



Fatal infection of influenza A virus in a harbor porpoise (*Phocoena phocoena*)



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INTRO / BACKGROUND

Europe and more recently, the Americas are experiencing unprecedented mortality in wild and domestic birds because of the highly pathogenic avian influenza A virus (HPAI) (H5N1) clade 2.3.4.4b. Spill over infection of influenza A viruses (IAV) to wild mammals including marine mammals such as seals have been repeatedly documented. However, reports in cetaceans are scarce.

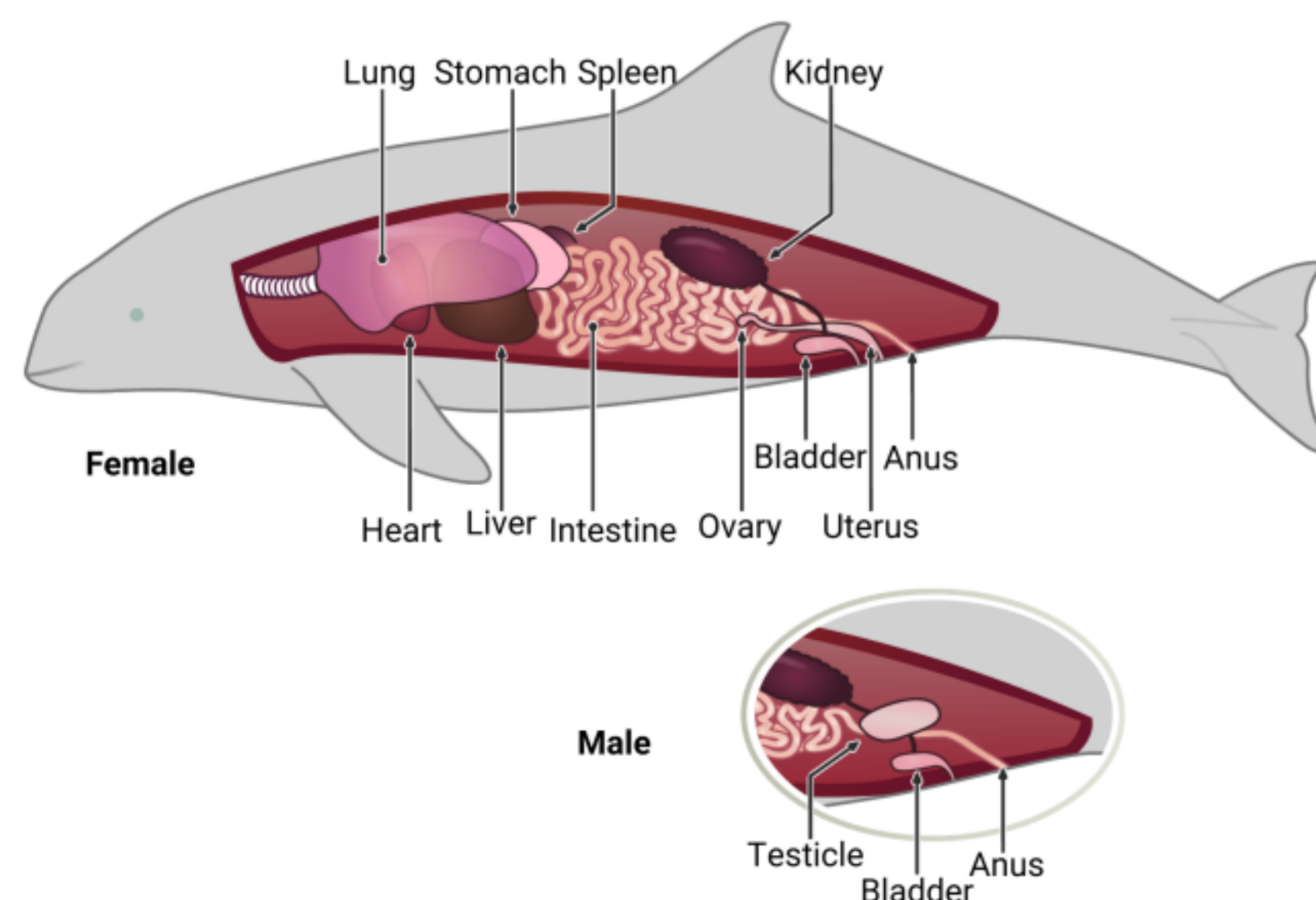
In June 2022, an immature male harbor porpoise presenting clinical signs suggestive of neurological disease was observed in shallow waters off the Swedish west coast and drowned shortly thereafter.



Use QR code to access film sequence of the distressed porpoise.
Photo: Fabian Sanchez

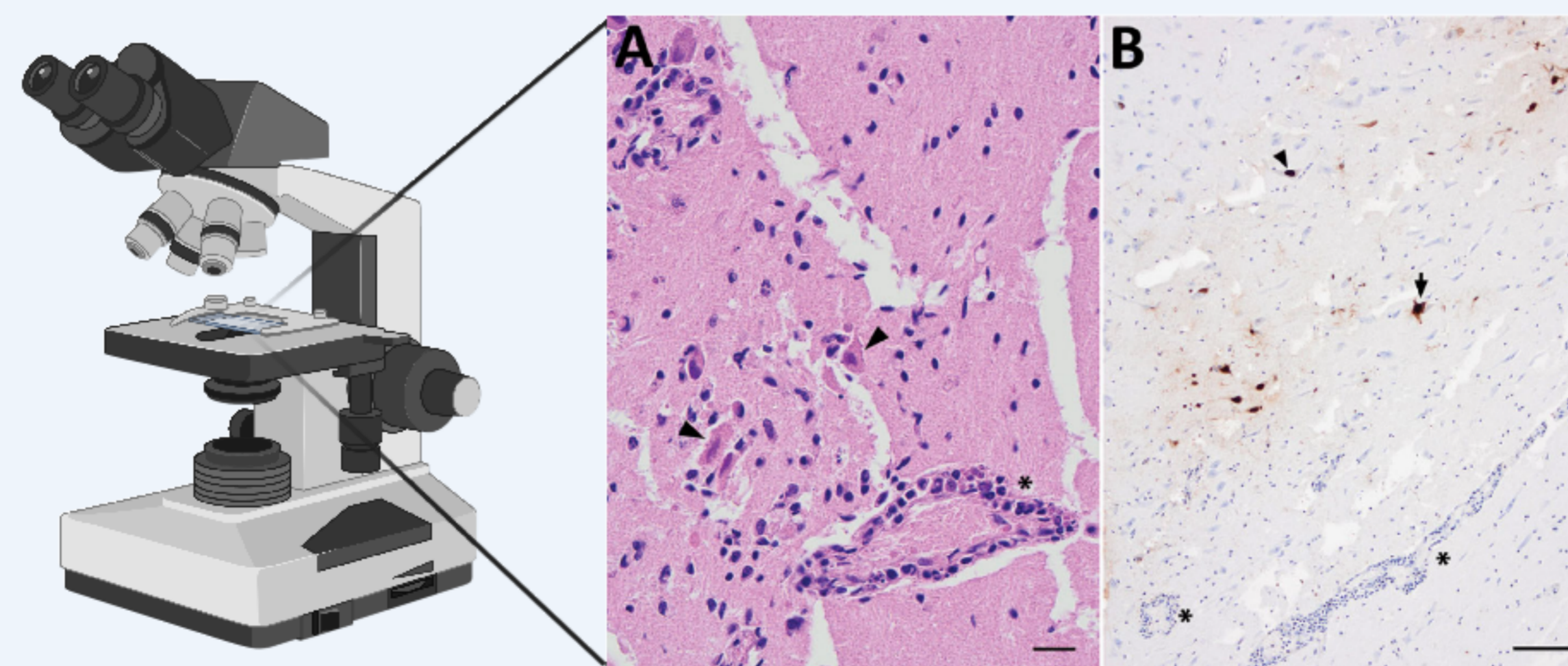
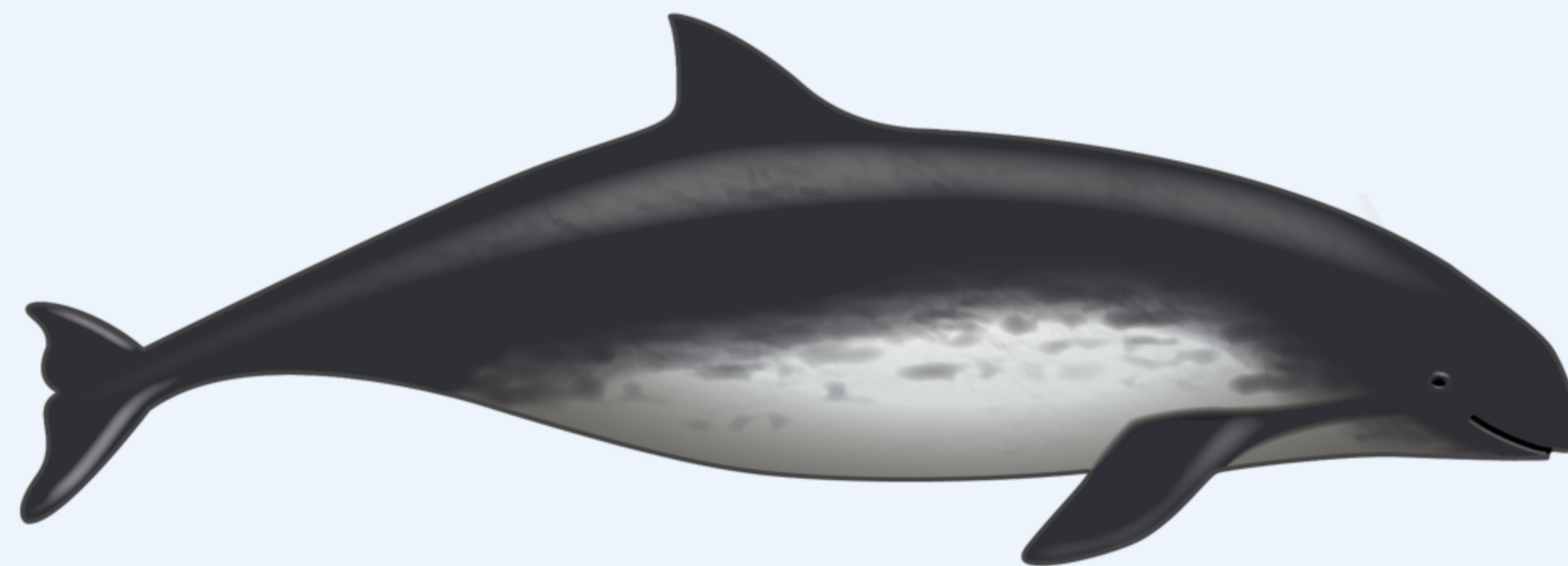
METHODS

Necropsy was performed at the National Veterinary Institute (SVA), Uppsala, Sweden, within the marine mammal disease surveillance program. Stranded porpoises in Sweden are screened routinely for cetacean morbilliviruses, which can be neurotropic in cetaceans, and IAV, which is neurotropic in other species.

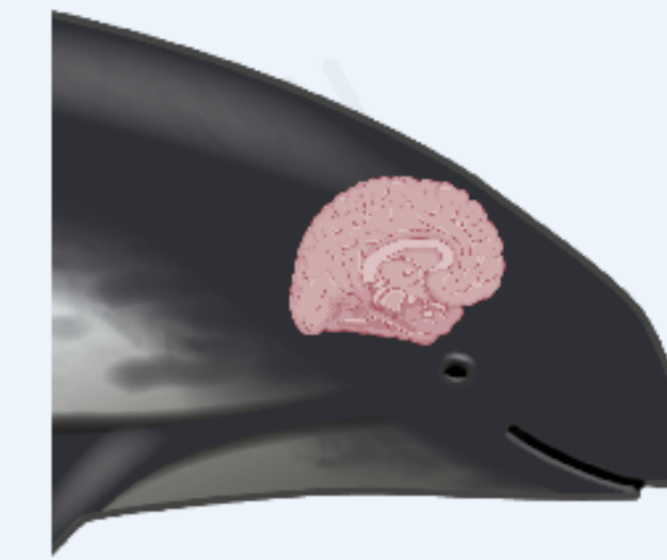


RESULTS

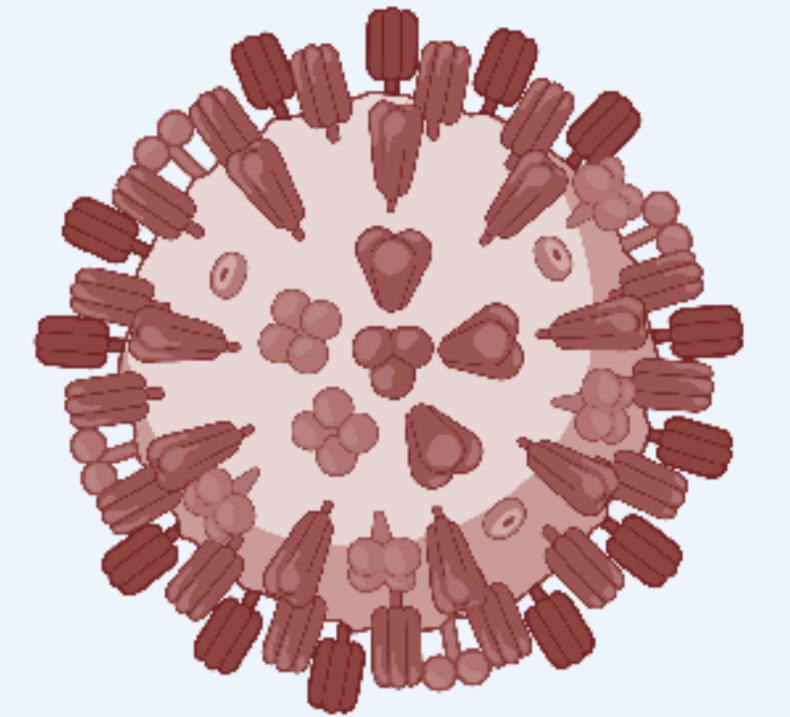
Stranded harbor porpoise died from viral infection in the brain caused by highly pathogenic avian influenza A (H5N1)



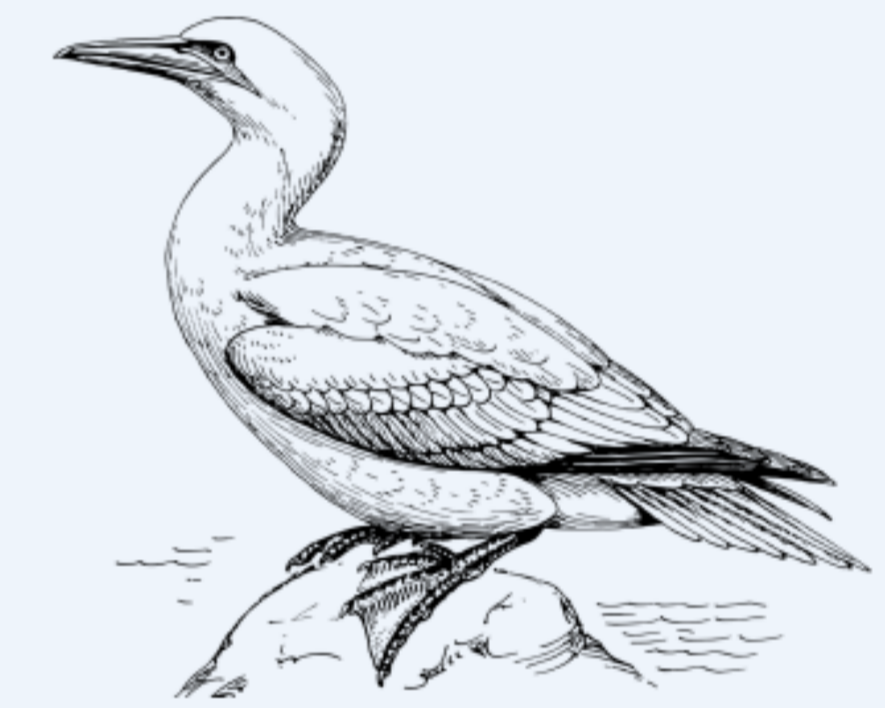
Microphotograph of brain tissue samples from harbor porpoise infected with HPAI H5N1. A) Histopathologic lesions of lymphoplasmacytic meningoencephalitis with neuronal necrosis (arrowheads), perivascular cuffing and vasculitis (asterisk). Scale bar represents 20 μ m. B) Immunohistochemical labeling of influenza A nucleoprotein in neuronal nuclei (arrowhead) and cytoplasm (arrow), as well as glial cells. Perivascular cuffing (asterisks) is seen in close association to influenza A immunolabeling. Scale bar represents 100 μ m.



Highest viral loads were detected in the brain and smaller loads in the lung, kidney, liver, and spleen. No virus was detected in the intestine, muscle, or blubber.



The virus was classified as HPAI H5N1 clade 2.3.4.4b. The genome contained no genetic motif of mammalian adaptation besides those already described for the clade.



The virus was closely related to strains recovered from wild birds, such as the northern gannet, from the same area, supporting spill over from wild birds.

CONCLUSION

- IAV infection in a harbor porpoise represents **expanding viral host range**.
- The route of transmission is unknown but includes **contact with infected birds** or indirect contact through contaminated water, suggesting that infection pressure in the ecosystem was high.
- The **potential zoonotic risk** of HPAI viruses for persons in close contact with infected animals should be considered.

ACKNOWLEDGEMENT / REFERENCES

Thorsson, E., Zohari, S., Roos, A., Banihashem, F., Bröjer, C., & Neimanis, A. (2023). Highly Pathogenic Avian Influenza A(H5N1) Virus in a Harbor Porpoise, Sweden. *Emerging Infectious Diseases*, 29(4), 852-855. <https://doi.org/10.3201/eid2904.221426>
 Porpoise illustrations: Valja infodesign, Carina Söe- Knudsen