TRANSMISSION DYNAMICS OF HIGHLY PATHOGENIC AVIAN INFLUENZA AMONG MULTIPLE WATERFOWL SPECIES AND POULTRY

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Outbreaks of highly pathogenic avian influenza (HPAI) pose a risk to human health and increase the probability of epidemics comparable to that of the 2016/2017 H5N8, European epidemic. Focusing on the overlap between stopover periods of different migratory species, we have modelled the transmission of HPAI between wild birds and domestic poultry at wetland regions in Croatia. Under a simplifying assumption of homogenous mixing, our deterministic compartmental model accounts for the direct mode of pathogen transmission among 4 bird populations. The modeled species include backyard poultry and mute swans (Cygnus olor), a sentinel species for HPAI outbreaks. Additionally, we modeled two distinct mallard populations (Anas platyrhynchos), asymptomatic carriers of HPAI, represented with migratory and non-migratory (resident) birds. Poultry was modeled at the farm level. The uncertainty and variability in model predictions was analyzed using Monte Carlo simulations. The preliminary results support that migration timing and the duration of overlap between mute swans and mallards strongly and positively affect the HPAI-induced mortality in wild birds and number of infected poultry farms. Our model will aid HPAI outbreak risk assessments based on real-time migration dates. Future work will evaluate the role of indirect transmission in the epidemiology of HPAI in the area.