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MULTIDISCIPLINARY TRACKING OF A HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1 OUTBREAK IN EUROPEAN GRIFFON VULTURES

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Julien Hirschinger, Ursula Höfle, Alberto Sánchez-Cano, Claire Guinat, Guillaume Croville, et al.. MULTIDISCIPLINARY TRACKING OF A HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1 OUTBREAK IN EUROPEAN GRIFFON VULTURES. 15. European Wildlife Disease Association conference (EWDA 2024), Sep 2024, Stralsund, Germany. <10.13140/RG.2.2.16088.81923>. <hal-05008992>

HAL Id: hal-05008992

<https://hal.science/hal-05008992v1>

Submitted on 28 Mar 2025

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HAL Authorization

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INTRODUCTION AND OBJECTIVES

H5N1 highly pathogenic avian influenza virus (HPAIV) has significantly impacted wild bird populations globally. In 2022, a notable outbreak affected Griffon vultures in Spain and France, leading to moderate mortality and reduced breeding success.

Objectives: To elucidate the dynamics of this unprecedented outbreak using an integrated approach combining virological, serological, phylogenetic, and ecological data.



METHODS

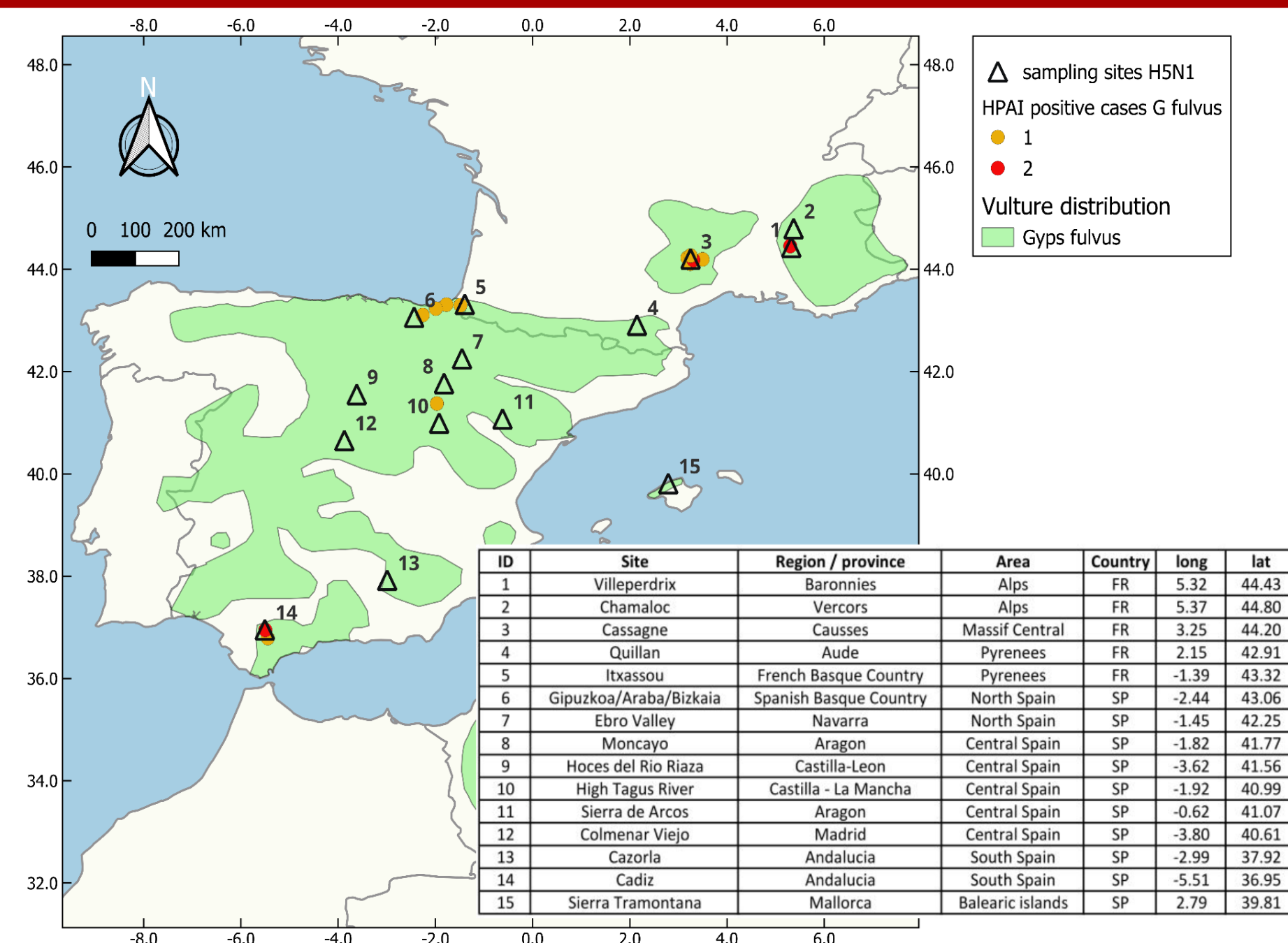


Figure 1. Sampling sites of live individuals (black triangles) and HPAIV-positive vulture carcasses (dots) from March 2020 to August 2023. The color of the dots indicates the number of cases per site. The light green shaded area represents the Griffon vulture breeding range. The table provides details of site names, regions/provinces, areas, site IDs, and geographic coordinates.

RESULTS

OUTBREAK DYNAMICS

H5 specific ELISA test adult Griffon vulture France/Spain

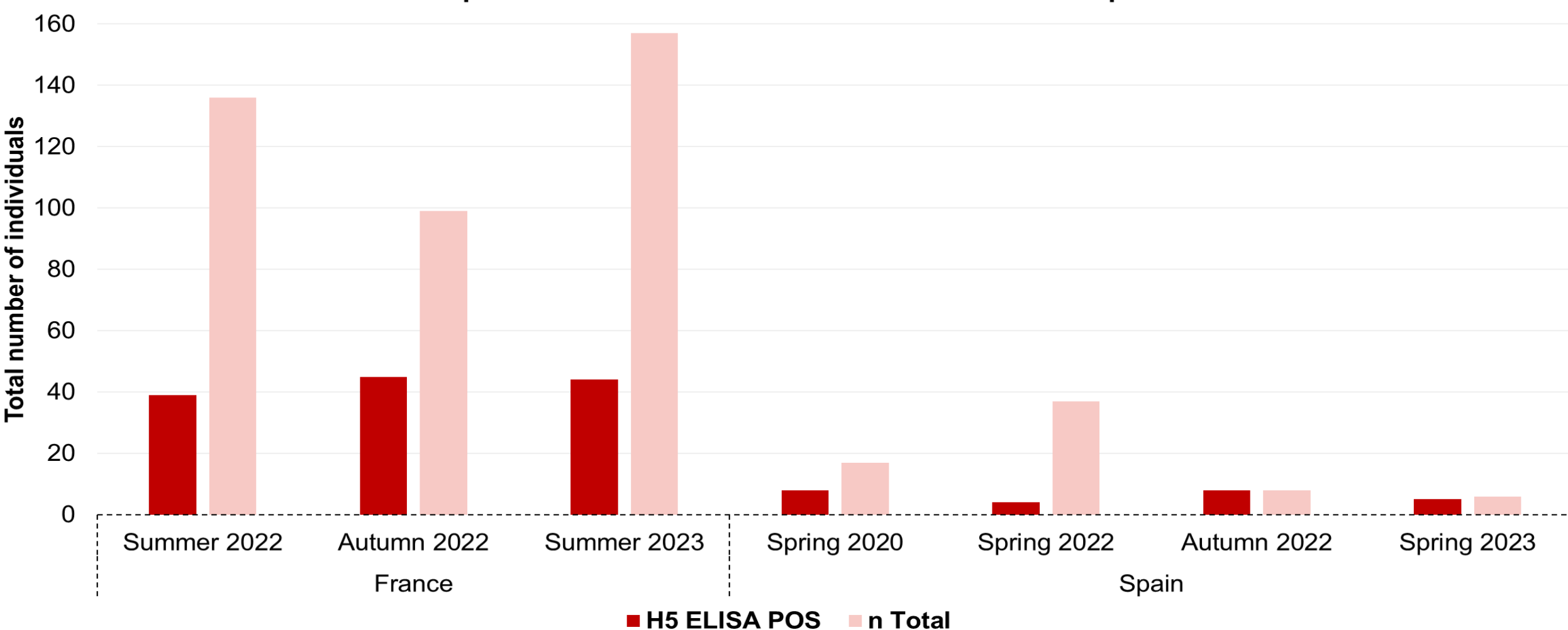


Figure 2. Results of H5 specific ELISA tests (AIV) of serum samples collected in Adult Griffon vultures in Spain and France from 2020 to 2023.

- ❖ Live vultures sampled between March 2020 and August 2023 in France (n = 393) and Spain (n = 196) tested negative for H5N1 HPAIV by specific RT-qPCR.
- ❖ Between April and August 2022, five Griffon vultures in Spain and eleven in France were confirmed to have died from H5N1 HPAIV by specific RT-qPCR.

ORIGIN AND SPATIAL SPREAD OF INFECTION

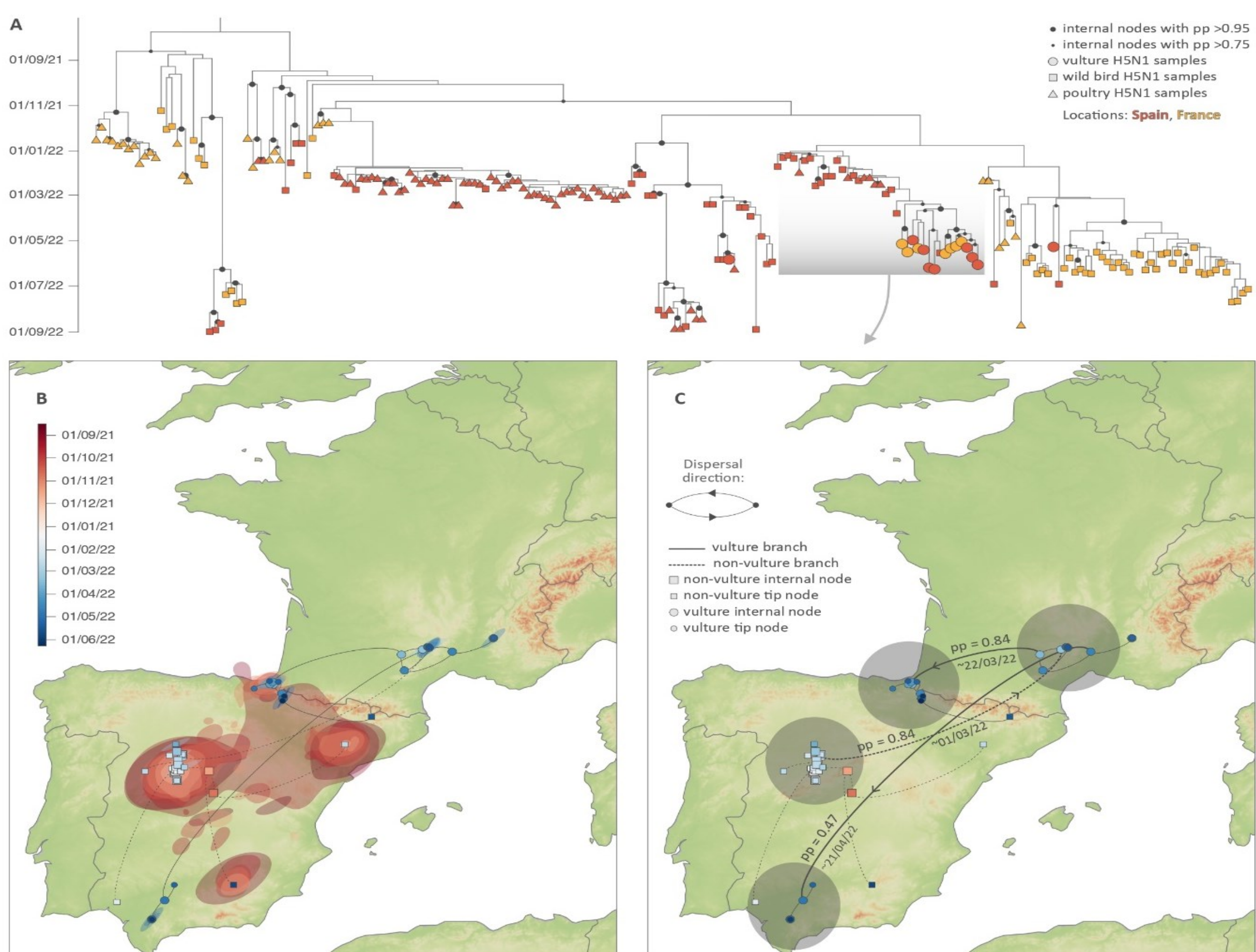


Figure 3. A: Maximum clade credibility (MCC) tree from time-scaled phylogenetic analysis of HA gene sequences from H5N1 HPAIV-infected birds in Spain and France (Nov 8, 2021 - Sep 1, 2022). The grey square highlights the clade with infected vultures. B: Map showing the MCC tree of this clade and 80% highest posterior density (HPD) regions, indicating uncertainty in Bayesian phylogeographic inference, colored by time. Full curves represent vulture clade branches; dashed curves represent others. C: Map of the same MCC tree, showing posterior probability and mean estimates of lineage dispersal events among the four main regions.

DISPERSAL OF HPAIV BY GRIFFON VULTURE MOVEMENTS

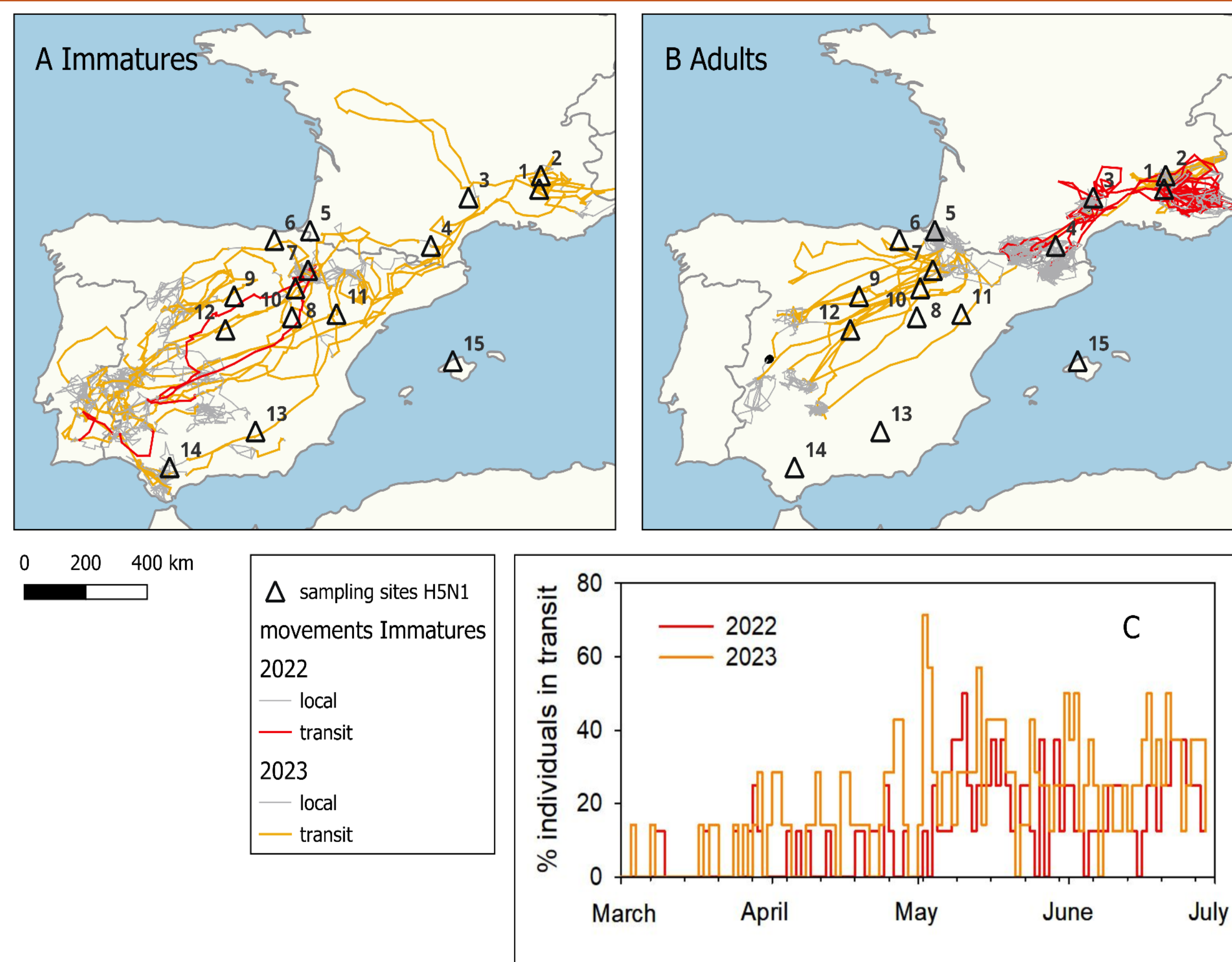


Figure 4. Movements of 16 Griffon vultures from March 1 to June 30 in 2022 and 2023. Maps A (immatures) and B (adults) show long-ranging transit movements (red for 2022, orange for 2023) and local movements (grey). Inset C displays the daily proportion of individuals (all ages pooled) in transit for both years.

CONCLUSIONS

- Transmission pathways:** Long-distance movements of immature birds played a crucial role in spreading the virus across regions.
- Disease dynamics:** This outbreak shows the ability of H5N1 HPAIV to spread rapidly through a population after a single introduction.
- Broader ecological implications:** The potential danger of HPAIV H5N1 in these specialist necrophagous bird populations would lead to longer persistence of the carcasses they eliminate and increased risk of pathogen persistence and spread in the environment if their incidence increases in the future.

Conclusion: H5N1 HPAIV has to be considered as a severe threat for endangered bird species, especially those with colonial and scavenging behavior.

Integration of the epidemiology of the virus with the ecology of the host species is key to a better understanding of the outbreak dynamics and its possible impact on wildlife conservation..