A view from the past: shortwings and sky islands of the Western Ghats[1]

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What are sky islands and how do they affect species?

The Western Ghats in southern India, a 1,600 km mountain chain that runs along the western coast of the Indian peninsula, is a global biodiversity hotspot (Myers *et al.* 2000), and has a wide gradient of elevations. Most of the southern Western Ghats form highest elevation regions of this mountain range rising well above 1,500 m **(Fig. 1)**. There are taxa that are often restricted to, and found only in, these high-elevation regions. For such taxa that never come down to the lower-elevation regions, it is as if they are living on islands, except that these are continental islands. Such islands have been called sky islands that have been defined as a, 'continental or inland terrain made up of a sequence of valleys and mountains,' (Warshall 1994). The critical parameters in these sky islands are the conditions in the valleys and the ecological specificity of the sky island species. If the valleys are ecologically hospitable to some sky island species, they may serve as bridges, but if not, they become barriers. The Western Ghats in southern India is one of the twenty such sky island complexes in the world.

Western Ghats sky islands: what can we expect here?

The Western Ghats are a very old mountain system. The largest geographical gap in this almost-continuous mountain chain is the *c*. 40 km wide Palghat Gap, and the smaller Shencottah Gap, further south of it. Both these geographical gaps are actually shear zones that have existed for over 500 million years. Even the topography of the Western Ghats is relatively very old, having taken shape about 65 million years ago (Ma) (Gunnell *et al.* 2003). This clearly indicates that the geographic canvas for a bird species was already set even before any passerine bird came into this landscape. Passerines are thought to have evolved between 55–60 Ma. The Madrean sky island system in the USA and the Eastern Arc sky islands in Africa are perhaps some of the best-studied sky islands. It is evident from studies here that some species are particularly affected by their geographical isolation while some are not. Most of the high-elevation parts of these mountains, however, have been formed approximately over the last million years making the Western Ghats sky islands some of the oldest formations in the subcontinent. This makes the Western Ghats landscape an interesting region to examine the effect of geographical isolation on sky island species, many of which are endemic to these mountains.

There are clearly two major ways that species could colonise and occupy these sky islands, considering that the islands existed before the birds came.

1. The species or its ancestor arrived at one end of this linear sky island system and hopped from one sky island to the other, eventually colonising all the islands **(Fig. 2A)**.

2. The species or its ancestor could have arrived at the foothills of the Western Ghats and gradually moved up the elevational gradient **(Fig. 2B)**. There is evidence from other sky islands that both these models of colonisation are possible for different species. If the species had indeed used different sky islands as 'stepping stones' to colonise all the Western Ghats sky islands, the populations on the closest islands would be genetically most similar while the northernmost and southernmost populations would be most genetically differentiated. Moreover, in terms of the age of populations, the oldest population would be at one end of this linear sky island system while the youngest, at the other end. It would also be interesting to see how the deep and ancient geographical gaps that typically occur along the Western Ghats affect such species.

The study species: White-bellied Shortwing Brachypteryx major

We chose to investigate the evolutionary history of the White-bellied Shortwing *Brachypteryx major*. It is one among the several threatened, endemic avian species of the Western Ghats that has not been studied scientifically in any detail (Robin & Sukumar 2002). Of the six shortwing species in the world, this is the only one found in southern India and remains restricted to the Shola forests of the Western Ghats. It has also been recently added to the Red Data Book as a globally threatened species (BirdLife International 2001). The nominate race *B. m. major* is found north of the Palghat Gap while *B. m. albiventris,* which mainly differs from it in plumage colouration, is found south of it **(Figs. 3, 4)**. Whether these races interbreed remains an important question although a single museum specimen at the Museum of Natural History, Tring, UK, exhibits plumage characters of both races (BirdLife International 2001). This is yet another question that can be effectively addressed by a study on the population genetics of this interesting bird species.

The shortwing, being a high-elevation species, is particularly vulnerable to severe fragmentation and loss of habitat. Species that form small insular populations are particularly vulnerable to extinction and there has thus been concern that this species too could be lost forever. It is, therefore, important to unravel the genetic connectivity between such populations of the species in order to focus research and conservation efforts in a way that would allow us to implement better-informed adaptive management measures for the species in the foreseeable future.

[1] This note was prepared on invitation for *Indian BIRDS* to summarise for readers the author's findings published in the online journal, *PLoS ONE* (Robin, *et al*. 2010)

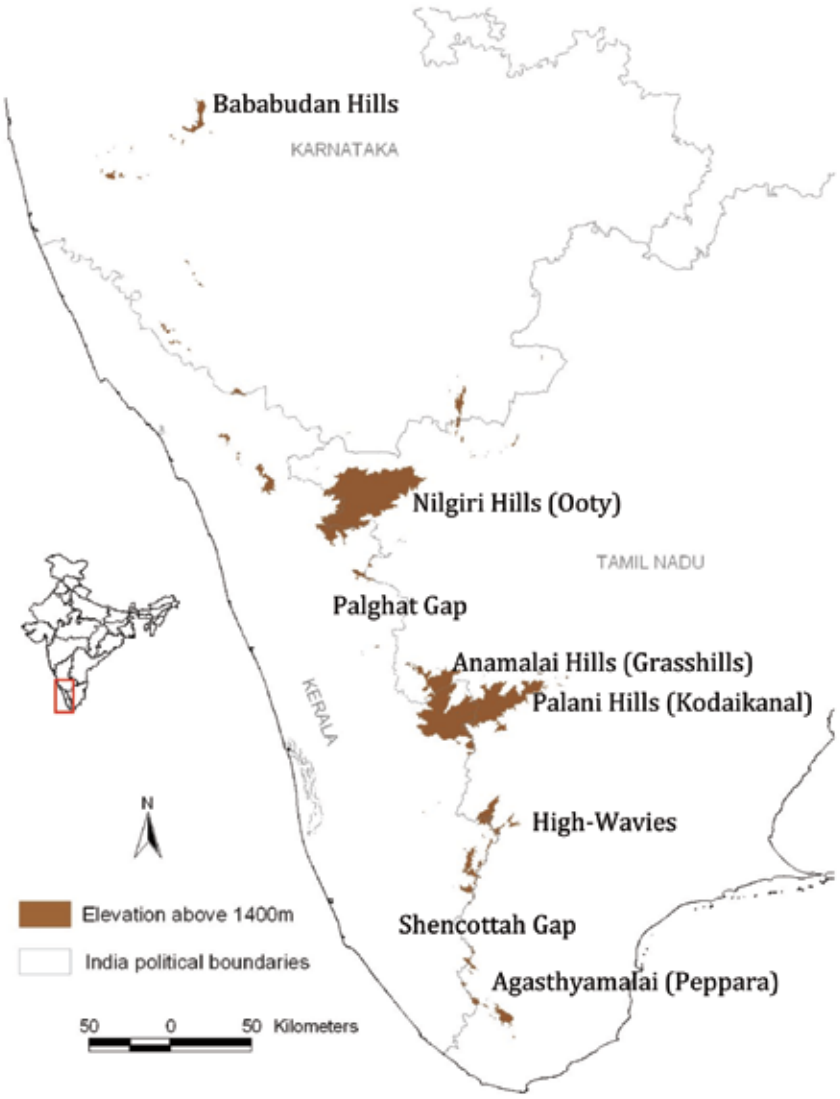

Fig. 1. The sky islands of the Western Ghats mountains, south-western India

A brief methodology

This aspect of our long-term study primarily involved obtaining genetic samples (a drop of blood) from 33 individual shortwings from different sky islands of the Western Ghats (detailed in Robin *et al.* 2010). In the lab we extracted DNA from these samples and generated sequences of different segments of mitochondrial and nuclear DNA. Mitochondrial DNA is maternally inherited and its mutation rate is very low. Broadly speaking, this implies that it may take thousands of years for changes to show up in the mitochondrial sequence. This marker is thus used to investigate genetic differences between taxa that could have risen over millions of years. Mitochondrial mutation rates have been examined for different bird species and it has been found that there is an almost constant rate of mutation over millions of years across several species. This clock-like definitive mutation rate is often referred to as a molecular clock and can be used to our advantage. One can examine the extent of mutations we find in different groups and arrive at an estimate of how long ago in time these groups diverged, giving us a molecular date for the splits between different groups. Since mitochondria are maternally inherited, it is likely that we could miss out signals that arise because of different dispersal patterns between males and females. Hence, we also sequenced a nuclear marker to counter this possible effect of differential sex. Certain sequences in the mitochondria like Cytochrome Oxidase 1 or COX1, often called the barcoding gene, have recently been developed as standards to identify and separate taxonomically different species. It has been estimated, for example, based on data from 260 North American birds, that species differ from one another by 7.9% in the DNA sequence of the barcoding gene (Hebert *et al.* 2004). This information has since been used as a cut-off to identify and classify different species and we proposed to use this to examine the differences in shortwings across the Palghat Gap.

Results & discussion

Effects of geographical gaps

We found that populations of shortwing that were geographically closest to each other were not genetically the closest. In fact, we found that the populations across the Palghat Gap showed the maximum genetic difference though they were geographically adjoining populations. Such a difference was also seen across the Shencottah Gap, once again indicating that geographical closeness need not imply genetic similarity. Only the High Wavies population was found to be very close to the Anamalais–Kodaikanal complex population, reflecting a similarity within regions not separated by ancient gaps. The genetic differences in the barcoding region across the populations on either side of the Palghat Gap were larger than the threshold set from North American bird studies and hence the populations could be considered different species. Our analysis, controlling for the effect of geographical gaps and geographical distances, shows that

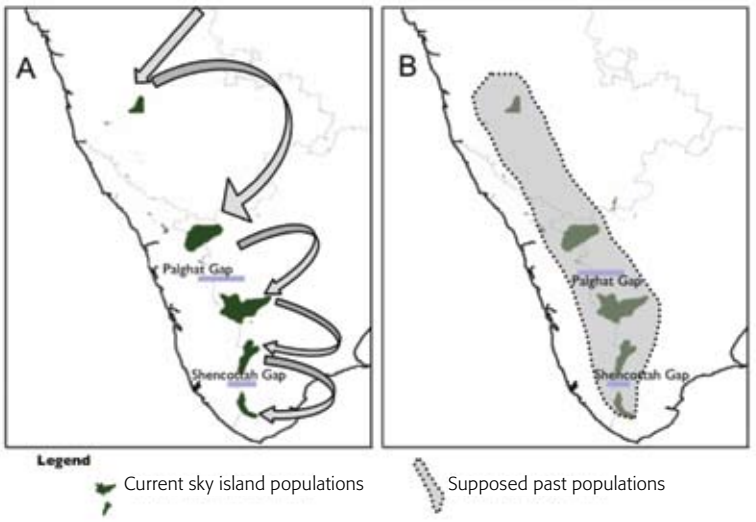

Fig. 2. Possible ways that populations could colonise sky islands of the Western Ghats.

geographical gaps have had a major role in shaping the structure of populations of shortwings.

Population structure

On the whole, the genetic structure of the shortwing groups does not reflect their population structure. Populations like those of the High Wavies and the Anamalais–Kodaikanal complex appear to have been genetically connected in the recent past, although they are on different sky islands. This formed a single genetic population of the 'central sky island complex.' All the other sky island populations appear to be genetically isolated from one another. The connectivity between the High-Wavies and the Anamalai-Kodaikanal population is interesting as there does not seem to be any connectivity between these regions at the 1,500 m elevation. There is, however, connectivity between these regions at an elevation between 1,000 m and 1,500 m. Our previous studies, including widespread surveys, have shown that shortwings prefer, and are found in high densities in regions above 1500 m but they also seem to marginally utilise the regions between 1000 m and 1500 m where they are found in low densities (Robin & Sukumar 2002; Robin *et al.* 2006). This may be the reason why the High Wavies population is genetically connected to the Anamalai–Kodaikanal population.

Our study did not have a large sample size from the north of the Palghat Gap, which implies that we do not have the fine resolution for a similar story on that side of the Gap. Our future work would thus be targeted in that direction.

Evolutionary history of the shortwing

Based on the estimated timing of the splits of different populations, it appears that all shortwing populations were a single population that split into two, on either side of the Palghat Gap, about 5 Ma. Since that period there has been no mixing of individuals across the Palghat Gap. The next split was across the Shencottah Gap where the populations split about 1.5 Ma. Interestingly, we found that the timing of these splits correlated with ancient global climatic events. We have always known that ice ages affect different species in the northern latitudes, but there has been little information on how tropical species from regions like the Western Ghats are affected. The Last Glacial Maxima, or the last Ice Age, about 20,000 years ago has been even popularly depicted in movies (such as Ice Age) to affect several species. During the Ice Age, while much of the northern hemisphere was turning into ice, and sea levels were falling, the tropics faced a severe dry spell, causing the wet forests to retreat to the higher reaches of the mountains. Our data indicate that during that time, all the shortwing populations on different sky islands had perhaps shrunk. It must be noted that when such glacial refugia[2] are formed, the entire population of shortwings across different sky islands could have formed a single refugia, but this did not happen in this case. Instead, several independent refugia formed on each mountain-top. Ever since the Ice Age receded, the forests may have expanded and shortwing populations have been increasing since then. Conlusive and detaied studies will reveal its larger impact in this habitat. It must be noted that this increase in population is at an evolutionary scale, in thousands of years, while it is still possible that recent anthropogenic fragmentation and deforestation could be causing a decline in the population of this species.

[2] Glacial refugia are small patches of suitable habitat left behind by the action of ice ages.

Clement Francis

Fig. 4. Rufous-bellied Shortwing *B. major*, Avalanche, Ooty, Tamil Nadu.

The other conclusion that can be highlighted from this study is that evidently the species did not have a linear mode of colonisation **(Fig. 2A)** but, a mode that was more consistent with option B **(Fig. 2B)**, where the species occupied lower lying areas and then moved up into the sky islands. The reason for this appears to have been global climatic events. These movements are not independent of geography, as the splits in the populations evolved merely because the topographic canvas that existed had deep valleys, like the Palghat Gap, and Shencottah Gap between these populations.

Taxonomy

This study was not directed at understanding the taxonomic status of the species, but was aimed towards an understanding of its phylogeography, and evolutionary history. In the process we found that the populations of shortwings had clearly separated into two different species over the last five million years. Unfortunately, we cannot ascertain the genus-level status of the species. There is only a single sequence of a *Brachypteryx (B. montana*) individual from north-eastern India that is available publicly. Our genetic studies indicate that *B. major* is not close to *B. montana*; other *Brachypteryx* spp., have, however, not been examined. This means that *Brachypteryx* could be close to *Myiomela, Cinclidium* or some other chats. As there is currently no genetic information available for all these congeneric spp., we currently cannot conclude to what genus this species belongs. We are collaborating with other groups of researchers who are working on similar taxa, to be able to examine this very soon. Meanwhile, we have proposed that a *status quo* be maintained

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Fig. 3. White-bellied Shortwing *B. albiventris*, Munnar, Kerala.

on the genus-level status of the bird while its species-level split should be recognised. We have proposed, following Ali & Ripley (1987), that the northern species, i.e., found north of the Palghat Gap, be called the Rufous-bellied Shortwing *B. major*, and the southern species, i.e., found south of the Palghat Gap, the White-bellied Shortwing *B. albiventris*.

Conservation implications

The newly-split northern species of the shortwing now has a much smaller range, and its conservation status will need to be re-examined. One of the larger implications of the study has been the possible impact of climate change on the evolution of this taxon. While one cannot conclusively state what might happen to this species in future climate change scenarios, one can draw broad conclusions, based on the evidence that at the Last Glacial Maxima, with a drying up of the forested habitats, the shortwing populations had crashed. It appears that some populations like the one in the Bababudan Hills (Karnataka), with inherently low population densities, might be the first ones to disappear, should we see any major impact of climate change. It is essential then, that a programme be initiated urgently, and efforts dedicated to monitoring the species in this area in the years to come.

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Birds of three different forest habitats in Nainital district (Western Himalaya), Uttarakhand, India

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Abstract

The present study was made to estimate the avifauna in terms of species richness and diversity and guild structure in forest habitats of Nainital district of Uttarakhand (350–2450m asl; 29°N). Field studies were conducted during January 2006 to December 2007. A total of 88, 106 and 95 species, respectively were recorded from Nainital, Bhowali and Haldwani forest habitats. A checklist of 160 avian species was recorded in the Nainital district forest habitats. This study could provide a base line structure for further studies on species distribution in different forest habitats in Nainital district.

Introduction

On a global scale, the Himalayan regions are rich in biodiversity because of various factors including the diverse forest types such as broad leaf mixed, dry deciduous, moist deciduous and conifer that are found here. Therefore, conservation of forest areas of Himalayan region is imperative. These forests also have a large number of endemic and globally threatened species. The avifauna of this region has been extensively documented from Jerdon's (1862–1864) pioneering investigation to Ali & Ripley's (1983) authoritative *Handbook*. Thereafter, some other studies have also been conducted in recent years to prepare the checklist of the avi fauna in some parts of Uttarakhand state (Sankaran 1995; Sharma *et al*. 2001; Sathyakumar 2003; Singh *et al*. 2004; Sultana *et al*. 2007; Joshi & Bhatt 2009; Naithani & Bhatt 2010; Bhatt & Joshi 2011).

In the context of avian diversity many studies have identified the factors such as vegetation structure profile, tree diversity, weather conditions, *etc*., responsible for variation in avifauna from habitat to habitat in India (Beehler *et al*. 1987; Daniels 1989; Johnsingh *et al*. 1986). These studies also emphasised the value of avifaunal studies in quantifying and monitoring forest degradation.

The history of ornithology from this hilly region is brief. The last comprehensive field work in the area was by Hudson (1930) who compiled a checklist. After Hudson, detailed work was carried out by the famous Indian ornithologist Salim Ali, who published his work in a book entitled "Indian Hill Birds" (1984). However, few studies concentrated on the avian species abundance and community structure in forest habitats of the Himalayan region.

In the light of this background, we decided to prepare an avian species checklist for three different forest habitats in Nainital district of Western Himalaya.