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An assessment of the efficiency of protection status through determinations of biodiversity hotspots based on endemic bird species, Taiwan

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ABSTRACT

Evaluations of species richness patterns have been performed at diverse scales, and biodiversity hotspots, especially endemism hotspots, have received much attention in conservation biology. We estimated the distributions of endemic bird species based on a 12-yr avian inventory project in Taiwan, identified biodiversity hotspots of endemism on a regional scale based on predictions from the ensemble forecasting framework and frequency histogram approach, and assessed the efficiency of protected areas. The results indicated that the predicted endemism hotspots were mostly located in mid- and high-elevation areas along the Central Mountain Range of Taiwan. An observed endemism hotspot was defined as one in which at least five of Taiwan's 17 endemic bird species were present. This criterion was used because the 5% of the sampled grid squares that were the richest in endemic bird species all had 5 endemic bird species or more. Seventy to seventy-one percent of the observed biodiversity hotspots matched the predicted biodiversity hotspots. This outcome was obtained whether the richness biodiversity in a grid square was based on summed predicted probability or summed predicted richness. The majority of the protected areas for these Taiwanese endemic bird species were national parks, protecting 24.1% of the predicted hotspot areas, whereas nature reserves and wildlife refuges protected less than 7%. Most of the predicted endemism hotspots were not adequately protected. We conclude that the ensemble forecasting framework and the frequency histogram approach are useful for selecting critical habitats and biodiversity hotspots for endemic species and for appraising the efficiency of the protection status provided by governments.

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Introduction

Worldwide biodiversity levels are in a state of decline (Butchart et al., 2010; Rands et al., 2010; Hoffmann et al., 2011), and the past 60 years have witnessed a steeper decline than that occurring at any previous time in human history (Edwards & Richardson, 2004; Domisch, Jaehnig, & Haase, 2011). Anthropogenic threats, such as pollution, habitat destruction, introduced species, and climate change, are leading to irreversible losses of biodiversity, and ecosystem services are also expected to be affected by these losses of animal or plant species from the food chain (Worm & Emmett, 2003).

Protecting species' critical habitats and biodiversity hotspots (Myers, 1988; Myers, Mittermeier, Mittermeier, da Fonseca, & Kent, 2000) are effective methods of sustaining and increasing biodiversity (Dobson et al., 2006; Schmitz, Hawlena, & Trussell, 2010). Studies have found that in protected habitats, plants and animals are more than twice as likely to move toward recovery as species in unprotected habitats (Myers, 1988; Myers et al., 2000). However, identifying critical habitats and hotspots remains highly challenging because the comprehensive data on species distribution and abundance that are required for such identification are often lacking (Clemens, Weston, Haslem, Silcocks, & Ferris, 2010; Clemens, Herrod, & Weston, 2014). To overcome this limitation, species

distributions are predicted by either (1) associating individual species occurrences with known habitat preferences, constructing relationships between environments and species distribution at the individual species level, and then combining distribution information from different species (Austin, 2002; Elith et al., 2006; Araújo & New, 2007; Elith & Leathwick, 2009) or (2) using a cross-covariance matrix to find linear combinations of environments and a group of species' distributions that have a maximum correlation with each other at the community level (Ferrier & Guisan, 2006; Johnson & Wichern, 2007). Both approaches provide critical but slightly different elements for use in identifying species' critical habitats. A major drawback is that cross-covariance matrices cannot furnish any information about the detailed composition of species community assemblages and/or the biotic interactions that may affect species' spatial co-occurrence patterns, whereas the individual species-level approach can (Baselga & Araújo, 2009; Chapman & Purse, 2011; Dubuis et al., 2011). For this reason, the individual species-level approach (i.e., species distribution models, SDMs) is currently used relatively more widely to estimate species richness and to identify further hotspot locations. Here, we used the individual species-level approach for Taiwanese endemic bird biodiversity.

Species distribution models predict the distributions of species by correlating habitat characteristics with species occurrences (presence only or presence/absence; Elith et al., 2006; Stockwell, 2007). Such SDMs were first applied in terrestrial systems, and the utilization and complexity of species distribution models have increased rapidly. A wide variety of methods associated with SDMs have been developed over the past 20 years and applied to various conservation cases (e.g., Manel, Dias, & Ormerod, 1999; Elith et al., 2006; Ferrier & Guisan, 2006; Araújo & New, 2007; Meynard & Quinn, 2007; Phillips & Dudik, 2008; Baselga & Araújo, 2009; Ko, Lin, Ding, Hsieh, & Lee, 2009; Araújo, Alagador, Cabeza, Nogués-Bravo, & Thuiller, 2011; Chapman & Purse, 2011; Barbet-Massin, Thuiller, & Jiguet, 2012; Wu, Walther, Chen, Lin, & Lee, 2014). The results of individual SDMs are accumulated to estimate modeled species richness. The sum of the continuous probability/suitability values furnished by the individual SDMs represents a direct estimate of total species richness. Alternatively, a threshold for converting continuous probability/suitability values to binary values (presence/absence) can be set for each species, and all individual SDMs are then overlapped to derive a possible value for species richness. On average, the latter (i.e., threshold) approach usually exhibits a statistical artifact that may cause the over-prediction of species richness (i.e., commission errors, Guisan & Rahbek, 2011; Calabrese, Certain, Kraan, & Dormann, 2014). In contrast, the former approach may shape a lower possible species richness due to a low contribution of the species' predicted probability/suitability (although the species may be present) to the sum. To fill the aforementioned gaps, we chose a percentage-based highest scoring prediction of grid locations rather than the traditional number calculated from species-based thresholds to determine predicted species biodiversity hotspots in this study.

The purpose of this study was to (1) use multiple individual-species distribution models and structure a frequency histogram approach to determine the locations of endemism hotspots for bird species in Taiwan and (2) evaluate whether the current protected areas are suitably located. We considered that endemic bird species would furnish an ideal metric and serve well as both conservation concern and critical links to the biotic community within the forest space (i.e., provision of ecosystem functions; Whelan, Wenny, & Marquis, 2008). We interpreted areas with high endemism at a regional scale as biodiversity hotspots (Myers, 1988; Pressey, Humphries, Margules, Vane-Wright, & Williams, 1993; Myers et al., 2000; Orme et al., 2005).
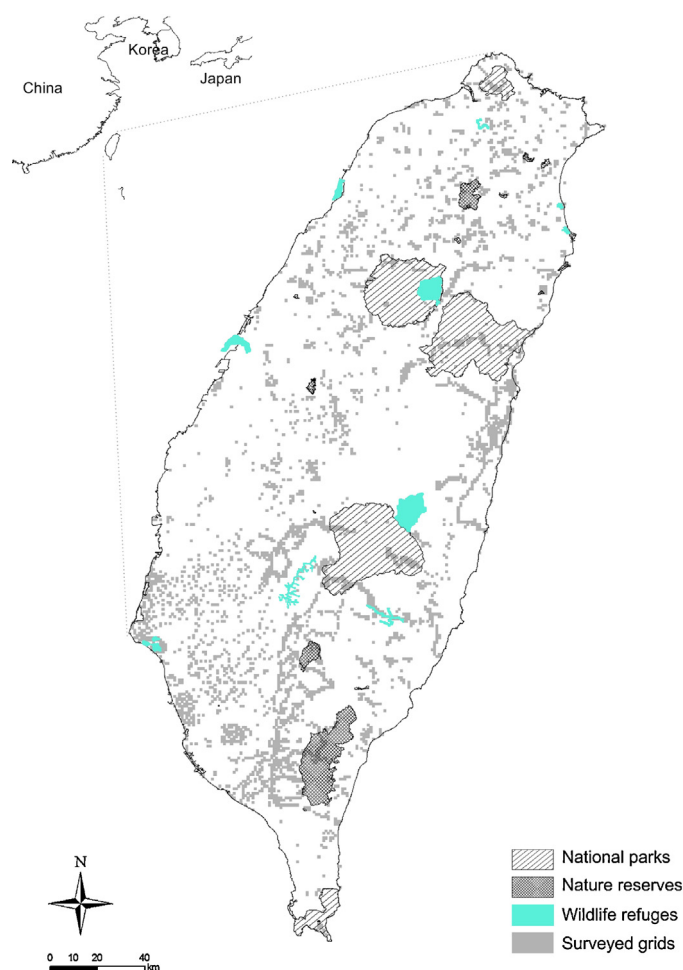

Fig. 1. The location of Taiwan, grid squares surveyed in this study, and protected areas in Taiwan.

Methods

Study area

Taiwan, an island with an area of more than 36,000 km^2, is located in the western Pacific Ocean and the importance of Taiwan's rich variety of endemic species has been noted frequently in Asian and global studies (Fig. 1; Myers et al., 2000; Ceballos & Ehrlich, 2006). Among the taxa belonging to Taiwan's biota, bird species are a well-defined and complex group, and standardized bird inventories in Taiwan have been implemented for more than 10 years (e.g., Koh, Lee, & Lin, 2006). Moreover, the Taiwanese endemic bird species are the subject of frequent studies (Nieh, 1999; Lee, Ding, Hsu, & Geng, 2004; Koh et al., 2006; Ko, Lin, & Lee, 2010; Wu et al., 2014) and are often used as indicators to represent potential patterns of changes that may affect other species (Ko et al., 2009).

Study species

Seventeen endemic bird species were selected in this study (Table 1). Among them, six species are listed as near threatened or vulnerable species on the International Union for Conservation of Nature (IUCN) Red List; http://www.iucnredlist.org/). Fifteen of the bird species were recognized as endemic species before 1990, and the endemic status of the other two species was recently confirmed: the Taiwan Hwamei (*Garrulax taewanus*) in 2006 and the Taiwan Barbet (*Megalaima nuchalis*) in 2008. These species belong