

Impact of H5 vaccination in ducks on influenza virus evolution

Inhalt

High pathogenicity avian influenza (HPAI) H5Nx viruses of clade 2.3.4.4b have become spread globally in the last few years. In early 2024, the USA reported the first outbreak of HPAI H5N1 clade 2.3.4.4b genotype B3.13 in dairy cattle. In France, HPAI H5N1 of clade 2.3.4.4b (genotype DI) caused numerous outbreaks in wild and domestic birds. Since 2022, around 32 million birds have been culled across France due to detection of H5N1 virus. This led to a drastic change in EU regulations including the implementation of vaccination programs in domestic ducks in France that started in autumn 2023.

Based on the hypothesis that vaccine-induced immunity pressure can lead to emergence of escape mutant viruses, this study aimed to understand the impact of vaccination on virus evolution. We constructed an attenuated reverse genetics (6+2) HA “delta”(HA with a LP cleavage site) genotype B3.13 virus on a PR8 backbone. This RG virus was passaged twice in embryonated eggs from vaccinated ducks. Across 4 replicates, NGS was performed to assess viral genetic diversity. No hemagglutinin mutation was observed, but a neuraminidase N42D mutation was consistently detected.

Additional passages in eggs from vaccinated ducks will be conducted using RG H5 (6+2) viruses representing different genotypes from different countries. Overall, we will assess the possible emergence of antigenically drifted H5N1 viruses and study their putative impact in the context of vaccination failure and phenotypic changes

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Junior scientist status

Yes, I am a junior scientist.

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