

Natural variables separate the endemic areas of *Clonorchis sinensis* and *Opisthorchis viverrini* along a continuous, straight zone in Southeast Asia

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Figure1

Figure2

Figure3

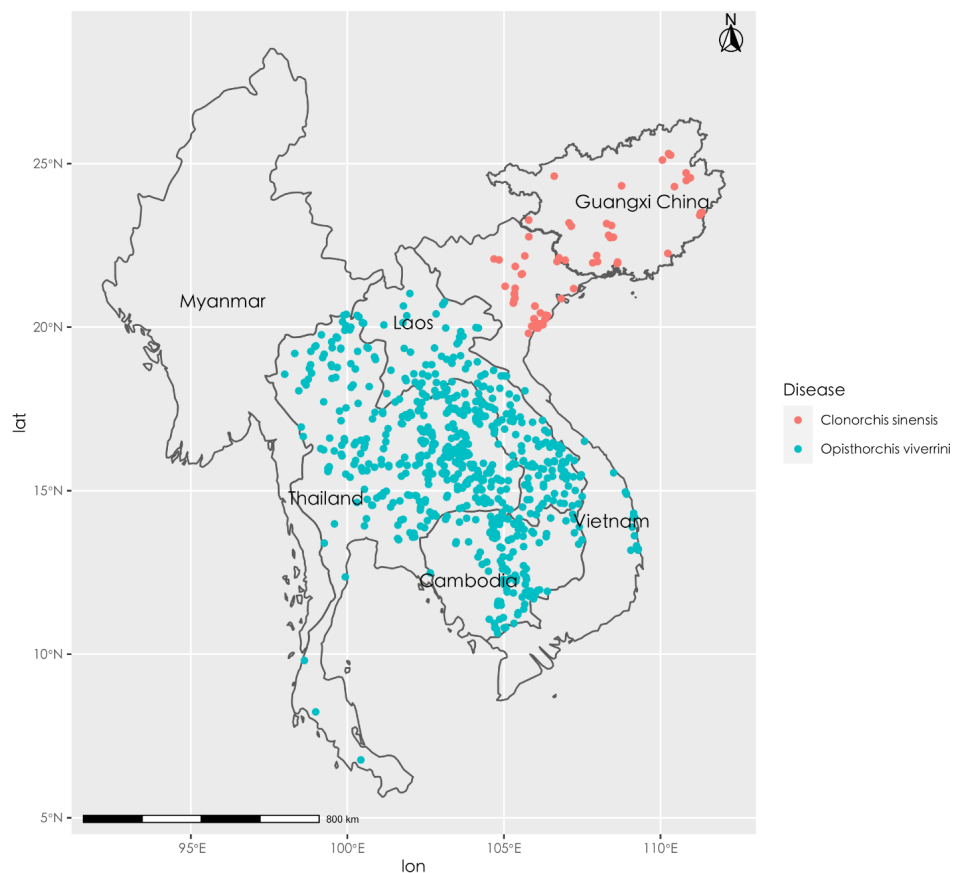


Figure 1 Geospatial Distribution of *Clonorchis sinensis* and *Opisthorchis viverrini* infections with human in the Mekong River Basin of study areas. The occurrences of *Clonorchis sinensis* are marked in red, indicating a concentration in the Guangxi region of China, while the instances of *Opisthorchis viverrini* infection are denoted in blue, highlighting a widespread presence throughout Thailand, Laos, Cambodia, and Vietnam

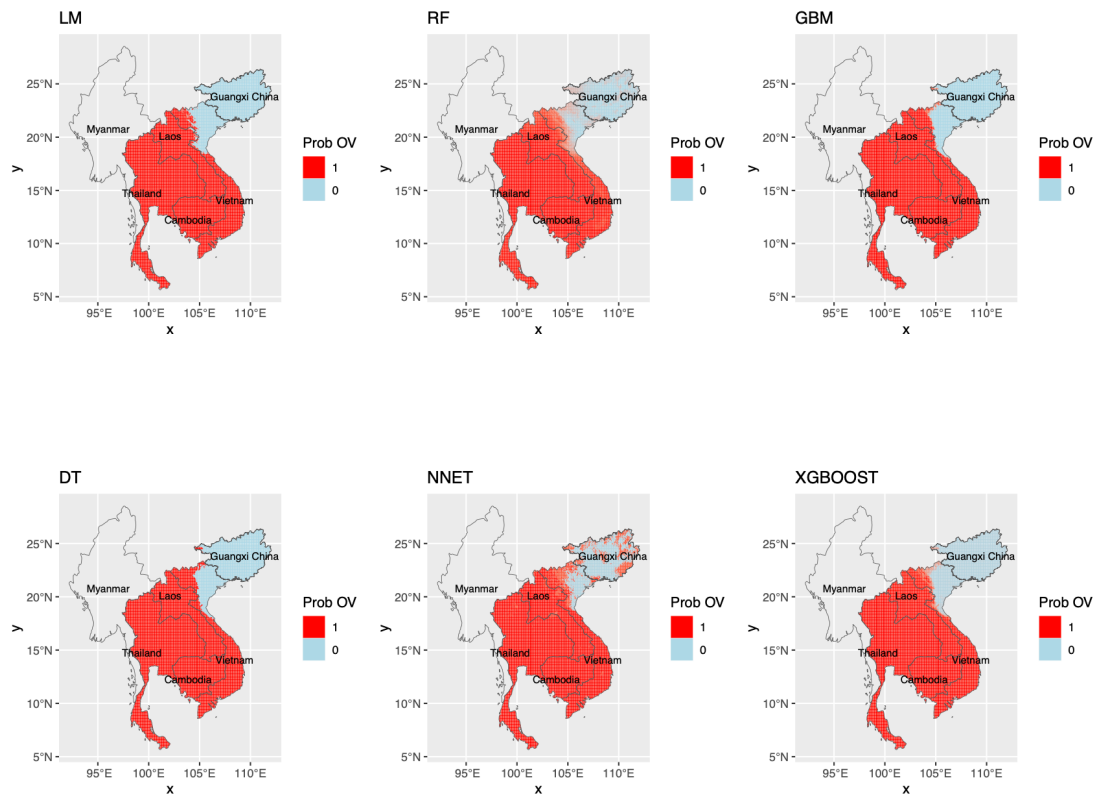


Figure 2. Predictive risk mapping of *Opisthorchis viverrini* infection across the Mekong River Basin Using Various Machine Learning Models. Linear Model (LM), Random Forest (RF), Gradient Boosting Machine (GBM), Decision Tree (DT), Neural Network (NNET), and eXtreme Gradient Boosting (XGBOOST). The shaded areas indicate the predicted probability of OV infection, with red representing a higher likelihood and blue representing a lower likelihood.

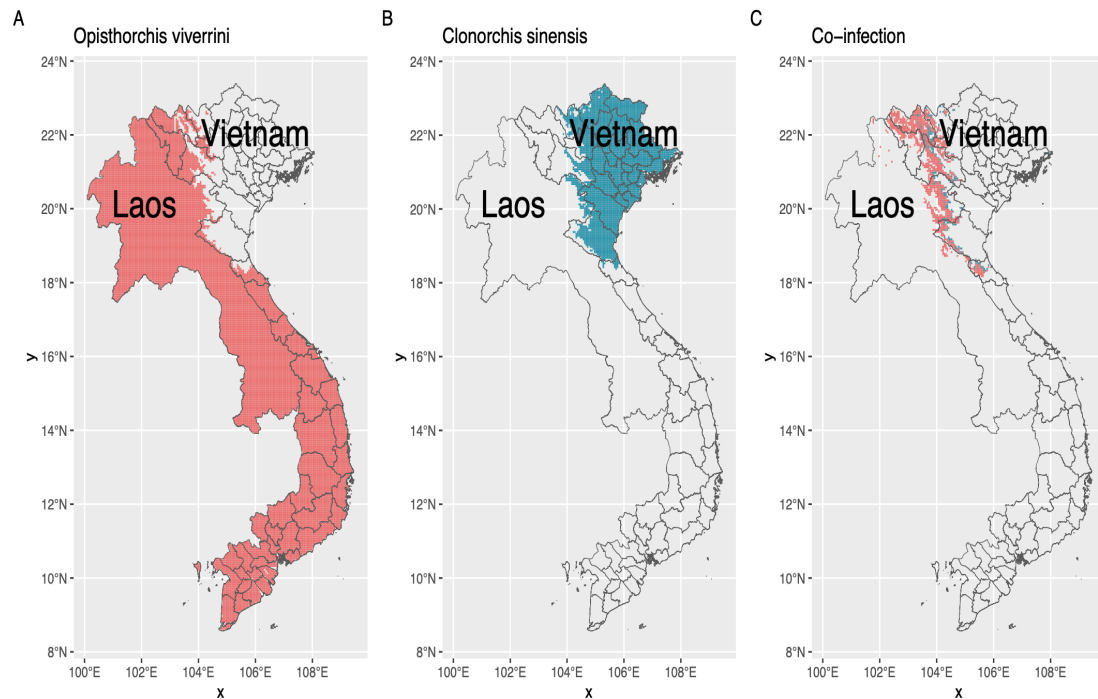


Figure 3. Predicted Distribution of *C. sinensis* and *O. viverrini*, and Co-infection in the Greater Mekong Subregion in Laos and Vietnam by Random Forest. A) *O. viverrini*: The red shaded areas, predominantly covering parts of Laos and Vietnam, indicate regions where the RF model predicts a higher risk of *O. viverrini* infection. B) *C. sinensis*: In contrast, the blue shaded areas suggest the RF model's prediction for the prevalence of *C. sinensis*, primarily within Vietnam. C) Co-infection: The third map showcases the zones with potential for co-infection, where the model indicates the presence of both *O. viverrini* and *C. sinensis*, noted by the intermingling of red and blue shades.