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基于 MaxEnt 模型模拟肯尼亚茜草科河骨木属植物的潜在分布及其在植物志中的应用初探

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摘要: 物种分布模型目前被广泛应用于生物学、生态学和保护生物学的各个领域。该文以肯尼亚茜草科河骨木属(*Afrocanthium*)为例, 利用最大熵模型(MaxEnt)模拟植物在当前气候情景下的潜在分布, 并将这些分布图利用于正在编写的《肯尼亚植物志》中。结果显示, 基于足够的原始标本记录, 模型能够很好地模拟出每种植物的潜在分布区域。相比传统和新一代植物志仅提供标本信息点或是粗略分布图, 《肯尼亚植物志》预采用的潜在分布图, 将为志书使用者提供更加全面、实用的信息。

关键词: 物种分布模型; 气候因子; MaxEnt 模型; 肯尼亚植物志

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Simulating potential distribution of *Afrocanthium* (Rubiaceae) in Kenya based on MaxEnt and its application in the *Flora of Kenya*

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Abstract: Species distribution models are widely used in the fields of biology, ecology, and conservation biology. Taking *Afrocanthium* of Rubiaceae in Kenya as an example, this paper briefly introduces the potential distribution of plants under current climate scenarios using the maximum entropy model (MaxEnt), and the possible use of these distribution maps in the forthcoming *Flora of Kenya*. Results showed that the model well simulated the potential distribution areas of each species based on sufficient original sample records. Compared with traditional and next-generation Floras, which only provide sample information points or rough distribution maps, the potential distribution maps, which will be used in the upcoming *Flora of Kenya*, will provide more comprehensive and practical information.

Key words: Species distribution models; Climate factors; MaxEnt; *Flora of Kenya*

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The distribution range of species along geographical gradients reflects their ecological adaptability, diffusion ability, and evolutionary history, and understanding the spatial distribution patterns of species is one of the core issues in biogeography and macroecology^[1, 2]. Climate and environmental factors are key elements leading to physiological metabolism and biological reproduction in organisms^[3, 4]; therefore, the geographical distribution of species is closely related to climate at the macro scale^[5, 6]. Species distribution models (SDMs) can combine species distribution information and corresponding climatic and environmental information, which can then be used to estimate the distribution of target species. The models have been applied in many studies, such as the distribution of species under climate change, monitoring and management of large-scale natural resources, protection of endangered species, maintenance of biodiversity, and protected area planning, as well as in the prediction of invasive regions of alien species^[7-14].

During the development of SDMs, several modeling tools and methods have emerged. These include Ecological Niche Factor Analysis (ENFA), Maximum Entropy Model (MaxEnt), Generalized Linear Models (GLM), and Generalized Additive Model (GAM)^[15]. Compared with other models, the MaxEnt machine learning algorithm model is one of the most widely used species distribution models due to its fast and straightforward operation and good prediction results. In this model, the potential distribution of species is estimated by fitting the probability distribution with the maximum entropy value based on known sample points and corresponding environmental variables^[16]. Recently, MaxEnt has been used to simulate the distribution of different plants, such as *Asclepias* L.^[8], *Rhododendron* L.^[9], *Canacomyrica monticola* Guillaumin^[17], *Solidago canadensis* L.^[18], *Stipa purpurea*

Griseb.^[19], *Justicia adhatoda* L.^[20], *Cornus kousa* Bürger ex Hance^[21], *Vanda bicolor* Griff.^[22], and *Didymodon* Hedw.^[4]. These studies have played a guiding role in understanding the potential distribution of related species, formulating conservation measures for endangered species, and preventing large-scale spread of invasive species.

The study of flora and plant diversity can be traced back to the publication of *Species Plantarum* by C. Linnaeus in the 18 th century, and the establishment of the taxonomic system using binomial nomenclature and a series of taxonomic hierarchical elements including phylum, class, order, family, genus, and species^[23-25]. Traditional Floras generally record most plant species in a country or specific area, as well as their names (scientific names, generic names and aliases), sources of literature, morphological characteristics, origin, ecological habits, geographical distribution, and economic significance. Also, keys for and descriptions of families, genera, and species are recorded with illustrations or color photographs^[26]. In contrast, iFlora combines modern botany, bioinformatics, molecular genetics, digital image technology, GIS, and remote sensing with computer information technology, which will result in a leap-forward in the development of digital flora and fauna^[27, 28]. Information on the geographical distribution of species is an essential component for readers, yet the vast majority of current Floras or plant monographs only provide sample collection points for each species^[29, 30] or a general distribution map based on lower administrative divisions^[28, 31]. Although this information provides the existing distribution of each species, it does not stipulate the potential distribution of a species, which limits the use of Floras in the management, protection, and control of specific plants.

The *Flora of Tropical East Africa* is the most comprehensive plant taxonomic publication co-

vering the three East African countries (Kenya, Tanzania, and Uganda). It was compiled over 60 years and finally completed in 2012, recording some 12 500 species of vascular plants in the area^[32]. Following the completion of the *Flora of Tropical East Africa*, a large-scale project to publish the *Flora of Kenya*, jointly initiated by botanists in both China and Kenya, began in 2015, which plans to record ~7000 – 8000 species of Kenyan plants over the next 10 to 15 years^[32]. Based on the functional orientation of this project, that is, accurate identification, precise arrangement, and easy access and guidance by the Kenyan people, we hope that the *Flora of Kenya* will provide potential distribution maps of most species using species distribution models based on existing distribution information from specimens and field investigations.

In Kenya, there are presently 265 species in 74 genera in Rubiaceae, which is the sixth largest family of angiosperms. These numbers may reach more than 280 species in 80 genera based on recent investigations and statistics^[32]. Members of *Afrocanthium* (Bridson) Lantz & B. Bremer were documented in the *Flora of Tropical East Africa* as *Canthium* subg. *Afrocanthium* Bridson, which was given a generic rank by Lantz

and Bremer in 2004^[33]. There are about 17 species of this genus restricted to eastern and southern tropical Africa and South Africa, five of which are found in Kenya, namely *Afrocanthium keniense* (Bullock) Lantz, *A. kilifiense* (Bullock) Lantz, *A. lactescens* (Hiern) Lantz, *A. peteri* (Bridson) Lantz, and *A. pseudovercicillatum* (S. Moore) Lantz. Except for *A. peteri*, with only four specimens in collection records, we attempt to simulate the distribution of the other four species of *Afrocanthium* with more than 20 collection entries based on existing distribution points using the Maximum Entropy Model (MaxEnt). Furthermore, we discuss the application of species distribution simulation in Flora publication, which will provide guidance for the compilation of the *Flora of Kenya*.

1 Materials and Methods

1.1 Study area

Kenya is a coastal country in the eastern part of the African continent. It is located in the equatorial region from 34° to 42° E, bordering Somalia in the northeast, Tanzania in the south, Uganda in the west, Ethiopia in the north, South Sudan in the northwest corner, and the Indian Ocean in the southeast (Fig. 1) ^[34].

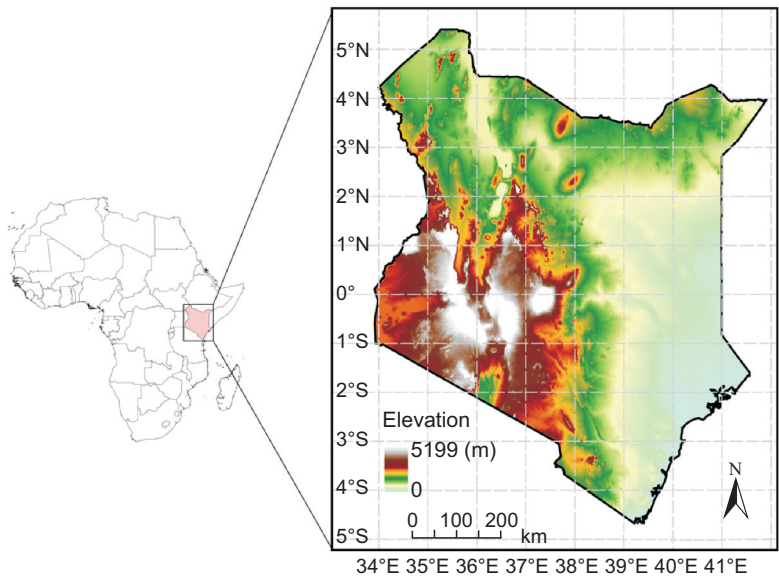


Fig. 1 Locality and elevation map of Kenya

1.2 Data sources

We compiled a comprehensive distribution database for the four *Afrocanthium* species by extracting information from specimens including collection date, location, longitude, latitude, and altitude. Most specimens were kept in the East African Herbarium (EA) and Kew Herbarium (K), with information also obtained from online databases, such as the Global Biodiversity Information Facility (<https://www.gbif.org/>). As SDMs can exhibit significant deviations from the simulation results of species with little information on distribution, we deleted data of *Afrocanthium petersi*, given there were only four records. Finally, 133 valid and accurate distribution information points were obtained.

1.3 Climate data

In total, 19 bioclimatic variables were downloaded from the WorldClim database (<https://www.worldclim.org>), i.e., Annual Mean Temperature (BIO1), Mean Diurnal Range (BIO2), Isothermality (BIO3), Temperature Seasonality (BIO4), Max Temperature of the Warmest Month (BIO5), Min Temperature of the Coldest Month (BIO6), Temperature Annual Range (BIO7), Mean Temperature of the Wettest Quarter (BIO8), Mean Temperature of the Driest Quarter (BIO9), Mean Temperature of the Warmest Quarter (BIO10), Mean Temperature of the Coldest Quarter (BIO11), Annual Precipitation (BIO12), Precipitation of the Wettest Month (BIO13), Precipitation of the Driest Month (BIO14), Precipitation Seasonality (BIO15), Precipitation of the Wettest Quarter (BIO16), Precipitation of the Driest Quarter (BIO17), Precipitation of the Warmest Quarter (BIO18), and Precipitation of the Coldest Quarter (BIO19). We first tailored these variables to match our research area using the Extraction mask tool in ArcGIS, then performed correlation analysis for the 19 variables using ENMTools to avoid possible correlation among bioclimatic factors affecting prediction accuracy.

When the correlation coefficient was greater than 0.8, the more biologically significant factor was retained. Finally, eight bioclimatic variables were selected for subsequent analysis, including four temperature-related variables, i.e., BIO1, BIO2, BIO3 and BIO7, and four precipitation-related variables, i.e., BIO12, BIO15, BIO18, and BIO19.

1.4 MaxEnt modeling

The longitude and latitude distribution data of each species (or all genera as a whole) and the eight bioclimatic variables were imported into MaxEnt. We used default settings for MaxEnt parameters and randomly selected 25% of the distribution points as test datasets and 75% as training datasets.

2 Results

Based on the MaxEnt model, under modern climate scenarios, the contribution rates of the eight bioclimatic variables to the predicted *Afrocanthium* distribution area were: BIO2 (28.5%) > BIO19 (26.6%) > BIO12 (16.8%) > BIO13 (11.2%) > BIO7 (5.8%) > BIO1 (5.5%) > BIO15 (5.3%) > BIO18 (0.3%), and the cumulative contribution rate of BIO2, BIO19, BIO12, and BIO13 reached 83.1% (Table 1).

The potential distribution of *A. keniense* was mainly concentrated in the central Kenyan plateau regions (Fig. 2: a), whereas that of *A. kilifiense* and *A. pseudoverticillatum* was concentrated in the eastern coastal plains of Kenya (Fig. 2: b, d) and that of *A. lactescens* was concentrated in central and southern Kenya (Fig. 2: c). Thus, the simulated potential distribution areas for the four *Afrocanthium* species were related to the original sampling data (Fig. 2: e).

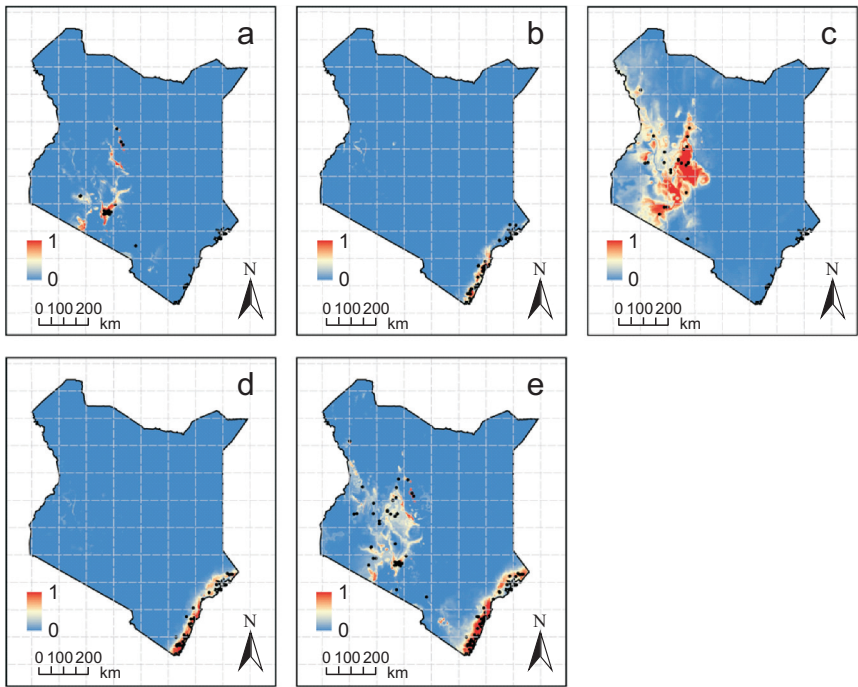
3 Discussion

The topography and physiognomy of Kenya can be roughly divided into four parts: the eastern coastal plain area, northern and northeastern desert and semi-desert area, central plateau area,

Table 1 Contributions of eight climatic factors to prediction of potential distribution areas of *Afrocanthium* species in Kenya

Species	Percentage of contribution (%)							
	BIO1	BIO2	BIO3	BIO7	BIO12	BIO15	BIO18	BIO19
<i>Afrocanthium keniense</i>	22.2	1.9	7.1	2.4	4.0	14.9	30.8	16.8
<i>A. kilifiense</i>	2.7	39.5	26.9	0.0	1.3	0.0	0.6	29.0
<i>A. lactescens</i>	47.3	8.3	0.2	0.4	4.9	4.9	0.0	33.9
<i>A. pseudoverticillatum</i>	0.0	38.5	23.2	2.3	1.4	0.0	0.6	34.0
Total genus	5.5	28.5	11.2	5.8	16.8	5.3	0.3	26.6

Note: Bold numbers are two climatic factors showing the greatest contribution to each species.



a; *Afrocanthium keniense*; b; *A. kilifiense*; c; *A. lactescens*; d; *A. pseudoverticillatum*; e: Superposition of potential distribution area and sampling points for all four *Afrocanthium* species.

Fig. 2 Potential distribution maps of *Afrocanthium* (Rubiaceae) species in Kenya based on species distribution model (MaxEnt)

and southwestern lakeside plain area. Although the potential distribution of different species of *Afrocanthium* was affected by different bioclimatic variables, the two most important ones affecting each species were temperature- and precipitation-related variables (Table 1). This indicates that temperature and precipitation are the main factors affecting the geographical distribution of *Afrocanthium* in Kenya, and also supports the idea that these climatic factors determine species distribution at the large-scale^[35]. The simulated potential distribution area of *A. kilifiense* and *A. pseudoverticillatum* was located along the eastern

coastal plains of Kenya, which is a narrow plain that runs along the Indian Ocean coast from north to south, with a width of about 30 – 50 km and an elevation of not more than 180 m above sea level^[34]. As a hotspot of global biodiversity, this region is one of the most diverse areas in Kenya and harbors a large number of coastal plants^[32, 36]. In regard to *A. keniense*, the simulated potential distribution area was mainly in the central Kenyan plateau regions, mostly > 1500 m above sea level. The central part of this region is transected by the Great Rift Valley of East Africa from north to south, forming the eastern and western pla-

teaus. Most of the alpine and plateau lakes in Kenya are also concentrated on both sides of the Great Rift Valley^[32]. For *A. lactescens*, the simulated potential distribution area was concentrated in central Kenya (Eastern Nairobi) and southern Kenya (Masai Mara). Only a small number of *Afrocanthium* specimens were collected from the semi-desert area of northern Kenya, including *A. peteri*, which was not simulated due to the small number of specimens. Thus, it can be concluded that the main distribution areas of this genus in Kenya are the eastern coastal and central plateau areas, which is closely related to their suitable temperature and precipitation, as well as complex topography and landform.

Statistical analysis of more than 6000 previously published papers showed that, in the past 20 years, species distribution models have been widely used in many areas, including climate change, biodiversity conservation, habitat restoration, and species migration^[37]. There has been a substantial upward trend since 2005 due to the rapid development of computer technology and statistical science, as well as the sharing and acquisition of data such as geological, remote sensing, global 156 elevation model, and climate interpolation data^[15, 37]. In recent years, many researchers have used species distribution models and related software to predict suitable habitat or potential distribution of species, especially the prediction of new distribution regions for endangered species^[14]. Researchers have even conducted supplementary field surveys based on model results and revised the simulations by combining study results^[38]. It should be noted that based on sufficient original records and detailed climatic and environmental data, the distribution model can simulate current distribution areas of some species with wide distribution ranges^[37]. The potential distribution maps of these species can provide a more detailed and valuable reference for researchers than relying solely

on information maps of distribution points.

Floras of a country or given region should be a summary of all plant data in the area, providing crucial information and a scientific basis for the rational development and utilization of plant resources. Since its launch in Montreal, Canada, in May 2012, next-generation intelligent Flora (iFlora) integrates modern botany, DNA sequencing, and information technologies to provide botanical experts, government departments, industries, and the public with convenient and accurate identification of plants and access to relevant information^[28]. However, the absence of fine or potential distribution maps for each plant in both classical and next-generation Floras has dramatically reduced the amount of information provided by such publications. Based on existing sample information, the potential distribution of each plant could be simulated by species distribution models and combined with field survey data, and the obtained plant distribution maps could be fully adopted in the compilation of new Floras.

Several researchers in Kenya have used MaxEnt to simulate the potential distribution of individual species. For example, Kuria *et al.*^[39] used 270 distribution points of *Strychnos heningsii* Gilg, an endangered medicinal plant of Loganiaceae, to simulate its potential distribution areas and found that the arid low-altitude regions of Kenya, such as the coast, Masai Mara, and Marsabit, are ideal for *ex situ* conservation of this species. This indicates that the species distribution models have a specific practical basis in Kenya. Thus, as an international cooperation project, the compilation of the *Flora of Kenya* could maximize the use of such models. This is to say, we could use species distribution models to model the potential distribution areas for most plants with a wide range of distribution and a large number of specimens (e.g., Fig. 2: a–d), and even simulate the overall distribution of a genus or family (Fig. 2: e). At the same time, to

take into account the sample information points used by the compiler, it is suggested that superimposed maps of the simulated distribution and sample collection points should be cited in the process of compiling floras. This would not only reflect the actual distribution locations but also the potential distribution of species in the relevant areas.

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