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Bioclimatic models estimate areas of suitable habitat for *Armillaria solidipes* in Wyoming

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Armillaria species range from beneficial saprobes to damaging root pathogens, and their ecological roles and impacts vary with environment and host. *Armillaria solidipes* (= *A. ostoyae*) causes tree mortality and significant growth loss in coniferous forests of Wyoming and throughout the world. For *Armillaria* root disease management, it is important to identify species involved and predict their current and potential distributions. The study objective was to identify forest areas at potential risk to disease caused by this pathogen, based on climatic conditions and known occurrence of *A. solidipes*. DNA-based identification and 19 location-specific climatic variables were used to develop models to predict areas suitable for the occurrence of disease caused by *A. solidipes*. Maximum entropy distribution models were based on 1) 39 locations of *A. solidipes* only in Wyoming, and 2) 320 locations throughout western North America. These models will be used to predict geographic distribution of suitable habitat for *A. solidipes* under predicted current and future climates. This information will contribute to habitat-specific management strategies for reducing impacts of this important forest pathogen.

Keywords: *Armillaria* root disease , forests , climate change , DNA-based identification , distribution models

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