Mapping priorities for conservation in Southeast Asia

A.C. Hughes

Landscape Ecology Group, Centre for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Menglun, Xishuangbanna, Yunnan 666303, China

A B S T R A C T

Southeast Asian biodiversity is a global priority for conservation, due to the high levels of diversity and endemism, combined with some of the greatest levels of threat. Conservation planning is essential to ensure that hotspots of biodiversity and endemism have the protection needed to prevent deforestation, hunting and other forms of exploitation in some of the Southeast Asia's most diverse areas, yet this requires data which in many cases does not exist.

Growing volumes of online available data provides the ability to develop accurate models of species distributions, and gain new perspectives on regional diversity patterns and provide essential baseline data for planning and conservation.

Here, using the best available information I develop maps of the ranges of 2471 vertebrate (birds, mammals, reptiles and amphibians) and 1198 plant species, and explore patterns of biodiversity and the adequacy of protection. Each taxon shows different patterns of diversity, and no taxa provided an effective surrogate for diversity patterns in different groups. I show that for the majority of biodiversity hotspots fall outside protected areas, with between 10 and 55% of areas with at least >75% of the maximum number of species unprotected. The percentage of species ranges protected areas also varies by taxa, from a maximum of 40% to reptiles with a mean of only 13.5% of species ranges protected. Furthermore comparison between my predictions and IUCN maps of diversity differed greatly for all taxa examined, with IUCN hotspots covering a much larger portion of the region and potentially overestimating the ranges of many species. Further efforts are needed to better protect centres of diversity, and the inclusion of these methods into regional conservation planning may greatly assist in increasing the effectiveness of conservation.

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1. Introduction

Southeast Asia is a global biodiversity hotspot (De Bruyn et al., 2014), however relative to other parts of the tropics there has been considerably less research across much of the Southeast Asian region (Martin et al., 2012). Southeast Asian biodiversity patterns are also highly complex, reflecting the complex biogeography of the region and demarcated and partitioned by a number of biogeographic divides (Hughes et al., 2011; Barley et al., 2015). The lack of baseline data, and limited surveys and inventories (both spatially and taxonomically) make assessing the efficacy of protected areas in protecting biodiversity highly challenging (Collen et al., 2008). In recent years the rate of species description across the region has continued to rise (Chapman, 2009), and groups analysed in detail show high rates of crypsis and taxonomic uncertainty, for example only around 50% of Southeast Asian bat species have officially been classified (Francis et al., 2010).

However the Southeast Asian region is also an undisputed hotspot of threat (Wilcove et al., 2013) and the global hotspot of threat to mammals (Schipper et al., 2008). The drivers of these threats are complex; however hunting and deforestation are among the most devastating to regional biodiversity (Hughes, 2017, Harrison et al., 2016). The region also has the highest rates of deforestation globally (Rosa et al., 2016) and some of the highest levels of landscape destruction and degradation of all global biodiversity hotspots (Sloan et al., 2014). This is especially troubling given the high regional endemicity and the potential loss of species given that Southeast Asia includes 4 of the 34 world biodiversity hotspots (De Bruyn et al., 2014).

For the majority of species across Southeast Asia there is no reliable source of range data (Verde Arregoitia, 2016), as no published data, or rigorous taxonomic data exists for the majority of species with a body size too small to be accurately be classified by camera traps (most rodents, insectivores, bats, amphibians and reptiles (Rovero et al., 2014; Ahumada et al., 2011, 2013; Beaudrot et al., 2016)). Developing regional priorities for conservation, or evaluating the adequacy of current protection on species relies upon having enough data on which to base these decisions. However with such high uncertainty in species

E-mail address: Achughes@xtbg.ac.cn.

distributions combined with rapid drivers of species loss; an evaluation of the adequacy of current protected areas is essential.

Multiple mechanisms have been advocated to develop these priorities, but the use of indicator taxa in the lieu of more complete knowledge of biodiversity patterns is one of the most widely utilised (Rodrigues and Brooks, 2007). Typically priorities have been based upon "charismatic" and easily fundable species such as the tiger (Smith et al., 2012), yet analysis shows that these "landscape species" are particularly poor surrogates of biodiversity (Jones et al., 2016). Therefore other methods to explore biodiversity patterns and develop appropriate targeted conservation strategies may be effective to the long-term survival of many species.

Given that no reliable maps exist for the majority of species, a possible way to make the best use of existing data is to collate distribution data and through combining it with environmental layers of various facets of the environment, to project the ranges of species across the region (Guisan et al., 2013; Platts et al., 2014). Once individual species distribution maps have been created it is possible to use these predicted distribution maps to ascertain centres of biodiversity, and then assay the adequacy of protected areas in these regions to explore the level of coverage and ensure that biodiversity hotspots are adequately protected. Endemism is another important point to be considered, and conserved; however mapping endemism relies on taxonomic data which does not yet exist for many of small mammal and amphibian species.

To secure a future for these species and ecosystems, protection is needed; both for biodiversity hotspots, and centres of endemism (Orme et al., 2005). Assaying the protected area coverage of biodiversity centres for these taxa is essential. Factors such as deforestation, hunting, mining, reservoir construction and numerous other factors act at higher rates and intensities outside protected areas on the majority of occasions, and as many of these species are already known from only small areas they are significantly at risk if their range does not fall within any protected areas (Li et al., 2016).

Here I explore how current knowledge of species ranges based on IUCN "expert drawn" maps compares to those produced through species distribution models and discuss the potential limitations, assumptions and challenges of both utilising both approaches. Using these two methods of exploring spatial patterns of biodiversity I compare the results, and explore the possibility of using any of the major taxa analysed (amphibians, birds, mammals and reptiles) as surrogate indicators for other taxa.

We also explore the distribution of biodiversity hotspots for four major vertebrate groups, in addition to non-flowering plants. Once biodiversity hotspots have been compared I then explore the level of protection, both for biodiversity overall and in terms of protected area coverage for each species for which sufficient data exists. Ultimately I discuss strategies for better protecting the biodiversity of one of the world's often forgotten biodiversity hotspots, and make recommendations for new spatial priorities and for sensitive approaches which provide a more effective mechanism for protecting regional biodiversity.

2. Materials and methods

2.1. Species distribution records

Distribution data for all taxa for the last two decades were downloaded from GBIF and cleaned to remove all suspect records for all birds, mammals, reptiles and amphibians for the mainland Southeast Asian region. Additional data for bats was included using the database compiled by Hughes et al. (2012), in addition to further data for China (Zhang et al., 2009, 2010). Duplicate records (i.e. repeated records of a species at a single locality) were removed from analysis, species with three or less points were also removed. Small sample sizes for species were included because this analysis seeks to optimise the retention of biodiversity by focussing on the most diverse areas, rather than on

each species individually. Species range predictions using low numbers of localities will be conservative and are likely to be smaller than actual ranges, they may to a degree "cancel out" errors in other maps with similar errors, and will help define biotic hotspots. Once species with 1–2 records and duplicates (multiple captures of a species at the same site) were removed there was 12,928 records for 308 species of mammal (average 41.97 records per species) 14,642 records for 304 species of amphibian (average 48.16 records per species) 1941 records for 83 reptile species, and 286,603 records for 1820 species of birds. A selection of non-angiosperm plants were also analysed including 11,690 localities for 1198 species. Details of the exact number of records per family are available in Supplements 1.

2.2. Environmental layers

GIS layers for the whole of mainland Southeast Asia were compiled using a number of data sources, and scaled to 1 km resolution grids for the whole study area. Attention was made to try to include variables that sufficiently represented the conditions encountered by individuals of each species, to try to develop more "accurate" maps of each species distributions. During this analysis the following layers were used: aridity, potential evapotranspiration, a number of bioclimatic layers (bio1, bio12, bio13, bio14, bio15, bio2, bio3, bio4, bio5, bio6), canopy height, elevation, standard deviation of elevation variability using high resolution data, distance from karsts (digitised by hand for the region, and calculated using the path distance function in Arcmap), vegetation cover, humidity, lights at night (for 2012), net primary productivity (annual standard deviation in monthly primary productivity), population density, distance from rivers, and soil pH. Data sources are available in Supplements 2.

Environmental variables were selected to represent the conditions species experience based on their tolerances and dependencies. In the case of the bioclimatic variables I aimed to retain all factors which are likely to either be directly physiologically limiting, or to change access to important resources, whilst minimising the correlation between variables. Some bioclimatic variables are likely to show high levels of redundancy due to correlations between different bioclimatic variables. Therefore all bioclimatic variables were tested using a correlation matrix developed by using spatial principal component analysis in Arcmap. In cases where a variable was likely to have lower explanatory ability or relevance (i.e. minimum temperature of the coldest quarter compared with the minimum temperature of the coldest month) or correlated with a large number of other variables (i.e. daily temperature range) redundant bioclimatic variables were removed, and the remaining bioclimatic variables used (as listed above).

Initial vertebrate models showed bias due to increased sampling effort in the vicinity of roads (and thus correlated with lights at night), and as a result three vegetation layers were created to replace the lights at night layer and better elucidate the relationship between species and habitat requirements, whilst minimising observer biases. Three "vegetation intactness" layers were created, percentage coverage of forest per km^2, distance to forest and mean tree density per km^2.

Forest was mapped using continuous 30 m resolution tree density data (Sexton et al., 2013) combined with road data (open street map) and deforestation data (Global forest watch: www.globalforestwatch.org). 30 m resolution continuous tree cover data was downloaded from 2005 imagery data and tiled using the "mosaic to new raster" function in Arcgis. Areas which had been deforested between 2000 and 2014 and roads were then removed using spatial analyst tools. Three different vegetation layers were then created from this updated 2014 tree density map. To create a forest layer the continuous tree-cover layer was reclassified to forest and non-forest using 60% tree density as a minimum threshold to signify forest cover. This threshold was selected because when maps of rubber (Li and Fox, 2012) were used to test for