The implications for conservation of a major taxonomic revision of the world's birds

Ashley T. Simkins^{1,2*}, Graeme M. Buchanan³, Richard G. Davies² & Paul F. Donald^{1,4}

¹BirdLife International, David Attenborough Building, Pembroke Street, Cambridge CB2 3QZ, UK.

²School of Biological Sciences, University of East Anglia, Norwich Research Park, Norwich NR4 7TJ, UK.

³RSPB Centre for Conservation Science, 2 Lochside View, Edinburgh Park, Edinburgh EH12 9DH, UK.

⁴Conservation Science Group, Department of Zoology, University of Cambridge, David Attenborough Building, Pembroke Street, Cambridge CB2 3QZ, UK.

*Correspondence: Ashley T. Simkins, BirdLife International, David Attenborough Building, Pembroke Street, CambridgeCB2 3QZ, UK. Email: ashley.simkins@birdlife.org

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Abstract

A recent comprehensive revision of the taxonomy that underpins the global IUCN Red List for birds led to an increase of 10.7% (over 1,000 species) in the number of recognised bird species. We assessed the implications for conservation of this revision by (i) comparing extinction risk between newly recognised and un-revised species, (ii) calculating the extent to which newly recognised species' ranges are covered by Important Bird and Biodiversity Areas (IBAs) and protected areas, and (iii) identifying new hotspots of extinction risk, where high numbers of newly recognised threatened species intersect areas of low protected area coverage. Unexpectedly, newly recognised species derived from taxonomic division (splitting) were on average significantly less threatened in terms of their IUCN global threat categories than species whose taxonomic status remained unchanged, despite their significantly smaller mean range size. Newly recognised species listed as globally threatened had higher average coverage of their ranges by IBAs and protected areas than their prerevision 'parents', although 25 and 21 species had no coverage by IBAs or protected areas respectively. The absolute number of globally threatened species increased slightly overall, particularly in Java and the Philippines, already recognised as hotspots of extinction risk, and in southern Amazonia, which emerged as a new hotspot of extinction risk. All three regions have low levels of protection and should be prioritised for expansion of the protected area network. Our results suggest that while major taxonomic revisions may lead to an increase in the absolute number of species requiring conservation attention, they do not necessarily lead to a rise in average extinction risk, a decrease in the coverage of species' ranges by sitelevel conservation designations or a significant increase in the number of priority areas for conservation investment.

INTRODUCTION

A recent major taxonomic revision of all the world's birds (del Hoyo & Collar 2014, del Hoyo & Collar 2016) resulted in a net increase of 10.7% in the number of recognised bird species (Fig. 1), and represents one of the most fundamental taxonomic revisions of an entire class of animals attempted in recent times. It was based on a thorough examination of the published literature, a review of a large number of cases judged by the authors as worthy of independent study (Burfield et al. 2017), and the application of a scoring system to assign species rank (Tobias *et al.* 2010). The resulting list forms the taxonomic basis of bird assessments for the IUCN Red List, and all species recognised by the revision have subsequently been evaluated against the Red List criteria (BirdLife International 2016). Such a significant revision and increase in the number of recognised species could clearly have significant implications for conservation. It might profoundly influence the distribution and degree of extinction risk between species and may lead to a redistribution of the sites or regions in greatest need of conservation intervention. This may require a commensurate change in the allocation of conservation investments and priorities, and could potentially undermine current networks of protected areas and sites of recognised conservation significance, such as Important Bird and Biodiversity Areas (IBAs) (Donald et al. 2019b) and Key Biodiversity Areas (KBAs) (IUCN 2016), which were identified on the basis of the prerevision taxonomy and its associated measures of extinction risk. This is likely to be particularly true when taxonomic revision leads to a significant increase in the number of species recognised through the subdivision of previously recognised forms, since such taxonomic division (also known as taxonomic inflation or splitting) inevitably leads to a reduction in average range sizes and populations; most threatened bird species have small

ranges (BirdLife International 2017). This in turn could compromise efforts to measure changes over time in extinction risk to report on international policy objectives, such as the Red List Index (Butchart *et al.* 2007). Large increases in the total number of recognised species, whether resulting from changes in species concepts, the application of new methods or the description of new species, may therefore have significant implications for conservation, particularly when the revised taxonomy is that which underpins the relevant Red List assessment (Agapow *et al.* 2004, Isaac *et al.* 2004, Zachos 2013).

We therefore assess the implications for conservation of this major taxonomic revision of the world's birds by (i) comparing levels of extinction risk between the revised taxa, their 'parents' and species whose taxonomic limits were not revised, (ii) comparing their degree of spatial overlap with IBAs and protected areas and (iii) mapping the distribution of newly recognised and globally threatened species to identify emerging hotspots of extinction risk.

METHODS

Changes in extinction risk

We compared the revised taxonomy of del Hoyo and Collar (2014, 2016) with the prerevision arrangement to classify species to groups according to the type of revision, classifying species as being (i) unchanged by the revision, (ii) splits of previous recognised species, (iii) mergers of previously recognised species or (iv) species that were wholly new to science and hence had no taxonomic equivalent in the pre-revision taxonomy. Sample sizes for each of these classes of species are shown in Fig. 1.

To compare Red List status between the different taxonomic treatment groups identified in Fig. 1, we used cumulative link mixed models, fitted using the 'clmm' command in the package 'ordinal' (Christensen 2018) of R version 3.3.1 (R Core Team 2013). Red List category was fitted as an ordered factor with five levels: Least Concern < Near Threatened < Vulnerable < Endangered < Critically Endangered. These models represent a significant improvement over methods that model numbers subjectively assigned to different categories (e.g. Least Concern = 1, Near Threatened = 2, etc.) because they account for the non-linear progression of extinction risk across categories and effectively handle the modelling of small numbers of categories (Christensen 2018). However, they present challenges in terms of data presentation, since no "mean" value of category can be estimated and no R² equivalent is available. We therefore present plots of the raw data and tables of models, rather than the more usual plots of model outputs. The first analysis compared Red List categories between all pre-revision species and all post-revision species, excluding species new to science that had no taxonomic equivalent in the pre-revision taxonomy, to assess overall change in mean extinction risk before and after the taxonomic revision. We then modelled extinction risk between post-revision species groups. These models included taxonomic family nested within order as a random effect to account for the known non-independence of extinction risk across higher taxonomic levels in birds (e.g. Bennett & Owens 1997). Finally, we modelled extinction risk between pre-revision classes to assess whether species that went on to be split differed in mean extinction risk to species that were un-revised. The last analysis was confined to passerines (c. 60.3% of all species), since taxonomic cross-walk tables were not maintained for non-passerines, and in this model family alone was included as a random effect. A general linear model (ANOVA) was

used to compare breeding range size between the different groups of species shown in Fig. 1.

Changes in range overlap with IBAs and protected areas

We assessed the spatial coverage of the ranges of species as recognised before and after the taxonomic revision with protected areas (UNEP-WCMC 2017) and with IBAs (BirdLife International 2018, Donald et al. 2019b). All IUCN protected areas with associated polygons were included (Levels I-VI; IUCN 2019) and no distinction was made between the different types of protected areas (to reduce the complexity of the dataset and processing requirements, and because of uncertainty about how well the different classes are recorded). Species range maps were sourced from BirdLife International & Handbook of the Birds of the World (2017). Polygons were filtered to include only the native breeding ranges of each species, and only where they are extant, probably extant or possibly extinct. We used only breeding distributions because range- and biome-restriction, two important components in identifying IBAs, are based on breeding distributions only, and because the overwhelming majority of newly recognised species are non-migratory. Species classified as Extinct, Extinct in the Wild or Data Deficient were omitted from the range overlap analyses, as they had no range (if Extinct) or because they could not be placed on the continuum of extinction risk (if Data Deficient). The original ranges of species that were split during the taxonomic revision were reconstructed by merging the ranges of all the species they were split into. After filtering to remove Extinct, Extinct in the Wild and Data Deficient species, 1,894 newly recognised species were used for the intersection analysis, 187 of which were classified as globally threatened by BirdLife International. Six further species were excluded

during the filtering process due to discrepancies in the data (*Apteryx australis, Branta canadensis, Branta hutchinsii, Callaeas cinereus, Saltator plumbeus* and *Tangara whitelyi*). Spatial analysis used a Behrmann equal area projection. The protected area layer was simplified to a maximum tolerance of 300 m to facilitate analysis of this large dataset.

Range maps for each of the newly-split bird species and their pre-revision 'parent' species were intersected with maps of IBAs and protected areas in turn in ArcGIS via ArcPy (ESRI 2017). The area of each intersection and the percentage overlap of each species' range with protected areas and IBAs was calculated. The difference between the percentage of each of the newly split species' range and their "parent" species' range that overlapped with IBAs and protected areas was calculated by subtracting the "parent" range overlap from the new species' overlap (for an illustration of how spatial divisions can either increase or decrease the relative coverage of ranges by protected areas or IBAs, see Fig. S1). We used one-sample *t*-tests to test whether the change in average overlap of the ranges of newly split species (combined, and threatened and non-threatened separately) with IBAs and protected areas was significantly different from zero.

Species richness maps were produced in ArcGIS (ESRI 2011) by overlaying species maps onto a grid with a cell size of 100 km by 100 km and calculating the number of species that overlapped each grid cell. Species richness maps were generated for all species newly recognised as a result of taxonomic division of previously recognised species ('splits'), for splits that were assessed as being globally threatened (Vulnerable, Endangered or Critically Endangered) and for the proportion of all currently recognised species that is made up by taxonomic splits. A bivariate map was produced to highlight areas where high richness of newly recognised species coincides with little or no protected area coverage.

RESULTS

Changes in extinction risk

Results of the cumulative link mixed models indicated that the taxonomic revision did not lead to a significant change in the average threat status of the world's birds (Table 1a). Indeed, species that were revised by taxonomic splitting were significantly less threatened on average than those whose taxonomic status was unchanged (Table 1b, Fig. 2), although their average range size was significantly smaller (Fig. 3). Species that were new to science, and so had no taxonomic antecedents, were significantly more threatened than any other group in the new taxonomy (Table 1b; Fig.2). When these new-to-science species were excluded, there was no significant difference in average extinction risk between the 10,048 species recognised before the taxonomic revision and the 11,086 recognised after (Table 1). However, when the newly discovered species are included in the post-revision list, the average extinction risk is significantly higher than in the pre-revision species list. Species (passerines only) that went on to be split (indicated by p_s in Fig. 1) were significantly less threatened before the taxonomic revision than those that were un-revised (Table 1c), and their ranges were significantly larger (t = -4.272, P < 0.001).

Global distribution of taxonomic changes

Taxonomic splits were made primarily in areas of already high species richness, such as the northern Andes, the Himalayas and the islands of South East Asia (Fig. 4). However, the proportion of post-revision species that comprised splits of previously recognised species, a measure of the extent of taxonomic revision, was highest in species-poor areas North Africa and the Middle East, where taxonomically revised species were few in absolute number but comprised as much as 50% of the local bird community, though the islands of South East Asia again scored highly in this measure (Fig. 5).

Range overlap with IBAs and protected areas

The average overlap by IBAs of the ranges of splits was significantly higher than that of their 'parent' species, for all split species, split threatened and split non-threatened species (Table 2). There was no change in the average percentage of all species' ranges captured by protected areas, but in the case of threatened species the average overlap increased significantly (Table 2). Of the 187 globally threatened splits, 64 (34%) had <10% of their ranges covered by IBAs (Table S1) and 84 (45%) had <10% covered by protected areas (Table S2). The areas of highest richness of newly split threatened species (Amazonia, Philippines and Java) coincided with areas of low protected area coverage (Fig. 6).

DISCUSSION

Our results show that a major taxonomic revision of all the world's birds, which resulted in a more than 10% increase in the number of recognised species through taxonomic division, did not lead to an elevation of mean global extinction risk across birds, or to a reduction in the average coverage of species' ranges by IBAs or protected areas. Unexpectedly, newly recognised species resulting from the splitting of formerly recognised species, which necessarily had smaller ranges and populations than their 'parent' species, were on average significantly *less* threatened than species whose taxonomic status remained unchanged. This counterintuitive finding may owe much to the fact that the

previously recognised species that went on to be split (p_s in Fig. 1) were significantly less threatened and had larger range sizes initially than those species whose taxonomic status was not changed. Furthermore, we found that the mean coverage of newly recognised species' ranges by IBAs (and in the case of threatened species, by protected areas) was significantly higher for splits than for their pre-split 'parent' species. We considered the possibility that the extinction risk of taxonomic splits might be underestimated, owing to poorer knowledge of their threats and population trends than was the case for their 'parents'. However, this seems unlikely; many of the metrics used in assigning species Red List category, such as range size, forest loss, prevalence of threats from hunting or invasive species etc., are known equally well for revised and un-revised species.

The 35 species in the post-revision taxonomy that were new to science, and thus had no taxonomic antecedents in the pre-revision list, were significantly more threatened on average than any other group. This is likely to reflect the fact that in a well-studied group like birds any remaining undiscovered species will tend to be rare and have small ranges, a pattern already noted by Collar (2000). As there was no significant difference in average extinction risk between pre-revision and post-revision species when this small group of newto-science species is excluded (Table 1), any decline in the global Red List Index (Butchart *et al.* 2007) immediately following the taxonomic revision is likely to reflect the discovery to science of a small number of species with high extinction risk, rather than an effect of taxonomic revision.

Despite the average proportional increase in IBA and protected area coverage of the ranges of newly split species relative to their "parents", of the 187 split species that were identified as globally threatened, 34% and 45% had less than 10% coverage of their ranges by IBAs and protected areas, respectively (Table S1 and S2), and 25 (13%) and 21 (11%)

respectively had no coverage. These species may therefore require further conservation investment, and IBA and protected area expansion needs to be considered in these areas if they are species that may benefit from site-based conservation. This is particularly the case in southern Amazonia, Java and the Philippines, where clusters of newly recognised, globally threatened species occur in areas of low protected area coverage. Java and the Philippines were already recognised as being hotspots of globally threatened bird species richness (Orme *et al.* 2005, Grenyer *et al.* 2009), and the addition of new threatened species makes the need for the creation of new protected areas in these regions even more imperative.

The emergence of a hotspot of newly recognised globally threatened species in southern Amazonia was unexpected, since most bird species in the region previously had sufficiently large ranges and populations that they do not meet thresholds for being classified as globally threatened, and there were previously relatively few globally threatened bird species in this region (Grenyer *et al.* 2009). This new hotspot of globally threatened bird species in southern Amazonia may be explained by a combination of reduced range size following splitting, severe loss of forest intactness, which has been shown to be a strong predictor of extinction risk in birds (Donald *et al.* 2019a), and high levels of deforestation, which is used in the calculation of extinction risk under Red List Criterion A (Tracewski *et al.* 2016). In all three areas where the numbers of newly recognised species that are listed as globally threatened are highest, there were clear gaps in protected area coverage, and the IBA and protected area networks need to be reassessed and new sites created for those species that benefit from site-based conservation.

Conservation and taxonomy are intimately linked, particularly at the species rank, and the delimitation of species limits therefore has a major influence on conservation priority-setting and expenditure (Collar 1997, Agapow *et al.* 2004, Mace 2004, Burfield *et al.*

2017). However, species lists are inherently unstable and there has been a significant increase in recent decades in the number of generally recognised forms, even in wellstudied groups of organisms. This increase results from new discoveries, from closer or wider examination of existing material and from the application of a range of new species delimitation approaches, foremost among them molecular methods, that have a tendency to reduce previously recognised species concepts into more and geographically smaller units (e.g. Isaac et al. 2004, Padial & De la Riva 2006, Zachos 2013). The use of taxonomy in conservation is further complicated by the lack of generally agreed and unified taxonomic lists; for birds, for example, there are at least four widely used global taxonomies and numerous regional ones, with differing degrees of agreement between them, and the number of scientific articles published each year that propose changes to currently accepted species concepts is growing rapidly (Burfield et al. 2017, Garnett & Christidis 2017). At the heart of this debate lies the conundrum that taxonomic names are used for two purposes one to identify a concept or hypothesis that may be tested, modified or discarded as further research dictates, the other to define a non-volatile entity on which to attach biological information (Thiele & Yeates 2002, Hey et al. 2003). Garnett & Christidis (2017), following an earlier suggestion by Godfray (2002), suggested that a lack of global oversight in taxonomic decision-making "threatens the effectiveness of global efforts to halt biodiversity loss" and poses so significant a threat to the conservation of biodiversity that a central authority should be established to make ultimate decisions. Underlying their argument is the assumption that splitting existing species into more taxonomic units, which inevitably have smaller populations and ranges than their antecedents, will result in an increase in extinction risk. In response, Thomson et al. (2018) argued, among other things, that that there is little evidence that taxonomic revision influences conservation in a predictable or

consistent way, and indeed that failing to revise species limits may have adverse impacts on conservation. As an illustration of this, Gippoliti et al. (2018) suggested that "taxonomic inertia" was more harmful to the conservation of African ungulates than taxonomic revision, for example through the neglect of threatened but unrecognised lineages and inappropriate translocation and captive breeding programmes. Morrison et al. (2009) suggested that the implications for conservation of taxonomic re-evaluation are idiosyncratic and that if anything, splitting tends actually to increase levels of protection. However, there are few quantitative assessments of the conservation implications of major taxonomic revisions available for assessing these various claims, and none covering a whole class of organisms. Our results suggest that the clear benefits of improving our understanding of the taxonomic units that underpin conservation priority-setting are not necessarily balanced by a cost in terms of higher extinction risk, a reduction in the performance of site-based networks in capturing species' ranges or a significant increase in the number of areas of high conservation threat that require a response. It is unclear how our findings might apply to taxonomic revisions of other groups, in which the taxonomic level at which species are defined may differ systematically from birds, but they support previous assertions (e.g. Morrison et al. 2009, Thomson et al. 2018) that major taxonomic revisions do not have predictable impacts on conservation.

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Table 1. Post-hoc comparisons of extinction risk, from cumulative link mixed models (clmm) of IUCN Red List categories, between species grouped according to their type of taxonomic revision. Models in (b) also included taxonomic family nested within order as a random effect. Contrasts show post-hoc comparisons of each pair of species groups, denoted by the letters shown in Fig. 1. Estimates are the difference between the regression parameters of each pair of groups and its sign indicates which member of each pair in the contrast is the more threatened; positive values indicate that the first group is less threatened (i.e. species are less likely to appear in higher classes of extinction risk) than the second, negative values that the first group is more threatened. The original regression parameters are estimates of a latent variable and lack units (Christensen 2018). For the pre-revision comparisons (c), only passerines were included and family was included as a random effect (see text). In model (a), species new to science (denoted as "n" in Fig. 1) and which had no taxonomic antecedent were excluded; when they were included, the average extinction risk of post-revision species was significantly higher (P < 0.05) than that of pre-revision species.

	Contrast	Estimate	SE	Р
(a) All species				
pre- vs. post-	pre- vs. post-	-0.032	0.033	0.327
revision	revision			
(b) Post-revision	m vs. n	1.966	0.560	0.003
	m vs. s	-0.047	0.319	0.999
	m vs. u	0.262	0.313	0.837
	n vs. s	-2.014	0.469	<0.001
	n vs. u	-1.704	0.466	0.001
	s vs. u	0.310	0.067	<0.001
(c) Pre-revision	p_m vs. p_s	-1.138	0.344	0.003
(passerines	p_m vs. u	0.114	0.300	0.924
only)	psvs.u	1.252	0.176	<0.001

Table 2. Average percentage coverage and average change in percentage coverage by IBAs and protected areas of the ranges of newly split species, broken down by IUCN Red List category. The change in coverage was calculated by subtracting the 'parent' species' coverage from the split species' coverage. Asterisks indicate where the average change in coverage for newly recognised split bird species (all species and threatened and non-threatened species separately) following the taxonomic review is significantly different from zero (*P < 0.05, **P < 0.01, ***P < 0.001).

Newly split species	Average % coverage (± SE)		Change in % coverage (± SE)		
				Protected	
	IBAs	Protected areas	IBAs	areas	
All	16.116±0.374	19.063±0.424	+2.493±0.310***	+0.383±0.332	
Threatened	23.251±1.795	24.830±2.159	+5.727±1.608***	+3.800±1.584*	
Non-threatened	15.334±0.360	18.431±0.404	+2.139±0.294***	+0.009±0.324	



Figure 1. Summary of the taxonomic revision, giving sample sizes for each group of species.

The letters inside the boxes refer to those used to denote groups in Table 1.



Figure 2. The proportion of species falling in each IUCN threat category within each of four classes of taxonomic revision (see Fig. 1). Critically Endangered includes a small number of species listed as Critically Endangered (Possibly Extinct) and Critically Endangered (Extinct in the Wild).







Figure 4: Species richness of all newly split bird species (those indicated by "s" in Fig. 1).



Figure 5: The distribution of relative taxonomic reassignment, represented as the proportion of the post-revision bird community that was made up by newly recognised splits.



Figure 6: Bivariate map showing richness of globally threatened newly recognised (split) species and percentage cover by protected areas for each grid cell. Areas in orange indicate where high numbers of newly recognised globally threatened species coincide with areas of low protected area coverage, blue indicate where protected area coverage is high but the number of newly recognised globally threatened species is low, white indicates where both are low and black denotes where they are both high.