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Abstract

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A probabilistic model predicting host specificity and host range expansion in mites parasitic on mammals*

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The emergence of new mammalian diseases through the switching of parasitic organisms to novel hosts has significant wildlife, livestock, and human health impacts, however, new host switches are notoriously difficult to predict. The factors influencing the host switches are not fully understood because complete unbiased large-scale datasets of host-parasite relationships are lacking. Building a large-scale model to identify these factors and predict potential host switching (host range expansion) could hold substantial benefits from theoretical and applied perspectives (e.g., disease emergence prediction). Here we analyzed a large, curated database of host-parasite relationships of 1906 species of acariform mites forming permanent associations with 1235 species of mammals, including humans, and built a probabilistic predictive model of host-specificity for these mites. There was a total of 3,125 unique host-parasite records. We used a linear regression with mixed effects as follows:

$$Y \sim B0+B1*x_1+B2*x_2+\ldots\ (1|\text{Geographic range}) + \varepsilon$$

where, Y= response variable (dependent); B0 = intercept; B1,B2 = regression coefficients; x_1, x_2 = independent variables (predictors); ε = error, random effects; (1|Geographic range) = intercept is different for each category of the geographic range variable.

Proximity to the host immune system (correlated with the feeding type) and host domestication were the first and second most important factors increasing the host specificity in these host-parasite systems. These characteristics are also risk factors for parasite transmission to other hosts. Our analysis predicted that a high likelihood for consecutive, host-rank-dependent host switches. Spatial co-occurrence of hosts and higher mean temperatures also significantly increased the risk of host switching. Other ecological or climatic factors had no significant correlation with host specificity. We demonstrated with a specific application of our model for the prediction of parasite's host range expansion following changes in ecological characteristics. Our model can be used to predict the probability for host specificity in mites parasitic on mammals, which is a property related to emerging infectious diseases.

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Keywords: Host switch, permanent parasites, full-time parasites, Acariformes, host-related factors, parasite-related factors, environmental factors

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