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"Biogeography applied to the study of zoonotic diseases"

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When the ecology of a pathogen is complex and unresolved, as is the case of the Ebola virus, imposing restrictions to the selection of species considered in a model might under-represent the zoological substrate conditioning the pathogen distribution. We addressed the mapping of favourable areas for the Ebola virus in the wild by combining two biogeographical approaches: SDM and the analysis of mammalian distribution types in (e.g. chorotypes). Mammalian chorotypes in Africa were employed as surrogates of the types of distribution shown by reservoirs, victims and any wildlife species in the virus spillover cycle. We found that a model based on mammalian chorotypes defined the favourable areas for the presence of Ebola virus with higher accuracy than did a model based on environmental variables (i.e. climate, forest type). We concluded that mammalian biogeography contributes significantly to explaining the distribution of Ebola virus in Africa, although vegetation may also underscore clear limits to the presence of the virus. So, a final map of favourable areas according to the information provided by both models was built.