

# Mapping the distributional potential of the Crimean-Congo haemorrhagic fever vector *Hyalomma marginatum*

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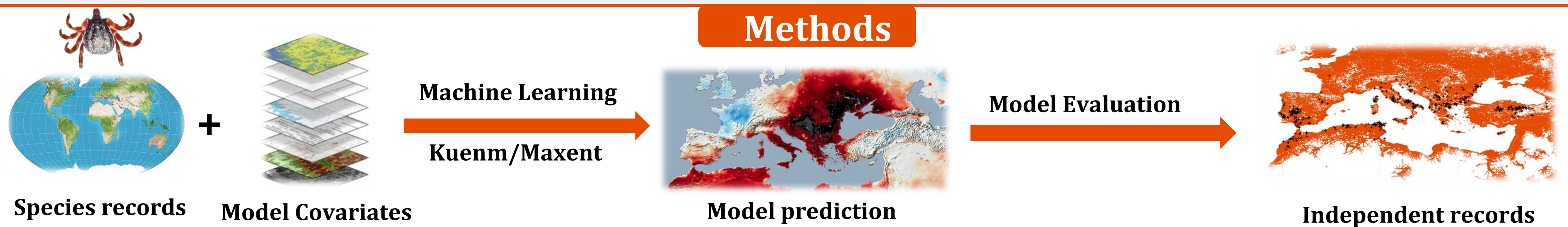


## BACKGROUND

Crimean-Congo haemorrhagic fever (CCHF) is the most widely distributed tick-borne viral disease in humans caused by the **Crimean-Congo haemorrhagic fever (CCHFV)**. The historical known distribution of the CCHFV vector *Hyalomma marginatum* in Europe included most of the Mediterranean and the Balkan countries, Ukraine, and southern Russia and are absent in Central Europe, likely due to environmental conditions. Further expansion of its potential distribution is possibly occurred in and out of the Mediterranean region. The **distribution of CCHFV is related to the distributional potential of its vector species**. **Climate change**, transportation of immature ticks through **international animal trade**, and **migratory birds** have also significant impacts on modifying the distributional potential of *H. marginatum* and allowing the emergence of CCHF into new geographic regions such as Central Europe.

**HYPOTHESIS** → We hypothesized that several abiotic, biotic, and socio-economic factors may influence the ability of *H. marginatum* to colonize areas in Europe.

**AIM** → To assess the current potential distribution of *H. marginatum*, the principal vector of CCHFV, in Europe, with a particular focus on Central Europe by using ecological niche modeling approach.



## RESULTS

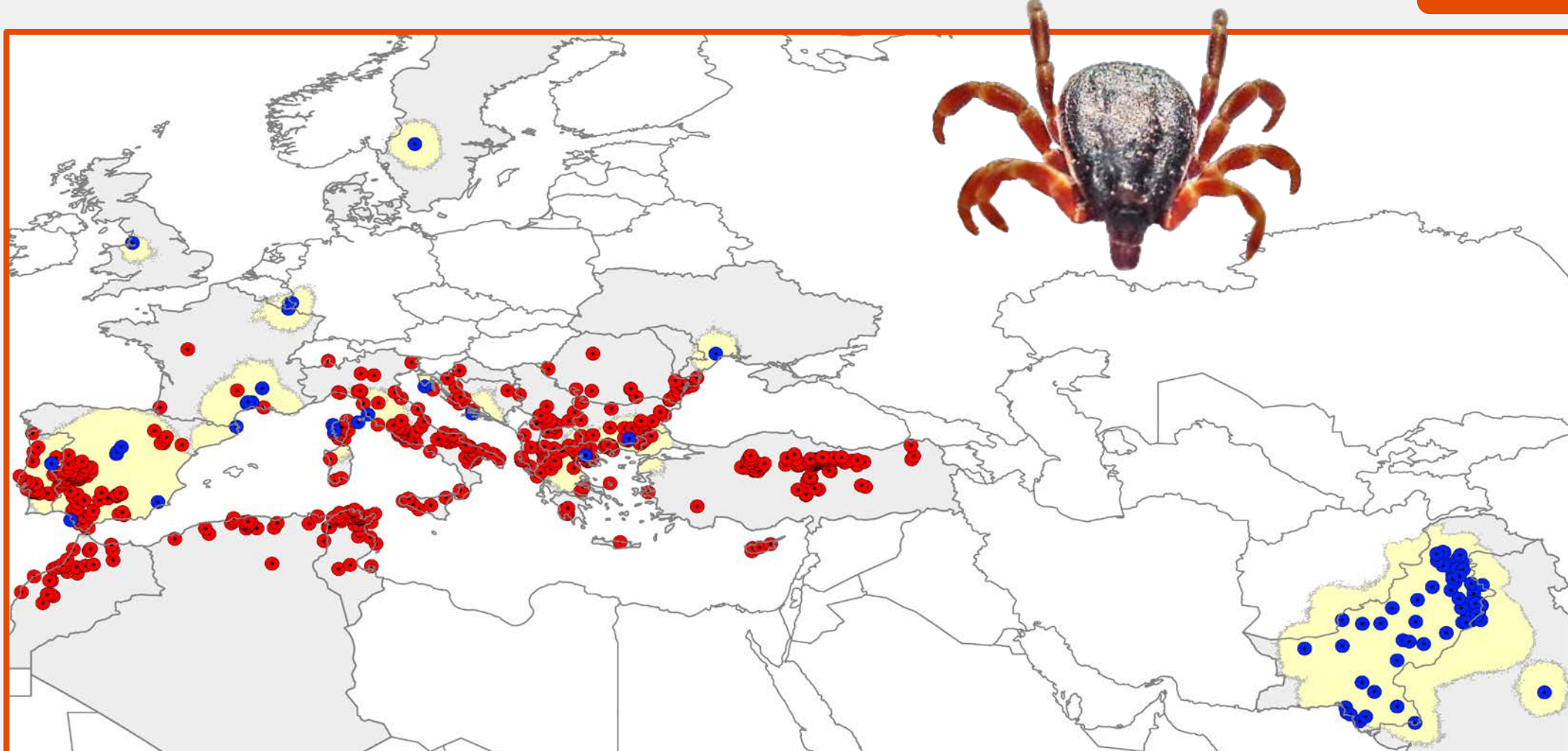


Figure 1. *Hyalomma marginatum* occurrence records used in model calibration and final model evaluation across Europe, North Africa, Western and South-Central Asia.

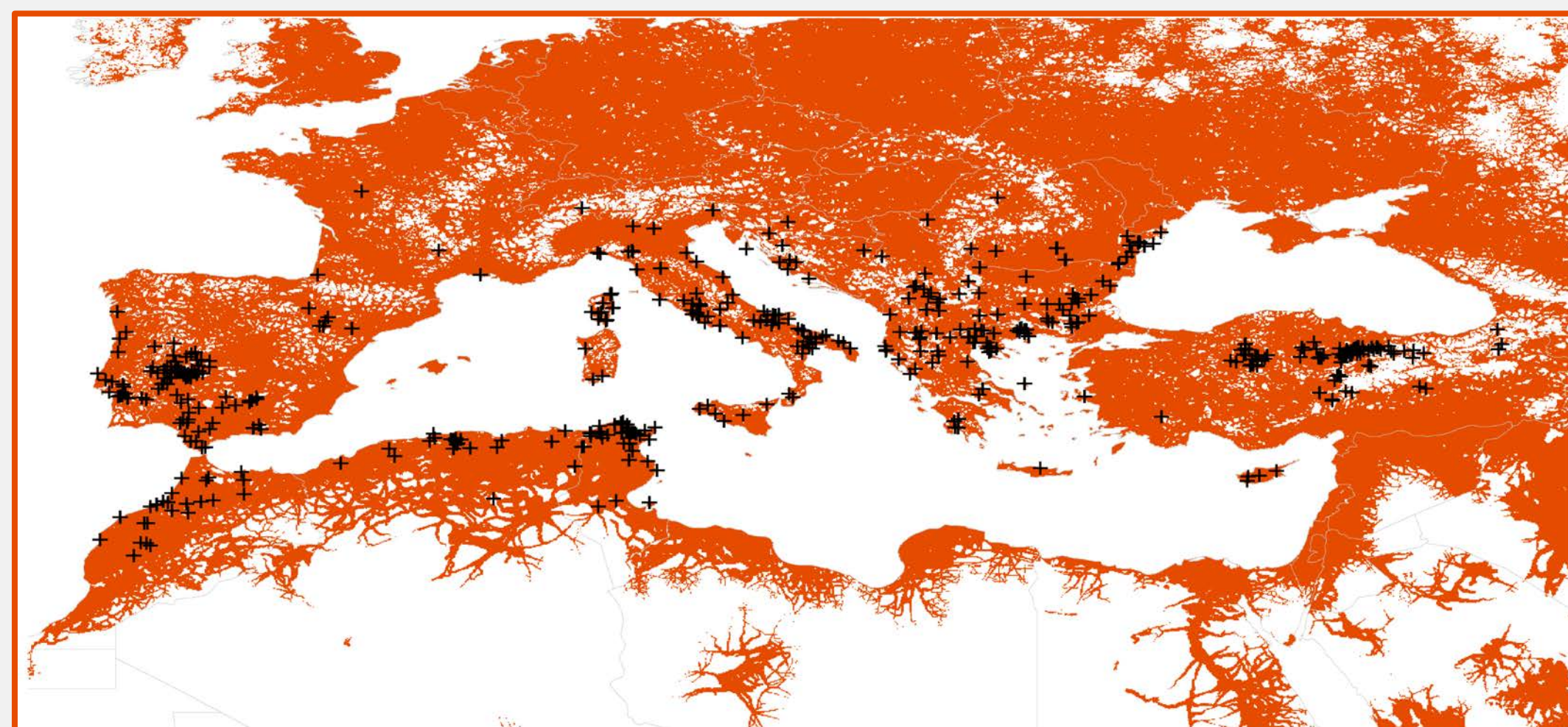


Figure 3. Relationship of *Hyalomma marginatum* ecological niche modeling prediction to the distribution of the independent set of *Hyalomma marginatum* occurrence records.

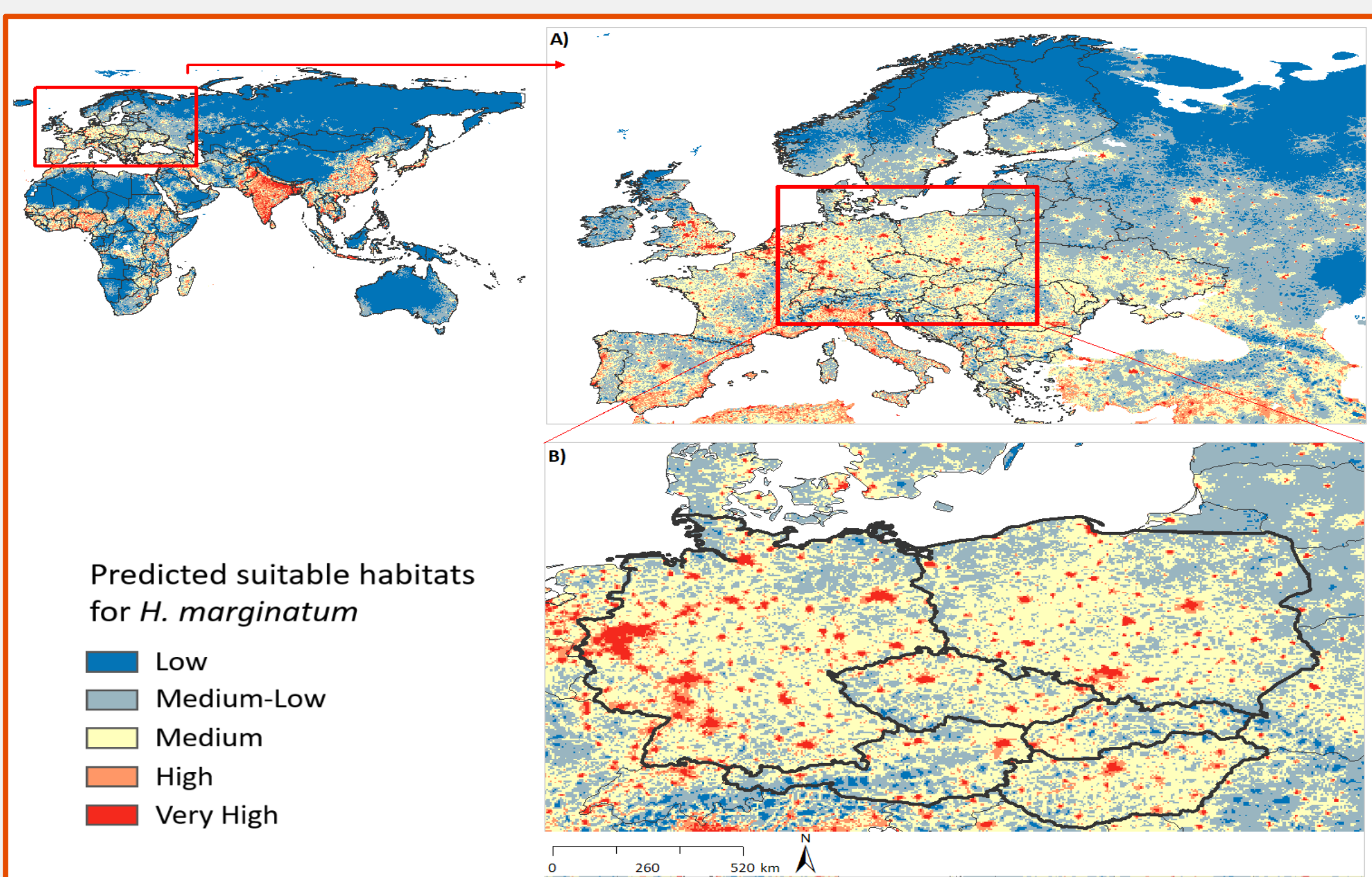


Figure 2. Predicted potential distribution of Crimean-Congo haemorrhagic fever vector *Hyalomma marginatum* on a global scale (left top), and close-ups of Europe (A) and Central Europe (B), to provide additional detail to predictions in the region.

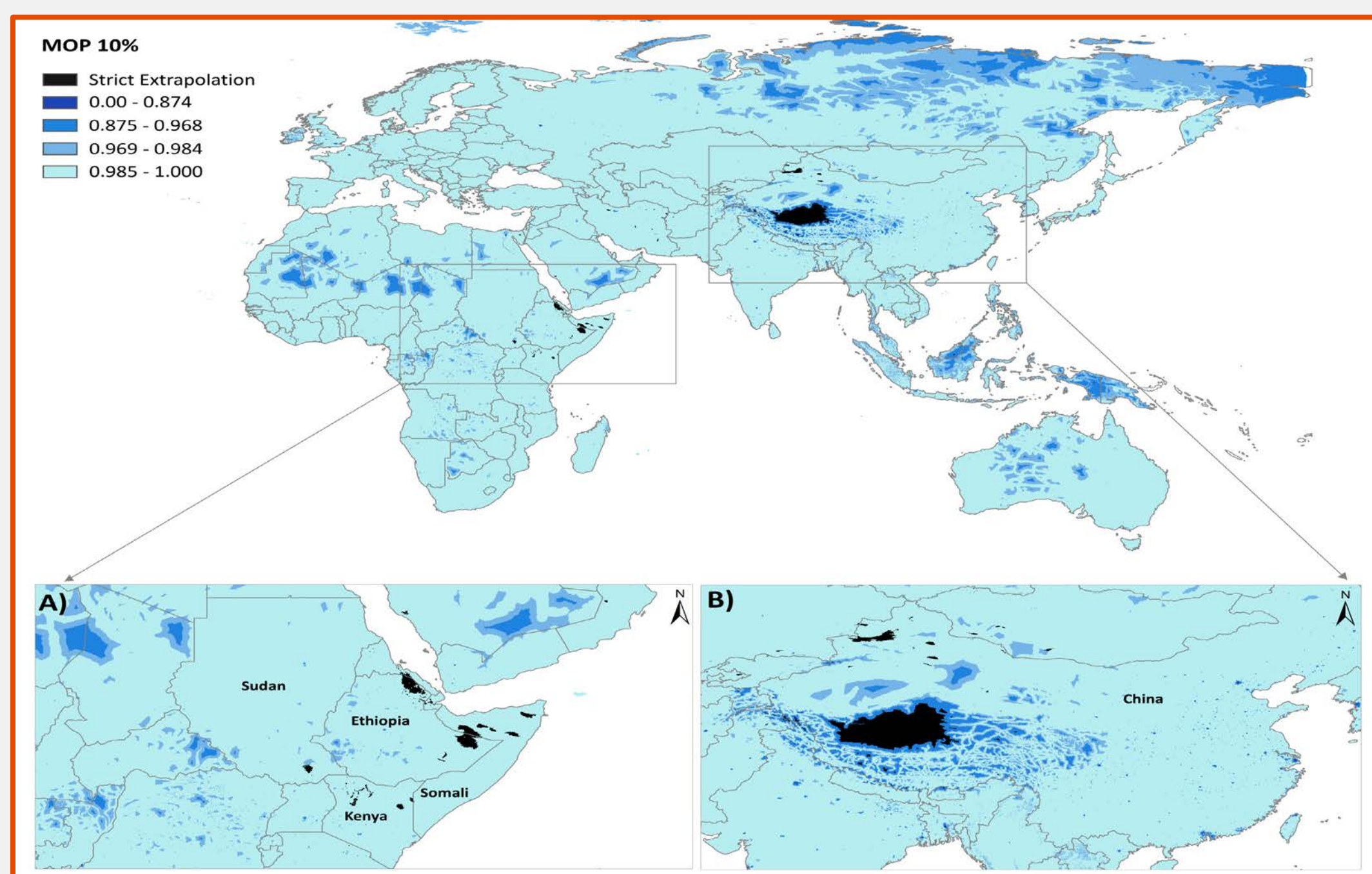


Figure 4. Mobility-oriented parity (MOP) 10% extrapolation risk analysis for the ecological niche model of *Hyalomma marginatum*, and close-ups of East Africa (A) and Eastern Asia (B), to provide additional detail to strict extrapolations occurred in the areas.

## CONCLUSIONS

- The model predicted **higher suitability** for the species in Central, Western, Eastern, and Northern Europe compared to previous studies.
- **Extensive medium to very high suitability** for the species was identified in **all countries across Central Europe and in southern areas of Scandinavia**.
- The rapidly changing climate in northern Europe may allow the subadult ticks carried by migratory birds to develop into adult stage, increasing the risk of attachment and feeding on large mammals, including humans.
- The study used the MOP metric to identify areas with **high uncertainty in the model projections**, especially in **Southwest and Northwest China**.
- **Future studies** will involve detailed mapping of CCHF disease and *H. marginatum* distribution **under different climate change scenarios**, as well as improved modeling studies incorporating effects of vertebrate hosts and tick species life traits.