Age, Not Population, Predicts Avian Influenza Exposure in Barnacle Geese During an HPAI Outbreak

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Highly pathogenic avian influenza (HPAI) H5N1 clade 2.3.4.4b has caused substantial mortality in wild waterfowl, yet it remains unclear which individuals and populations face the greatest exposure risk. This study tested whether population origin and individual characteristics predict serological evidence of HPAI exposure in Barnacle geese (*Branta leucopsis*), a species that has experienced significant HPAI-associated mortality. Using serological data from 337 individuals across five UK populations differing in migratory status, habitat, density and connectivity, we combined molecular sexing with body condition metrics. Overall seroprevalence was 67.1%, and age was the strongest predictor of serostatus: juveniles were substantially less likely than adults to be seropositive. Seroprevalence was similar across four of the five populations despite marked ecological differences between them; the fifth, North Yorkshire, showed both lower seroprevalence and a lower proportion of H5-positive samples among AIV-positive birds, indicating a distinct exposure history. Body condition was associated with serostatus only in the highest-density population. We found no evidence of sex differences or a coastal–inland gradient. These findings suggest that, during this outbreak, individual age was a more consistent predictor of exposure than population-level ecology, and that serological patterns in HPAI-affected systems likely reflect both exposure and differential mortality. Though distinguishing outbreak-driven homogenisation from survival filtering as the underlying mechanism will require longitudinal sampling across outbreak and inter-outbreak periods. Distinguishing outbreak-driven homogenisation from survival filtering will require longitudinal sampling across both outbreak and inter-outbreak periods.