Supplementary Materials

Tracking HPAIV H5 Through a Geographic Survey of Antarctic Seabird Populations

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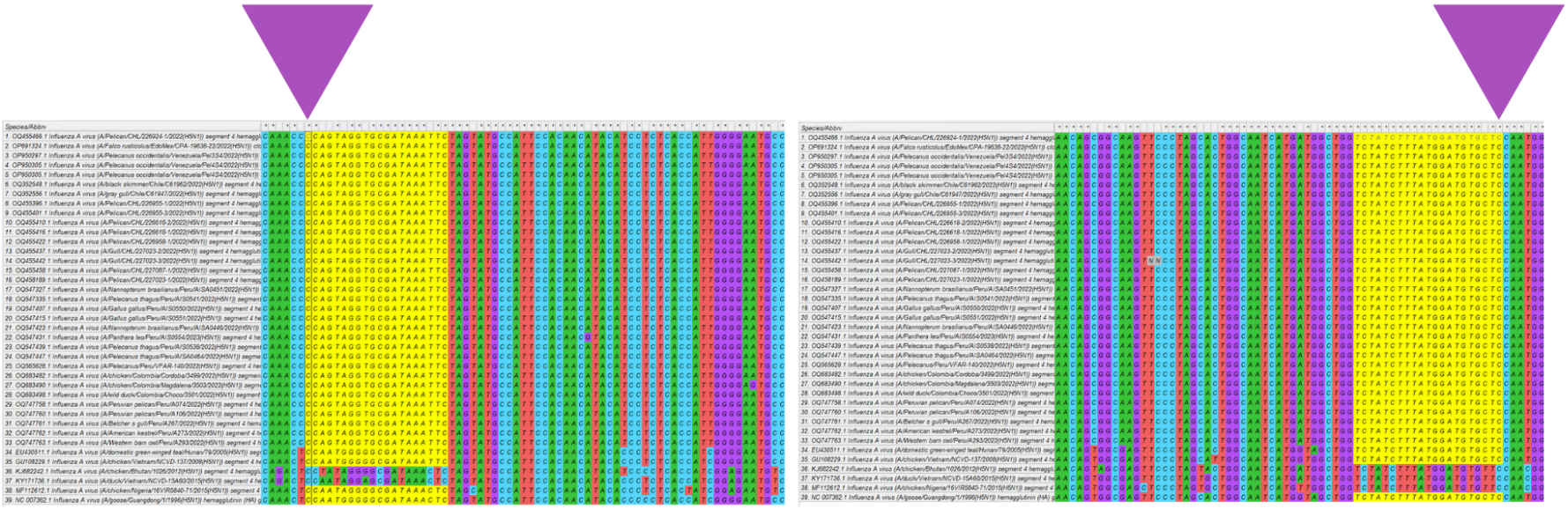
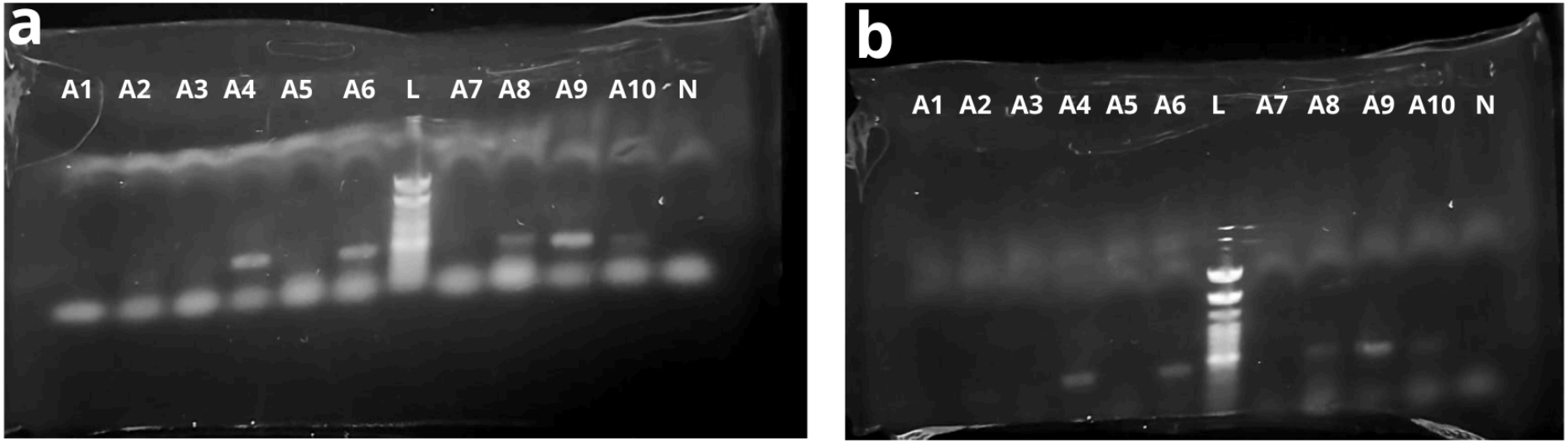
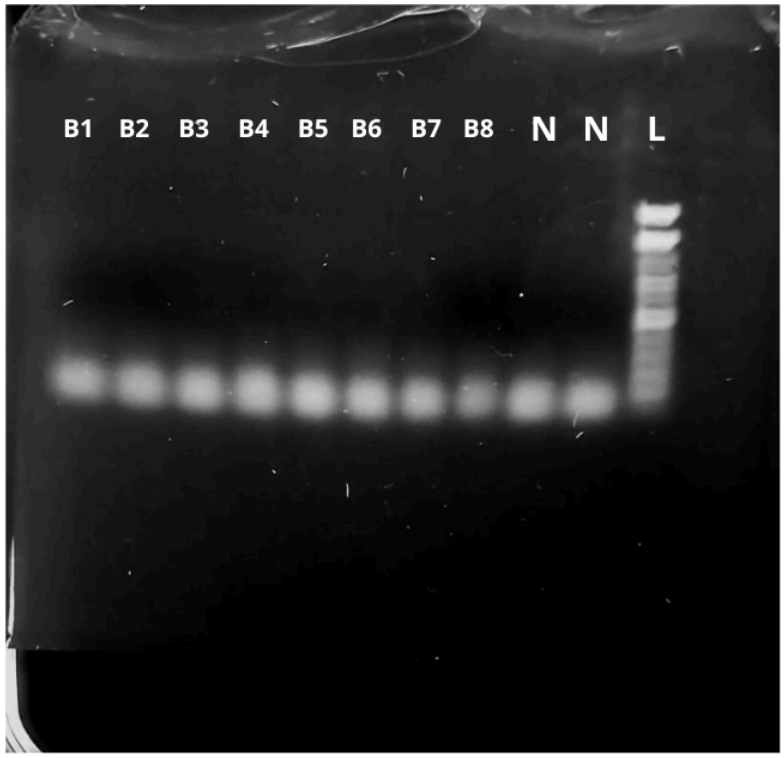


Supplementary Figure 1. Alignment of 39 H5 sequences: 33 from highly pathogenic H5N1 viruses in South America (Chile, Peru, Venezuela), and 6 control sequences from earlier H5 strains, including Asian lineages. A conserved region (yellow) targeted for primer design yields a 782 bp amplicon.The purple triangle showing the beginning and end of the amplicon Alignment and primer design were performed using MEGA11 (Tamura et al., 2021). Forward (H5-918F): CCA RTR GGK GCK ATA AAY TC. Reverse (AH5-R1686): GAG CAC ATC CAT AAA GAT AGA.



Supplementary Figure 2. Agarose gel electrophoresis showing PCR amplicons obtained on board during fieldwork under suboptimal conditions. The electrophoresis system used was a compact, low-capacity unit, and the ship's motion, combined with unstable power regulation, led to uneven heating of the gel, causing asymmetrical melting and distortion. Panel (a) shows the gel after 30 minutes of electrophoresis; panel (b) after 50 minutes. Despite the distorted migration, distinct bands of the expected size can be observed, confirming successful amplification. Adelie penguins samples (A1-10), Ladder 100 pb (L), Negative control (N).



Supplementary Figure 3. Agarose gel electrophoresis showing RT-PCR results for HPAIV H5 in samples collected from Cape Burks and Stephen Island. All samples shown yielded negative amplification. Samples B1–B7 correspond to Adélie Penguins (*Pygoscelis adeliae*) and sample B8 corresponds to a South Polar Skua (*Stercorarius maccormicki*). These individuals were sampled at Cape Burks and Stephen Island, respectively. No suspected HPAIV H5 cases were detected at these sites. L: 100 bp molecular ladder; N: negative control.