

Investigating the role of pheasants as a bridging host for the introduction of clade 2.3.4.4 H5N6 highly pathogenic avian influenza viruses into chickens

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Abstract

Clade 2.3.4.4 H5Nx highly pathogenic avian influenza viruses (HPAIVs) have spread worldwide, resulting in six European epizootics since 2014, with accompanying poultry outbreaks being economically damaging and demanding statutory disease responses. These HPAIVs have also incurred into wild and farmed pheasants, from which infection could spread into commercial poultry wherever populations overlap. To investigate, we directly infected a group of pheasants (n=6) with a wild pheasant-origin H5N6 HPAIV from Denmark (A/pheasant/Denmark/12106-3/2018 (H5N6-2018)) where 100% (6/6) infection resulted, as ascertained by H5N6-2018 shedding. The directly-infected pheasants served as donors to model an H5N6-2018 transmission chain as a natural infection route: Four additional groups (n=6 in each) of contact pheasants were introduced stepwise through four successive cohousing stages. Throughout this transmission chain, all pheasants in each contact group shed viral RNA, confirming infection, and thereby demonstrating a successful transmission chain in this species. H5N6-2018 transmission was further extended to spread efficiently to a 5th contact group of chickens (6/6). However, attempted onward transmission to a 6th contact group of chickens was inefficient (2/6). All infected pheasants and chickens succumbed to infection as a typical HPAI outcome, although species differences in mean death time was observed, with species differences also observed for the H5N6-2018 tissue tropism. We demonstrated that H5N6-2018 may be transmitted efficiently in pheasants and might function as a bridging host between wild birds and farmed chickens, although onward spread in chickens was inefficient suggesting species adaptation may play a role in susceptibility and maintenance within different avian hosts.