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RESEARCH ARTICLE

Evolutionary distinctness of Important Bird Areas (IBAs) of Sri Lanka: Do the species-rich wet zone forests safeguard Sri Lanka's genetic heritage?

Dilini K. Abeyarama and Sampath S. Seneviratne*

Avian Evolution Node, Department of Zoology and Environment Sciences, Faculty of Science, University of Colombo, Colombo 03

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Abstract: Different components of biodiversity cannot be treated equally due to the limitations of knowledge and resources, and the heterogeneity in the distribution of biodiversity in the landscape. Therefore, biodiversity should be prioritized in effective site-based conservation. Parameters related to ecology, sociology and economics are primarily used for this prioritization process. Genetic and evolutionary history is broadly ignored. Using Important Bird Areas (areas of high avian diversity or density, defined based on several key criteria of species richness and abandons) as a model, here we attempted to use several key evolutionary tools in biodiversity prioritization with the aim of testing their applicability in an island nation where evolutionary relationships of species are yet to be fully appreciated. We developed a DNA-based phylogenetic tree for the 342 total species of birds recorded in Sri Lanka's 71 IBAs. We used DNA sequence archives at www.birdtree.org for closely-related crown nodes of Sri Lankan species and higher-order phylogenetic backbone for represented taxonomic orders to construct the phylogenetic tree. Using this tree, we calculated the Phylogenetic Diversity (PD), Evolutionary Distinctness (ED) and the extinction risk of deep lineages (EDGE scores) for each IBA. *Batrachostomus moniliger* (Ceylon Frogmouth) is the most ED species while *Otus thilohoffmanni* (Serendib Scopes-owl) is the most EDGE species for Sri Lanka. Sri Lanka's premier dry zone National Parks, Yala, Bundala and Udawalawe are the top ranked IBAs in PD, ED and EDGE scores. Except Sinharaja MAB Reserve and Knuckles, all other wet zone IBAs, which are characterized by their high endemicity and biodiversity were not ranked among the top ten IBAs for above evolutionary parameters. Mixing of both continental and insular lineages in the dry zone due to its proximity to mainland, the presence of wetlands that support migratory lineages and the movement of wet zone taxa along the riverine forests towards the dry zone could have increased the PD and ED scores in dry zone IBAs. However, wet zone IBAs are better at keeping the avian genetic composition that is unique to Sri Lanka by holding most of the avian endemics. For islands like Sri Lanka, global indices do not reflect the local evolutionary and conservation status. Effective site-based conservation programs that are aimed at preventing local extinctions therefore, must recognize the heterogeneity of biodiversity across the landscape. Our results show that the evolutionary parameters such as PD, ED and EDGE score are effective tools to refine the conventional indices used in habitat prioritization for Sri Lanka.

Keywords: Conservation prioritization, evolutionary distinctness, Important Bird Areas, *in-situ* conservation, phylogenetic diversity, risk of extinction, Sri Lanka.

INTRODUCTION

As a result of excessive consumption of natural resources and the climate change, world is experiencing a sharp drop in biodiversity and an unprecedented rate of extinction of both fauna and flora (Vitousek *et al*., 1997). Conservation of species is therefore paramount in curtailing biodiversity decay. With limited amount of knowledge and resources available, effective conservation requires prioritization of biological entities such as the species and ecosystems. Commonly used ecological parameters such as species richness and number of endemic species do not consider the evolutionary history of the species. Not all species are ecologically equally important, yet they are important in other aspects such as form, function, evolutionary uniqueness and aesthetic appeal, where an extinction of such species causes a considerable loss of biodiversity because biodiversity is not only species richness but also the history of life as a whole (Jetz *et al*., 2014).

The evolutionary history of a clade (a distinct group of organisms) can be traced back using a phylogenetic tree (Pagel, 1999), in which the tips and nodes of the tree stand for descendant taxa and their common ancestors respectively (Vellend *et al*., 2011). Nee and May (1997) suggested that the more distal nodes (*i.e*. species) a branch carries, the lower the amount of evolutionary history captured by each of its representative nodes in that particular part of the tree of life (Figure 1).

Several phylogenetic parameters have been introduced to measure how much evolutionary history is captured by a species or a geographic area such as: Phylogenetic Diversity (PD), Evolutionary Distinctness (ED), and Evolutionary Distinct and Globally Endangered Score (EDGE Score) (Faith, 1992a; Isaac *et al*., 2007; Vellend *et al*., 2007; Jetz *et al*., 2014). PD is the minimum sum of branch length of a particular set of taxa in the phylogenetic tree (Faith, 1992a). The branch length between two given nodes (*i.e*. taxa) is the estimate of time at which two nodes started to evolve independently of each other (Vellend *et al*., 2011). ED is a measure of how much a particular species is isolated in a phylogenetic tree. The higher the ED of a given species, the lower the number of closely related species it has in the phylogenetic tree (Jetz *et al*., 2014). The EDGE score (Isaac *et al*., 2007) is an index derived from combining ED scores with the IUCN red list categories (Butchart *et al*., 2004). EDGE scores can

**Corresponding Author's Email:* sam@sci.cmb.ac.lk
http://orcid.org/0000-0003-2159-4410

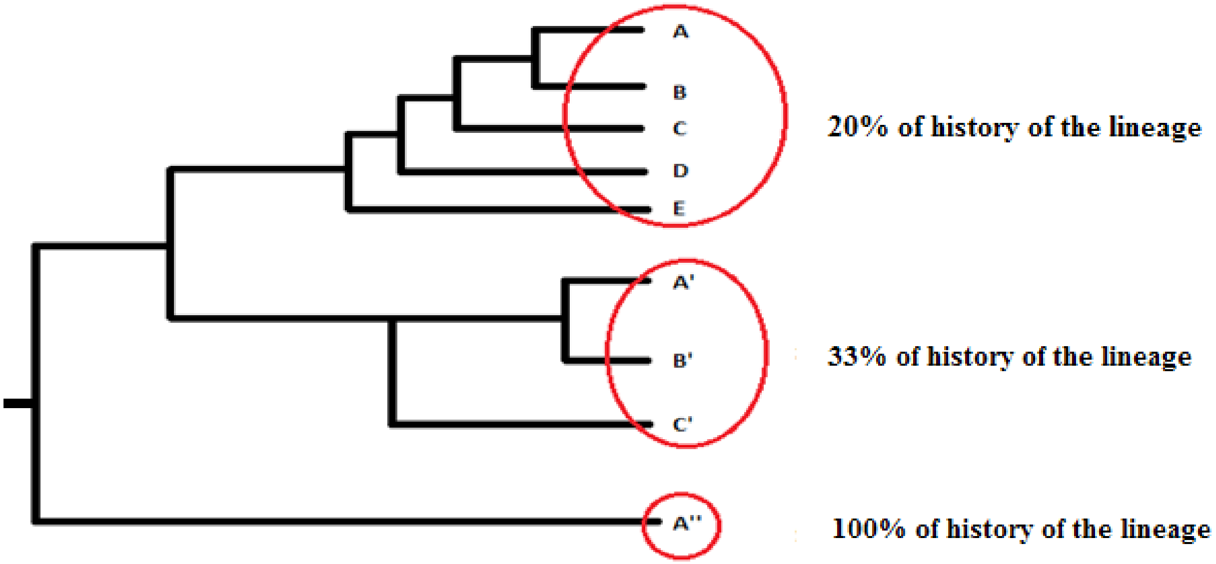

Figure 1: A schematic phylogenetic tree illustrating the unequal representation of evolutionary history captured by each of the nine distal nodes (A to A") after (Nee & May, 1997).

be directly used to set conservation priorities (Isaac *et al*., 2007).

Mean Pairwise Distance (MPD) is another phylogenetic measurement that is used to determine whether the species found in a given area are more closely related than predicted by their form and function**.** MPD is measured as a summation of the evolutionary relatedness of all the pairs of species found in that area (Webb *et al.,* 2002).

Effective conservation could be achieved through site-based conservation measures (Jetz *et al*., 2014). Since the global distribution and abundance of taxa is not uniform (Brusatte *et al.* 2015, Jetz *et al.* 2014), similar to what has been recognized in IUCN red listing criteria (National Red List, 2012), the conservation prioritization should recognize the heterogeneity of evolutionary and ecological criteria across the landscape. Therefore, global PD, ED or EDGE values do not fit to assess the level of accumulation of lineages and risk of local extinctions of globally widespread species in the regional or national level (*e.g.* in an island like Sri Lanka). There are numerous criteria available for site selection. For example biodiversity indices such as Simpson Index (Simpson, 1949), legislative descriptions such as National Parks and sites marked for species based conservation such as 'Important Bird Areas' (IBAs) can be used to compare sites.

IBAs are sites that have international significance on the conservation of birds and were introduced by a global consortium of bird-related organizations called BirdLife International (BirdLife International, 2016). IBAs have both regional and global significance; they have been selected based on scientific and objective standards associated with globally threatened species, restricted-range species, biome-restricted species and large bird aggregations (BirdLife International, 2016). There are 71 IBAs in Sri Lanka and all of them are located within the protected area network of Sri Lanka (Field ornithology group of Sri Lanka, 2003).

Birds have evolved within the lineage led to dinosaurs over a period of ~100 million years (Brusatte *et al*., 2015). About the past 50MYA they underwent an explosive radiation which led to the present diversity of ~10,000 species (Jarvis *et al.,* 2014, Jetz *et al*., 2012). Does each of these extant species capture the same evolutionary history in the bird tree? Do all IBAs carry similar evolutionary history of the birds that they harbor? Which IBAs have higher evolutionary significance or carry a higher number of unique or endangered lineages, and hence require greater conservation attention? Using IBAs as a model, here we attempted to use several key evolutionary tools such as PD, ED and EDGE, to rank IBAs in the aim of testing their applicability as a tool for conservation for Sri Lanka. We hypothesized that the species-rich wet zone IBAs have greater PD, ED and EDGE scores compared to their less celebrated dry zone counterparts. We use the help of low-cost global data archives and statistical freeware to perform our bioinformatics analysis.

METHODS

A total species list, which contains all recorded species across 71 IBAs was obtained from the IBA database of the Field Ornithology Group of Sri Lanka. Vagrant species and species unlikely to utilize the focal habitat (e.g. seabirds in montane IBAs) were removed from the dataset. The final list of 342 species was fed into the option 'Phylogeny subsets' of 'www.birdtree.org' and a set of 5000 phylogenetic trees was generated. Hackett *et al.* (2008) described the deep order- and family-level affinities of birds. We used the option 'Hackett All Species: a set of 10,000 trees with 9,993 OTUs each' in the www.birdtree.org site, which uses the database of species of Hackett *et al.* (2008) as the backbone. To generate the grand tree for all 342 species recorded, the program followed four main steps. For the construction of the tree it combined relaxed molecular clock trees of well supported clades with a backbone which contained representatives from each clade (Jetz *et al*., 2012). As the first step, each species was assigned to one of the 158 clades which arise from the 158 tips of the backbone trees. Then relaxed-clock trees were constructed for each clade. The species that do not have genetic information were plugged in to their relevant clades using the information obtained by combining the relaxed clock trees and available taxonomic information (Jetz *et al*., 2012). The final tree was constructed by merging trees from either of the previous two steps with time calibrated relaxed molecular clock backbone trees (Jetz *et al*., 2012; BirdLife International, 2016).

A consensus tree (Figure 2) was generated from the file of 5,000 phylogenetic trees generated by www.birdtree.org using 'TreeAnnotator v1.8.2' of the software BEAST (BEAST v1.8.2). R platform (R Development Core Team) was used to measure the Evolutionary Distinctiveness (ED) and EDGE scores for each species. Using the R codes E1 (see below), the ED of all 342 species was calculated.

Originality<-evol.distinct(tree,type="fair.proportion"

(E1)

The ED of IBAs was calculated using the equation E2,

ED of an IBA= ∑ ED of each species in the IBA

(E2)

EDGE score was calculated for each species using E3 (Isaac *et al*., 2007)

$$\mathrm{EDGE} = \ln(1+\mathrm{ED}) + \mathrm{GE} * \ln(2) \qquad \text{(E3)}$$

Where GE = Red list category weight (Least Concern=0, Near Threatened and Conservation Dependent=1, Vulnerable=2, Endangered=3, Critically Endangered=4).

Then the EDGE scores for each of the IBAs were calculated separately by summing the EDGE scores of all the bird species in the IBA (E4).

EDGE score of an IBA= ∑ EDGE of all species in the IBA (E4)

We ranked all 342 species based on their ED and EDGE values. The global ED and EDGE scores of birds were taken from Jetz *et al.* (2014). The MPD could not be calculated due to several technical limitations.

Species Richness (SR) and abundance are two of the most widely used ecological parameters in the measurement of biodiversity (Gugerli *et al*., 2008). Number of endemics in a given area is another parameter that can be used to

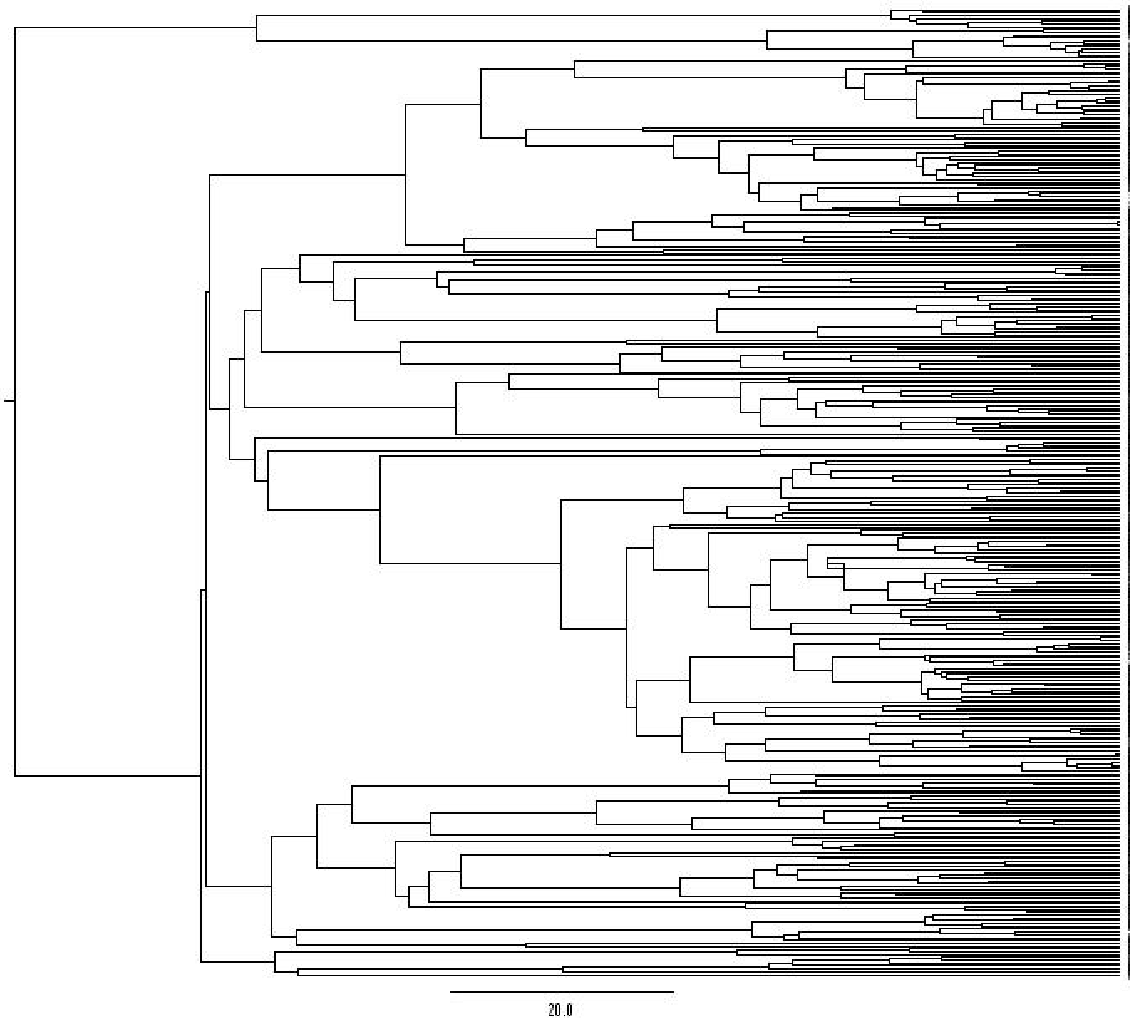

Figure 2: Phylogenetic tree of total 342 bird species reported in IBAs of Sri Lanka.

measure biodiversity. SR of each IBA was obtained taking the total number of species in the total area of each IBA. Number of endemic species (EM) of an IBA was obtained by counting the total number of endemic species of birds found in each IBA.

RESULTS

The most evolutionarily distinct (ED) species that are found in 71 IBAs of Sri Lanka are (Table 01) as follows: Ceylon Frogmouth (*Batrachostomus moniliger*), Malabar Trogon (*Harpactes fasciatus*), Indian Pitta (*Pitta brachyura*), Greater Flamingo (*Phoenicopterus roseus*) and Little Grebe (*Tachybaptus ruficollis*). The most evolutionary distinct endangered lineages (EDGE) found in IBAs (Table 02) are: Serendib Scops-owl (*Otus thilohoffmanni*), Green-billed Coucal (*Centropus chlororhynchus*), Ceylon Whistling-thrush (*Myophonus blighi*) and Lesser Adjutant (*Leptoptilos javanicus*).

When considering both the resident and migratory species, the below 10 IBAs topped the list of IBAs with highest PD; Yala National Park, Bundala NP, Udawalawe NP, Kalametiya Sanctuary, Wasgomuwa NP, Sigiriya Sanctuary, Wilpattu NP, Gal Oya NP, Minneriya-Girithale NP and Maduru Oya NP (Figure 3). When only the resident species were included for the analysis, the below IBAs topped the list of IBAs with the highest PD; Yala NP, Udawalawe NP, Wasgomuwa NP, Bundala NP, Gal Oya NP, Sigiriya Sanctuary, Wilpattu NP, Maduru Oya NP, Minneriya-Girithale NP and Sinharaja MAB Reserve. Therefore, Sinharaja MAB Reserve is the only wet zone IBA in the list of top IBAs with highest PD (Table 03 and Table 04).

In the analyses with migratory species and without migratory species, a higher percentage of IBAs that ranked top 10 under four parameters SR, PD, ED and EDGE score are forest IBAs located in the dry zone (Figure 3). However, when considering the number of endemics per IBA, the top 10 IBAs are all forest IBAs in the wet zone (Table 05- 07).

Table 01: Species that has the highest evolutionary distinctness (ED) in Sri Lanka

Local Rank	Scientific Name	Common Name	IUCN status
01	*Batrachostomus moniliger*	Ceylon Frogmouth	Least Concern
02	*Harpactes fasciatus*	Malabar Trogon	Least Concern
03	*Pitta brachyura*	Indian Pitta	Least Concern
04	*Phoenicopterus roseus*	Greater Flamingo	Least Concern
05	*Tachybaptus ruficollis*	Little Grebe	Least Concern
06	*Pelecanus philippensis*	Spot-billed Pelican	Near Threatened
07	*Upupa epops*	Eurasian Hoopoe	Least Concern
08	*Pandion haliaetus*	Osprey	Least Concern
09	*Elanus caeruleus*	Black-winged Kite	Least Concern
10	*Phodilus badius*	Oriental Bay-owl	Least Concern

Table 02: Species that has the highest EDGE score in Sri Lanka

Local Rank	Scientific Name	Common Name	IUCN status
01	*Otus thilohoffmanni*	Serendib Scops-owl	Endangered/ Endemic
02	*Centropus chlororhynchus*	Sri Lanka Green-billed Coucal	Vulnerable/ Endemic
03	*Myophonus blighi*	Sri Lanka Whistling-thrush	Endangered/ Endemic
04	*Leptoptilos javanicus*	Lesser Adjutant	Vulnerable
05	*Pelecanus philippensis*	Spot-billed Pelican	Near Threatened
06	*Urocissa ornata*	Sri Lanka Magpie	Vulnerable/ Endemic
07	*Phaenicophaeus pyrrhocephalus*	Sri Lanka Red-faced Malkoha	Vulnerable/ Endemic
08	*Anthracoceros coronatus*	Malabar Pied Hornbill	Near Threatened
09	*Columba torringtoniae*	Sri Lanka Wood-pigeon	Vulnerable/ Endemic
10	*Threskiornis melanocephalus*	Black-headed Ibis	Near Threatened

Table 03: Top 10 IBAs with highest phylogenetic diversity (PD). Both resident and migratory species of birds were included for this analysis.

Rank	PD	IBA	SR	No: of Endemics	ED of IBA	EDGE score
1	**7146.08**	**Yala NP**	**265**	**15**	**6716.26**	**851.514**
2	6599.51	Bundala NP	237	8	5910.93	759.557
3	6394.98	Udawalawe NP	220	14	5705.46	714.051
4	5861.09	Kalametiya Sanctuary	205	6	5060.33	651.369
5	5836.75	Wasgomuwa NP	199	17	5169.09	649.623
6	5822.66	Sigiriya Sanctuary	190	11	4946.32	615.532
7	5815.05	Wilpattu NP	190	7	4840.92	612.845
8	5806.31	Gal Oya NP	187	16	5060.84	615.03
9	5671.78	Minneriya - Girithale NP	173	11	4646.39	567.236
10	5507.71	Maduru Oya NP	174	14	4528.13	564.414

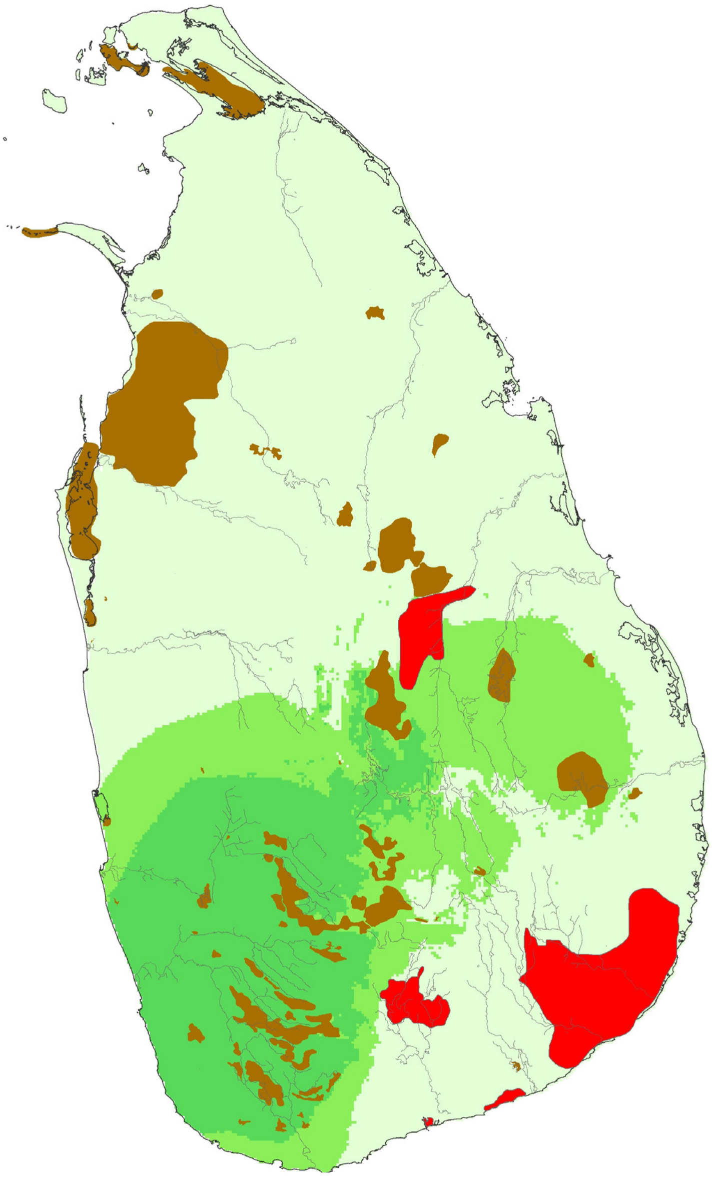

Figure 3: IBAs of Sri Lanka. The top five most evolutionarily diverse (PD, ED and EDGE) IBAs are highlighted in red color. Main climatic zones and main river systems of the island are also indicated in the map.

Table 04: Top 10 IBAs with highest phylogenetic diversity (PD). Only resident species of birds were included for this analysis.

Rank	PD	IBA	SR	ED of IBA	EDGE
1	**5759.48**	**Yala NP**	**187**	**5118.95**	**618.803**
2	5323.99	Udawalawe NP	167	4529.83	547.876
3	5165.79	Wasgomuwa NP	168	4533.63	555.482
4	5059.09	Bundala NP	154	4183.55	509.339
5	5049.8	Gal Oya NP	162	4443.86	537.055
6	5032.27	Sigiriya Sanctuary	155	4202.66	510.355
7	4912.51	Wilpattu NP	144	3933.69	476.221
8	4856.28	Maduru Oya NP	147	3952.02	483.06
9	4735.8	Minneriya - Girithale NP	136	3816.81	453.016
10	4724.16	Sinharaja MABR	159	4088.88	524.846

DISCUSSION

Species in the older and species-poor lineages tend to carry a greater amount of phylogenetic history than those in speciose, recently branched out lineages (Isaac *et al*., 2007). Using several phylogenetic parameters such as Phylogenetic Diversity (PD), Evolutionary Distinctness (ED) and Evolutionary Distinct Endangered Lineage (EDGE) scores, we measured how much evolutionary history is captured by Sri Lanka's IBAs. We tested whether the avian evolutionary history of the island is confined to a particular climatic zone. When we ranked IBAs based on PD, ED and EDGE scores the majority of the top 10 ranked IBAs are located in the dry zone (Fig. 03). Although wet zone IBAs are poor at representing the evolutionary history (PD and ED) of birds of the island, their high endemicity represents the genetic heritage unique to the island.

The PD of an IBA increases with the increment of the number of species in that IBA with some distinguished omissions. For example, the SR of two IBAs Anuradhapura Sanctuary and Sinharaja MABR are 172 and 182 where the PD of them are 5492.97 and 5241.96 respectively. The reason for this is that not all the species contribute equally for PD (Brusatte *et al*., 2015). The species that have evolved long ago have greater contribution to PD while the recently diverged species have lesser contribution (Hackett *et al*., 2008; Table 01). The species that have low ED scores are not isolated in the avian phylogenetic tree and they have many closely related species. However the birds that have very high ED scores such as *B. moniliger* (Ceylon Frogmouth) are isolated groups in the phylogeny and they do not have closely related forms near them in Sri Lanka. The species such as *S. bengalensis* (Lesser-Crested Tern) and *S. bergii* (Great-Crested Tern) that have similar ED scores are sister to each other. Closely related (non-sister) forms could also have approximately similar ED scores (Table 01).

The cumulative ED score of an IBA represents how much evolutionary history is captured by that particular area (Jetz *et al*., 2014). The higher the species richness, the higher will be the ED captured by that area. When that IBA is home for more evolutionarily isolated species (species with high ED) the ED value of the IBA could increase more than the average. For an example, the two IBAs Newgalkanda and Padaviya Tank harbor 66 species in each, but the ED are very different between the two IBAs (1464.891 and 1739.62 respectively). Padaviya Tank IBA must be carrying more evolutionary isolated species than that by the Newgalkanda IBA.

Yala NP is rank 1st in SR, PD, ED and EDGE score in both analyses done with and without migratory species (Table 05-07). The reason could be its very high SR. Species richness tends to push PD and adds a bias. Using MPD one could reduce this bias. However due to technical difficulties, we could not correct this bias. When only resident species were included in the analysis, the order of IBAs with regards to PD, changes. In our study at Bundala NP, which ranked 2nd when migratory species were included, ranked 4th when they were removed. Being a wetland IBA and a key overwintering location for migratory species, the reason for this shift is that Bundala NP gets several extra lineages as migratory species, which elevates its PD.

The local and global ED ranking are very different, for example, *P. brachyura* (Indian Pitta) which ranks 3rd in the local rankings comes 10th if we use global rankings. But *P. haliaetus* (Osprey) which ranks 8th under local rankings will come 1st with the global rankings. The reason for this is that in the local context Indian pitta represents a monotypic genus and therefore its ED is high, but when all bird species of the world are considered the pittas represent a polytypic genus.

Sri Lanka is a distinctly identifiable geological entity (a continental island) with a unique geological history. As a result, it harbors a unique faunal and floral assemblage (e.g. Ripley and Beehler 1990, Bossuyt *et al* 2004, Wickramasinghe *et al* 2017). Even though there are ~10,000 species of birds in the world, the island of Sri Lanka only carries a 1/20th of the global diversity that is ~ 500 species (Rasmussen and Anderton, 2005). To evaluate the evolutionarily significance of Sri Lanka's avifauna, one should only consider the 500 or so species found in Sri Lanka. To simplify the concept, let us breakdown this approach into few simple steps: (a.) Let us go to Sri Lanka in time T_0 where no birds found. (b.) In time T_1 one species

Table 05: IBAs with highest scores in SR, EM, PD, ED and EDGE scores with respect to the climatic zone. Both resident and migratory species are included in the analysis. Colour key: Tangerine- arid zone, coral- dry zone, dark green- wet zone hill country, and green- wet zone low country.

Rank	IBA	SR	IBA	No: of Endemics	IBA	PD	IBA	ED of IBA	IBA	EDGE score
1	Yala NP	265	Peak Wilderness Sanctuary	33	Yala NP	7146.08	Yala NP	6716.26	Yala NP	851.51
2	Bundala NP	237	Sinharaja MABR	33	Bundala NP	6599.5	Bundala NP	5910.93	Bundala NP	759.56
3	Udawalawe NP	220	Thangamale Sanctuary	30	Udawalawe NP	6394.98	Udawalawe NP	5705.46	Udawalawe NP	714.05
4	Kalametiya Sanctuary	205	Delwala FR	29	Kalametiya Sanctuary	5861.09	Wasgomuwa NP	5169.09	Kalametiya Sanctuary	651.37
5	Wasgomuwa NP	199	Kithulgala	29	Wasgomuwa NP	5836.75	Gal Oya	5060.84	Wasgomuwa NP	649.62
6	Wilpattu NP	190	KDN Complex	29	Sigiriya Sanctuary	5822.65	Kalametiya Sanctuary	5060.33	Sigiriya Sanctuary	615.53
7	Sigiriya Sanctuary	190	Delgoda-Kudumiriya FR	29	Wilpattu NP	5815.05	Sigiriya Sanctuary	4946.32	Gal Oya NP	615.03
8	Gal Oya NP	187	Morapitiya-Runakanda FR	28	Gal Oya NP	5806.31	Wilpattu NP	4840.92	Wilpattu NP	612.85
9	Sinharaja MABR	182	Horton Plains NP	27	Minneriya - Girithale NP	5671.78	Sinharaja MABR	4690.01	Sinharaja MABR	600.23
10	Maduru Oya NP	174	Gilimale-Eratna Sanctuary	27	Maduru Oya NP	5507.71	Minneriya - Girithale NP	4646.39	Minneriya - Girithale NP	567.24

Table 06: IBAs with highest scores in SR, PD, ED of IBA and EDGE scores with respect to climatic zones. Only the resident species are included in the analysis. Colour key: Tangerine- arid zone, coral-dry zone, dark green- wet zone hill country and green- wet zone mid & low country.

Rank	IBA	SR	IBA	PD	IBA	ED of IBA	IBA	EDGE score
1	Yala NP	187	Yala NP	5759.48	Yala NP	5118.95	Yala NP	618.803
2	Wasgomuwa NP	168	Udawalawe NP	5323.99	Wasgomuwa NP	4533.63	Wasgomuwa NP	555.482
3	Udawalawe NP	167	Wasgomuwa NP	5165.79	Udawalawe NP	4529.83	Udawalawe NP	547.876
4	Gal Oya NP	162	Bundala NP	5059.09	Gal Oya NP	4443.86	Gal Oya NP	537.055
5	Sinharaja MABR	159	Gal Oya NP	5049.8	Sigiriya Sanctuary	4202.66	Sinharaja MABR	524.846
6	Sigiriya Sanctuary	155	Sigiriya Sanctuary	5032.27	Bundala NP	4183.55	Sigiriya Sanctuary	510.355
7	Bundala NP	154	Wilpattu NP	4912.51	Sinharaja MABR	4088.88	Bundala NP	509.339
8	Maduru Oya NP	147	Maduru Oya NP	4856.28	Maduru Oya NP	3952.02	Maduru Oya NP	483.06
9	Wilpattu NP	144	Minneriya - Girithale NP	4735.8	Wilpattu NP	3933.69	Wilpattu NP	476.221
10	Knuckles Conservation Forest	139	Sinharaja MABR	4724.16	Minneriya - Girithale NP	3816.81	Knuckles Conservation Forest	454.764

Table 07: IBAs with highest scores in SR, EM, PD, ED and EDGE scores with respect to the habitat type (forest or wetland). Both resident and migratory species are included in the analysis. Colour key: Green- forest IBAs, blue- wetland IBAs and cyan- forest and wetland IBAs.

Rank	IBA	SR	IBA	No. of Endemics	IBA	PD	IBA	ED of IBA	IBA	EDGE
1	Yala NP	265	Sinharaja MABR	33	Yala NP	7146.08	Yala NP	6716.26	Yala NP	851.51
2	Bundala NP	237	Peak Wilderness Sanctuary	33	Bundala NP	6599.5	Bundala NP	5910.93	Bundala NP	759.56
3	Udawalawe NP	220	Thangamale Sanctuary	30	Udawalawe NP	6394.98	Udawalawe NP	5705.46	Udawalawe NP	714.05
4	Kalametiya Sanctuary	205	Delwala-Panilkanda-Walankanda FR	29	Kalametiya Sanctuary	5861.09	Wasgomuwa NP	5169.09	Kalametiya Sanctuary	651.37
5	Wasgomuwa NP	199	Kithulgala FR	29	Wasgomuwa NP	5836.75	Gal Oya NP	5060.84	Wasgomuwa NP	649.62
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7	Sigiriya Sanctuary	190	Delgoda-Kudumiriya FR	29	Wilpattu NP	5815.05	Sigiriya Sanctuary	4946.32	Gal Oya NP	615.03
8	Gal Oya NP	187	Morapitiya-Runakanda FR	28	Gal Oya NP	5806.31	Wilpattu NP	4840.92	Wilpattu NP	612.85
9	Sinharaja MABR	182	Gilimale-Eratna FR	27	Minneriya - Girithale – Kaudulla	5671.78	Sinharaja MABR	4690.01	Sinharaja MABR	600.23
10	Maduru Oya NP	174	Horton Plains-Ohiya-Pattipola	27	Maduru Oya NP	5507.71	Minneriya - Girithale NP	4646.39	Minneriya - Girithale NP	567.24

of bird (SP1) had colonized in Sri Lanka. Therefore, now the evolutionary history (PD) of birds in this island is represented by SP1. There are nearly 10,000 species of birds found in the rest of the world, however none represented in the focal area, therefore the SP1 solely represents the bird lineage in Sri Lanka at T_1. As a result ED of SP1 should be very high. (c.) In T_2 another species of bird (SP2) got colonized in the island. Now the total PD is represented by SP1 and the extra phylogenetic info brought in by SP2. With that the ED of the SP1 drops by half. (d.) With the colonization of the SP3 in T_3 the PD improves further and ED of each of the three species reduced. Regarding the phylogenetic position of SP3 the reduction of ED will vary in the three species (Isaac *et al*., 2007; Vellend *et al*., 2007). (e.) After T_n (say today) there are 500 species of birds found in Sri Lanka. Those birds represent the total phylogenetic diversity of birds in the island and each one of the 500 species will have its own ED for the area – that is the fraction of evolutionary information that the species is represented. Bird lineages that are represented by few species will have high ED, while the members of the more speciose lineages will have low ED for the area. Note that still there are nearly 10,000 species of birds in the rest of the world. Since they are not present in Sri Lanka, they do not contribute to either of the tested parameters.

No matter how speciose a lineage is in the global arena, the species' evolutionary value depends on the number of members represented by that lineage in the focal geographic area. Therefore, the evolutionary weightage of species varies from region to region. Consequently, to assess the evolutionary distinctness of Sri Lankan birds found in IBAs one should not consider species that are not found in the island or away from IBAs. We want to see the phylogenetic information that each species brings in to these IBAs.

This approach is similar to the IUCN Red list approach. The red list has two independent versions: the Global Red List and the National Red List (National Red List 2012). For the national list one should only use the species found in the focal area (*i.e.* Sri Lanka). A globally least concern (LC) species can be critically endangered (CR) in the national list. Similarly, globally endangered species (EN) could be LC in the national list. The national status is evaluated independent of the global status (National Red List 2012).

We believe that for effective site-based conservation and management, one should honour the heterogeneity of these measures across the landscape. In order to prevent local extinctions of globally widespread species, especially in small islands, conservation efforts should focused on the regional and local diversity irrelevant to the global figures.

The EDGE score of a species depends on both the ED and the IUCN red list status (Isaac *et al*., 2007). For a species to have a high EDGE score, that species should be an evolutionary isolated species, a globally threatened species or both. *O. thilohoffmanni* (Serendib Scops-owl) has the highest ED for Sri Lanka, it has a relatively low ED score. But it is an endangered species. The EDGE score for *B. moniliger,* which has the highest ED value for the country, has a low EDGE score due to its better IUCN red list status (Table 02). None of the top 10 ranked species under ED is endemic to Sri Lanka; however, the majority of the top 10 EDGE species are endemic (Tables 01-02). Most of our endemic forms are diverged recently as insular populations (Rasmussen and Anderton, 2005; Ripley and Beehler, 1990) hence low ED, and that most of them have poor red list status (National Red List 2012) hence the higher EDGE score.

IBAs in Sri Lanka are distributed in three main climatic zones as wet zone, dry zone and arid zone (Fig. 03). Top IBAs with highest SR are located in dry zone. Just two top-ranked IBA are found in the wet zone (Table 05-06). None of the IBAs out of the 10 IBAs with highest PD are located in the wet zone either (Table 05-06). Top 10 IBAs under ED and EDGE scores are also dominated by dry zone IBAs (Fig. 03). Only Sinharaja MABR and Knuckles CR represented the wet zone under these parameters. However, when the number of endemics were considered, the opposite is true (Table 05-06). In general, the sizes of the IBAs in dry zone are bigger than that of the IBAs in wet zone (Fig. 03: unpublished data – FOGSL IBA database). Because of that higher carrying capacity of dry zone IBAs, they carry slightly higher number of species (SR). Furthermore, most of the IBAs in the coast (Figure 3) receive migratory waterbirds, which increase the SR of these IBAs as well.

Most of these lineage-rich dry zone IBAs are fed by rivers that are originated from the wet zone (Figure 3). Allowing the mixing of wet zone (hydrophilic) lineages with the dry zone (hydrophobic) lineages, which makes the riverine forests of the dry zone harbor an assortment of both wet and dry zone taxa. The high PD, ED and SR observed in these IBAs could be a result of this lineage-rich riverine forests. Although wet zone IBAs of Sri Lanka are not best at harboring the evolutionary history of birds, they are the bests in up keeping the avian endemics and EDGE species of the country.

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REFERENCES

BirdLife International. (2016). *BirdLife Data Zone*. Retrieved 2016, http://datazone.birdlife.org/site/ibacriteria

Bossuyt, F., Meegaskumbura, M., Beenaerts, N., Gower, D.J., Pethiyagoda, R., Roelants, K., Mannaert, A., Wilkinson, M., Bahir, M.M., Manamendra-Arachchi, K. and Ng, P.K. (2004). Local endemism within the Western Ghats-Sri Lanka biodiversity hotspot. *Science* **306**(5695): 479-81. doi: 10.1126/science.1100167

Brusatte, S. L., O'Connor, J. K. and Jarvis, E. D. (2015). The origin and diversification of birds. *Current Biology* **25**(19): R888-R898.

Butchart, S. H., Stattersfield, A. J., Bennun, L. A., Shutes, S. M., Akçakaya, H. R., Baillie, J. E. and Mace, G. M. (2004). Measuring global trends in the status of biodiversity: Red List Indices for birds. *PLOS Biology* **2**(12): e383.

Faith, D. P. (1992a). Conservation evaluation and phylogenetic diversity. *Biological conservation* **61**(1): 1-10.

Field ornithology group of Sri Lanka. (2003). Preliminary IBA site. Colombo: Field Ornithology Group of Sri Lanka.

Gugerli, F., Englisch, T., Niklfeld, H., Tribsch, A., Mirek, Z., Ronikier, M. and IntraBioDiv Consortium. (2008). Relationships among levels of biodiversity and the relevance of intraspecific diversity in conservation–a project synopsis. *Perspectives in Plant Ecology, Evolution and Systematics* **10**(4): 259-281.

Hackett, S. J., Kimball, R. T., Reddy, S., Bowie, R. C., Braun, E. L., Braun, M. J. and Huddleston, C. J. (2008). A phylogenomic study of birds reveals their evolutionary history. *Science* ***320***(5884): 1763-1768.

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C. and Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PlOS one* ***2***(3): e296.

Jarvis, E.D., Mirarab, S., Aberer, A.J., Houde, P., Li, C., Ho, S.Y.W. and Fairclo, B.C.(2014). Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science* **346** (6215): 1320-1331.

Jetz, W., Thomas, G. H., Joy, J. B., Hartmann, K. and Mooers, A. O. (2012). The global diversity of birds in space and time. *Nature*, **491**(7424): 444-448.

Jetz, W., Thomas, G. H., Joy, J. B., Redding, D. W., Hartmann, K. and Mooers, A. O. (2014). Global distribution and conservation of evolutionary distinctness in birds. *Current Biology*, ***24***(9): 919-930.

National Red List 2012 of Sri Lanka; Conservation Status of the Fauna and Flora. Weerakoon, D.K. and S. Wijesundara Eds., Ministry of Environment, Colombo, Sri Lanka.

Nee, S., and May, R. M. (1997). Extinction and the loss of evolutionary history. *Science*, **278**(5338): 692-694.

Pagel, M. (1999). Inferring the historical patterns of biological evolution. *Nature* **401**(6756): 877.

Rasmussen, P. C. and Anderton, J. C. (2005). Birds of South Asia: The Ripley Guide, Lynx Edicion, Barcelona, Spain.

Ripley, S. D. and Beehler, B. M. (1990). Patterns of speciation in Indian birds. *Journal of Biogeography* **17**: 639-648.

Simpson, E. H. (1949). Measurement of diversity. *Nature*. **163**: 668. doi: 10.1038/163688a0

Vellend, M., Cornwell, W. K., Magnuson-Ford, K. and Mooers, A. Ø. (2011). Measuring phylogenetic biodiversity. *Biological diversity: frontiers in measurement and assessment. Oxford University Press, Oxford, UK*, 194-207.

Vitousek, P. M., Mooney, H. A., Lubchenco, J. and Melillo, J. M. (1997). Human domination of Earth's ecosystems. *Science* **277**(5325): 494-499.

Webb, C. O., Ackerly, D. D., McPeek, M. and Donoghue, M. J. (2002). Phylogenies and community ecology. *Annual Review of Ecology and Systematics* **33**:475-505.

Wickramasinghe, N., Robin, V. V., Ramakrishnan, Reddy, S. and Seneviratne, S. S. (2017). Non-sister Sri Lankan white-eyes (genus *Zosterops*) are a result of independent colonizations. *PLOS ONE* **12**(8): e0181441.