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Building ecological niche models of Bacillus anthracis with constrained diversity index-defined phylogenies and bespoke environmental covariates across spatial scales

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Ecological niche models (ENMs), including several genetic algorithms and machine learning approaches, are used to prediction the distribution of Bacillus anthracis from local to global scales. Bacillus anthracis, the bacterial cause of anthrax, has a near global distribution limited by specific soil and environmental conditions constraining its range. As a spore-former, B. anthracis can persist for years resulting in repeat outbreaks in areas meeting these ecological conditions. Phylogenetically, B. anthracis is divided into five major lineages and 19 sub-lineages (defined by single nucleotide repeats [SNPs]). Within these sub-lineages, B. anthracis can be differentiated into several genotypes using many typing systems, including variable number tandem repeats (VNTR) in a multi-locus VNTR analysis (MLVA) and core genome multi-locus strain typing (cgMLST). While cgMLST is promising for tracking evolution in local populations, a much smaller subset of strains has been whole genome sequenced, limiting cgMLST value in mapping B. anthracis. In contrast, available MLVA data reflect a larger population of B. anthracis strains in the global collection. Some studies informed ENMs with MLVA-specific sub-lineages and showed environmental and spatial differences. No models have examined which specific VNTRs differentiate spatially, or which spatial scales are best modeled with specific genotypes. Here, we use ENMs, MLVA-25 phylogenies, and constrained-Simpson Indices to model patterns of B. anthracis lineages from global to local with a bespoke remote sensing approach to matching ideal covariates to spatial scales. This integrative approach improved model performance and better explained diffusion and evolutionary patterns across landscapes and a diversity of sub-lineages.

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