Introducing the Featherflu™ H5N1 Bird Flu Research Foundation

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FEATHERFLU™

BIRD FLU RESEARCH FOUNDATION

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Abstract

Migratory waterfowl are now the primary epizootic vector for HPAI/H5N1 viral incubation and dispersal along the North American Pacific Flyway—all California condor nesting & release sites lie directly in their path (Ramey (2022)).

History of Condor Population Decline

In 1982 California condors went extinct in the wild and only (22) twenty-two remained alive in captivity (Robinson et al. (2021, 2939)). According to (2021), ``endangered species frequently suffer from a lack of genetic diversity, potentially leading to inbreeding depression and reduced adaptability”[(2021)).

The California condor has 40 pairs of chromosomes (compared to 23 pairs for humans) and the California condor's fully-sequenced genome prepared by Robinson et al. (2021) in their Robinson et al. (2021) complete & contiguous rendering of the California condor genome by means of a `high-quality"\footnote{\citeauthor{RobCB31} used` a long read chromatin mapping interaction mapping chromosome-length assembly (Hi-C) method" to fully and contiguously sequence the genome (?, p. 2939).} sequencing method which revealed the California condor shares a common ancestor with the American poultry-farmed chicken whose genetic divergence occurred $\approx$ 70 million years before present (?, p. 2939).

References

Ramey, Hill, A. M. 2022. "Highly Pathogenic Avian Influenza Is an Emerging Disease Threat to Wild Birds in North America." *The Journal of Wildlife Management* 86 (2): 1–21. https://doi.org/https://doi.org/10.1002/jwmg.22171.

Robinson, J. A., R. C. K. Bowie, O. Dudchenko, E. L. Aiden, and S. L. et al. Hendrickeson. 2021. "Genome-Wide Diversity in the California Condor Tracks Its Prehistoric Abundance and Decline." *Current Biology* 31 (7): 2939–46. https://doi.org/https://doi.org/10.1016/j.cub.2021.04.035.