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An ecological niche model of highly pathogenic avian influenza virus H5N1 occurrence in domestic poultry in Asia

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The control of highly pathogenic avian influenza virus (HPAIV) H5N1 in Asia – a region of widely diverse agro-ecological and socio-economic systems – continues to present formidable challenges to health practitioners. However, the use of an ecological niche-based spatial modeling method – maximum entropy (Maxent) – may help to extend our understanding, and thus control, of the disease. The objective of this study was to model the risk of HPAIV H5N1 occurrence in domestic poultry in Asia. Maxent was used to assess the correlation between five variables and the occurrence of HPAIV H5N1 outbreak data. The contribution of each variable to the model was determined together with the general trend of disease risk across the values of each variable. A risk map delineated areas of high and low risk, each of which were in turn characterized with respect to the individual variables. The predictive accuracy of the model was excellent (area under the curve (AUC) 0.903). Two of the five variables together accounted for just under 85% of the variation in HPAIV H5N1 occurrence – densities of domestic waterfowl (50%) and humans (33%) – with proximity to areas suitable for rice-growing (7%), proximity to roads (7%) and chicken density (3%) accounting for the remainder. Areas with the highest predicted risk included Bangladesh, parts of Vietnam and central Thailand and most of Java. High-risk areas were characterized by high densities of domestic waterfowl and humans, medium-to-high chicken density and were close to roads and areas suitable for rice-growing. Conversely, low risk areas were generally characterized as having no domestic waterfowl, low human and chicken densities and were far from areas suitable for rice-growing. By allowing regions of different risk to be characterized with respect to predictor variables, Maxent can extend our understanding of HPAIV H5N1 and enables the optimization of finite resources in designing risk-based disease surveillance systems.