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Weak support for disappearance and restricted emergence/persistence of highly pathogenic influenza A in North American waterfowl

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Krauss et al. (1) use lack of detection of highly pathogenic (HP) H5 clade 2.3.4.4 (henceforth “H5”) influenza A viruses (IAVs) from >22,000 wild bird samples collected in North America in 2014–2015 to argue that HP H5 IAVs disappeared from waterfowl and that unresolved mechanisms restrict emergence and perpetuation of HP IAVs in natural reservoir species. Here we offer an alternative interpretation.

The majority of negative data presented by Krauss et al. (1) is from samples collected before HP H5 IAV outbreaks in North America (8,962 samples), states/provinces where outbreaks were not reported (11 of 16 locations), or from seabirds, shorebirds, and gulls (4,330 samples), none of which have been implicated in the ecology of HP H5 IAVs, nor are considered “waterfowl” (order Anseriformes). Given that the majority of this negative data could be considered inapt for assessing the “disappearance” of HP H5 IAVs in North American waterfowl, Krauss et al. provide weak support for their thesis. In contrast, detections of HP H5 IAVs were reported in waterfowl inhabiting the Pacific Americas flyway concurrent with the authors’ sample collection efforts (2), in addition to sporadic detections in wild birds in the Mississippi flyway (3), a region for which Krauss et al. (1) estimate 95% confidence of detection. As such, additional data from outbreak-affected areas would be useful to assess if HP H5 IAVs disappeared from waterfowl in North America after June 2015. Although HP IAVs were not isolated from >45,000 independent wild bird samples collected during July 2015–June 2016, providing evidence that such viruses either circulate below detection levels or were eradicated in North America (3), the

detection of HP H5N2 IAV in a mallard sampled in Alaska during August 2016 suggests that such viruses may not have disappeared.

Furthermore, Krauss et al. (1) propose that cryptic mechanisms restrict HP IAVs from arising and being maintained in wild birds; however, without specific definitions for “emergence” and “perpetuation,” previously published data seemingly contradict this premise. Although HP IAV phenotypes evolve in gallinaceous birds, HP H5 IAV reassortants may have been generated in wild waterfowl, as is supported through assessment of the genetic ancestry of H5N1 and H5N2 subtype viruses detected in North America (4). Additionally, numerous investigations provide evidence for wild bird involvement in the maintenance and dispersal of HP H5 IAVs during seasonal outbreaks in South Korea (5, 6), introductions into Europe and North America (7, 8), and spread throughout the Pacific Americas flyway (2). Furthermore, pathological data provide evidence that HP H5 IAVs are well-adapted to waterfowl (9, 10), indicating lack of biological barriers to infection.

As the disappearance of HP H5 IAVs in North American waterfowl remains unclear, and mechanisms of viral persistence are largely unknown, we feel it is important to: (i) more thoroughly assess the presence/absence of HP H5 IAVs, given implications for biosecurity in North America and the need to develop appropriate surveillance/response plans; and (ii) recognize that migratory birds likely played some role in the generation of novel reassortant HP H5 IAVs and dispersal of viruses to new regions.

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2 Bevins SN, et al. (2016) Widespread detection of highly pathogenic H5 influenza viruses in wild birds from the Pacific flyway of the United States. *Sci Rep* 6:28980.

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