Host tree-based scenario modelling for predicting a key edible insect, mopane worm Gonimbrasia belina (Westwood, 1894) distribution in Southern Africa

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Abstract

Gonimbrasia belina, known as the mopane worm, is a large edible caterpillar in tropical and subtropical regions. However, little is known about the bioecology of this species as influenced by its host trees. This study evaluated the importance of different potential host trees in understanding mopane worms' behaviour and spatial distribution. To assess their relative importance, the study compared models incorporating various mopane worm host trees and predictor variables. Using the species distribution modelling (SDM) package in R, an ensemble of random forest (RF), support vector machine (SVM), and boosted regression tree (BRT) algorithms were used to assess the spatial extent of mopane worm distribution in Southern Africa. Four host tree-based scenarios were developed to assess their contribution to the relative distribution of the mopane worm i.e. (1) by excluding all the potential host trees as explanatory variables and considering only the environmental variables, (2) focusing on the primary host tree, Colophospermum mopane as an explanatory variable together with the other environmental variables, (3) incorporating all the host trees, including C. mopane and (4) examining all other host trees excluding C. mopane. Results demonstrated that incorporating all host trees enhanced the models' predictive abilities (mean AUC = 0.87) underscoring the significant impact of the alternative host trees on the mopane worm distribution patterns beyond just the C. mopane. This study highlights the significance of host trees in predicting the behaviour and distribution of mopane worm populations, providing valuable insights and decision-making for mopane worm use as an alternative protein source, conservation efforts, and land management practices.

Keywords: edible insects; ensemble; entomophagy; mopani forest; species distribution modelling