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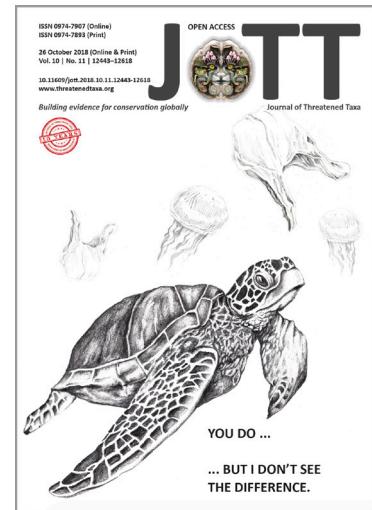
COMMUNICATION

HABITAT DISTRIBUTION MODELING FOR REINTRODUCTION AND CONSERVATION OF *ARISTOLOCHIA INDICA* L. - A THREATENED MEDICINAL PLANT IN ASSAM, INDIA

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Abstract: A detailed study on the regeneration ecology of *Aristolochia indica* L. was carried out to prevent this threatened medicinal plant from its future extirpation in Assam, India. The population stock of the species has been depleting fast in its natural habitats as a consequence of certain factors such as habitat fragmentation, over-exploitation due to its high medicinal properties, and other anthropogenic activities. For improving the conservation status of the species, potential area and habitat for its reintroduction were predicted using Maximum Entropy distribution modelling algorithm. The model was developed using environmental parameters and locality data in the natural range of Karbi Anglong District of Assam, India. The model predicted that the suitable habitats for the reintroduction of *A. indica* L. were restricted to parts of Assam, Nagaland, Meghalaya, and Arunachal Pradesh which have been identified to offer suitable environmental conditions for persistence of the species. Population status was positively correlated with higher model thresholds in the undisturbed habitats confirming the usefulness of the habitat model in population monitoring, particularly in predicting the successful establishment of the species.

Keywords: *Aristolochia indica*, Assam, conservation, habitat distribution modelling, India, MaxEnt, NDVI, reintroduction, threatened.

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Author Contribution: BS carried out the survey and execution of experiments. PSB prepared the manuscript. BT conceived and designed the experiment and critically analyzed the data. All authors read and approved the final manuscript.

INTRODUCTION

Rapidly changing climate, habitat fragmentation & loss, invasion of alien species & pathogens, over-exploitation, and rapid urbanization are the most important factors responsible for ecosystem degradation worldwide that alter the structural and functional integrity of ecosystems (Barnosky et al. 2011; Baruah et al. 2016). In addition to these, rising temperatures and rapid economic development, and can potentially affect ecosystems, rapidly disassemble communities, and negatively impact native biodiversity (Sanders et al. 2003; Lin et al. 2007; Thuiller et al. 2007; Kelly & Goulden 2008; Walther 2009). Such alterations have brought approximately one-fifth of plant species to the brink of extinction (Brummitt & Bachman 2010). Species (re)introduction is one of the successful ecological engineering techniques for the restoration of depleted species populations and degraded habitats & ecosystems (Leaper et al. 1999; Martinez-Meyer et al. 2006; Kuzovkina & Volk 2009; Ren et al. 2009; Rodríguez-Salinas et al. 2010; Polak & Saltz 2011). In order to reintroduce and rehabilitate the threatened species in terrestrial ecosystems, a detailed knowledge on the distribution of their potential habitats is essential. Habitat distribution modeling, therefore, helps to identify the areas for species reserves & reintroduction, and in developing effective species conservation measures. Habitat distribution modeling is a computer-based tool which uses algorithms to relate known occurrences of a species across landscapes to digital raster geographic information system (GIS) coverage summarizing environmental variation across the landscapes to develop a quantitative picture of the ecological distribution of the species. New insights into the factors governing the distribution of species have been developed using habitat distribution modeling or ecological niche modeling (ENM) (Guisan & Zimmermann 2000; Elith et al. 2006; Kozak et al. 2008). The technique of ENM uses computer algorithms that predict species distribution in a geographic space based on the mathematical representation of the ecological niche of the species. ENM considers environmental factors such as temperature, precipitation, soil, vegetation & land cover as ecological conditions and uses the dataset from GIS databases such as www.worldclim.org & www.diva-gis.org. Availability of high-resolution satellite imageries, downscaling tools for environmental variables, and interpolated spatial datasets on climate and vegetation has enhanced the accuracy of prediction of the models manifold. ENM facilitates interpolation as well as extrapolation of species distributions in

geographic space across different time periods. This has made it possible to prepare species distribution maps with a high level of statistical confidence and to identify areas suitable for reintroduction of threatened species (Irfan-Ullah et al. 2006; Martinez-Meyer et al. 2006; Kumar & Stohlgren 2009; Ray et al. 2011; Sarma et al. 2015; Sarma & Tanti 2017).

Identification of suitable habitats for the reintroduction of species is the next logical step in species conservation effort. Therefore, the present work was undertaken to model the potential habitat distribution of *Aristolochia indica* L., a threatened medicinal plant species in northeastern India, in its native range.

MATERIALS AND METHODS

Plant materials

Aristolochia indica L. is a climber which belongs to the family Aristolochiaceae. The plant is a shrubby or herbaceous vine with a woody rootstock (Kanjilal et al. 2009). The leaves are glabrous, variable, usually obovate-oblong to sub-pendurate entire with undulate at the margins, cordate acuminate at the base. Flowers few, in axillary racemes with a perianth upto 4 cm long having a glabrum pale green inflated (Das et al. 2010). It is mostly distributed along tropical, subtropical, and Mediterranean regions of the world (Sarma & Tanti 2015; Neinhuis et al. 2005; Wanke et al. 2007). The plant is used to treat cholera, intermittent fever, bowel troubles, ulcers, leprosy, and poisonous bites (Krishnarajuet al. 2005; Kanjilalet al. 2009). It is also used for its emmenagogue, abortifacient, antineoplastic, antiseptic, anti-inflammatory, and antibacterial properties (Achari et al. 1981; Das et al. 2010).

Habitat distribution modeling

Sixteen primary distributional records of the species were collected through field surveys. The coordinates of all the occurrence points were recorded to an accuracy of 10–40 m using a Global Positioning System (GarminEdge-1000). The coordinates were then converted to decimal degrees for use in modeling the distribution of potential habitats of the species in its native range. Over the years, a variety of environmental datasets have accumulated in public domain websites, which can be used in distributional modeling of species. Use of different formulation of environmental datasets, however, yields different results for the same set of species (Peterson & Nakazawa 2008). Hence, selection of appropriate data type and pixel resolution

is a prerequisite prior to predictive modeling (Parra et al. 2004). In the present study, normalized difference vegetation index (NDVI) was used to summarize the habitat boundaries for the species in northeastern India. All the analyses were conducted at the spatial resolution of 250m.

Validation of model robustness

Following standard methods, the potential habitat of *A. indica* L. was defined as 'a habitat which bears a set of ecological conditions that allows the species to persist and regenerate.' For habitat modeling, the pixel dimension was a 250×250 m grid cell and the model was developed using maximum entropy modeling (Max-Entversion 3.3.3e, Phillips et al. 2006). MaxEnt estimates the maximum entropy probability distribution function to predict the geographic location of a species based on environmental variables and reconstructs the boundaries of the ecological niche by placing constraints on the probability distribution based on the environmental parameters of the grid-cell presence record (Phillips et al. 2006). It is one of the 'presence-only' group of species distribution modeling methods that has been widely used. The strong attributes of MaxEnt are:

- (i) It holds a strict mathematical definition.
- (ii) It gives a continuous probabilistic output.
- (iii) It simultaneously handles both continuous and categorical environmental data.
- (iv) It investigates variable importance through jackknife procedure.
- (v) It has the capacity to handle low sample sizes.
- (vi) Its simplicity for model interpretation (Elith et al. 2006; Phillips et al. 2006; Pearson et al. 2007).

It also facilitates replicated runs to allow cross-validation, bootstrapping, and repeated sub-sampling in order to test model robustness.

Of the 16 records, 75% were used for model training and 25% for testing. To validate the model robustness, we executed 20 replicated model runs for the species with a threshold rule of 10 percentile training presence. In the replicated runs, we employed a cross-validation technique where samples were divided into replicate folds and each fold was used for test data. Other parameters were set to default as the program is already calibrated on a wide range of species datasets (Phillips & Dudík 2008). From the replicated runs, average, maximum, minimum, median, and standard deviation were generated. Model quality was evaluated based on area under curve (AUC) value and the model was graded following Thuiller et al. (2005) as poor ($AUC < 0.8$), fair ($0.8 < AUC < 0.9$), good ($0.9 < AUC < 0.95$), and very good

($0.95 < AUC < 1.0$). Further, potential area of distribution and/or reintroduction were categorized into five classes based on logistic threshold of 10 percentile training presence, i.e., very-high (0.762–1), high (0.572–0.761), medium (0.381–0.571), low (0.325–0.570), and very low (0–0.324).

Population status vis-à-vis model thresholds

Extensive field surveys were carried out in order to explore the robustness and pertinence of the model in predicting the population status of the species in each occurrence locality as predicted under various model thresholds. The total population of the species was ascertained through a direct count of all the individuals of seedlings, saplings, and mature individuals in each 250×250 m grid of occurrence within the predicted localities. The population data of *A. indica* L. in each locality was then correlated with the corresponding threshold level of the distribution models to assess whether regions covered in the higher thresholds maintain higher populations thus approving better habitat conditions for species establishment and vice versa.

Assessment of habitat status and identification of areas for reintroduction

Assessment of the actual habitat type of the species in the localities of occurrence as well as in the entire predicted potential area was done through repeated field surveys. We also superimposed the predicted potential areas on Google Earth Ver. 6 (Deka et al., 2018) imageries for habitat quality assessment. The predicted suitability maps were exported in KMZ format using Diva GIS ver. 7.3 (Baruah et al. 2016). KMZs are zipped Keyhole Markup Language (KML) files that specify a set of features such as place marks, images, polygons, 3D models, or textual descriptions for display in Google Earth. The exported KMZ files were overlaid on satellite imageries in Google Earth to ascertain the actual habitat condition prevailing in the areas of occurrence (Adhikari et al. 2012; Deka et al. 2017).

RESULTS

Calibration of models

The model calibration test for *A. indica* L. yielded satisfactory results ($AUC_{test} = 0.95 \pm 0.002$). The highest percent contribution was given by eu7_1_eur (July), i.e., 29.3%. eu7_1_eur had the maximum influence on the habitat model. Jackknife analysis revealed that

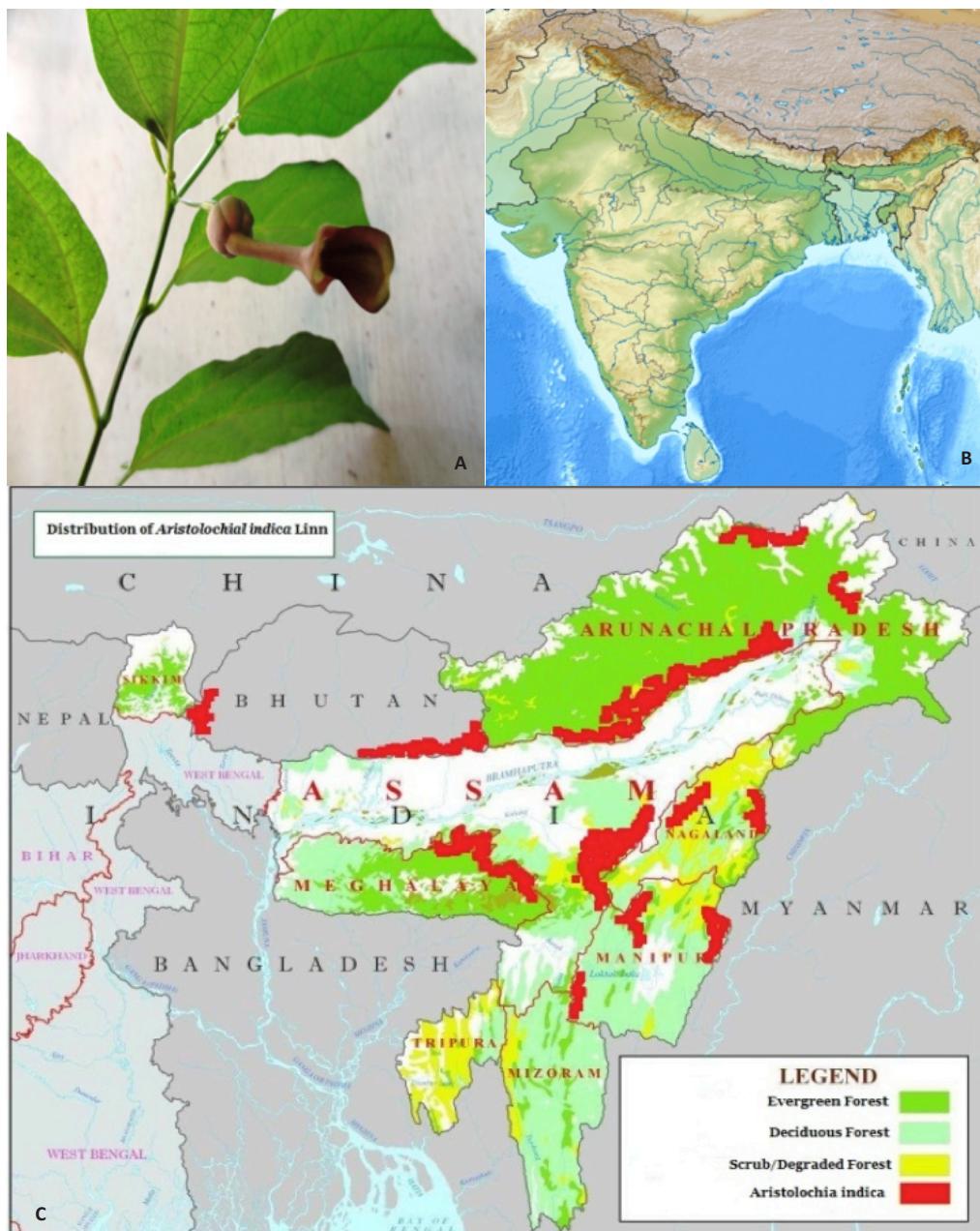


Image 1. A - *Aristolochia indica* L. plant in natural habitat; B - map of India; C - map showing potential habitat distribution of *A. indica* in northeastern India. The red patches in the map represent the occurrence localities of the species.

the environmental variable with the highest gain, when used in isolation, is eu7_1_eur, which therefore appears to have the most useful information by itself. The environmental variable that decreases the gain the most when it is omitted is eu2_1_eur(February), which therefore appears to have the most information that is not present in other variables. Bioclimatic variables did not show any major contribution to the development of the model.

Potential habitat distribution area for reintroduction

In our field survey, we found the species only in some parts of Karbi Anglong District of Assam, India. When we superimposed the data with Google Earth, the suitable habitats where the species can be conserved and reintroduced were distributed in various parts of Assam, Nagaland, Meghalaya, and Arunachal Pradesh. Besides, some areas of Bhutan were also suitable for the reintroduction (Image 1).

Table 1. List of NDVI and variable contribution used in the model

Variable	Percent contribution	Permutation importance
eu8_1_eur	25.7	0
eu7_1_eur	29.3	64.2
eu2_1_eur	20	5.7
eu10_1_eur	12.5	17.3
eu3_1_eur	6.1	1.7
eu11_1_eur	4.5	9.2
eu5_1_eur	1.4	1.2
eu4_1_eur	0.3	0.3
eu6_1_eur	0.2	0.3
eu12_1_eur	0.1	0.1
eu1_1_eur	0	0
eu9_1_eur	0	0

Analysis of variable contributions

Table 1 gives estimates of relative contributions of environmental variables to the MaxEnt model. To determine the first estimate, in each iteration of the training algorithm, the increase in regularized gain is added to the contribution of the corresponding variable, or subtracted from it if the change to the absolute value of β is negative. For the second estimate, for each environmental variable, in turn, the values of that variable on training presence and background data are randomly permuted. The model is re-evaluated on the permuted data and the resulting drop in training AUC is shown in the table, normalized to percentages. As with the variable jackknife, variable contributions should be interpreted with caution when the predictor variables are correlated. Values shown are averages over replicate runs (Table 1).

Figure 1 shows the results of the jackknife test of variable importance. The environmental variable with the highest gain, when used in isolation, is eu7_1_eur, which therefore appears to have the most useful information by itself. The environmental variable that decreases the gain the most when it is omitted is eu2_1_eur, which therefore appears to have the most information that isn't present in the other variables. Values shown are averages over replicate runs (Baruah et al. 2018; Das et al. 2018).

DISCUSSION

Model output and field surveys revealed that suitable natural habitats of the species concurred

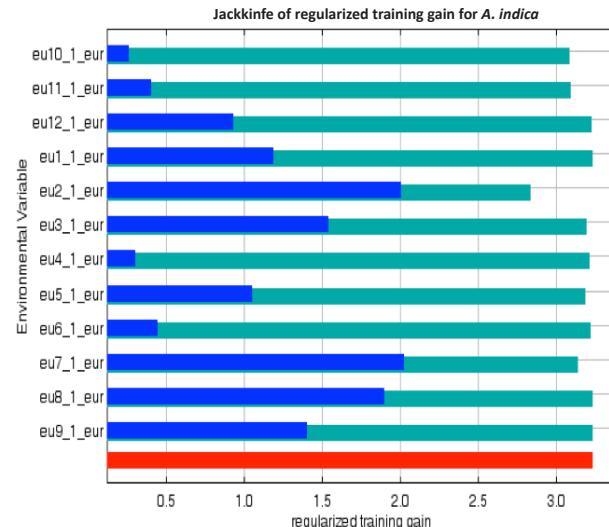


Figure 1. Jackknife test of variable importance for *A. indica* L.- individual variable contribution (blue bar), contribution when a given variable is excluded (green bar), whole set of variables (red bar)

with the distribution of humid subtropical forests. NDVI parameters offered a reasonable explanation on the underlying role of other environmental factors that determined the habitat suitability of the species. Various environmental factors such as geology, soil, and climate have a plausible influence on vegetation indices of a given place at a given time (Soleimani et al. 2008). The effects of such underlying environmental factors are reflected through the spatial and temporal variation in vegetation indices such as NDVI. Hence, NDVI also act as powerful and informative surrogate variables, representing the complex formulations of the underlying environmental factors that determine the boundaries of the potential habitat of species. Overall, the results of actual habitat assessment through Google Earth superimposition and field surveys were identical. Habitat status assessment through primary field surveys and secondary surveys using Google Earth satellite imageries revealed that the predicted potential areas of the species under all suitability threshold levels, i.e., low to very high suitability, encompass a mosaic of disturbed/undisturbed forest patches, scrubs, grasslands, and human-generated land use elements such as rural/urban settlements, settled cultivation areas, homestead gardens, and small groves, which essentially are components of the anthropobiome (Tanti et al. 2010). Species reintroduction plans should therefore carefully select appropriate areas under such a setting. In the present study, some areas consisting of continuous and intact patches of subtropical broadleaved and degraded

forest patches offer potential habitats at higher levels of probability. Hence, such forest areas could serve as habitats for in situ conservation and reintroduction. Predicted less suitable areas such as small groves and homestead gardens, however, could also be used for reintroduction of the species provided that adequate measures are taken for habitat protection. To achieve this, awareness and active participation of local people, non-government organizations (NGOs), and community based organizations are warranted. The present study demonstrates that habitat distribution modeling could be of great help in predicting the potential habitats of threatened species for reintroduction. Results of the study also suggest the strong relationship between the population size and model thresholds, thereby indicating the high potential value of ENM in population studies. The areas identified in the present study for the reintroduction of *A. indica* would not only help in ecorestoration of degraded forests and habitats where the species had existed before but also in rehabilitating the species population and improving its conservation status. Therefore, the results would be quite useful for natural resource managers in the management of this species and conservation of overall biological diversity in the region.

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