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Invasion of the Himalayan hotspot by *Acacia farnesiana*: how the human footprint influences the potential distribution of alien species

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The invasion of alien species in their non-native range has resulted in inevitable consequences. Thus, the potential distribution of alien species must be delineated

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to anticipate and reduce their negative effect on native ecosystems. The potential distribution can be predicted using invasive species distribution models (iSDMs). Thus far, few studies have investigated the human influence on the distribution of alien species when modelling their potential distribution. In the present study, we predict the potential distribution of Acacia farnesiana in the Himalayan hotspot using a popular iSDM. The effect of human influence was studied by comparing the potential distribution predicted using only bioclimatic variables and that using both bioclimatic and human footprint variables. We found that using both bioclimatic and human footprint variables, the potential distribution of target species could be 55.38% larger than that of using only bioclimatic variables. This proves the positive effect of human activities on distribution of invasive species. Among the six considered bioclimatic variables, the mean temperature of the coldest quarter, the precipitation of the coldest quarter, and temperature seasonality are the most influential factors in determining the potential distribution of A. farnesiana.

Keywords: *Acacia farnesiana*, alien species, human footprint, potential distribution.

THE spread of alien species that have been deliberately or unwittingly introduced into new habitats has resulted in inevitable consequences to various native ecosystems^{1,2}. The ecological consequence of alien species is a major one. For example, in South Africa, cattle grazing over the past six centuries has enabled invasive scrub and small trees to displace much of the original grassland, resulting in a massive reduction in forage for native bovid and other grazers³. Since the introduction of rabbits to Australia from Europe, these animals have become the most significant factors contributing to native species loss and have been identified to be responsible for serious erosion problems because they consume surface plants and leave the topsoil exposed and vulnerable to sheet, gully and wind erosion⁴. The invasion of alien species can also adversely affect the following: natural ecosystems^{5,6}, agriculture and forestry production⁷, recreation activities such as fishing, hiking and hunting8, human health9,10 and genetic pollution¹¹

The negative effects of invasive species on various ecosystems can be reduced if detailed information related to the actual distribution of these species is obtained. These negative effects can also be anticipated if the potential distribution of the species is delineated. Although the actual distribution of invasive species cannot be reliably obtained because of the expensive investigation cost, the potential distribution can be modelled using invasive species distribution models (iSDMs). The iSDMs have been used to project the potential distribution of invasive species, investigate the relationship between invasive species and environmental conditions, and provide useful information for conservation planning and ecosystem restoration practices¹. The iSDMs predict the potential distribution in the following way: first, the relationship between species occurrence and predictive variables (biotic, abiotic and anthropogenic) at locations within the native range of the target species is constructed. Then the constructed relationship is applied to the invasive range to obtain the potential invasive distribution¹². However, the relationship constructed in this way may be problematic because the invasive species are capable of adaptation at invasive range. This indicates that the relationship constructed at the native range does not consider the relationship between species and environment condition at the invasive range¹³. As a result, when modelling the potential distribution of invasive species, the presence of samples at the invaded region must be included to delineate the relationship between species and environmental conditions.

The iSDMs can be used in different stages of invasion for different purposes: at the emerging (early) stage, the potential distribution of target species predicted by iSDMs is useful for the conservation planning of native species; at the widespread (late) stage, the geographic range shift of invasive species modelled by iSDMs under changing climate is needed to identify areas in which early warning detection and control programmes are critical to implement. During modelling, the selection of predictive variables lies at the core of the modelling approach because different variables or a combination of variables can lead to varied prediction results¹⁴. The bioclimatic variables, such as Worldclim, have been used to delineate the potential distribution of target species under different climatic conditions¹⁵. Although bioclimatic variables are good predictors and are widely used for modelling the potential distribution of invasive species, they may be insufficient if more reliable predictions corresponding to potential distribution are required because human activities significantly influence the dispersal of species. Bioclimatically suitable habitats could reportedly be affected by intensive and diverse human activities. With the modification of human activities relative to species dispersal strategies, invasive species distributions are likely not at equilibrium with the bioclimatic conditions¹⁶. Among various indicators of human activities, human population density, GDP per capita and real estate gross state product have been shown to be correlated with the distribution of invasive species¹⁷. However, during potential distribution modelling of the invasive species, incorporating only one of these factors with other bioclimatic parameters to generate a predictor dataset is insufficient to delineate the spatial range of the target species¹⁸. As a result, a combination of the proxies related to various human activities may imply more information than separate ones and could thus be used to predict the potential distribution of invasive species.

The Himalayan mountain system, being the longest and the highest among all the mountainous system of the

world, harbours a rich and diverse spectrum of fauna and flora¹⁹. The list of plants native to the Himalayan region is extensive and of potential value. Most of these species are aromatic and medicinal plants used in perfumery and traditional medicine. However, many of these species are currently on the verge of extinction. Their extinction can be partly attributed to the anthropogenic elimination of native vegetation and the subsequent invasion of alien species. Acacia farnesiana, also called Huisache, Opoponax and needle bush, is a woody shrub species native to North and Central American tropics and subtropics that has invaded the Himalayan regions with the aid of direct and indirect human influences. The direct influence includes the introduction A. farnesiana to new habitats for medicine and recreation. Indirect influence was realized through anthropogenic elimination of native species²⁰. Owing to its flexible ecological requirement and high germination rate, A. farnesiana has invaded many of the subtropical and tropical arid lands in the world, including North Africa, Sahel, East Africa, Arabian Peninsula, Pakistan, India, and Australia. The species has since become naturalized in these areas. The invasion of A. farnesiana in the Himalayan region has been reported previously²¹, but a few questions remain: Where will A. farnesiana invade in the near future? Do human activities influence the potential invasion regions of this species? Based on the above observations, the present study aims to: (1) predict the potential distribution of A. farnesiana in the Himalayan hotspot area; (2) identify the most influential bioclimatic variables that can affect the geographic distribution of A. farnesiana, and (3) explore the manner in which the potential geographic distribution of A. farnesiana responds to human activities.

The Himalayan hotspot (71.18-98.40°E, 25.63-36.21°N) lies at the north slope of the Himalayan mountains (Figure 1). The Himalayan hotspot is home to the highest mountains of the world, including Mt Everest. The abrupt rise of the Himalayan mountains from less than 500 m to more than 8000 m, makes it home to diverse ecosystems that range from alluvial grasslands (among the tallest in the world) and subtropical broadleaf forests along the foothills to temperate broadleaf forests in the mid hills, mixed conifer and conifer forests in the higher hills, and alpine meadows above the tree line within only a couple of hundred kilometres^{22,23}. The Himalayan hotspot covers nearly 750,000 sq. km, while the remaining vegetation covers less than 186,000 sq. km. Within the range of the hotspot area, the number of endemic plants, birds, mammals and amphibians is 52, 8, 4 and 4 respectively²⁴

The presence samples of *A. farnesiana* were downloaded from the Global Biodiversity Information Facility (<u>www.gbif.org</u>), which is a data portal that provides open access to scientific data for biodiversity studies, and Global Invasive Species Database managed by the Invasive Species Specialist Group (<u>http://www.issg.org/</u>)



Figure 1. The Himalayan hotspot (71.18–98.40°E, 25.63–36.21°N) lying at the north slope of the Himalayan mountains. Triangles denote the presence of samples within and around the study area.

under the Species Survival Commission of the International Union for the Conservation of Nature. We collected a total of 1981 presence samples (30 within the study area) for A. farnesiana after excluding duplicate samples (only one sample in each pixel). When modelling the potential distribution of target species in the present study, we randomly selected 10% (195) of all the collected presence samples out of the study area (1951) and 30 samples from the study area as the final sample set (totally 225). Such selection strategy could avoid the overfitting induced by too much samples out of the study area and the underfitting induced by relatively less samples within the study area. These presence samples were divided into training (70%) and test (30%) datasets. The environmental variables included a human footprint layer (downloaded from NASA Socio-Economic Data and Application Center (SEDAC, http://sedac.ciesin.columbia. edu/), as well as six temperature- and precipitationrelated layers (downloaded from Worldclim website: www.worldclim.org, including mean diurnal range, maximum temperature of the warmest month, minimum temperature of the coldest month, mean annual precipitation, precipitation of the wettest month, and precipitation of the driest quarter). These variables provide a combination of means, extremes and seasonality that are known to influence species distribution²⁵ as well as the pairwise $r_{\text{Pearson}} < 0.75$ among these variables. The human footprint dataset is the human influence index normalized by biome and realm that is established from nine global data layers which cover human population pressure, land use and infrastructure, and human access (coastlines, roads), among others²⁶. The bioclimatic variables and the human footprint layer were resampled to a resolution of $5 \text{ km} \times 5 \text{ km}$ (0.0417 arc degree).

The potential distribution of A. farnesiana was predicted using the Maxent model, which employed the maximum entropy principle to discriminate a suitable geographic range for the distribution of target species associated with the presence of species from an unsuitable range associated with absences²⁷. The required data for the model included geographic locations of the presence samples of the target species and environmental variables in grid format. All collected presence samples (including samples within and around the study area) were used to determine the relationship between species and environmental condition. The model (version 3.3.3k) was run on default settings as follows: random test percentage = 25, regularization multiplier = 1, maximum number of background points = 10,000 and replicates = 10. The replicated run type was set as bootstrap. The prediction result of the Maxent model was converted from probability values to Boolean values (1 for predicted presence and 0 for absence), and the sensitivity plus specificity derived from the error matrix was maximized during the conversion²⁸. The model was run based on two sets of environmental variables to study the influence of human activities on the potential invasion of A. farnesiana. These include one with only the aforementioned six bioclimatic variables and another with seven variables that also include the human footprint layer aside from the six bioclimatic variables. The performance of the Maxent model was evaluated

The performance of the Maxent model was evaluated using the True Skill Statistic $(TSS)^{29}$. In recent years, the performance of the Maxent model is usually evaluated using the area under receiver operating character curve (AUC), which is suitable for evaluating the performance of species distribution models with continuous outputs. However, this method is under criterion because in a case

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Figure 2. Potential distribution of *Acacia farnesiana* predicted based on only bioclimatic variables (top) and on both bioclimatic variables and human footprint (bottom).

in which the occurrence samples are localized in a small area and have a small prevalence, a high AUC value will be obtained. Meanwhile, the TSS value is unaffected by the prevalence of the occurrence point or the size of the study area³⁰. The TSS value ranges from -1 to +1, where +1 indicates perfect agreement, and values of 0.4 or less indicate a performance no better than random. The performance corresponding to TSS values of 0.4–0.5, 0.5–0.7, 0.7–0.85, 0.85–0.9, and 0.9–1 is correlated to fair, good, very good, excellent and perfect respectively³⁰.

The TSS value for the Maxent model prediction with only the six bioclimatic variables is 0.714, whereas for prediction with the bioclimatic variables and human footprint layer, the TSS value is 0.734. These two values demonstrate that the predictions are reliable.

The general potential geographic distributions of *A*. *farnesiana* that are predicted using two datasets (only bioclimatic variables and both bioclimatic variables and human footprint) are similar, that is, the environmental condition at lower altitudinal regions is relatively more suitable for *A*. *farnesiana* than that at higher regions (Figure 2). In comparison, the potential distributions of *A*. *farnesiana* that are predicted using only bioclimatic variables cover a relatively narrower geographic range than the potential distribution predicted using both bioclimatic variables and human footprint layer (Figure 2). The land

areas of the former and latter ranges are 240,572 and 373,800 sq. km respectively. This finding indicates that with the influence of human activities, the potential distribution of target species could be 55.38% larger than that of under the climatic condition.

A more detailed comparison is displayed in Figure 3. The grey-shaded regions are similar predictions (suitable or unsuitable) of Maxent that are made using two predictor datasets. These regions show similar results (suitable or unsuitable) between two predictions. The ambershaded regions denote areas predicted to be suitable based on both bioclimatic variables and human footprint, but unsuitable based on only bioclimatic variables. The blue-shaded regions denote the areas predicted to be suitable based only on bioclimatic variables, but unsuitable based on both bioclimatic variables and human footprint.

The contributions of these predictors (six bioclimatic variables and the human footprint layer) reveal their on the potential distribution of the target species. For prediction based on only six bioclimatic variables, the minimum temperature of the coldest month, the precipitation of the driest quarter, and mean annual precipitation are variables with the highest contributions (with more than 10% of contribution) at 68.7%, 14.5% and 10.7% respectively, for a total contribution of 93.9%. Meanwhile, when the human footprint layer is included, the variables



Figure 3. The difference between potential distribution of *A. farnesiana* based on only bioclimatic variables and on both bioclimatic variables and human footprint. The grey-shaded regions show similar results (suitable or unsuitable) between two predictions. The amber-shaded regions denote areas predicted to be suitable based on only bioclimatic variables, but unsuitable based on both bioclimatic variables and human footprint. The blue-shaded regions denote the areas predicted to be unsuitable based only on bioclimatic variables, but suitable based on both bioclimatic variables and human footprint.

with the highest contributions are minimum temperature of the coldest month, human footprint and mean annual precipitation at 62.1%, 11.4% and 11.2% respectively, for a total contribution of 84.7%.

Although the predictions of potential distribution of A. farnesiana were based on two different predictor sets, the minimum temperature of the coldest month contributed the most during these two predictions, which indicates that the minimum temperature of the coldest month is a key bioclimatic variable in determining the geographic distribution of A. farnesiana. Similar studies also found a significant decrease in model performance when the minimum temperature during winter was excluded from the predictor $set^{31,32}$. It was also reported that woody plants of temperate regions commonly require a winter chilling period for rapid budburst the following spring³³. In addition to the temperature constraint, the potential distribution of A. farnesiana is also determined by mean annual precipitation, which fulfils the moisture requirement of plant growth. However, the seasonal distribution of annual precipitation can significantly affect the severity of drought experienced by plant species³⁴.

An integrated framework of natural environment and human activities has the potential to explain how ecosystems emerge from the continuous interactions between human and ecological processes³⁵. As shown in this study, the potential distribution of the species delineated using only six bioclimatic variables covers 240,572 sq. km within the study area, whereas the land area of potential distribution increased to 373,800 sq. km with the introduction of human footprint layer. Additionally, the contribution of the human footprint layer can exceed that of bioclimatic variables. Thus, this variable must be considered during species potential distribution modelling. Similar studies also highlighted the influence of the environmental factors, land use and human usage on the spatial pattern of invasive alien plant species, reporting that the spatial pattern of invasive alien species is mostly driven by human use, after accounting for environmental factors^{17,36,37}. However, how human activities could influence the distribution of species, that is, either positively or negatively, remains unclear. In this study, we found that the land area of potential distribution of alien species increased when we introduced human activities during distribution modelling. Human activities, including urbanization and agriculture, were also reported to act as a positive factor influencing the invasion of alien species at the initial stage^{17,37}. Given that the invasive species were introduced by humans, who eliminate some of the native species to assist the growth of invasive species, the positive assistance could be amplified because of the rapid reproduction and high dispersal capability of invasive species.

Apart from the bioclimatic and human activities, the distribution of invasive plant species may also be restricted by biotic factors, such as grazing, trampling and fertilization of vegetation³⁸. The intensity of these factors is required and can be spatialized by collecting the quantity and density of vegetation. However, the collection on native (and possibly the alien) vegetation may include misleading information, such that the subsequent modelling of the potential distribution of invasive plant species may be further influenced because of the propagation of errors. Additionally, the competition among native plant

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species may also affect the distribution of invasive species¹². Furthermore, the native competitor must be identified, and information related to its density and distribution must be delineated before modelling the potential distribution of invasive species. Generally, the aforementioned biotic factors can be classified into two categories: the horizontal (i.e. grazing and trampling) and vertical factors (i.e. competition and facilitation). Although the horizontal factors may have a greater influence on fine-scale potential distribution modelling of the species, the vertical factors are also important but on a mesoor macro-spatial scale³⁹.

The equilibrium issue should be considered when modelling the potential distribution of alien species. The equilibrium assumption posits that the modelled species is in equilibrium with its environment^{40,41}. In the studies related to the modelling of the potential distribution of invasive species, the equilibrium assumption does not hold, which means that extrapolation, both temporal and spatial, is problematic. As regards the temporal issue, the equilibrium assumption can be partly fulfiled when a long period of invasive species collection is followed and when the potential distribution of the species is modelled at different stages of invasion³⁵. The basic requirement of this approach are observed data, which correspond to the invasion history of the target species. As regards the spatial issue, the assumption can also be partly fulfiled if the species distribution model is run at different spatial scales, that is, global and regional, and when the output of the global model is used to weigh species occurrence records in the regional model⁴².

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Sono-, photo- and sonophotocatalytic decontamination of organic pollutants in water: studies on the lack of correlation between pollutant degradation and concurrently formed H_2O_2

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The degradation of trace amounts of phenol in water is studied under sono-, photo- and sonophotocatalytic conditions using ZnO as a catalyst. Sonophotocatalytic degradation is more than the sum of the respective sono- and photocatalytic degradation under otherwise identical conditions, indicating synergistic effect. The degradation proceeds through many intermediates and ultimately the parent compound is mineralized. The concentration of concurrently formed H_2O_2 increases and decreases periodically resulting in an oscillatory behaviour. The oscillation is more pronounced in sonocatalysis in which the degradation of phenol and corresponding formation of H_2O_2 are slower. In photocatalysis and sonophotocatalysis, where the degradation is faster, the amount of H_2O_2 is relatively more and the oscillation becomes weaker and tends towards stabilization. However, in all cases the degradation of phenol continues unabated until the mineralization is complete. The stabilized concentration of H₂O₂ is much less than the expected amount based on the degradation of the organic pollutant. Probable causes for the phenomena are discussed.

Keywords: Hydrogen peroxide, phenol, photocatalysis, sonocatalysis, zinc oxide.

ADVANCED oxidation processes (AOPs) based on the generation of highly reactive 'OH radicals which can attack the target molecules and mineralize them eventually to harmless CO₂, water and salts have been widely studied as viable candidates for the removal of chemical and bacterial pollutants from water. Some of these AOPs include wet-air oxidation, radiolysis, cavitation, photolysis, photocatalysis, fenton chemistry and electrochemical oxidation. They can be used either independently or in combination with other techniques in order to enhance the efficacy, economy and safety. In this context semiconductor-mediated sonocatalysis, photocatalysis and sonophotocatalysis have been promising with relatively higher rates of degradation for a variety of molecules^{1–12}. The expected advantage of sonophotocatalysis is the

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