

# Conservation biogeography in North-east India: hierarchical analysis of cross-taxon distributional congruence

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## ABSTRACT

Distributional similarity (congruence) between phylogenetically independent taxonomic groups has important biogeographical as well as conservation implications. When multiple groups show congruence, one or two of them can be used as surrogates of diversity in others; thus, simplifying some of the challenges of area prioritization for conservation action. Here we test for congruence in complementarity between amphibians, reptiles and birds across seven tropical rainforest sites in the Eastern Himalaya and Indo-Burma global biodiversity hotspots. The results show that while frogs and lizards are strongly congruent with each other, birds as a whole do not show congruence with either of them. However, certain bird subgroups delineated on the basis of broad ecological niche and life history attributes are significantly congruent with both frogs and lizards. Multiple Mantel regression between environmental variable and species distribution dissimilarity matrices indicate that along with differential response to between-site ecological differences, inherent life-history characteristics shared by certain groups contributes to observed patterns of congruence. Our analyses indicate that examining biologically distinct subsets of larger groups can improve the resolution of congruence analyses. This approach can refine area-prioritization initiatives by revealing fine-scale discordances between otherwise concordant groups, and vice versa. Given that monetary resources do not always allow inclusion of multiple groups in biodiversity inventorying efforts, performing such analyses also makes economic sense because it can provide better resolution even with single-group data. In the context of conservation in North-east India, the results highlight the biogeographical complexity of the region, and also point at future priorities for biodiversity inventorying and conservation prioritization, both in terms of areas as well as taxonomic groups.

## Keywords

Amphibians, birds, congruence, conservation biogeography, North-east India, reptiles.

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## INTRODUCTION

With limited resources available for biodiversity conservation worldwide, it is necessary to minimize species' loss by prioritizing areas (Balmford & Long, 1995; Myers *et al.*, 2000; Mittermeier *et al.*, 2004). Ideally, for achieving adequate representation of biodiversity, multiple taxonomic groups should be used. However, due to practical constraints on data availability for multiple groups, a majority of area-prioritization studies assume some level of similarity in species geographical distributions (congruence) and use available groups as surrogates for others (hereafter referred to as surrogacy; e.g. Kitching, 1996; Howard & Viskanic,

1998; Garson *et al.*, 2002; Moore *et al.*, 2003; Rondinini & Boitani, 2006). Two main distributional characteristics are currently used for assessing cross-taxon congruence and surrogacy: species diversity (or alpha diversity) and associated measures such as endemism and rarity, and turnover (also known as beta diversity, Whittaker, 1960; or community dissimilarity, e.g. Su *et al.*, 2004). Although diversity, rarity and endemism have traditionally been used in most conservation assessment and prioritization initiatives, the focus has increasingly shifted towards community dissimilarity. A number of recent studies have shown that the two distributional characteristics often yield disparate patterns of congruence (Howard & Viskanic, 1998; Oliver *et al.*,

1998; Su *et al.*, 2004; Oertli *et al.*, 2005; Steinitz *et al.*, 2005). For conservation area prioritization, community dissimilarity is a better criterion than alpha diversity because it maximizes the overall representation of biodiversity in the landscape. A number of algorithms have also been designed over the last decade that seek networks of sites that maximize community dissimilarity (often called 'complementarity' in the literature; Howard & Viskanic, 1998; Justus & Sarkar, 2002; Margules *et al.*, 2002; Sarkar *et al.*, 2002).

Irrespective of the criterion for congruence, the use of surrogacy is a popular approach. It is especially useful in the tropics, which on one hand are exceptionally diverse, and on the other, generally data poor and cash strapped. But despite the apparent advantages and widespread use of surrogacy, its efficacy remains unclear. In the last decade or so, a number of studies have focused on this, using richness, endemism, rarity, or community dissimilarity (or combinations of these) and found conflicting results (e.g. Prendergast *et al.*, 1993; Flather *et al.*, 1997; Moritz *et al.*, 2001; Lund & Rahbek, 2002; Moore *et al.*, 2003; Kati *et al.*, 2004; Lamoreux *et al.*, 2006). For example, with data on tropical insects, snails, plants, and vertebrates, Moritz *et al.* (2001) found that congruence is high and surrogacy a useful approach only in areas with a clear history of geographical vicariance, while Lamoreux *et al.* (2006) found good congruence between four vertebrate groups at a global scale.

Thus, given that the assumptions of surrogacy are frequently not met, more studies need to perform detailed analyses of distributional congruence between multiple taxonomic groups, and investigate the numerous factors that can contribute to observed levels of incongruence (or congruence). In part, the matter is of scale; at finer geographical resolution, distribution patterns often do not overlap. Another factor is taxonomic resolution; using a more coarse level classification of biotic groups often improves congruence (e.g. Negi & Gadgil, 2002). Contemporary habitat change and fragmentation can also lead to incongruence because such changes affect groups differently. In addition to all these factors, there are fundamental historical biogeographical processes that need consideration. Biogeographical analyses of distributional congruence between phylogenetically distinct taxonomic groups provide information about the relative importance of vicariant and non-vicariant processes such as dispersal, extinction, and non-allopatric speciation (Ronquist, 1997; Crisci *et al.*, 2003; Lomolino & Heaney, 2004). For example, in the simplest scenario where multiple taxonomic groups show significant congruence, a common geographical vicariance event is the most parsimonious explanation. The infusion of such biogeographical insights into conservation biology are an important step towards developing methods that preserve not just contemporary patterns of taxonomic diversity, but also the historical processes that underlie them (Moritz, 2002; Whittaker *et al.*, 2005).

In this paper, we focus on the fact that life history is a crucial factor from historical biogeographical as well as contemporary perspectives (e.g. Hilt & Fiedler, 2006). For example, a taxonomic group with poor dispersal abilities will be more sensitive to a vicariant palaeo-ecological event (such as desiccation in intervening areas of a contiguous range) than one that is more

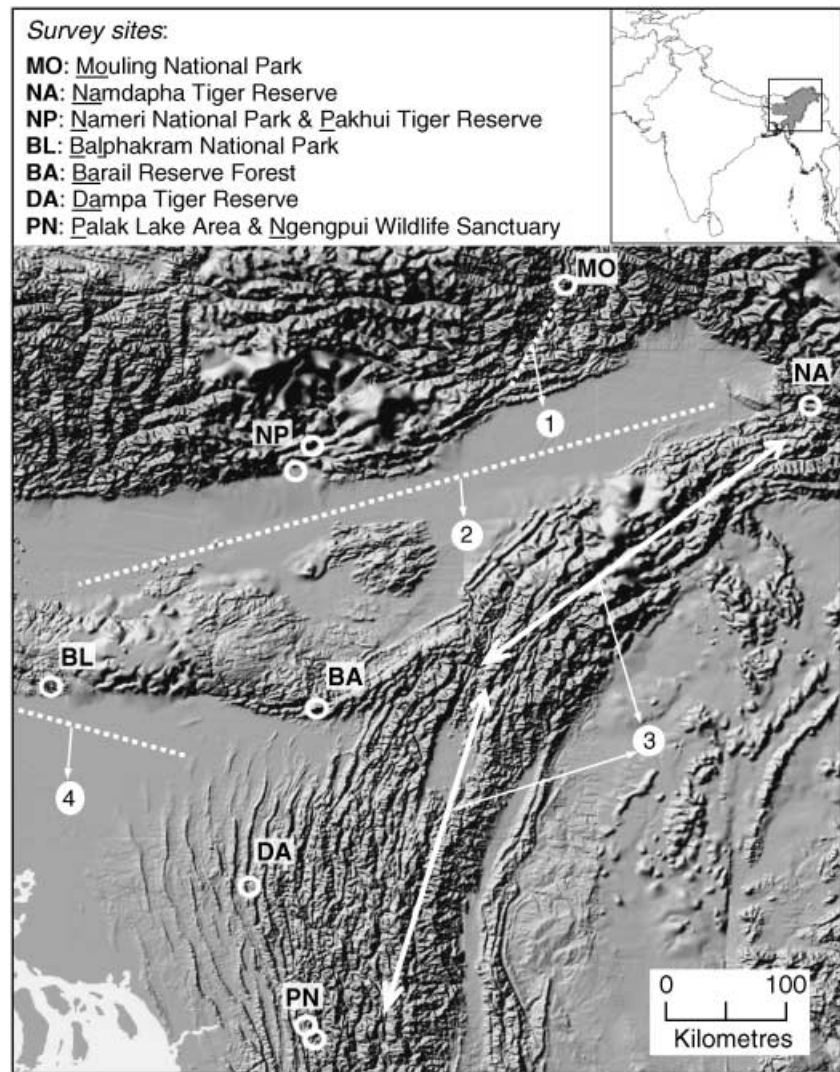
vagile, possibly resulting in distributional incongruence. We claim that better resolution can be achieved in conservation prioritization if groups of taxa with disparate life-history characteristics are contrasted objectively. Moreover, even in otherwise large phylogenetically inclusive groups (clades), biological disparities between subsets of taxa may lead to incongruence between them. This possibility is generally disregarded, with most surrogacy studies considering whole groups (such as all birds or mammals) in a region together.

We evaluate biogeographical congruence in richness and community turnover between amphibians, reptiles and birds across sites spanning the Himalaya and Indo-Burma global biodiversity hotspots (cf. Mittermeier *et al.*, 2004), paying particular attention to variation in biological characteristics within each phylogenetically inclusive group. To date, only a few papers have looked at subsets of taxa for biogeographical congruence from a surrogacy perspective (Moritz *et al.*, 2001; Kati *et al.*, 2004; Tognelli, 2005; Graham *et al.*, 2006). These studies have found that subsets defined either on the basis of taxonomy or life-history attributes frequently show lack of congruence and surrogacy values that differ from groups considered as a whole. Using hierarchical analyses, we test the effect of taxonomic pooling by estimating congruence at whole-group and strategically defined subgroup levels. Specifically, we ask: (i) How much distributional congruence do amphibians, reptiles, and birds show? (ii) Do subgroups with similar biological characteristics show higher congruence than whole groups? (iii) What independent factors correlate with observed patterns of congruence? We consider the conservation implications of the results in detail, with particular focus on gaps in existing information in the North-east Indian region.

## METHODS

### Study area

North-east India forms a significant portion of both the Himalaya and Indo-Burma biodiversity hotspots (Mittermeier *et al.*, 2004; Conservation International, 2005). The region can be broadly differentiated into the Eastern Himalaya (Olson & Dinerstein, 2002; GIS data from World Wildlife Fund, 2006) to the north, the North-east Hills (Meghalaya and Mizoram-Manipur-Kachin forest zones of Olson & Dinerstein, 2002) to the south, and the Brahmaputra River basin (BRB) (the Brahmaputra valley forest zone of Olson & Dinerstein, 2002) in between (also see Mani, 1974). Of these, Eastern Himalaya and North-east Hills are primarily montane zones with contrasting geological origin and morphology, while the BRB consists of the flood plains of the Brahmaputra River (Mani, 1974). North-east India has a relatively complex biogeography due to a combination of factors, including its age, unique plate tectonic and palaeo-climatic history, location at the confluence of distinct realms (Afrotropic, Palearctic, and Indo-Malay; cf. Olson & Dinerstein, 2002), wide physiognomic range (e.g. altitude ranging from c. 100 to > 7000 m above sea level) and habitat diversity (from tropical to alpine; Champion & Seth, 1968; Puri *et al.*, 1989). On



**Figure 1** Map showing digital elevation model of North-east India (the shaded region of the inset map of South Asia) with study sites indicated by white rings. Major biogeographical features are numbered, with dashed lines for barriers, and bidirectional arrows for potential dispersal routes: (1) The Siang River and valley, (2) the Brahmaputra River and basin, (3) Rakhine-Yoma ranges (including the Barail range), (4) upper plains of the Ganga-Brahmaputra delta. See text for more discussion.

the whole though, distribution data across multiple plant and animal groups indicate that the region's biological affinities are closest to South-East Asia (Mani, 1974).

Although both the Himalaya and the Indo-Burma hotspots are considered data-deficient, existing knowledge about plant and vertebrate biodiversity provide some indication of their value (Mittermeier *et al.*, 2004). In case of the Himalaya hotspot, of the 10,000 species of plants known from the region, about 3160 (32%) are endemic (including 71 genera and 5 families that are endemic). In the case of the Indo-Burma hotspot, 7000 (52%) of 13,500 vascular plant species known from the region are endemic.

### Species distribution data sets

Species distribution data were obtained during an 8-month survey between October 2000 and May 2001, by S.S.P. and A.C.B. in seven areas of North-east India (Fig. 1; Pawar & Birand, 2001). Sites were chosen in contiguous low to mid-elevation (100–1500 m above mean sea level) tropical moist broadleaf forest across the

region (Fig. 1). This choice of elevation range eliminated taxa resident to higher mountains from the analysis, but rendered the data collection tractable and allowed more exhaustive sampling within the chosen range. Faunal sampling was focused mainly on surveying mature and primary forests, and comparable effort was invested across sites (Pawar & Birand, 2001). Both diurnal and crepuscular-nocturnal surveys were carried out. Typically all three groups were sampled on diurnal walks during one composite survey extending from dawn to forenoon, with the initial morning hours dedicated to birds. Crepuscular-nocturnal walks began late in the evening and rarely extended beyond 2100 h. The period up to dusk was devoted to detecting pre-roosting birds combined with searches focused along forest streams and ponds for amphibians.

To minimize seasonal effects on faunal sampling, and to compile more comprehensive species lists, the primary data were supplemented with records from local and regional field museums and private collections, from previous studies by S.S.P. (Pawar *et al.*, 2004), T.R.S.R. (Raman *et al.*, 1998; Raman, 2001), M.F.A. (unpublished data), S.S. (unpublished data),

and published species lists. A majority of these secondary sources consisted of records that had been collected after 1990 (see Pawar & Birand, 2001). Hence, the effects of temporal distributional changes are expected to be minimal. While incorporating data from secondary sources, particular care was taken to exclude records that were obvious geographical outliers, as well as those that lay outside the chosen altitudinal range for the study. In the case of museum data, each specimen was examined and its taxonomic status verified.

Given the multiple sources of data used to compile species lists, and comparable field survey effort across sites, we consider the species lists for each area to be reasonably comprehensive (especially in the case of birds) and henceforth use raw species number as a measure of species richness. From the raw data set, we retained only species that are at least partially dependent on primary forest. Non-forest species are generally widespread, can track recent anthropogenic changes in the landscape, and are therefore likely to shroud more historical biogeographical patterns. Species were classified as being forest-dependent based on literature (Ali & Ripley, 1983; Grimmett *et al.*, 1999) and our own observations. As an additional measure to minimize errors, we excluded from all analyses the following taxonomic subsets, which were very difficult to adequately sample or record consistently during the study: fossorial reptiles and amphibians, snakes, turtles, diurnal raptors and all nocturnal birds. Thus, in effect, our analyses are restricted to anuran amphibians (frogs), saurian reptiles (lizards), and diurnal, non-raptorial birds. The final data set consisted of 125 frog, 90 lizard, and 1016 bird records. Of these, 23 (19%) frog (two from museums), 13 (15%) lizard (five from museums), and 570 (56%) bird records (none from museums, all from published species' lists) were from secondary sources.

### Classification of biotic groups and subgroups

To examine congruence hierarchically, two levels of subgroups were defined among birds based on broad ecological and life-history characteristics. The first level consisted of six subgroups: three based on trophic and three on spatial (vertical habitat) niche. These two characteristics have been considered crucial in defining functional subcommunities of forest birds in North-east India (Raman *et al.*, 1998; Raman, 2001), and in general are strongly related to life-history characteristics such as body size and dispersal ability. For example, previous studies have shown strong evidence that understorey and terrestrial (e.g. Stratford & Stouffer, 1999; Sekercioglu *et al.*, 2002; Laurance & Gomez, 2005) and frugivorous (e.g. Githiru *et al.*, 2002) birds are relatively more dispersal limited. The three trophic groups were herbivores (frugivores, nectarivores, granivores, and pollen feeders) (HB), insectivores (IB), and omnivores (OB). The three spatial groups were terrestrial and lower understorey (TB), lower canopy and upper understorey (LB), and upper canopy species (UCB). The second level of subdivision consisted of seven subgroups based on combinations of the trophic and spatial niches: terrestrial and lower understorey omnivores (TOB) and insectivores (TIB); lower canopy and upper understorey omnivores

(LOB), insectivores (LIB), and herbivores (UCHB); and upper canopy omnivores (UCOB), and insectivores (UCIB). A few frugivores and nectarivores were present among LB and TB subgroups, but not in sufficient numbers to merit the designation of separate group at those strata. These species were hence clubbed with omnivores into the subgroups LOB and TOB. Classification into subgroups was based on our own observations, along with natural history notes from Grimmett *et al.* (1999) and Ali & Ripley (1983). We also considered migratory habits to gain additional information about potential dispersal limitations. Across the seven level 2 subgroups, the distribution of this characteristic was: TOB and UCHB — mostly residents; TIB, UCOB and LIB — residents and local migrants; and LOB and UCIB — residents, local migrants and long-range migrants. The bird species list and subgroup memberships are given in Appendix S1 in Supplementary Material.

The frog and lizard groups were not subdivided for two reasons. First, both show small within-group variation in broad trophic niche and physiology (both are insectivorous ectotherms). Second, although subclassification based on structural habitat use and diel activity is possible (see Pawar *et al.*, 2004, for one such classification of an assemblage from North-east India), doing so would result in subgroups with extremely small species numbers relative to bird subgroups (see Results section). Because community dissimilarity indices (see section on data analysis) are at least somewhat sensitive to species richness (Clarke & Warwick, 1994), we chose to retain frogs and lizards as single groups because these then have richness values comparable to the bird subgroups (see Results section). Species lists for frogs and lizards are given in Appendix S1. Among all the taxonomic groups and subgroups, frogs and lizards are the most dispersal limited.

### Environmental and landscape data

Centered on each of the seven sites, we delineated square landscapes of 4000 km<sup>2</sup>. This landscape size ensured that all the survey localities within each site were covered. For each landscape, we then extracted the following features.

#### *Unweighted geographical distance*

Straight-line distance between sites was calculated to examine the effects of spatial autocorrelation.

#### *Weighted geographical distance*

To examine the potential role of major rivers as dispersal barriers, we calculated the shortest distances between sites that circumvented the two main river basins in the region: the Brahmaputra, and the Barak-Surma river system (Mani, 1974). Weighted distances were calculated between each pair of sites using a digital elevation model (1-km resolution), by tracing the shortest route that did not involve either descent into any of these basins (defined as any cell with value < 100 m) or ascent to very high elevations (defined as any cell with value > 2000 m).

### *Altitudinal features*

We used altitudinal data derived from the Shuttle Radar Topography Mission (SRTM) elevation database, at a 30 arc-second (approximately 1 km, yielding 5244 pixels across all sites) resolution (Hijmans *et al.*, 2005). To summarize altitudinal attributes, we calculated the following statistics using all the pixels in each landscape: mean, coefficient of variation, median, skewness, skewness of first three quartiles, and kurtosis.

### *Temperature and precipitation*

These data were we extracted from the derived BIOCLIM variables of the 1-km resolution WORLDCLIM database (Hijmans *et al.*, 2005). This data set contains interpolated data for different climatic attributes including annual extremes, means, and variances. Temperature data consisted of BIOCLIM 1–11, and precipitation of BIOCLIM 12–19. Each variable was summarized by its mean and coefficient of variation across all cells in each landscape.

### *Forest type and secondary habitat cover*

These data were extracted from the 1-km resolution AVHRR-Global Land Cover Classification data set of the Global Land Cover Facility (Hansen *et al.*, 1998). These satellite-derived data consist of 13 categories, including degraded habitat features. Of these, five that contained information on broad forest type (categories 1–2 and 4–6; see Hansen *et al.*, 1998) were separated from another five that represented secondary habitat categories (7–11), yielding the two separate data sets: one representing forest type composition and the other the proportion of secondary/degraded land cover. The remaining three categories (3, 12–13) were not represented by any pixels in the seven sites.

## **Statistical methods and analyses**

### *Congruence*

Correlation in species richness between groups and subgroups across sites was estimated by the Spearman's rank correlation test. To estimate congruence in community dissimilarity, we first calculated between-site community distance matrices, and then tested for associations between them with the Mantel procedure (Manly, 1997). This method for measuring congruence was first used by Oliver *et al.* (1998). The dissimilarity matrices for all faunal groups and subgroups were calculated with the Jaccard coefficient (Clarke & Warwick, 1994) between all possible pairs of sites, using species' presence-absence data. For Mantel's tests, the Pearson's correlation coefficient was used, and one-tailed *P*-values (under an alternative hypothesis of only positive correlation) of statistical significance were estimated with  $10^6$  randomizations. As a scalar value to compare turnover in species composition across sites for different groups, we used the mean of the respective between-site dissimilarity matrix. This metric, originally suggested by Whittaker (1972), is not widely used but

gives results comparable to standard turnover indices (Legendre *et al.*, 2005).

### *Biogeographical patterns*

For a detailed comparison of biogeographical patterns, we used nonmetric multidimensional scaling (NMDS; Clarke & Warwick, 1994) on each faunal dissimilarity matrix, restricting the ordination to two dimensions. NMDS algorithms attempt to find a solution in a prescribed number of dimensions (two in our case), such that the order of distances in the rescaled space correspond to the order of the corresponding dissimilarities in the data matrix. The iterative spatial optimization for each NMDS model was initiated with the actual geographical configuration of the seven sites (Fig. 1), i.e. with the actual spatial distance matrix. Iterations were curtailed at 10,000 runs or at a convergence threshold of  $10^{-5}$  between successive Kruskal's stress values, whichever was reached earlier. Stress reflects how well the rescaled model fits the actual disparities in the distance matrix, with smaller values implying a better fit. NMDS analyses were performed with the XLSSTAT-PRO™ software. To avoid redundant comparisons between different hierarchical levels of bird subgroups the NMDS analyses were performed only for the finest scale subclassification (the seven level 2 subgroups).

### *Correlates of distribution patterns*

To examine factors underlying distribution and congruence patterns, we performed multivariate Mantel regression (Manly, 1997) between faunal and environmental dissimilarity matrices. Matrices based on environmental dissimilarities were derived from the altitudinal, temperature, precipitation forest type and land cover data by calculating Euclidean distances between all pairs of sites. Regression models were built with the stepwise procedure using the Permute! software (Legendre *et al.*, 1994). This method involves forward selection followed by backward elimination. At each step, the statistical significance of each partial regression slope as well as multiple  $R^2$  is estimated by comparing against null distributions calculated by repeated randomization of the dependent variable matrix. Addition and removal of variables are based upon pre-designated Bonferroni-corrected *P*-values. We used  $P = 0.1$  for selection as well as elimination, estimating significance from  $10^3$  randomizations. Similar to the NMDS, redundant comparisons between different hierarchical levels of bird subgroups were avoided by performing analyses only for the finest scale subclassification (the seven level 2 bird subgroups).

## **RESULTS**

### **Congruence in species richness**

In all, 44 species of frogs, 26 species of lizards, and 248 species of birds were included in the analysis. Species richness across sites for the different groups and subgroups are given in Table 1. Richness was found to be highest in different areas for different

**Table 1** Species richness of forest frogs, lizards and birds across surveyed sites. Key to the acronyms for the bird subgroups are given in the methods section

	Total species richness	Site-specific species richness						
		NP	NA	MO	BL	BR	PN	DA
<b>Groups</b>								
Frogs	44	20	21	19	15	15	18	17
Lizards	26	11	14	11	13	10	16	15
Birds	248	155	183	133	117	178	104	146
<b>Level 1 bird subgroups</b>								
TB	63	30	45	30	20	42	23	31
LB	122	78	93	68	59	95	55	77
UCB	63	47	45	35	38	41	26	38
HB	42	29	28	19	28	33	22	27
IB	109	72	81	62	51	79	45	69
OB	97	54	74	52	38	66	37	50
<b>Level 2 bird subgroups</b>								
TOB	25	9	19	13	7	17	10	12
TIB	38	21	26	17	13	25	13	19
LOB	48	25	37	27	19	33	15	22
LIB	48	34	38	29	22	39	26	36
UCHB	26	19	18	12	18	23	14	19
UCOB	29	23	21	17	19	19	13	17
UCIB	34	24	24	18	19	22	13	21

**Table 2** Correlation in species richness between frogs, lizards, birds, and bird subgroups across the seven sites. Spearman rank correlation was used. Only correlation coefficients with a two tailed *P*-value < 0.05 are shown. The following redundant correlations that were not performed: all those above the diagonal, those that involved subgroups vs. their own super sets (e.g. all birds vs. any of their level 1 or level 2 subgroups), and those between the two sets of level 1 subgroups (TB, LB, UCB vs. HB, IB, OB; because the two sets include the same species classified in two different ways)

	Frogs	Lizards	Birds	TB	LB	UCB	HB	IB	OB	TOB	TIB	LOB	LIB	UCHB	UCOB
Lizards															
Birds															
TB															
LB				0.87											
UCB					0.79										
HB															
IB															
OB								0.96							
TOB															
TIB															
LOB										0.82	0.88				
LIB										0.79	0.92	0.79			
UCHB															
UCOB															
UCIB											0.87				0.90

groups and subgroups. For frogs, the two richest areas are in the Eastern Himalaya (NP, NA) and for lizards in the North-east Hills (PN, DA). Among the level 2 bird subgroups, TOB, TIB, and LOB are the richest in NA and BR, whereas all the other

subgroups show relatively less difference across sites. Correlation in species richness (Table 2) was significant only among certain bird subgroups, with frogs and lizards not correlated with any of the other groups or bird subgroups.

**Table 3** A comparison of forest frog, lizard and bird species turnover across sites. Turnover was measured as the average pairwise Jaccard dissimilarity between all pairs of sites. This measure ( $\pm$  standard deviation) for each group is given in parentheses next to its name in the first column. Only pairwise comparisons (using Dunn's nonparametric rank sum test) with a two-tailed  $P$ -value  $< 0.05$  are shown (asterisks). Certain redundant comparisons were not performed, as explained in Table 2

	Frogs	Lizards	Birds	TB	LB	UCB	HB	IB	OB	TOB	TIB	LOB	LIB	UCHB	UCOB
Frogs (0.65 $\pm$ 0.21)															
Lizards (0.49 $\pm$ 0.12)	*														
Birds (0.49 $\pm$ 0.10)	*														
TB (0.59 $\pm$ 0.11)		*													
LB (0.47 $\pm$ 0.11)	*			*											
UCB (0.44 $\pm$ 0.10)	*			*											
HB (0.41 $\pm$ 0.12)	*														
IB (0.49 $\pm$ 0.11)	*														
OB (0.51 $\pm$ 0.10)	*						*								
TOB (0.53 $\pm$ 0.12)	*														
TIB (0.63 $\pm$ 0.12)		*								*					
LOB (0.53 $\pm$ 0.11)	*										*				
LIB (0.41 $\pm$ 0.11)	*	*								*	*	*			
UCHB (0.40 $\pm$ 0.12)	*	*								*	*	*			
UCOB (0.42 $\pm$ 0.10)	*									*	*	*			
UCIB (0.48 $\pm$ 0.13)	*										*			*	

**Table 4** Congruence in distribution over seven sites for the three faunal groups and five bird subgroups estimated with Pearson's correlation coefficients between pairs of dissimilarity matrices. Only correlation coefficients with  $P$ -values  $< 0.05$  are shown, and those with  $P < 0.005$  are shown in bold typeface. The key to acronyms for the subgroups is in Table 1. Certain redundant correlations were not performed, as explained in Table 2

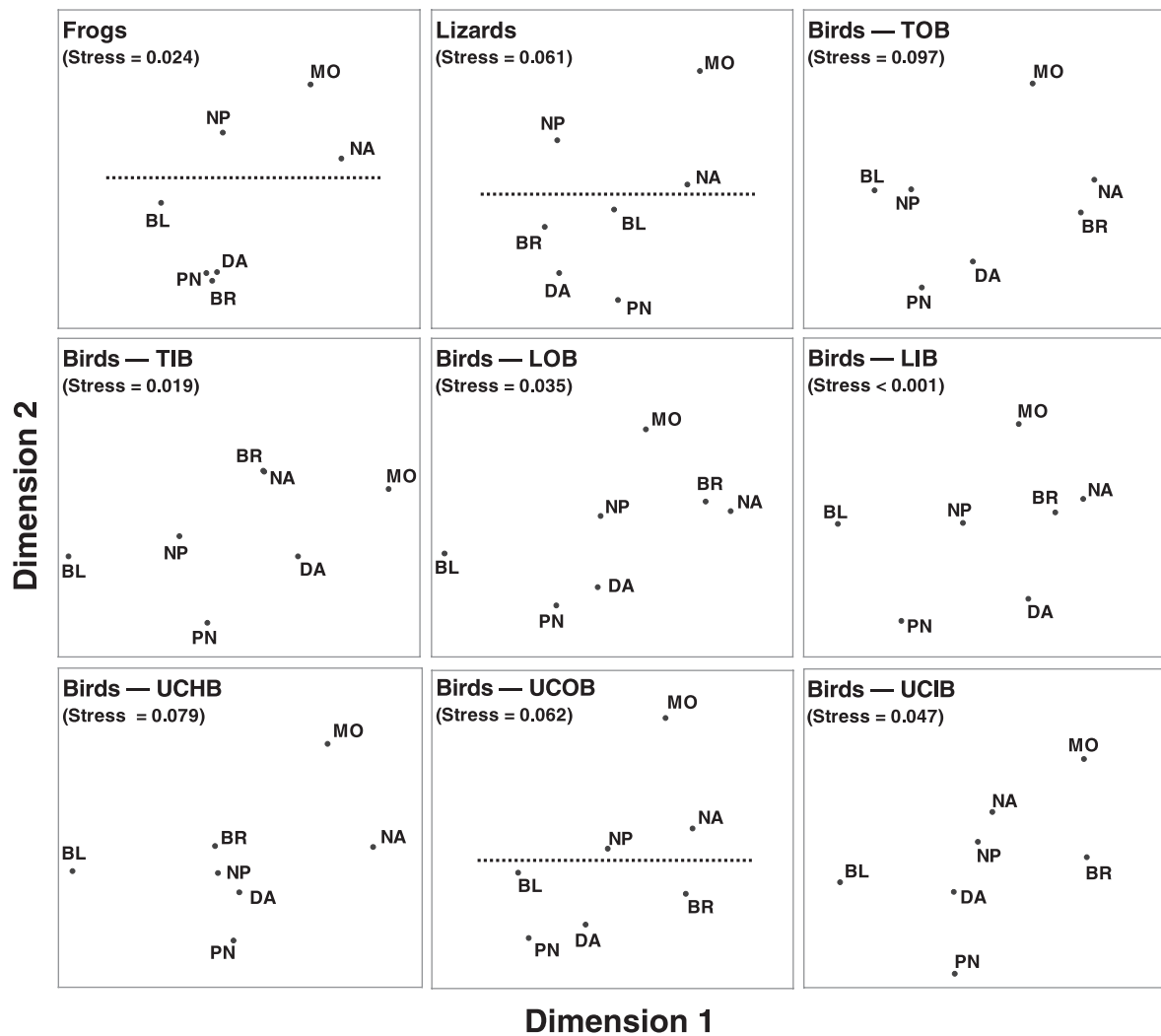
	Frogs	Lizards	Birds	TB	LB	UCB	HB	IB	OB	TOB	TIB	LOB	LIB	UCHB	UCOB
Lizards	<b>0.70</b>														
Birds															
TB															
LB				<b>0.85</b>											
UCB	0.39	0.37		<b>0.78</b>	<b>0.81</b>										
HB	0.39														
IB							<b>0.64</b>								
OB	0.42						<b>0.76</b>	<b>0.74</b>							
TOB	0.42														
TIB										<b>0.58</b>					
LOB										<b>0.72</b>	<b>0.69</b>				
LIB										<b>0.58</b>	<b>0.81</b>	<b>0.76</b>			
UCHB	0.43									<b>0.72</b>	<b>0.75</b>	<b>0.64</b>	<b>0.74</b>		
UCOB	0.54	<b>0.60</b>								<b>0.69</b>	0.42	<b>0.64</b>	<b>0.61</b>	<b>0.76</b>	
UCIB										0.47	<b>0.70</b>	<b>0.65</b>	<b>0.72</b>	<b>0.62</b>	<b>0.65</b>

**Congruence in community dissimilarity**

Pairwise comparisons in turnover (measured as the average pair wise Jaccard dissimilarity across sites) between groups and subgroups were tested using Dunn's rank sum test (Dunn, 1964), and are shown in Table 3. Turnover was highest for frogs (0.65, significantly more than lizards and all bird subgroups except TB and TIB). Among the spatial-niche based level 1 bird subgroups, terrestrial birds had the greatest turnover, the difference being

accounted for by the TIB level 2 subgroup (0.63, significantly more than lizards and all other bird subgroups). Among the trophic-niche based level 1 bird subgroups, omnivorous birds had the highest turnover, the difference being accounted for by TOB and LOB level 2 subgroups. Thus, within birds, turnover is highest for the relatively more terrestrial birds, and lowest for canopy birds (see Table 3).

The results of the between-group Mantel tests (Table 4) show that frogs and lizards show significant congruence in community



**Figure 2** NMDS representation of observed biogeographical patterns for different faunal groups. Kruskal’s stress values are given in parentheses. All the solutions have been plotted on the same scale. See Table 1 for the key to acronyms of bird subgroups. Compare with the actual geographical configuration of sites in Figure 1. The apparent barrier effect of the BRB for frogs, lizards, and the bird subgroup UCOB are shown with a dotted line.

dissimilarity ( $P$ -value < 0.05). Birds as a whole show poor congruence with frogs and lizards, but certain bird subgroups at both levels are congruent with them: UCB (level 1, spatial niche), HB, OB (level 1, trophic niche), TOB, UCHB, UCOB (level 2) with frogs, and UCB (level 1), UCOB (level 2) with lizards. All bird subgroups show significant congruence with each other, with the weakest associations being between terrestrial and canopy bird subgroups (low correlation coefficients and large  $P$ -values compared to other tests between bird-subgroups).

**Biogeographical patterns**

The NMDS of between-site dissimilarity matrices of faunal groups and subgroups converged on solutions with stress values < 0.1 in all cases (Fig. 2). These graphs are a representation of biogeographical relationships between sites for the different faunal groups and subgroups. Frogs and lizards clearly show a

similar pattern, with sites north of the BRB (NP, NA, MO) clustering separately from sites to the south (PN, DA, BR, BL). Except UCOB, no bird subgroups show patterns that suggest an effect of the BRB. In terms of areas, MO, and to a lesser extent BL, consistently appear the most distinct across all configurations (Fig. 2), indicating that they have distinct assemblages across all biotic groups.

**Correlates of distribution patterns**

Multiple stepwise Mantel regression with dissimilarity matrices indicates that different groups and subgroups were affected by disparate environmental and geographical features (Table 5). The proportion of dissimilarity explained ranged from 27% to 63%. Neither temperature nor land-cover were significant predictors for any of the biotic groups or subgroups. Only the regression model for frogs included river barrier weighted distance.



**Table 5** Correlates of distribution patterns for different faunal groups tested with stepwise Mantel regression (forward selection followed by backward elimination) on dissimilarity matrices. Temperature and land cover were not significantly associated with any group, and are not shown. The standardized partial regression coefficients are shown for each variable, along with their one-tailed *P*-value in parentheses. The last column shows the overall  $R^2$  along with significance values in parentheses

Biotic group/subgroup	Independent variable					
	Distance	Weighted distance	Altitudinal attributes	Precipitation pattern	Forest types	Total $R^2$
Frogs	0.50 (0.008)	0.36 (0.019)				0.60 (0.002)
Lizards					0.79 (0.001)	0.62 (0.001)
TOB			0.60 (0.004)			0.37 (0.008)
TIB				0.52 (0.007)		0.27 (0.013)
LOB				0.61 (0.003)		0.38 (0.005)
LIB				0.55 (0.003)	0.33 (0.033)	0.48 (0.003)
UCHB	0.39 (0.008)			0.57 (0.002)		0.63 (0.001)
UCOB			0.54 (0.009)		0.36 (0.027)	0.61 (0.001)
UCIB				0.59 (0.004)		0.34 (0.004)

## DISCUSSION

### Congruence and sources of discordance

While we find poor congruence between frogs and all birds and lizards and all birds, both frogs and lizards show significant congruence with bird subgroups at both levels of hierarchically nested subgroups. These results show how detailed hierarchical analyses can reveal hidden patterns of congruence and provide insights into potential sources of discordance. For example, while at first glance birds as a whole are not congruent with frogs, three level 1 bird subgroups (upper canopy, herbivorous, and omnivorous birds; Table 4) are congruent with them. This pattern is further clarified by examination of level 2 bird subgroups, which indicate that the congruence is accounted for by the distributional similarity between frogs and terrestrial omnivorous birds, upper canopy herbivorous birds, and upper canopy omnivorous birds (Table 4). Recent studies have also found qualitatively similar results, but with very different taxonomic groups, and without the fine-scale subclassification used here (e.g. Moritz *et al.*, 2001; Tognelli, 2005; Graham *et al.*, 2006).

The NMDS analyses and the between-group Mantel tests also show that average between-site turnover alone is a poor indicator of underlying distributional similarities. For example, although lizards have a significantly lower average turnover than frogs (Table 3), the Mantel tests show that the two groups actually have congruent distribution patterns (Table 4), the NMDS plots (Fig. 2) indicating that the BRB may in part account for this congruence (both plots show a separation of sites on either side of the BRB). One factor that has been previously found important in determining congruence in community dissimilarity is dispersal ability (Moritz *et al.*, 2001; Graham *et al.*, 2006). Moritz *et al.* (2001) found a greater congruence between poorly dispersed groups such as flightless insects and snails relative to flying insects, while Graham *et al.* (2006) found that a subgroup consisting of dispersal limited terrestrial-breeding Microhylid

frogs was more affected by historical geographical isolation than other groups and subgroups (including birds, mammals and reptiles). In this study, we find multiple instances of congruence between potentially poorly dispersed groups and subgroups: between frogs and lizards (clearly the two most dispersal limited sets of taxa among all the groups and subgroups), frogs and TOB and UCHB bird subgroups, and between lizards and UCOB subgroup. Moreover, in the case of frogs, straight as well as weighted distances emerge as important factors determining distributions in the multiple regression analysis (with an high overall  $R^2$ ; Table 5). How dispersal limitation might have an influence in the case of frogs is illustrated by comparing assemblages in the BL and NP areas. Although both these areas are relatively close geographically (see Fig. 1), they lie on either side of the BRB, and have very different frog assemblages (see the NMDS configuration in Fig. 2). We therefore infer that the interaction of dispersal limitation and the importance of local barriers such as river basins in speciation partly account for these patterns of congruence.

The Brahmaputra and Barak-Surma river systems are a dominant feature of North-east India (Fig. 1). Such features create barriers in two main ways: as a physical hurdle to dispersal (especially for more terrestrial biota) and because their associated basins generally differ ecologically. The BRB in particular, origins of which can be dated back to at least the late Tertiary period (Mani, 1974; Uddin & Lundberg, 1999) is likely to have influenced the distribution of taxonomic groups that are relatively dispersal limited (e.g. plants; Bell & Donoghue, 2003). In the case of birds, Ripley & Beehler (1990) inferred that rivers and associated basins in the Indian Subcontinent were an important feature governing speciation in 42% of all the species pairs they analysed, and identified the BRB as the single most important feature in North-east India. Of the 12 river-influenced genera common to their analysis and ours, two belong to TOB, four to UCHB, and four to UCOB groups, all of which consist of resident birds that are potentially dispersal limited. This influence of

local barriers on such bird subgroups is also supported directly by our results; the only bird subgroup to be associated with between-site distance in the multiple regression analysis is UCHB (Table 5), and the only bird subgroup that shows an effect of the BRB in the NMDS analysis is UCOB. In the case of the terrestrial bird subgroups TOB, TIB, and lower canopy–upper understorey subgroups LOB, LIB, the north–south orientated Rakhine-Yoma ranges (including the Barail Hills) have probably been an important route to disperse around the BRB, as suggested by the close compositional relationships between the NA and BR sites (see NMDS configurations in Fig. 2).

In all the bird plots, BL at the west and MO at the northern edge of North-east India stand out clearly. The distinctness of BL arises partly from its proximity to Peninsular India, many forest bird taxa having dispersed there across the plains of the Ganga-Brahmaputra delta from further west. MO on the other hand lies in the Siang River relatively deep inside the Eastern Himalayan ranges, and many higher elevation birds are found here. In contrast, BL is not so distinct in the frog and lizard NMDS plots, while MO is. The reason for this is that while MO has many higher montane elements in its frog and lizard fauna, BL, although relatively close to Peninsular India, shares no forest species from that region. In fact, the herpetofauna of the entire North-east India do not share a single rainforest species with Peninsular India (but do share some with areas to the east and south). This emphasizes the fact that North-east India is relatively isolated biogeographically from the western Indian Subcontinent, more so for some biotic groups than others.

That groups and subgroups show much less congruence in species richness compared to community dissimilarity is also a result consistent with previous studies (e.g. Howard & Viskanic, 1998; Oliver *et al.*, 1998; Su *et al.*, 2004; Oertli *et al.*, 2005). The key to understanding this apparent contradiction between the two measures of congruence is detailed biogeographical analyses. Ecological differences probably play an important part in this, but are difficult to pinpoint without detailed historical and phylogenetic analyses (e.g. Graham *et al.*, 2004, 2006). However, our results do provide some insights. The most notable among these is that the ostensibly dispersal restricted lizards show association (Table 5) not with geographical distance, but instead with forest types. There are key ecological differences between the Eastern Himalaya and the North-east Hills; the three areas in the Eastern Himalaya (NP, MO, NA) lie at the foothills of some of the highest mountain ranges of the world, and receive more frequent, aseasonal rainfall than the sites in the North-east Hills. Because lizards are less moisture-dependent than frogs, they are less dispersal limited and their distributions are probably more influenced by forest types, which in part reflect the physiographic and climatic differences between the Eastern Himalaya and North-east Hills. This is also indicated by the fact that lizard diversity peaks in the relatively more seasonal forests of the North-east Hills (PN, DA; see Table 1), while frog diversity peaks in two sites of the Eastern Himalaya (NP, NA).

The bird groups TIB, LIB, UCIB, and LOB show association with precipitation. All these groups have local or longer-range migrants, and their distributions are not likely to be affected by

local barriers, but rather by ecological differences directly or indirectly related to precipitation. The primarily nectarivorous, frugivorous, and omnivorous bird groups TOB and UCOB on the other hand, show association with altitudinal attributes. Both these groups are largely resident, with some local altitudinal migrants. Whether altitudinal attributes of the landscape affect these groups directly, or indirectly by through some ecological factors is difficult to discern at our level of resolution.

That none of the groups or subgroups was found associated with land cover change (as estimated by current secondary habitat cover) is in part accounted for by the fact that we only looked at forest species. In the case of birds, local as well as long-distance migratory species are likely to be affected by landscape changes (for example, by destruction of altitudinal migratory routes). However, with the current level of resolution, it is possible that we were unable to detect such effects on local forest species assemblages.

### Implications for conservation prioritization

Our results provide general as well as regional insights for the use of the surrogacy approach in conservation planning. As mentioned earlier, the surrogacy approach has been questioned because an increasing number of studies have found lack of congruence, especially at more local scales (e.g. Prendergast *et al.*, 1993; Moritz *et al.*, 2001; Kati *et al.*, 2004). This study was conducted at a geographical resolution comparable to these analyses (relative to global or interregional analyses), and scale is probably an important factor contributing to the observed levels of incongruence. It is not yet clear as to what geographical scales are most appropriate for conservation planning. In a recent study, Lamoreux *et al.* (2006) conclude from large-scale global analysis of congruence between vertebrate groups that surrogacy is a useful approach. However, in most cases, priorities are set at relatively local scales (generally within the bounds of political entities), and more studies are needed at finer geographical scales before general patterns begin to emerge.

Geographical scale apart, this study clearly demonstrates the need to consider taxonomic resolution. Some studies have suggested the approach of coarsening taxonomic resolution to achieve congruence between biotic groups (e.g. Negi & Gadgil, 2002; Baldi, 2003). For example, Negi & Gadgil (2002) investigated congruence between lichens, mosses, liverworts, woody plants and ants in the temperate zone of the Western Himalayan region, and found a number of conflicting patterns, including negative relationships in species richness and turnover between certain groups. However, they found broad congruence at higher taxonomic levels (genera, subfamilies and families), and suggested use of the surrogacy approach after such coarsening of taxonomic resolution. On the contrary, this study and a few others (e.g. Moritz *et al.*, 2001; Tognelli, 2005; Graham *et al.*, 2006) point in the opposite direction; finer-scale analyses can yield more insights. Once fine-scale patterns of congruence and their underlying factors are revealed, surrogacy-based solutions can be made more comprehensive by modifying them to include the observed disparities. As more taxonomic groups are included

in such hierarchical analyses, general patterns will become clearer. That broad-life history traits can be used to choose informative subsets of otherwise phylogenetically inclusive groups indicates one source of generality.

#### *A regional perspective*

Despite awareness of their biological diversity, the Eastern Himalaya and Indo-Burma region remain notoriously data-poor regions for a wide variety of plant and animal taxa (Mittermeier *et al.*, 2004). This study is the first evaluation of cross-taxon distributional congruence in Indo-Burma, and only the second in the entire Himalayan biodiversity hotspot (Negi & Gadgil, 2002). As further studies are undertaken and more phylogenetic data become available, it will become possible to differentiate between underlying factors and processes that influence distributional congruence in this biogeographically complex region (see Biswas & Pawar, 2006, for an overview).

Our results do raise questions about current conservation prioritization initiatives in North-east India, both in terms of optimal sizes as well as ranking of areas. The Biodiversity Conservation Prioritization Project has undertaken conservation prioritization and evaluation in India, including some hill states of North-east India (Singh *et al.*, 2000). These efforts aim at including multiple biotic groups, but in practice, data limitation have restricted them to a subjective ranking of values using taxa for whom information is available (e.g. Singh *et al.*, 2000). Moreover, these methods focus almost exclusively on single species attributes such as endemism and range restrictedness (e.g. Khoshoo, 1984; Singh *et al.*, 2000).

The other major conservation prioritization initiative in North-east India has been the 'Important Bird Areas' (IBA) program, which assumes that birds are effective indicator taxa for other biota (ICBP, 1992; Islam & Rahmani, 2004). This approach has led to the identification of a number of potential IBAs in the region, a majority of which are in the BRB and nearby hills (Islam & Rahmani, 2004). This suggests that the IBA prioritization effort may be biased towards the better-documented areas of North-east India in comparison to the relatively inaccessible tracts in the North-east Hills and Eastern Himalaya. Moreover, the general efficacy of birds as surrogates for biodiversity at different spatial scales remains untested, and has only recently come under scrutiny (Pain *et al.*, 2005; O'Dea *et al.*, 2006; Tushabe *et al.*, 2006). Our study shows that birds as a whole might not be good surrogates for amphibians and reptiles. Moreover, if one considers the high turnover rate shown by frogs, lizards and certain bird subgroups relative to others, there is a high probability that many species in these groups are not included in the current conservation area network. A preliminary assessment using niche modelling based on extensive herpetological surveys in Indo-Burma area combined with algorithmic area prioritization support this conjecture (Pawar *et al.*, unpublished data). Evaluations based on plant diversity within North-east India also point at the need to include more biotic groups in area prioritization efforts. Thus, in general, there is an urgent need to expand current prioritization in the North-east Indian region both in terms of

biodiversity coverage, and the methods for analysing cross-taxon congruence.

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## SUPPLEMENTARY MATERIAL

The following supplementary material is available online at <http://www.blackwell-synergy.com/doi/abs/10.1111/j.1366-9516.2006.000298.x>

**Appendix S1.** Lists of frog, lizard, and bird species

**Appendix S1** Species lists of frog, lizard and bird species included in the study. MO: Mouling National Park; NA: Namdapha Tiger Reserve; NP: Nameri National Park & Pakhui Tiger Reserve; BL: Balphakram National Park; BA: Barail Reserve Forest; DA: Dampa Tiger Reserve; PN: Palak Lake Area & Ngengpui Wildlife Sanctuary.

## FROGS

Family	Scientific name	NP	NA	MO	BL	BR	PN	DA
Bufo	<i>Bufo cf. burmanus</i>	0	1	0	0	0	0	0
Bufo	<i>Bufo himalayanus</i>	1	1	1	0	0	0	0
Bufo	<i>Bufo macrotis</i>	1	1	0	0	0	0	0
Bufo	<i>Bufo melanostictus</i>	1	1	1	1	1	1	1
Bufo	<i>Pedostibes kempiae</i>	0	0	0	0	0	1	1
Megophry	<i>Leptobrachium smithi</i>	0	0	0	1	1	1	1
Megophry	<i>Xenophrys lateralis</i>	1	0	0	0	0	0	0
Megophry	<i>Xenophrys parva</i>	1	0	0	1	1	1	1
Megophry	<i>Xenophrys robusta</i>	0	1	1	0	0	0	0
Megophry	<i>Xenophrys cf. boettgeri</i>	0	0	1	1	0	0	0
Microhyl	<i>Kaloula pulchra</i>	0	0	0	0	1	1	1
Microhyl	<i>Microhyla berdmorei</i>	1	1	0	1	0	1	1
Ranidae	<i>Amolops cf. formosus</i>	1	0	1	0	0	0	0
Ranidae	<i>Amolops cf. viridimaculatus</i>	0	0	1	0	0	0	0
Ranidae	<i>Amolops gerbillus</i>	1	1	1	0	0	0	0
Ranidae	<i>Amolops marmoratus</i>	0	1	1	1	1	1	1
Ranidae	<i>Limnonectes laticeps</i>	1	0	0	1	1	1	1
Ranidae	<i>Occidozyga (P.) sp.</i>	0	0	0	1	1	1	1
Ranidae	<i>Occidozyga (Phrynoglossus) borealis</i>	1	0	1	0	0	0	0
Ranidae	<i>Rana (Ingerana) cf. tasanae</i>	0	1	0	0	0	0	0
Ranidae	<i>Rana alticola</i>	0	0	0	0	0	1	0
Ranidae	<i>Rana danieli</i>	1	1	0	1	0	1	1
Ranidae	<i>Rana garoensis</i>	0	0	0	1	0	0	0
Ranidae	<i>Rana leptoglossa</i>	0	0	0	1	1	1	1
Ranidae	<i>Rana livida</i>	0	0	0	0	1	1	1
Ranidae	<i>Rana taiphensis</i>	1	0	0	1	0	0	0
Rhacophor	<i>Chirixalus doriae</i>	0	1	0	0	0	0	0
Rhacophor	<i>Chirixalus simus</i>	1	0	0	0	0	0	0
Rhacophor	<i>Chirixalus vittatus</i>	1	0	0	0	0	1	0
Rhacophor	<i>Philautus andersoni</i>	1	1	1	0	0	0	0
Rhacophor	<i>Philautus cf. annandalii</i>	1	1	1	0	0	0	0
Rhacophor	<i>Philautus parvulus</i>	0	1	0	0	1	1	1
Rhacophor	<i>Philautus. sp1</i>	0	1	1	0	0	0	0
Rhacophor	<i>Philautus. sp2</i>	0	0	0	0	1	1	1
Rhacophor	<i>Polypedates leucomystax cf. sexvirgatus</i>	1	1	0	1	1	1	1
Rhacophor	<i>Polypedates sp. (cf. himalayanus)</i>	1	1	1	0	0	0	0
Rhacophor	<i>Rhacophorus bipunctatus</i>	0	1	1	0	1	0	1
Rhacophor	<i>Rhacophorus cf. jerdoni</i>	0	0	1	0	0	0	0
Rhacophor	<i>Rhacophorus maximus</i>	1	1	1	1	1	1	1
Rhacophor	<i>Rhacophorus namdaphaensis</i>	0	1	0	0	0	0	0
Rhacophor	<i>Rhacophorus naso</i>	0	0	1	0	0	0	0
Rhacophor	<i>Rhacophorus sp.</i>	0	0	0	0	1	0	0
Rhacophor	<i>Theلودerma (Nyctixalus) moloch</i>	0	0	1	0	0	0	0
Rhacophor	<i>Theلودerma asperum</i>	1	1	1	1	0	0	0

## LIZARDS

Family	Scientific name	NP	NA	MO	BL	BR	PN	DA
Agamidae	<i>Acanthosaura sp.</i>	0	1	0	0	0	0	0
Agamidae	<i>Calotes chincollium</i>	0	0	0	0	0	1	0
Agamidae	<i>Calotes emma</i>	0	0	0	1	1	1	1
Agamidae	<i>Calotes jerdoni</i>	1	1	1	0	0	0	0
Agamidae	<i>Calotes mystaceus</i>	0	1	0	0	0	0	0
Agamidae	<i>Calotes versicolor</i>	1	1	0	1	1	1	1
Gekkonidae	<i>Cosymbotus platyurus</i>	1	1	1	1	1	1	1
Gekkonidae	<i>Cyrtodactylus khasiensis</i>	0	1	1	1	0	0	0
Agamidae	<i>Draco maculatus</i>	0	1	1	1	1	1	1
Agamidae	<i>Draco sp.</i>	0	0	0	0	0	0	1
Gekkonidae	<i>Gekko gecko</i>	1	1	0	1	1	1	1
Gekkonidae	<i>Hemidactylus garnoti</i>	0	0	0	0	0	1	0
Gekkonidae	<i>Hemidactylus frenatus</i>	1	0	1	1	1	1	1
Agamidae	<i>Japalura planidorsata</i>	0	0	0	1	1	0	1
Agamidae	<i>Japalura cf. andersoniana</i>	1	0	1	0	0	0	0
Scincidae	<i>M. dissimilis</i>	1	0	0	0	0	0	0
Scincidae	<i>Mabuya macularia macularia</i>	1	1	1	1	1	1	1
Scincidae	<i>Mabuya multifasciata</i>	1	1	0	1	0	1	1
Scincidae	<i>Mabuya sp.</i>	0	0	0	0	0	1	1
Agamidae	<i>Oriocalots paulus</i>	0	0	1	0	0	0	0
Gekkonidae	<i>Ptychozoon lionotum</i>	0	0	0	0	0	1	0
Agamidae	<i>Ptyctolaemus gularis</i>	1	1	1	1	1	1	1
Scincidae	<i>Sphenomorphus courcyanum</i>	0	0	1	0	0	1	0
Scincidae	<i>Sphenomorphus indicum</i>	1	1	1	1	1	1	1
Scincidae	<i>Sphenomorphus maculatus</i>	1	1	1	1	1	1	1
Lacertidae	<i>Takydromus sexlineatus cf sexlineatus</i>	1	1	0	1	1	1	1
Scincidae	<i>Tropidophorus assamensis</i>	0	0	0	0	0	1	1

## BIRDS

Family	Scientific name	Subgroup level-1	Subgroup level-2	NP	NA	MO	BL	BR	PN	DA
Sylviidae	<i>Abroscopus albogularis</i>	IB	LIB	0	1	1	0	1	0	1
Sylviidae	<i>Abroscopus schisticeps</i>	IB	LIB	0	0	1	0	0	0	1
Sylviidae	<i>Abroscopus superciliaris</i>	IB	LIB	1	1	0	0	1	1	1
Bucerotidae	<i>Aceros nipalensis</i>	HB	UCHB	1	1	0	0	1	0	0
Bucerotidae	<i>Aceros undulatus</i>	HB	UCHB	1	1	0	0	1	1	1
Sylviidae	<i>Actinodura egertoni</i>	OB	LOB	1	1	1	0	1	0	0
Corvidae	<i>Aegithina tiphia</i>	IB	UCIB	1	1	1	1	0	1	1
Sylviidae	<i>Aethopyga nipalensis</i>	HB	LOB	1	0	1	1	1	0	0
Sylviidae	<i>Aethopyga saturata</i>	HB	LOB	1	1	1	1	1	1	1
Sylviidae	<i>Aethopyga siparaja</i>	HB	LOB	1	1	1	1	0	1	1
Sylviidae	<i>Alcippe castaneiceps</i>	OB	LOB	0	1	1	0	1	0	0
Sylviidae	<i>Alcippe cinerea</i>	OB	LOB	0	1	1	0	1	0	0
Sylviidae	<i>Alcippe nipalensis</i>	OB	LOB	1	1	1	1	1	1	1
Sylviidae	<i>Alcippe poioicephala</i>	OB	LOB	0	0	0	0	1	0	1
Sylviidae	<i>Alcippe rufogularis</i>	OB	LOB	0	1	0	0	1	0	0
Pycnonotidae	<i>Alophoixus flaveolus</i>	HB	LOB	1	1	1	1	1	1	1
Bucerotidae	<i>Anorrhinus tickelli</i>	HB	UCHB	0	1	0	0	1	0	0
Bucerotidae	<i>Anthracoceros albirostris</i>	HB	UCHB	1	1	0	1	1	1	1
Sylviidae	<i>Anthreptes singalensis</i>	HB	LOB	1	0	0	1	1	1	1
Sylviidae	<i>Anthus hodgsoni</i>	IB	TIB	1	0	0	1	0	1	0
Sylviidae	<i>Arachnothera longirostra</i>	OB	LOB	1	1	1	1	1	1	1
Sylviidae	<i>Arachnothera magna</i>	OB	LOB	1	1	1	1	1	1	1
Phasianidae	<i>Arborophila atrogularis</i>	OB	TOB	1	1	0	0	1	1	1
Phasianidae	<i>Arborophila rufogularis</i>	OB	TOB	0	1	1	0	0	0	0
Phasianidae	<i>Arborophila mandelii</i>	OB	TOB	0	0	1	0	0	0	0
Phasianidae	<i>Bambusicola fytchii</i>	OB	TOB	0	0	0	0	1	0	1
Picidae	<i>Blythipicus pyrrhotis</i>	IB	LIB	1	1	1	1	1	1	1
Muscicapidae	<i>Brachypteryx hyperythra</i>	IB	TIB	0	1	0	0	1	0	0
Muscicapidae	<i>Brachypteryx leucophrys</i>	IB	TIB	1	1	0	0	0	0	0
Muscicapidae	<i>Brachypteryx montana</i>	IB	TIB	1	1	0	1	1	0	0
Muscicapidae	<i>Brachypteryx stellata</i>	IB	TIB	0	0	1	0	0	0	0
Bucerotidae	<i>Buceros bicornis</i>	HB	UCHB	1	1	0	1	1	1	1
Cuculidae	<i>Cacomantis merulinus</i>	OB	UCIB	1	1	0	0	0	0	1
Picidae	<i>Celeus brachyurus</i>	IB	LIB	1	1	1	1	1	1	1
Columbidae	<i>Chalcophaps indica</i>	HB	LOB	1	1	0	1	1	1	1
Irenidae	<i>Chloropsis aurifrons</i>	OB	UCOB	1	1	0	1	1	1	1
Irenidae	<i>Chloropsis cochinchinensis</i>	OB	UCOB	1	1	0	1	1	1	1
Irenidae	<i>Chloropsis hardwickii</i>	OB	UCOB	1	1	1	1	1	1	1
Cuculidae	<i>Chrysococcyx xanthorhynchus</i>	OB	LIB	0	0	0	0	0	1	1
Picidae	<i>Chrysocolaptes lucidus</i>	IB	UCIB	1	1	0	1	0	1	1
Muscicapidae	<i>Cinclidium frontale</i>	IB	TIB	0	1	0	0	0	0	0



Corvidae	<i>Cissa chinensis</i>	IB	LIB	1	1	1	1	1	1	1
Cuculidae	<i>Clamator coromandus</i>	OB	LIB	0	1	0	0	0	1	0
Muscicapidae	<i>Cochoa purpurea</i>	HB	LOB	0	1	0	0	1	0	0
Muscicapidae	<i>Cochoa viridis</i>	HB	LOB	1	1	0	0	1	0	0
Columbidae	<i>Columba hodgsonii</i>	HB	LOB	0	0	1	0	0	0	0
Columbidae	<i>Columba pulchricollis</i>	HB	LOB	0	1	0	0	1	0	0
Muscicapidae	<i>Copsychus malabaricus</i>	IB	TIB	1	0	0	0	0	1	0
Corvidae	<i>Coracina macei</i>	IB	UCIB	1	1	1	1	1	0	1
Corvidae	<i>Coracina melaschistos</i>	IB	UCIB	1	1	0	1	1	0	1
Cuculidae	<i>Cuculus canorus</i>	OB	UCIB	0	0	0	0	1	0	0
Cuculidae	<i>Cuculus micropterus</i>	OB	UCIB	1	0	0	1	1	1	1
Muscicapidae	<i>Culicicapa ceylonensis</i>	IB	LIB	1	1	1	1	1	1	1
Sylviidae	<i>Cutia nipalensis</i>	OB	LOB	0	0	1	0	0	0	0
Muscicapidae	<i>Cyornis concretus</i>	IB	LIB	0	0	0	0	1	0	1
Muscicapidae	<i>Cyornis poliogenys</i>	IB	LIB	1	0	0	1	1	1	1
Muscicapidae	<i>Cyornis unicolor</i>	IB	LIB	1	1	0	0	0	0	0
Corvidae	<i>Dendrocitta formosae</i>	OB	UCOB	1	1	1	1	1	1	1
Corvidae	<i>Dendrocitta frontalis</i>	OB	UCOB	1	1	0	0	0	0	0
Corvidae	<i>Dendrocitta vagabunda</i>	OB	UCOB	1	0	0	1	0	0	0
Picidae	<i>Dendrocopus canicapillus</i>	IB	LIB	1	1	0	1	1	0	1
Picidae	<i>Dendrocopus macei</i>	IB	LIB	1	1	1	1	1	0	0
Motacillidae	<i>Dendronanthus indicus</i>	IB	TIB	0	0	1	1	1	1	1
Sylviidae	<i>Dicaeum concolor</i>	OB	UCOB	1	0	0	0	1	0	1
Sylviidae	<i>Dicaeum cruentatum</i>	OB	UCOB	1	0	0	1	1	0	1
Sylviidae	<i>Dicaeum ignipectus</i>	OB	UCOB	1	1	1	0	1	0	0
Corvidae	<i>Dicrurus aeneus</i>	IB	LIB	1	1	1	1	1	1	1
Corvidae	<i>Dicrurus annectans</i>	IB	LIB	0	0	0	0	0	1	1
Corvidae	<i>Dicrurus hottentottus</i>	HB	UCHB	1	1	1	1	1	1	1
Corvidae	<i>Dicrurus leucophaeus</i>	OB	UCOB	1	1	1	1	1	0	1
Corvidae	<i>Dicrurus paradiseus</i>	OB	UCOB	1	1	0	1	1	1	1
Corvidae	<i>Dicrurus remifer</i>	OB	UCOB	1	1	1	1	1	1	1
Picidae	<i>Dinopium shorii</i>	IB	UCIB	0	0	0	1	0	0	0
Columbidae	<i>Ducula aenea</i>	HB	UCHB	1	0	0	1	1	1	1
Columbidae	<i>Ducula badia</i>	HB	UCHB	1	1	1	0	1	1	1
Muscicapidae	<i>Enicurus immaculatus</i>	IB	TIB	1	1	0	1	1	1	1
Muscicapidae	<i>Enicurus leschenaulti</i>	IB	TIB	1	1	0	1	0	1	1
Muscicapidae	<i>Enicurus maculus</i>	IB	TIB	0	1	1	0	1	0	1
Muscicapidae	<i>Enicurus schistaceus</i>	IB	TIB	1	1	1	0	1	0	1
Muscicapidae	<i>Enicurus scouleri</i>	IB	TIB	1	1	1	1	1	0	0
Muscicapidae	<i>Eumyias thalassina</i>	IB	LIB	1	0	1	1	0	0	1
Coraciidae	<i>Eurystomus orientalis</i>	IB	UCIB	1	1	0	0	1	1	1
Muscicapidae	<i>Ficedula hyperythra</i>	IB	TIB	1	1	1	0	1	0	1
Muscicapidae	<i>Ficedula monileger</i>	IB	TIB	0	0	0	0	1	0	0
Muscicapidae	<i>Ficedula sapphira</i>	IB	LIB	0	1	0	0	1	0	1

Muscicapidae	<i>Ficedula strophhiata</i>	IB	LIB	1	1	1	0	1	0	1
Muscicapidae	<i>Ficedula westermanni</i>	IB	UCIB	1	1	1	1	1	0	1
Phasianidae	<i>Gallus gallus</i>	OB	TOB	1	1	1	1	1	1	1
Sylviidae	<i>Gampsorhynchus rufulus</i>	IB	LIB	1	1	1	0	1	1	1
Sylviidae	<i>Garrulax caerulatus</i>	OB	TOB	0	0	0	0	0	1	0
Sylviidae	<i>Garrulax galbanus</i>	OB	TOB	0	1	0	0	0	0	0
Sylviidae	<i>Garrulax gularis</i>	OB	TOB	0	1	0	0	1	0	0
Sylviidae	<i>Garrulax leucolophus</i>	OB	TOB	1	1	1	1	1	1	1
Sylviidae	<i>Garrulax merulinus</i>	OB	TOB	0	0	0	0	1	0	0
Sylviidae	<i>Garrulax monileger</i>	OB	TOB	1	1	1	1	1	1	1
Sylviidae	<i>Garrulax pectoralis</i>	OB	TOB	1	1	1	1	1	1	1
Sylviidae	<i>Garrulax ruficollis</i>	OB	TOB	0	1	1	0	0	0	0
Sylviidae	<i>Garrulax rufogularis</i>	OB	TOB	0	1	0	0	1	0	0
Sylviidae	<i>Garrulax squamatus</i>	OB	TOB	0	1	1	0	0	0	0
Sylviidae	<i>Garrulax striatus</i>	OB	LOB	1	0	1	0	0	0	0
Picidae	<i>Gecinulus grantia</i>	IB	LIB	0	1	0	0	1	0	1
Sturnidae	<i>Gracula religiosa</i>	HB	UCHB	1	1	1	1	1	1	1
Trogonidae	<i>Harpactes erythrocephalus</i>	OB	LOB	1	1	1	1	1	1	1
Picidae	<i>Hemicircus canente</i>	IB	UCIB	0	0	0	0	0	0	1
Corvidae	<i>Hemipus picatus</i>	IB	UCIB	0	1	1	1	1	1	1
Pycnonotidae	<i>Hemixos flavala</i>	HB	UCHB	1	1	1	1	1	1	1
Sylviidae	<i>Heterophasia annectans</i>	OB	UCOB	0	1	1	1	1	0	0
Sylviidae	<i>Heterophasia capistrata</i>	OB	UCOB	0	1	0	1	0	0	0
Sylviidae	<i>Heterophasia gracilis</i>	OB	UCOB	0	0	0	0	1	0	0
Sylviidae	<i>Heterophasia picaoides</i>	OB	UCOB	1	1	1	0	0	0	0
Sylviidae	<i>Heterophasia pulchella</i>	OB	UCOB	0	1	1	0	0	0	0
Corvidae	<i>Hypothymis azurea</i>	IB	LIB	1	0	0	1	1	1	1
Pycnonotidae	<i>Hypsipetes leucocephalus</i>	HB	UCHB	1	1	1	1	1	0	1
Pycnonotidae	<i>Hypsipetes mccllellandii</i>	HB	UCHB	1	1	1	1	1	0	0
Pycnonotidae	<i>Iole virescens</i>	HB	UCHB	0	0	0	1	0	0	1
Irenidae	<i>Irena puella</i>	HB	UCHB	1	1	1	1	1	1	1
Sylviidae	<i>Leiothrix argentauris</i>	OB	LOB	1	1	1	0	1	0	0
Sylviidae	<i>Leiothrix lutea</i>	OB	LOB	0	1	0	0	0	0	0
Sylviidae	<i>Liocichla phoenicea</i>	OB	TOB	1	1	1	0	1	0	0
Phasianidae	<i>Lophura leucomelanos</i>	OB	TOB	1	1	0	1	1	1	1
Psittacidae	<i>Loriculus vernalis</i>	HB	UCHB	1	0	0	1	1	1	1
Muscicapidae	<i>Luscinia brunnea</i>	IB	TIB	0	0	1	0	0	0	1
Sylviidae	<i>Macronous gularis</i>	IB	LIB	1	1	0	1	1	1	1
Columbidae	<i>Macropygia unchall</i>	HB	LOB	1	1	0	0	1	1	1
Sylviidae	<i>Malacocinla abbotti</i>	IB	TIB	1	0	0	1	1	1	0
Megalaimidae	<i>Megalaima asiatica</i>	OB	UCOB	1	1	1	1	1	1	1
Megalaimidae	<i>Megalaima australis</i>	OB	UCOB	1	0	1	1	0	0	1
Megalaimidae	<i>Megalaima franklinii</i>	OB	UCOB	1	1	1	0	1	0	0
Megalaimidae	<i>Megalaima lineata</i>	OB	UCOB	1	1	0	1	1	1	1

Megalaimidae	<i>Megalaima virens</i>	OB	UCOB	1	1	1	1	1	1	1
Paridae	<i>Melanochlora sultanea</i>	OB	UCIB	1	1	1	1	1	1	1
Meropidae	<i>Merops leschenaulti</i>	IB	UCIB	1	0	0	1	1	0	0
Sylviidae	<i>Minla cyanouroptera</i>	OB	LIB	1	1	0	0	1	0	0
Sylviidae	<i>Minla ignotincta</i>	IB	UCIB	1	1	1	0	0	0	0
Picidae	<i>Mulleripicus pulverulentus</i>	IB	UCIB	1	1	0	0	1	1	1
Muscicapidae	<i>Muscicapa muttui</i>	IB	LIB	0	0	0	0	0	1	1
Muscicapidae	<i>Muscicapella hodgsoni</i>	IB	TIB	1	1	1	1	1	0	0
Muscicapidae	<i>Myiomela leucura</i>	IB	TIB	1	1	0	0	1	1	1
Muscicapidae	<i>Myophonus caeruleus</i>	IB	LIB	1	1	1	1	1	1	1
Sylviidae	<i>Napothera brevicaudata</i>	IB	TIB	0	1	1	0	1	0	1
Sylviidae	<i>Napothera epilepidota</i>	IB	TIB	0	1	0	0	0	0	1
Sylviidae	<i>Nectarinia asiatica</i>	HB	LOB	0	0	0	1	0	0	0
Sylviidae	<i>Nectarinia sperata</i>	HB	LOB	0	0	0	1	0	0	0
Sylviidae	<i>Nectarinia zeylonica</i>	HB	LOB	0	0	0	1	0	0	0
Muscicapidae	<i>Niltava grandis</i>	IB	LIB	1	1	1	0	1	0	0
Muscicapidae	<i>Niltava macgrigoriae</i>	IB	LIB	1	1	1	0	1	1	0
Muscicapidae	<i>Niltava sundara</i>	IB	LIB	1	1	0	0	1	0	1
Meropidae	<i>Nyctornis athertoni</i>	IB	UCIB	1	1	0	1	1	1	1
Corvidae	<i>Oriolus oriolus</i>	OB	UCOB	0	0	0	1	0	0	0
Corvidae	<i>Oriolus traillii</i>	OB	UCOB	1	1	1	1	1	1	1
Sylviidae	<i>Orthotomus cuculatus</i>	IB	TIB	0	1	1	0	1	0	0
Sylviidae	<i>Orthotomus gularis</i>	IB	TIB	0	0	0	1	1	0	1
Sylviidae	<i>Paradoxornis gularis</i>	OB	LOB	1	1	0	0	1	0	0
Sylviidae	<i>Paradoxornis nipalensis</i>	OB	LOB	0	1	1	0	0	0	0
Sylviidae	<i>Paradoxornis ruficeps</i>	OB	LOB	0	1	1	0	0	0	1
Paridae	<i>Parus monticolus</i>	OB	LOB	0	1	1	0	1	0	0
Sylviidae	<i>Pellorneum tickelli</i>	IB	TIB	1	1	0	1	1	0	1
Sylviidae	<i>Pellornum ruficeps</i>	IB	TIB	1	1	0	1	1	1	1
Corvidae	<i>Pericrocotus brevirostris</i>	IB	UCIB	1	1	1	1	1	1	1
Corvidae	<i>Pericrocotus cinnamomeus</i>	IB	UCIB	0	0	0	1	0	0	0
Corvidae	<i>Pericrocotus ethologus</i>	IB	UCIB	1	0	1	1	0	1	0
Corvidae	<i>Pericrocotus flammeus</i>	IB	UCIB	1	1	1	1	1	1	1
Corvidae	<i>Pericrocotus roseus</i>	IB	UCIB	0	0	0	1	0	0	0
Corvidae	<i>Pericrocotus solaris</i>	IB	UCIB	1	1	1	0	1	0	1
Cuculidae	<i>Phaenicophaeus tristis</i>	OB	LIB	1	1	0	1	1	1	1
Sylviidae	<i>Phylloscopus cantator</i>	IB	LIB	1	1	1	1	1	1	1
Sylviidae	<i>Phylloscopus chloronotus</i>	IB	UCIB	0	1	1	0	1	0	0
Sylviidae	<i>Phylloscopus maculipennis</i>	IB	LIB	0	1	1	0	1	0	0
Sylviidae	<i>Phylloscopus pulcher</i>	IB	UCIB	0	0	0	0	1	0	0
Sylviidae	<i>Phylloscopus reguloides</i>	IB	UCIB	1	1	0	1	1	0	1
Picidae	<i>Picumnus innominatus</i>	IB	LIB	1	1	1	1	1	1	1
Picidae	<i>Picus canus</i>	IB	LIB	1	1	1	1	1	0	1
Picidae	<i>Picus chlorolophus</i>	IB	UCIB	1	1	1	0	1	1	1

Picidae	<i>Picus flavinucha</i>	IB	UCIB	1	1	1	1	1	1	1
Pittidae	<i>Pitta cyanea</i>	IB	TIB	0	1	0	0	0	0	1
Pittidae	<i>Pitta nipalensis</i>	IB	TIB	1	1	0	0	0	1	1
Pittidae	<i>Pitta sordida</i>	IB	TIB	1	0	0	0	1	1	0
Sylviidae	<i>Pnoepyga albiventer</i>	IB	TIB	1	0	1	0	0	0	1
Sylviidae	<i>Pnoepyga pusilla</i>	IB	TIB	1	1	1	0	1	1	1
Phasianidae	<i>Polyplectron bicalcaratum</i>	OB	TOB	1	1	0	1	1	1	1
Sylviidae	<i>Pomatorhinus erythrocnemis</i>	OB	TOB	0	0	0	0	0	1	1
Sylviidae	<i>Pomatorhinus ferruginosus</i>	OB	TOB	0	1	1	0	1	0	1
Sylviidae	<i>Pomatorhinus hypoleucos</i>	OB	TOB	0	1	1	0	0	1	1
Sylviidae	<i>Pomatorhinus ochraceiceps</i>	OB	TOB	0	1	1	0	1	0	0
Sylviidae	<i>Pomatorhinus ruficollis</i>	OB	TOB	1	0	0	0	1	0	0
Sylviidae	<i>Pomatorhinus schisticeps</i>	OB	TOB	0	1	1	1	1	0	1
Eurylaimidae	<i>Psarisomus dalhousiae</i>	HB	LOB	1	1	1	1	1	1	1
Psittacidae	<i>Psittacula alexandri</i>	HB	UCHB	1	0	0	1	0	0	0
Psittacidae	<i>Psittacula finschii</i>	HB	UCHB	0	0	1	0	1	0	1
Psittacidae	<i>Psittacula roseata</i>	HB	UCHB	0	1	0	0	0	0	0
Sylviidae	<i>Pteruthius flaviscapis</i>	IB	LIB	0	1	1	0	1	0	0
Sylviidae	<i>Pteruthius melanotis</i>	IB	LIB	0	1	1	0	1	0	0
Pycnonotidae	<i>Pycnonotus melanicterus</i>	HB	UCHB	1	1	0	1	1	1	1
Pycnonotidae	<i>Pycnonotus striatus</i>	HB	UCHB	0	1	1	0	1	0	1
Corvidae	<i>Rhipidura albicollis</i>	IB	LIB	1	1	1	1	1	1	1
Corvidae	<i>Rhipidura hypoxantha</i>	IB	LIB	1	1	1	0	1	0	1
Picidae	<i>Sasia ochracea</i>	IB	LIB	1	1	1	1	1	1	1
Sylviidae	<i>Seicercus affinis</i>	IB	LIB	1	1	1	1	1	1	1
Sylviidae	<i>Seicercus burkii</i>	IB	LIB	1	1	1	1	1	1	1
Sylviidae	<i>Seicercus castaniceps</i>	IB	UCIB	1	1	1	0	1	0	0
Sylviidae	<i>Seicercus poliogenys</i>	IB	UCIB	1	1	1	0	1	0	0
Sylviidae	<i>Seicercus xanthoschistos</i>	IB	LIB	1	1	1	1	1	0	0
Eurylaimidae	<i>Serilophus lunatus</i>	HB	LOB	1	1	1	0	0	1	1
Sittidae	<i>Sitta castanea</i>	IB	UCIB	1	1	1	0	0	0	1
Sittidae	<i>Sitta formosa</i>	IB	UCIB	0	1	1	0	1	0	0
Sittidae	<i>Sitta frontalis</i>	IB	UCIB	1	1	0	1	0	0	1
Sylviidae	<i>Spelaeornis caudatus</i>	IB	TIB	0	0	1	0	0	0	0
Sylviidae	<i>Spelaeornis formosus</i>	IB	TIB	0	1	0	0	1	0	0
Sylviidae	<i>Sphenocichla humei</i>	IB	TIB	0	1	1	0	1	0	0
Sylviidae	<i>Stachyris chrysaea</i>	OB	LOB	1	1	1	0	1	0	0
Sylviidae	<i>Stachyris nigriceps</i>	OB	LIB	1	1	1	0	1	1	1
Sylviidae	<i>Stachyris oglei</i>	OB	LIB	0	1	0	0	0	0	0
Sylviidae	<i>Stachyris ruficeps</i>	OB	LIB	1	0	0	0	1	1	1
Sylviidae	<i>Stachyris rufifrons</i>	OB	LOB	1	1	0	1	0	1	1
Cuculidae	<i>Surniculus lugubris</i>	OB	UCOB	1	1	0	0	0	1	1
Paridae	<i>Sylviparus modestus</i>	IB	UCIB	0	0	1	0	0	0	0
Muscicapidae	<i>Tarsiger cyanurus</i>	IB	TIB	1	1	0	0	1	0	0

Corvidae	<i>Tephrodornis gularis</i>	OB	UCOB	1	1	1	1	0	1	1
Corvidae	<i>Terpsiphone paradisi</i>	IB	LIB	1	1	1	1	1	1	1
Sylviidae	<i>Tesia castaneocoronata</i>	IB	TIB	1	1	1	0	1	0	0
Sylviidae	<i>Tesia cyaniventer</i>	IB	TIB	0	1	1	0	1	1	1
Sylviidae	<i>Tesia olivea</i>	IB	TIB	1	1	1	1	1	1	1
Sylviidae	<i>Tickellia hodgsoni</i>	IB	LIB	1	1	0	0	1	0	1
Columbidae	<i>Treron apicauda</i>	HB	UCHB	1	1	1	1	1	1	1
Columbidae	<i>Treron bicinctus</i>	HB	UCHB	0	0	0	1	1	0	0
Columbidae	<i>Treron curvirostra</i>	HB	UCHB	1	0	0	1	1	1	1
Columbidae	<i>Treron phoenicopterus</i>	HB	UCHB	0	0	0	1	1	0	0
Columbidae	<i>Treron pompadora</i>	HB	UCHB	1	1	1	0	1	1	1
Columbidae	<i>Treron sphenura</i>	HB	UCHB	1	1	1	1	1	0	1
Sylviidae	<i>Turdoides striatus</i>	IB	TIB	0	0	0	1	0	0	0
Muscicapidae	<i>Turdus albocinctus</i>	OB	LOB	0	1	0	1	0	0	0
Muscicapidae	<i>Turdus boulboul</i>	OB	LOB	1	1	0	0	1	0	1
Muscicapidae	<i>Turdus dissimilis</i>	OB	LOB	0	1	0	0	1	0	0
Corvidae	<i>Urocissa flavirostris</i>	IB	LIB	0	0	1	0	0	0	0
Sylviidae	<i>Xiphirhynchus superciliaris</i>	OB	TOB	0	1	0	0	1	0	0
Sylviidae	<i>Yuhina bakeri</i>	OB	LOB	1	1	1	0	1	0	0
Sylviidae	<i>Yuhina castaniceps</i>	OB	LOB	0	1	1	0	1	0	1
Sylviidae	<i>Yuhina flavicollis</i>	OB	LOB	1	1	1	0	1	0	1
Sylviidae	<i>Yuhina nigrimenta</i>	OB	UCOB	1	1	1	0	1	0	0
Sylviidae	<i>Yuhina occipitalis</i>	OB	UCOB	0	0	1	0	0	0	0
Sylviidae	<i>Yuhina xantholeuca</i>	OB	LOB	1	1	1	1	1	1	1
Muscicapidae	<i>Zoothera citrina</i>	OB	LOB	1	0	1	1	1	0	1
Muscicapidae	<i>Zoothera dauma</i>	OB	LOB	0	1	0	0	1	1	1
Muscicapidae	<i>Zoothera dixonii</i>	OB	LOB	0	1	1	0	1	0	0
Muscicapidae	<i>Zoothera marginata</i>	OB	LOB	0	1	0	0	0	0	1
Muscicapidae	<i>Zoothera molissima</i>	OB	LOB	0	1	0	0	0	0	0
Muscicapidae	<i>Zoothera monticola</i>	OB	LOB	0	0	0	1	1	0	0
Zosteropidae	<i>Zosterops palpebrosus</i>	OB	UCOB	1	0	1	1	1	1	1