Enhancing the Validity of Proxy-Based Non-Endemic Viral Monitoring Through GIS-AHP–Assisted Ecological Niche Modeling

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Emerging infectious diseases require accurate spatial risk assessments, yet current strategies in disease ecology lack a clear and reliable framework when direct disease data is lacking. One issue exists when modeling Japanese Encephalitis Virus (JEV), a climate-sensitive flavivirus with a 95% risk of introduction into the Southern U.S. This study addresses this gap by developing a novel proxy-validation framework based on ecological niche similarity, applied through a case study of West Nile Virus (WNV) and JEV in Florida. A WNV ecological niche model was developed and trained using 299 cases, whilst employing Pearson's Correlation and a Clark-Evans-justified spatial bias file to reduce spatial autocorrelation and optimize performance. This displayed a high prediction-expectation agreement (CBI=0.967), indicating model outputs accurately represent WNV distribution. A GIS-AHP model of JEV was developed by deriving weights from studies in endemic areas and was measured as consistent (CR<0.10), indicating this output successfully modeled JEV in a non-endemic location in the absence of training data. Schoener's D, Hellinger's I, and Bhattacharyya Distance all revealed significant similarity in niche behavior and in risk distribution in this case study, indicating the viability of the WNV as a proxy virus for JEV. Ultimately, this framework allowed complementary spatial modeling efforts to be combined whilst strengthening support for alternative case data use, addressing a key knowledge gap in the field of virology. These results establish a novel framework that equips virologists with a more reliable and timelier tool to model non-endemic viral threats, strengthening early detection and improving public health responses.

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