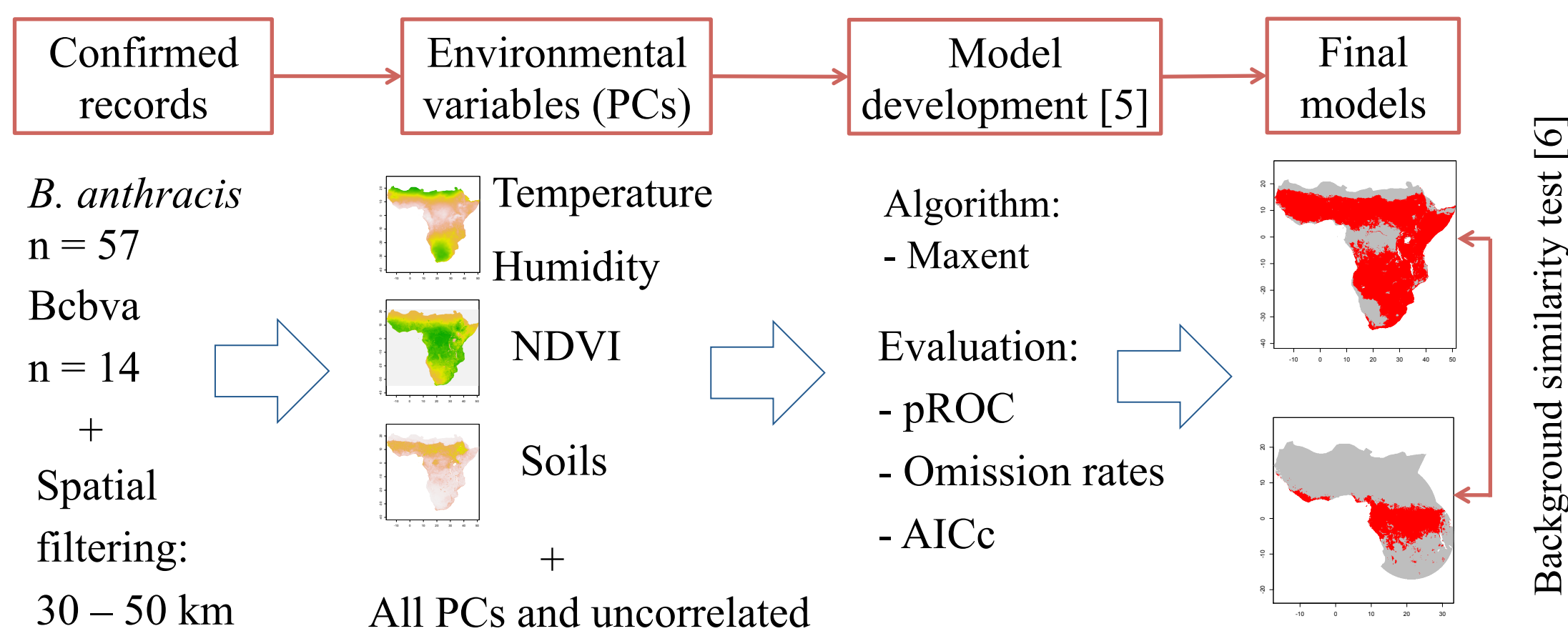
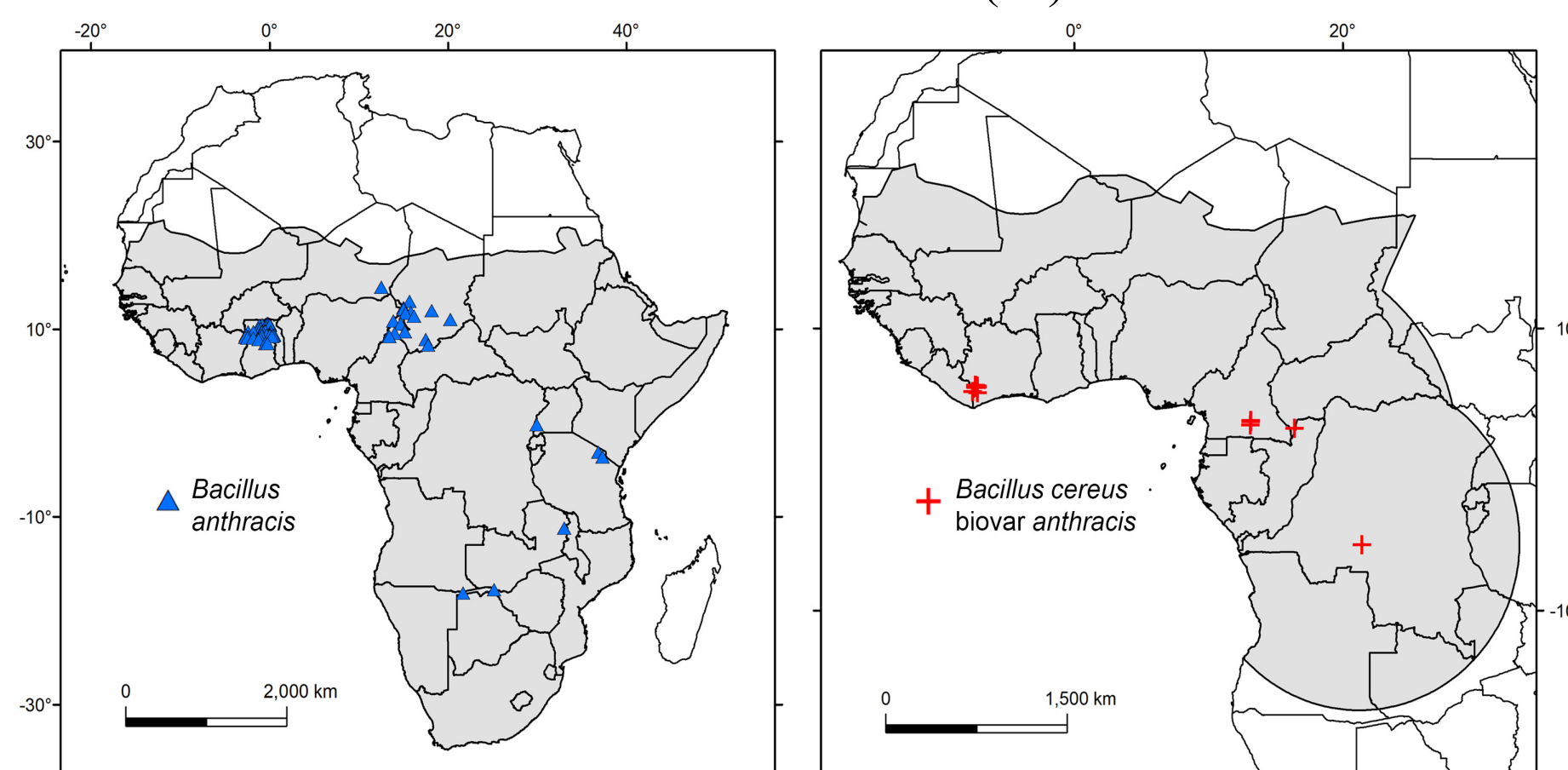


Bacillus anthracis is a well-known zoonotic bacterium that is the etiological agent of anthrax, also known as ‘Virgil’s plague’ is a disease that causes deadly infections in mammals (including humans), posing an important medical and economic burden worldwide [1]. Anthrax cases are rarely described in rainforest ecosystems, however in 2001 and 2004-2005 a series of carcass from chimpanzees (*Pan troglodytes troglodytes*) and gorilla (*Gorilla gorilla gorilla*) were identified as anthrax mortalities in forested natural reserves in Côte d’Ivoire and Cameroon [2]. Thus, a detailed molecular, morphological, and microbiological analysis revealed that the etiological agent was actually a new variety of a different *Bacillus* species, *B. cereus* biovar *anthracis* (Bcbva) [3,4]. Details on its ecology and geographic extend remain unknown; here we are using geographical information systems and ecological niche models to describe its potential distribution and to compare Bcbva’s environmental profile with that of *B. anthracis* in Africa.

Methods

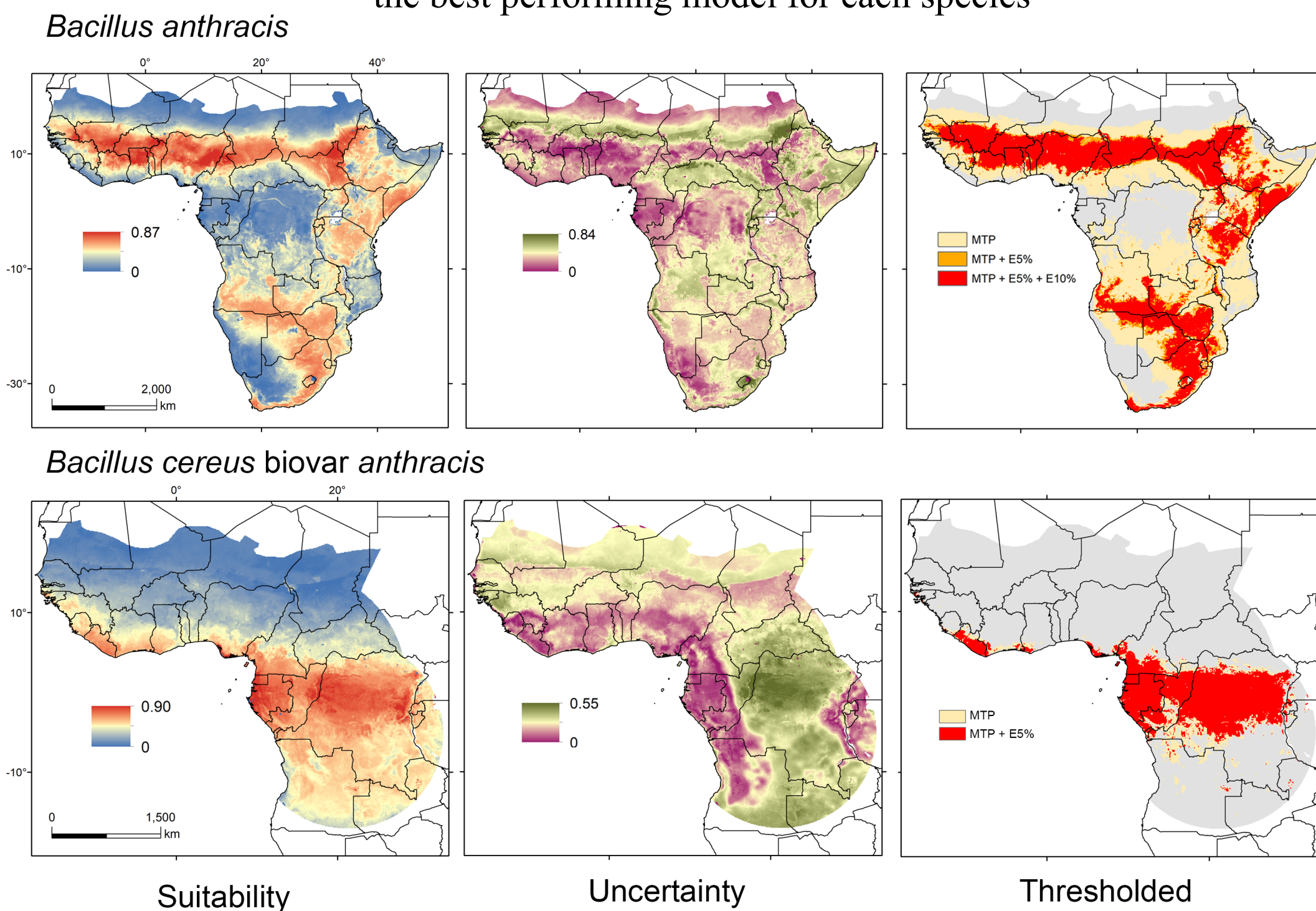


Confirmed records and accessible areas (M) for model calibration



Results & Conclusions

Potential distribution of *B. anthracis* and Bcbva. Panels show the best performing model for each species



Results.–

- We developed a total of 576 models for each species; from them, we depict those models showing the broader prediction with the lowest uncertainty (Occurrences thinned to 30 km with uncorrelated PCs).
- Suitability for *B. anthracis* was predicted in an east-west corridor across northern Africa, the majority of east African countries and in Namibia, South Africa, and Bostwana.
- Suitability for Bcbva was predicted for central Africa in areas neglected by *B. anthracis* models. Further, small regions of suitability were found in Liberia and southern regions of Ghana, Nigeria and Côte d’Ivoire.
- Our models suggests that *B. anthracis* could be using a different set of climates (temperature and humidity) and soils than Bcbva.

Conclusions.–

- To the best of our knowledge this is the first attempt to map the potential distribution of Bcbva.
- In-field surveys could be developed in areas identified by our models to collect Bcbva samples in order to develop reliable and easy-to-apply diagnostics for livestock, wildlife, and possibly humans.
- Although no human cases of anthrax due to Bcbva have been identified, cases reported along ecological transitions from forested to savanna habitats should be investigated thoroughly for correct diagnoses.

Acknowledgements

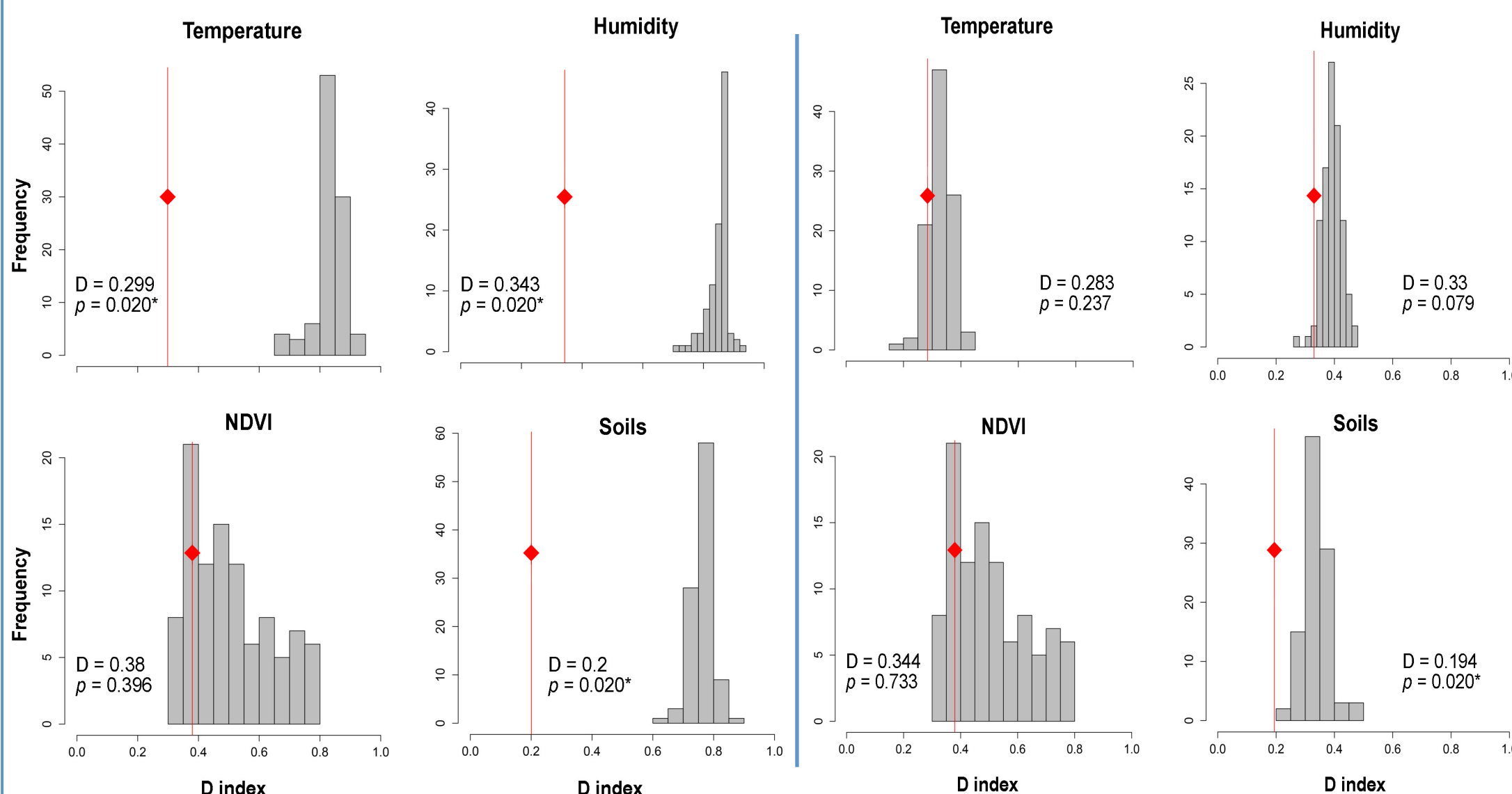
Models for this project were developed using the R package ‘[ku.enm](https://github.com/marlonecobos/kuenm)’ developed by Marlon E. Cobos (<https://github.com/marlonecobos/kuenm>)

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Comparison of each environmental profile between the species involved

B. anthracis vs. Bcbva



Bcbva vs. B. anthracis

