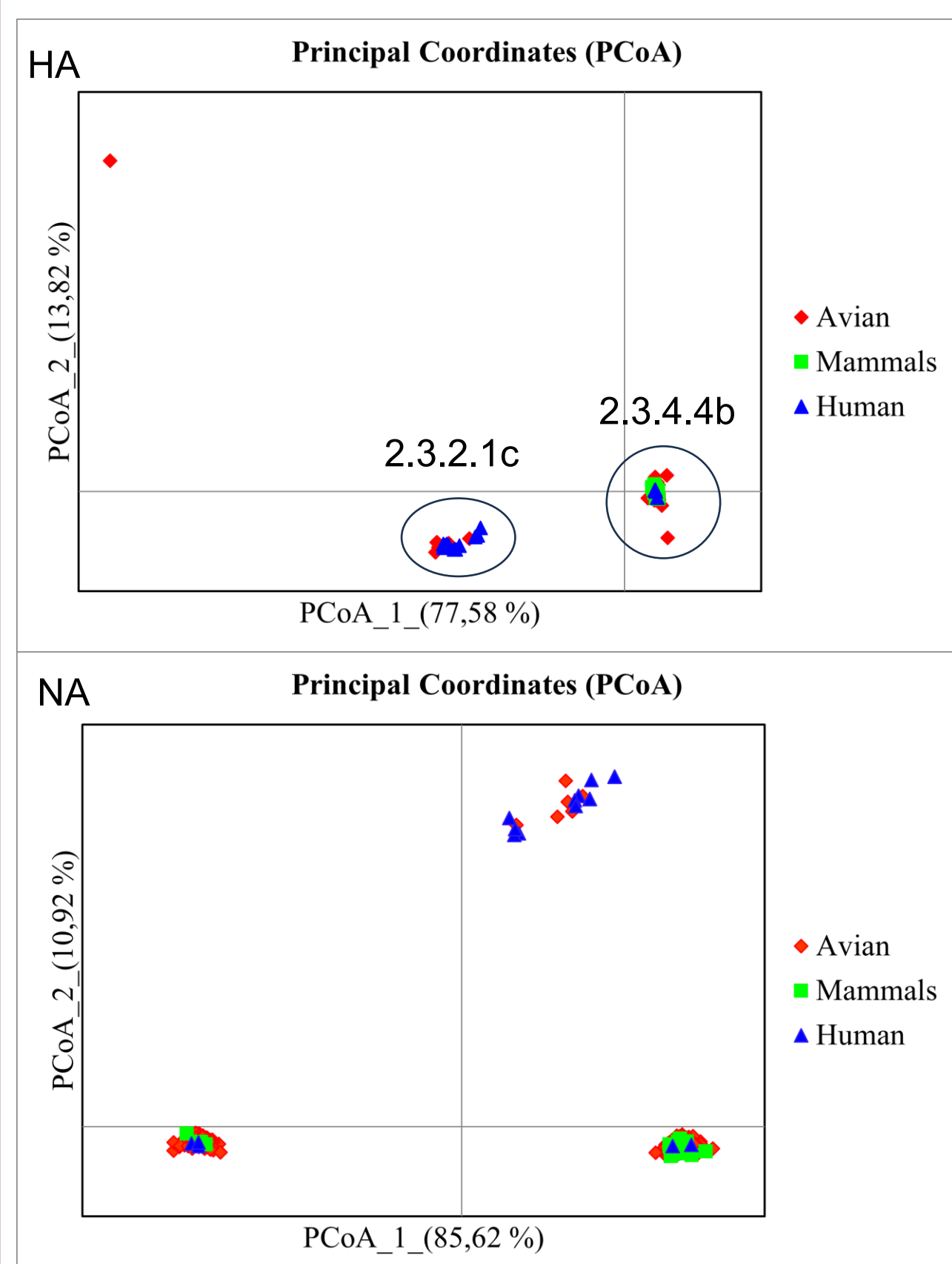
Objectives

- ➔ Monitor key mutations that could influence viral fitness (e.g., residue 226).
- ➔ Identify genetic traits that may facilitate spillover, including distinct genetic clusters
- ➔ Assess selective pressures shaping viral evolution

METHOD

- Molecular dating and Bayesian inference
- Phylogenetic and phylodynamic analysis
- Entropy and selective pressure

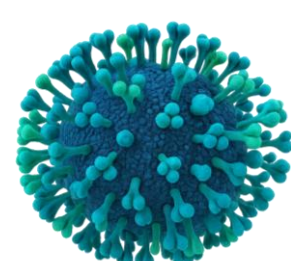
RESULTS



The results of our investigation show that the viral strains are not randomly distributed, but instead exhibit a **clear structuring by clade but not notable host-associated** genetic structure was detected.

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.

CONCLUSION



The study indicates that, at present, the virus demonstrates only a limited ability to adapt at the molecular level, in line with the fact that birds continue to serve as its main hosts. While some genetic variability was observed—likely shaped by agricultural practices and environmental factors—there is no compelling evidence of evolutionary changes tied to specific hosts. These results contribute to a better understanding of the processes underlying cross-species transmission and show how spillover events can impact animal populations and disturb ecological balance, providing important insights for wildlife health and conservation efforts.

