Introduction

Ends and beginnings: the taxonomic cycle

With this companion volume to del Hoyo & Collar (2014) the HBW-BirdLife International project to review and revise the taxonomy of the birds of the world reaches its first goal. A multiplicity of concerns and considerations has driven the endeavour, including the geographical patchiness of taxonomic research, the consequent neglect of many pressing and deserving cases (often highlighted by the species profiles in the *Handbook of the Birds of the World* [HBW] itself), the sometimes glacial speeds at which appointed regional committees take decisions, the potentially dramatic disparities of treatment resulting from choice and understanding of species concept, the poor standards of some published analyses, the often uncritical adoption of proposed changes by existing world checklists, the increasing availability and relevance of sound recordings, and BirdLife's enduring obligation to IUCN (International Union for Conservation of Nature) to evaluate the conservation status of all species of bird. We wanted to make fullest use of the results of recent studies, assembling and integrating modern assessments and evidence with the often detailed taxonomic notes already elaborated by the many and various HBW authors, paying particular attention to the findings of molecular research; but we also wanted to maintain as much independence of judgement as circumstances allowed, and to be proactive where nobody else was taking a lead.

Consequently this volume, like its predecessor, contains hundreds of original reworkings of long-established taxonomic arrangements, and hundreds more evaluations of recent work by others in the field of modern avian systematics, all using a single simple system to quantify levels of phenotypic differentiation while also being guided (and sometimes goaded!) by the findings of myriad molecular studies. By this means, although emphatically not pretending to provide a definitive solution to the seemingly intractable problem of species limits in birds, we hope to have achieved at least a moderate degree of consistency, even-handedness and transparency of treatment that will help to serve the contemporary interests and needs of science, conservation and recreational experience in equal and equitable measure.

We say "contemporary" with no very clear idea of the time-span this word might encompass. In the six-and-a-half years from the initiation of our project in late February 2010 to 31 August 2016, our last date for the consideration of new published evidence, at least 1,242 papers and articles appeared on the taxonomy of the passerines alone, a rate—0.5 per day—surely unprecedented in the history of avian systematics. (Simply keeping track of this material is a discipline in itself; assessing its import and incorporating its insights into a global framework is something else again.) It is not yet clear whether this extraordinary surge of information might be waning, although at some stage it surely must. Meanwhile, new connections, new interpretations, new insights—inflections of the verb "reveal" are ubiquitous in the titles of modern molecular papers on systematics—will constantly require new adjustments to be made to the world list of birds. Checklists are part of an enduring taxonomic cycle. What you have on your lap or table as you read these words is as much a beginning as an end.

Even so, the completion of this checklist marks the fulfilment of a specific ambition, fuelled over two decades with each new volume of HBW (and indeed over three-and-a-half decades of modern Red List assessments by BirdLife), to make a serious attempt at addressing the manifest, manifold inconsistencies, inequalities and inadequacies that have so long beset world lists of birds, and to establish a firm and unbiased foundation for the conservation of bird species across the planet. So many taxonomic notes in HBW contain comments about one subspecies or another that merits consideration for species rank; and so many of its plates and descriptions point to the potential and need for a fresh investigation of taxonomic status. Within the all-too-narrow constraints of time and resources we have sought to address as many of these issues as possible (although some, as we acknowledge further below, have proved beyond reach, but already with encouraging results from Volume 1, as with the rediscovery of the Blue-bearded Helmetcrest *Oxypogon cyanolaemus*: Rojas & Vasquez 2015). Of course the extensive body of recent work in avian systematics, running in parallel with our venture, has played by far the greater part; but through the combination of these endeavours we do not anticipate another undertaking on such a scale, at least for the foreseeable future.

Truly integrative taxonomy: building the broadest evidence base

There is an appealing and increasing recognition in modern avian taxonomy of the value of what has been termed an "integrative" approach to revisions, one which seeks to include all varieties of evidence in order to test and improve the robustness of the results obtained by one particular—almost invariably genetic—line of inquiry. Plumage pattern and structure, bare part colours and formations, morphometrics, vocalizations, ecological factors, behavioural traits and molecular findings all represent variables that can be assessed for information relevant to a taxonomic identity. Truly "integrative" work will endeavour to cover as many of these parameters as possible (see such exemplary studies as Payne & Sorenson 2007, Davison *et al.* 2012, Sangster *et al.* 2013, 2016, Alström *et al.* 2016). This is the fundamental premise on which this checklist is built.

The more these factors line up together, the more confident we can be of the taxonomic conclusion to which their alignment points. (Thus the plumage differences and morphometric disjunctions—so lightly and benightedly dismissed as "relatively minor" by the author of HBW's Turdidae—shown by the Eastern Slaty Thrush *Turdus subalaris* mark it emphatically, with a score of 9, as a species distinct from Andean Slaty Thrush *T. nigriceps*.) Moreover, it is also then more likely that other, as yet untested parameters will be found to show a difference. (The vocalizations of *T. subalaris* add a further score of 6 in their divergence from those of *T. nigriceps*.) The system of taxonomic evaluation that we use, the Tobias criteria (Tobias *et al.* 2010, del Hoyo & Collar 2014: 30–41), allows for the quantification of all the variables listed above, with the exception of genetics. The inability of the criteria to accommodate genetic evidence within the current scoring system is, as explained at length in the Introduction to Volume 1, a function of the inability of molecular science to establish a fixed level of genetic differentiation to serve as the species/subspecies boundary. However, the fact that genetics is not (or not yet) integrated into these criteria does not mean it is not integral to the evaluation process. On the contrary, the results and insights of recent molecular studies saturate this checklist: their evidence is constantly accounted for and incorporated. Indeed, the single greatest driver of our use of the Tobias criteria has been the findings of DNA studies.

So we take the view that the Tobias criteria have established the basis for a process of taxonomic revision which, while not fitting every circumstance and never claiming to be fault-free, is at once integrative, comprehensive, practical, robust, rapid, open and consistent. Consistency in particular is a vital aspiration—too easily lost sight of—in a global checklist. If species limits in allopatric taxa are, as we are commonly reminded, arbitrary constructs for human convenience, the Tobias criteria at least serve as one way to *standardise arbitrariness*. Whatever the judgement of the system or the reception of its results—and published criticism (Remsen 2015) has indicated potential areas for improvement but identified no irremediable weaknesses (Collar *et al.* 2016, Remsen 2016)—nothing is hidden from plain view: throughout this checklist the evidence we assemble in support of our decisions is laid out for scrutiny, contemplation, rejection, acceptance and/or adjustment. "Improved standardization and transparency of species taxonomy", Gill (2014) creditably asserted, "is essential". This is precisely what this checklist, autonomous in its explorations of fact and argument, and holistic in its use and open in its presentation of evidence, is attempting to provide.

Taxonomic democracy: taking account of *all* characters

Until relatively recently, morphology, internal as well as external, was the only means of assessing a taxon's relationships and distinctiveness. Now, however, two parameters have come to be regarded as fundamental to the robustness of taxonomic revisions: voice and DNA. These two variables have achieved a primacy of value which is, of course, entirely understandable: songs and calls are a principal way, along with outward appearance, by which bird species identify themselves, while DNA provides the best evidence of a population's internal coherence and composition. Even

so, the tendency to consider these parameters decisive to the point of veto—thereby rendering some characters "more equal than others"—is not wholly welcome or wise: voices, especially among the oscine passerines, vary with circumstance, and DNA has some intriguing, instructive mysteries, as when two clear species—or as many as five, in the case of the Tawny-bellied Seedeater *Sporophila hypoxantha*, Dark-throated Seedeater *S. ruficollis*, Pearly-bellied Seedeater *S. pileata*, Marsh Seedeater *S. palustris* and Black-bellied Seedeater *S. melanogaster* (Benites *et al.* 2014, Campagna *et al.* 2015)—prove genetically inseparable while other species possess startling genetic divides that have no effect on their behaviour or status (see, e.g., del Hoyo & Collar 2014: 28–29). Comments by certain molecular taxonomists—"genetic estimates of lineage divergence may not be… reliable indicators of species limits" (Humphries & Winker 2011); "levels of sequence divergence alone should not be used for describing species" (Schultz & Burns 2013)—reveal an awareness of this limitation. Indeed, the very techniques for producing evidence of molecular structure are still open for debate, as in the case of the California Gnatcatcher *Polioptila californica* (Zink *et al.* 2013, 2016, McCormack & Maley 2015, Anon. 2016).

The Tobias criteria spread the power to drive taxonomic change fairly evenly across all phenotypic characters (plumage, size, voice), allowing them to stand alone or to operate in (sometimes unexpected) combination to achieve species status for their bearers. A case in point is the Short-tailed Antbird *Poliocrania maculifer*, which we split here from Chestnut-backed Antbird *P. exsul* on the evidence of four colour characters and a markedly shorter tail yet with seemingly no difference in voice, despite song being the almost exclusive means by which changes to thamnophilid taxonomy have been effected over the past two decades. Equally, cued by the cautionary comments above about the acceptability of genetic evidence on its own or in large measure, the Tobias criteria have the capacity to reverse splits such as that of Highland Hepatic-tanager *Piranga lutea* from what we now simply call Hepatic Tanager *P. hepatica*, which was made in HBW on molecular grounds, given the very slight morphological and vocal differences these two taxa show. The system thus possesses the flexibility to liberate assessments, with no loss of analytical rigour, from the prevailing (if often seemingly unconscious) orthodoxy that places voice and DNA on a higher tier of taxonomic relevance.

In many cases the Tobias criteria may even constitute a useful independent test of the results of genetic analyses. If, as we suggest above, the number of variables that show differences predicts differences in other as-yet unmeasured variables (albeit not in the voice of the Short-tailed Antbird), it is plausible to assume that multiple phenotypic dissimilarities predict significant genetic distinctiveness. In this regard, an encouraging finding in this volume is the rather high degree of concordance between phenotypic and genetic evidence. Among the non-passerines there were several cases where simultaneous molecular and morphological analyses converged on the same answers (e.g. Hainan Peacock-pheasant *Polyplectron katsumatae*, Black-browed Barbet *Psilopogon oorti*), and more recently our split of Lesser Sri Lanka Flameback *Dinopium psarodes* has been supported by genetic evidence (Fernando *et al.* 2016). Among the passerines the list of species where genetic and phenotypic evidence coincides is notable: examples are to be found in virtually every family consisting of more than just a few species. We particularly acknowledge a good number of cases which, owing to the similarity of appearance of the taxa in question, were not ones we originally selected for further study but which, after being identified by genetic evidence, have proved also to meet the Tobias criteria, often because of the role played by voice: for example, Campina Thrush *Turdus arthuri* and Floodplain Thrush *T. debilis* from Black-billed Thrush *T. ignobilis*, Pacific Cacique *Cacicus pacificus* from Scarlet-rumped Cacique *C. microrhynchus*, and Amazonian Grosbeak *Cyanoloxia rothschildii* from Blue-black Grosbeak *C. cyanoides*.

This is not to pretend that phenotypic and genetic evidence is not sometimes in conflict. Rarely—or at least we hope this is so, but inevitably detection rates are low—the confusion is attributable to clerical error (mislabelled samples, misattributed specimens): we know of several unpublished cases that have led to published mistakes, and others have been openly acknowledged (Zou *et al.* 2008) or suspected (Davies & Peacock 2014). Meanwhile, the commonest problems involve paraphyly and polyphyly, and can often only be dealt with by calls for more research and denser sampling—a case in point is the seemingly intractable conundrum of the Great Grey Shrike *Lanius excubitor* complex, where the most recent molecular studies (Olsson *et al.* 2010) overturn some previous notions of relationship but also fail to provide an arrangement that can be reconciled with any species concept or with complete diagnosability. Other such cases where the Tobias criteria fail to vindicate claims based on the molecular evidence, but where circumstances compel us to judge that the molecular evidence must for the present prevail, include Olivaceous Mourner *Schiffornis olivacea* split from Northern Mourner *S. veraepacis*, Winter Wren *Troglodytes hiemalis* and Pacific Wren *T. pacificus* from Northern Wren *T. troglodytes*, Southern Variable Pitohui *Pitohui uropygialis* from Northern Variable Pitohui *P. kirhocephalus* and Highland Rush-warbler *Bradypterus centralis* from Little Rush-warbler *B. baboecala*. Perhaps the most baffling issue we have encountered in preparing this second volume concerns the identity and rank of a cluster of *Pomatorhinus* scimitar-babblers (White-browed *P. schisticeps*, Chestnut-backed *P. montanus* and Streak-breasted *P. ruficollis*), for which the genetic and morphological data are so wholly at variance that we feel obliged to stick with the *status quo* until renewed—and integrative—analyses can shed stronger light on an extraordinarily convoluted circumstance.

Overall, however, we see the frequent complementarity of phenotypic and genetic distinctiveness as evidence that the Tobias criteria are well rooted in established standards of taxonomic discrimination. This view seems to be slowly gaining traction with practitioners of molecular studies, albeit with reservations and conditions: Lifjeld *et al.* (2016) give a score of 11 to Gran Canaria Blue Chaffinch *Fringilla polatzeki*, while Campbell *et al.* (2016) "also consider a phenotypic score of 7, conservatively, to be a conceptual threshold for identifying what we term phenotypically highly divergent taxa". Such confluence and complementarity are encouraging. Molecular taxonomy thus need not be characterized either as a Cinderella, left out of consideration by a self-serving (and some might say self-sealing) system of evaluation, or as a Cyclops, dominating the modern taxonomic landscape with its unsparing, all-seeing eye. The combination of phenotypic and genetic analysis is clearly key to advances in avian systematics for the foreseeable future.

Representative sampling: the limits of confidence

Nevertheless, both phenotypic and genetic analysis depend on the number and distribution of the samples involved, and this issue crops up sufficiently often to be worth a brief commentary here. Statistically robust evidence of a consistent morphometric disjunction demands an adequate sample size. The magnitude of this depends on the scale of natural variation for each case, but we used a default minimum of 10 specimens of one sex for each test (Tobias *et al.* 2010), and our pursuit of this sample size has accounted for many months of work in various museums. (Here we should just repeat and refine information given in the Introduction to Volume 1: when an effect size is given with no indication of sample size or sex, this means that the sample was at least 10 and the sex of the sample was male.) The same requirements are of course highly desirable for the confident discrimination of constant vocal characters and when considering plumage differences in closely similar taxa. Inevitably there are shortfalls: many taxa are known from fewer than ten specimens, while many that are known by more have large proportions of them unsexed or scattered uneconomically among several distant museums. Similar problems attend the recordings of vocalizations.

The uneven spatial sampling of taxa is perhaps a less recognized problem. When evidence of clinality, involving voice, plumage and genetics, was first documented in a suboscine antbird, the Variable Antshrike *Thamnophilus caerulescens* (Isler *et al.* 2005), Brumfield (2005) was prompted to stress the cardinal importance of sampling over a wide area:

A more restricted sampling design in the present study might have led to the erroneous conclusion that *T. c. aspersiventer*, *T. c. dinellii*, and *T. c. paraguayensis* have reciprocally monophyletic mitochondrial lineages, making them full species according to some species concepts.

The warning continues to be missed, however. The elevation to species status of two clades in the Australian Raven *Corvus coronoides* (Jønsson *et al.* 2012) was declined by Dickinson & Christidis (2014) for lack of sampling intergradient material, a position we fully support irrespective of our agreement that levels of sequence divergence alone are not appropriate arbiters of species limits. We likewise resist a claim of species rank for northern Venezuela's Green-and-black Fruiteater *Pipreola riefferii melanolaema* on the basis of its 4.6% sequence divergence from subspecies *confusa* in distant Peru (Berv & Prum 2014), because south-western Venezuelan (i.e. geographically intermediate) specimens of nominate *riefferii* not only remain genetically unsampled but also "clearly present plumage transitional to *P. r. melanolaema*" (Kirwan & Green 2012). We do the same with the Chinese form *mutica* of Scaly-breasted Cupwing *Pnoepyga albiventer*, catapulted from synonym to species on the basis of "so pronounced" differences in molecular and bioacoustic markers compared to those in Nepal (Päckert *et al.* 2013), because our own sampling of songs

from geographically intermediate areas (Bhutan, north-east India) reveals a cline that reduces *mutica* to subspecific status. Certain recent proposed revisions by Pratt & Mittermeier (2016), who remark (without discernible supporting evidence) that the Tobias criteria "in many cases fail to include relevant behavioral and ecological data", fail to achieve an appropriate level of comprehensiveness, with Samoan Robin *Petroica pusilla* (nominate of a fourteen-race species) split on a vocal comparison with Fijian birds only, and Manu'a Starling *Aplonis manuae* given species rank on the basis of vocal evidence which our own review of all available sound recordings simply does not confirm.

But we have no intention of disguising or diminishing the fact that a significant proportion of the taxonomic judgements we make here is based on small sample sizes and assumptions. A striking case by way of illustration is that of the Slender-billed Cicadabird *Edolisoma tenuirostre*, a single species in HBW which in this checklist we break into eleven. This is based on as many specimens as we could access but which commonly did not reach the double figures we require; and in many cases also on just one or two sound recordings. In such circumstances, where morphology and voice are combining to point, with considerable strength, to a change in taxonomic ranking, the choice then arises whether to allow the weakness of the sample size to override the assumption that the material we are reviewing is representative. Our inclination has almost always been to opt for what we hope is a very small risk in accepting the evidence. However, wherever sample sizes have been too small to make a score with confidence we insert the word "allow" before the (typically in these cases conservatively) estimated number to acknowledge the increased degree of uncertainty in the overall assessment.

Quantifying voice: the new taxonomic dimension

The vocalizations of birds are often, as we note above, of crucial importance in determining taxonomic status. Among the non-passerines evaluated for species rank in Volume 1 of this checklist, at least 34 were given scores under the Tobias criteria for "different voice", comprising seven pigeons, seven owls, five woodpeckers, two guineafowl, two cuckoos, two kingfishers, two barbets and one penguin, snipe, rail, hornbill, trogon, motmot and parrot. The evidence for these differences was in the published literature, and the sources were cited; the scores themselves were based on a subjective assessment of the degree of distinctiveness conveyed by the descriptions.

Not all these taxa needed the awarded scores to achieve species rank, but the majority did. While we remain reasonably comfortable with the outcomes in these cases, it is obviously far from satisfactory in such important matters to depend so completely on the statements of others, which are themselves liable to subjective bias. This danger was underlined during work on the present volume when evaluating the distinctiveness of the race *longicaudata*, from Anjouan, of Madagascar Brush-warbler *Nesillas typica*. This form was split in a recent field guide (Sinclair & Langrand 2013) with the remark that its notes are more rapid and higher-pitched than those of the nominate, and in consequence *N. longicaudata* has been accepted by at least two world checklists. However, our own analysis of the voice of this form, using publicly available recordings, reveals no quantitative differences. We therefore retain *longicaudata* as a subspecies of *N. typica*. A similar case is that of the Golden-bellied Gerygone *Gerygone sulphurea*, where supposed differences in voice between populations prove to be no stronger than those within populations.

This analysis was just one product of an initiative never previously attempted in a world checklist, to incorporate quantitative analysis of vocalizations as a central component of the taxonomic decision-making process. Resources—including time—did not permit a truly comprehensive review of recorded material, but the decisive importance of vocalizations in the species-specific signals of almost all the passerines, coupled with our continuing adherence to the Tobias criteria (for acoustic parameters see Tobias *et al.* 2010: 734–735), required us at least to investigate as many cases as possible—more than eight hundred—where vocal evidence seemed likely to prove indispensable.

Quantifying vocal differences in birds is, of course, challenging. Vocalizations can vary within and between individuals, ages and sexes, and with time of day, time of year, circumstance and—manifestly—location. Sample size (see above!) is therefore a major issue. Moreover, determining homologous calls for comparison can be problematic. Quality of recordings matters. Recordists' competence in field identification matters more. Perhaps most taxing are the facts that oscine passerines learn their songs, and that many species and families—drongos, larks, shrikes, chats, starlings, thrushes, warblers—are highly imitative. As a consequence of all these things, a great deal of effort can be spent on analyses that ultimately fail to be convincingly robust.

These drawbacks were borne in mind during the process of evaluating vocal differences for use in this volume. Not all cases produced an outcome, owing to the scarcity or quality of the material. Occasionally we are able to point to previously unreported levels of distinctiveness which are highly suggestive but which require much closer investigation (e.g. Short-tailed Antthrush *Chamaeza campanisona*, Common Miner *Geositta cunicularia*, Wedge-billed Woodcreeper *Glyphorynchus spirurus*, White-eyed Tody-tyrant *Hemitriccus zosterops*, Mountain Elaenia *Elaenia frantzii*). However, in many dozens of cases the scoring for voice was decisive in elevating taxa to species rank. The findings are of necessity highly condensed in the taxonomic notes sections where phenotypic characters are enumerated and scored, but in the interests of transparency the full texts are to be published on the HBW Alive website very shortly.

Our null hypothesis

In an elegant, erudite and impassioned essay that appeared as Volume 1 was in press, Gill (2014) strove to make the case for a "reverse list" taxonomy of birds, arguing that the new null hypothesis in a polytypic species concept should be that: "distinct and reciprocally monophyletic sister populations of birds exhibit essential reproductive isolation and would not interbreed freely if they were to occur in sympatry". By this formulation Gill effectively presses the basic premises of the phylogenetic species concept (diagnosability and reciprocal monophyly) into the service of the biological species concept. Rather than treating isolated taxa on mountains and islands as conspecific with each other or with continental taxa, as under current arrangements, the working assumption would be that, unless and until shown otherwise, such taxa are presumed to be reciprocally monophyletic and therefore each a species. In a reversal of the decades-long tradition in which ornithologists of various backgrounds have slowly and laboriously, species by species, unpicked the overlumped global avifauna, the burden of proof would fall on the shoulders of those who would keep particular taxa lumped, not on those who want to see them split.

That this proposition has gained some traction is apparent in a recent molecular study of the Rufous-tailed Tailorbird *Orthotomus sericeus*. Lim *et al.* (2014) reasonably interpreted Gill's species-rank hypothesis to apply to all "physically separated, moderately divergent populations" of birds, and argued that the taxonomically undifferentiated population of the tailorbird on Palawan (Philippines) is in line for elevation because of its clear but moderate genetic distinctiveness from populations on Borneo: "If diagnosable differences in song or behavior are discovered…, it should then be named a different species".

This exercise of Gill's argument exposes its rather deep implications. How many "physically separated, moderately divergent populations" of birds are there in the world? In this case the moderate divergence is evident at the genetic level, so all that is needed is an additional phenotypic difference, no matter how small, to take Palawan birds from population to species in one bound. With sufficient sampling this may well happen (although our own comparisons have revealed nothing clear), as differences in voice in insular forms, at least of oscine passerines, are commonly not difficult to find, may simply relate to habitat, and can evolve at great speed (Baker 2006, Baker *et al.* 2006). Thus if the criteria for bestowing species rank can apply to any populations exhibiting physical separation and modest divergence in voice, even recently translocated North Island Saddlebacks *Philesturnus rufusater* appear to be on a path to eligibility (Parker *et al.* 2010).

Gill does, however, specify reciprocal monophyly, which (a) ought to prevent any absurdities resulting from voice shifts on newly colonized islands but (b) appears to lock non-molecular taxonomy out of all future consideration. Without genetic study, how will reciprocal monophyly or its absence ever be demonstrated? What criteria will govern the assumptions behind the new ranking of taxa as species? Or will the burden of proof simply require evidence of the absence of reciprocal monophyly? (Anyway, is there anything close to consensus that reciprocal monophyly is the new yardstick for implementing species-rank revisions? The five "capuchino" seedeaters mentioned above all behave as species by recognising each other by song and plumage, but do *not* exhibit reciprocal monophyly.)

A further question arises of how to judge the situation—what criteria to use—when the burden of proof is duly shouldered and evidence furnished to challenge the results of adopting the new null hypothesis. Irestedt *et al.* (2013) split Red-bellied Pitta *Erythropitta erythrogaster* into

17 species. Applying the Tobias criteria to the same complex, Collar *et al.* (2016) recognized 13. So by what standards are the rankings of the four taxa that the latter authors retained as subspecies or synonymized to be tested? It immediately becomes apparent that, rather than resolving this issue, the new null hypothesis has merely pushed it temporarily out of sight. But now, faced with evidence used to reject species rank for a taxon, a choice has to be made once again based on preference and belief. Ultimately, therefore, the studies and debates generated by the adoption of the new null hypothesis will be no shorter or less complex—or cost less in terms of human resources—than those in play at the moment, and they will still require taxonomists to choose between criteria for species discrimination. We salute Gill's intention with this initiative to seek to establish a broader platform for the conservation of avian diversity, but we suspect that in reality it will serve no practical purpose.

"A 'rapid assessment program' for assigning species rank?" Yes!

Remsen's (2016) sympathy for the need for greater speed and efficacy in evaluating species limits issues in birds gave him a good title, structured as a question, and we readily answer him in the affirmative. We deem it plausible that, in time, molecular studies might be able to resolve all taxonomic issues, including at the species and subspecies levels. But that time is not yet, and it seems unlikely to come for many years. Meanwhile we have to consider our options.

If Gill's new null hypothesis is a non-starter for reasons given above, the *status quo* he seeks to subvert is not acceptable either: it is, regrettably, too little, too late. Despite the spreading compass of molecular studies, great swathes of taxa remain unsampled, part-sampled or in need of re-sampling. Checklist committees serve an important purpose, but function reactively, appear to abide by majority votes that are sometimes cast before all the arguments are heard and weighed, and understandably struggle with the issue of urgency (as at August 2016—this observation is neutral and in no way a criticism—the South American Checklist Committee website indicated 252 cases of "Proposal needed" and 72 cases of "Proposal badly needed"). Checklist compilers, meanwhile, rely on the published findings of others, in some cases often with little or no discrimination over the quality involved (although they make occasional unexplained choices between competing viewpoints, resulting in disconcerting levels of avoidable contradiction and inconsistency).

All this underscores the necessity of our current exercise. We fully acknowledge its multiple imperfections, and we have no doubt made errors that will trouble our sleep for years to come. We admit, yet again, that the Tobias criteria are open to refinement and improvement, perhaps on a scale and of a type which will reverse some of the taxonomic decisions they have produced to date. And we need to emphasise that constraints of time and resources have prevented us from being able to apply the Tobias criteria to every case, especially when the issue is one of lumping rather than splitting. Many taxa in the Troglodytidae merit evaluation in this regard, and a good number of cases are scattered throughout other families, among them (merely by way of illustration) White-tailed Swallow *Hirundo megaensis* and Pearl-breasted Swallow *H. dimidiata*, Hildebrandt's Starling *Lamprotornis hildebrandti* and Shelley's Starling *L. shelleyi*, Japanese White-eye *Zosterops japonicus* and Lowland White-eye *Z. meyeni*, Adelaide's Warbler *Setophaga adelaidae*, Barbuda Warbler *S. subita* and St Lucia Warbler *S. delicata*, Scarlet-rumped Tanager *Ramphocelus passerinii* and Cherrie's Tanager *R. costaricensis*, and Black-capped Hemispingus *Kleinothraupis atropileus* and White-browed Hemispingus *K. auricularis*.

Nevertheless, this volume, like its predecessor, makes the case for significant numbers of species-level changes, and we respectfully await the verdict of history over their adoption. HBW treated 3,964 species of non-passerine and 6,008 species of passerine; these figures rise in the present work to 4,372 and 6,592 respectively; thus the number of bird species in the world rises in this exercise from 9,972 to 10,964, an increase of 11%. Somewhat over half this growth has been generated by the work of others; the remainder derives from our own endeavours after thousands of hours in museums and hundreds of hours analysing recordings of vocalizations and studying photographs and videos. We particularly hope that these "original" revisions will be subject to independent scrutiny, assessment and approval; in many cases fieldworkers may be motivated to collect the further evidence that will validate or refute them. But we feel confident, at least, that the emphasis in this checklist on phenotypic differentiation has identified numerous instances of previously neglected taxa whose newly recognized distinctiveness, whether as species or subspecies, will cause them to be accommodated into biodiversity conservation plans long into the future.

In terms of the future of this endeavour after the publication of the present volume, two points are worth conveying. First, the HBW/BirdLife team will continue to review newly published material to produce at least annual updates to the *Checklist* in the future, which will be reflected in HBW Alive, in the BirdLife Data Zone and on the IUCN Red List. Anyone can contribute to this process by highlighting new information we may have overlooked, or taxonomic decisions that may require review, via the Comments boxes on the species accounts in HBW Alive. While we cannot undertake to respond to individual comments, we will consider each one carefully. Second, we hope to undertake further research to inform the Tobias criteria themselves, potentially exploring: expanding the justification for the threshold score of 7 for species status, the feasibility and impact of evaluating hybrid-zone width as a proportion of the entire distribution width; broader issues relating to how to treat hybrid zones in the criteria; differences between bird families in the challenges they pose for the application of the criteria; and the feasibility of integrating genetic divergence into the criteria.

Technical aspects

However, in addition to reconsidering the taxonomic status of birds across the whole class, this checklist offers a great deal more. For well over two years our extended teams at both HBW/Lynx and BirdLife have been fully occupied working on the present volume.

Given the many and sweeping changes to avian taxonomy to be found in this volume, we have added extensively to the taxonomic texts imported from HBW but have also extensively used explanatory notes to accompany genus and family subheadings. These typically concentrate on indicating how and why the group in question differs in treatment from what was presented in HBW.

Recovering and embellishing one of the features used throughout HBW, in the present volume we include summary totals for each taxon from genus upwards. Thus, a genus will have two figures in blue, which represent species (in bold) and "taxa" (*sensu* HBW = total number of species-group taxa recognized, in other words all subspecies plus all monotypic species). Moving into family-group names, the numbers continue to expand leftwards, with the inclusion of genera, and (when applicable, further left still) tribes and subfamilies. So we might have a family with the figures 3sf·27·**273**·616, which would mean it contained three subfamilies, 27 genera, 273 species and 616 "taxa". As in HBW, these figures always refer to extant forms. When extinct forms are also involved, the numbers of extinct taxa are displayed in a like fashion but in a separate series of grey numbers, situated further to the right. These "extinct" figures continue leftwards until reaching the first "0". Thus, if the above family contained merely one extinct subspecies, the extinct figures would be †**0**·1; if it were one species and three subspecies, it would appear as †0·**1**·3. The complete family entry in this case would be: 3sf·27·**273**·616 †0·**1**·3. Note once again that the extinct taxa are not included within the blue figures for extant forms, so the total number of "recent" taxa in this family would be 619.

Our resident team of artists has been busy, and this volume contains a grand total of 12,629 bird illustrations, including 642 that are totally new, and a further 1,208 that have been improved from their original HBW versions. A few figures published in HBW have been omitted as being not sufficiently relevant or in a few cases misleadingly different.

Making the maps as accurate as possible involves extensive delving into an immense variety of sources, often to make very small changes that perhaps only a few will detect, and often struggling to make the best of what little is available to map some of the less well documented areas. Altogether 6,649 maps have been checked, rechecked and checked again by our teams at HBW/Lynx and BirdLife to provide what we would like to hope are probably the most accurate set of maps for any complete class of animals. A minor change on the maps this time is that arrows used to highlight small details of distribution now appear in red; this change has been made for purely practical reasons, as the black arrows previously used sometimes proved difficult to see against coastal outlines. Also on the subject of distributions, we ought perhaps to explain that we have attempted to respect local usage (as we understand it) in the positioning of the "R" (for River) before or after the actual name so it normally comes before the name in most of the world (R Xingu, R Indigirka, R Zambezi, R Danube), but after it in North America, Australia and New Guinea (Mississippi R, Murrumbidgee R, Fly R).

We have tried to be as informative as readability permits in backing up all new material or decisions, be they taxonomic, distributional or whatever, with extensive reference to the literature we have been consulting, and this amounts to some 2,809 references. A great many more papers and books have been referred to, but in a work of this scope, regrettably it is not practical to include them all.

The extensive internal rearrangements of numerous families in this volume have frequently had knock-on effects on the scientific names to be used. Some of the issues are explained below, along with a few other matters related to nomenclature (see page 21).

The English names of species have also come under new pressure as a consequence of the unprecedented levels of change in the composition of certain passerine families or groups, particularly in the New World (for example Fringillidae, Emberizidae, Cardinalidae and Thraupidae). Summer and Scarlet Tanagers turn out to be cardinals. The *Paroaria* cardinals prove to be tanagers. The Coal-crested Finch is a tanager. So are the two "diuca-finches", but they occupy different clades and arguably therefore should no longer be linked by a common name. The list of such misfits is fairly long and, assuming that these new arrangements will not be overturned by a further round of genetic analysis, it is obviously tempting to consider changing the English names of species to reflect their true identities. However, this is a sensitive issue and many birders and ornithologists seem likely to prefer stability over accuracy, or at least to favour a more measured and consensual transition from one usage to another. It is also potentially rather a complex issue: changing "White-winged Diuca-finch" to "White-winged Tanager" immediately runs into trouble with *Piranga leucoptera*, itself now a cardinal! Where opportunity arises and opposition seems unlikely, we have made a very small number of changes (the Coal-crested Finch becomes Coalcrest, for example); but otherwise we deem it more appropriate to assume a preference for a longer-term process of adjustment by the global ornithological community.

In order to avoid using up a great deal of space on what is a fairly minor feature, we have limited the "Other common names" to those used in recent world and regional checklists, and we do not list any that follow on fairly obviously from what is already listed.

As in Volume 1, we follow BirdLife International in indicating which Critically Endangered species are likely to have gone extinct (or extinct in the wild), but for which comprehensive searches are required to confirm that the last individual has died. The application of the Possibly Extinct and Possibly Extinct in the Wild tags to such taxa takes into account the time since the last record, the intensity, extensiveness and adequacy of searches, the extent, intensity and timing of threats, and the likely susceptibility of the taxon to these threats (Butchart *et al.* 2006, IUCN Standards and Petitions Committee 2016). We have also continued the approach in Volume 1 of identifying Extinct ("†") avian subspecies, updated from Szabo *et al.* (2012). It should be noted that the species-level assessments in particular need updating, but this has been postponed until publication of an important new series of papers that describe and apply a new quantitative approach to assessing such information within a statistical framework. Once published, there are likely to be a number of changes to the list of Extinct and Critically Endangered (Possibly Extinct) species. The Red List categories assigned to all species in this volume—including all the taxonomic revisions—are those published in BirdLife's 2016 update to the IUCN Red List.

For further information about the structure and technical workings of the current checklist, we would point readers towards the Introduction to Volume 1 (pages 43–51).

Acknowledgements

Volume 1 of this checklist contains long lists of people and institutions to whom and to which we owe an enormous debt of gratitude, and we should at once stress that many of the contributions from those people and institutions have been to the entire project, not merely the first volume. We hope that we may be forgiven for not repeating all these names here, where instead we simply focus on those who have been particularly important to the second volume and to the completion of the project. We should, however, also acknowledge the immense contribution made by the authors, artists and institutions involved with the production of the seventeen volumes of HBW, the foundation on which this checklist builds. To all of them we take this opportunity to register our sincere appreciation of their work.

The Natural History Museum (NHMUK), Tring, UK, has been fundamental to the fulfilment of this project, hosting us for several thousand hours of research time over the two-and-a-half years since work on Volume 2 began. For this privilege we particularly thank Robert Prŷs-Jones, whose very positive support has been of the greatest value (and which we attempt to acknowledge below: see page 21), Mark Adams, Hein van Grouw, Alison Harding and other staff members, including those in security who cheerfully supported our comings and goings at weekends and early and late in the working day. The American Museum of Natural History (AMNH), New York, USA, has also allowed us to work there over several weeks in the past three years, and we gratefully acknowledge the kind help of Paul Sweet, Thomas Trombone, Lydia Garetano, Mary LeCroy and Joel Cracraft. Two other museums have hosted us several times for several days: the Smithsonian Institution (United States National Museum, USNM), Washington DC, USA, where we thank Chris Milensky, Brian Schmidt and Christina Gebhart, and the Naturkundemuseum (ZMB), Berlin, Germany, where we thank Sylke Frahnert and Pascal Eckhoff. Other museums in which we undertook work on the project are Louisiana State University Museum of Natural Science (LSUMNS), Baton Rouge, USA, with thanks to Fred Sheldon and Van Remsen; Naturalis (RMNH), Leiden, Netherlands, with thanks to Steven van der Mije and Pepijn Kamminga; Muséum National d'Histoire Naturelle, Paris, France (Patrick Boussès and Jérôme Fuchs); Royal Museum for Central Africa (RMCA), Tervuren, Belgium (Alain Reygel and Michel Louette); and Royal Belgian Institute of Natural Sciences (RBINS), Brussels, Belgium (Tom Geerinckx, René-Marie Lafontaine and Pierre Devillers). We also had help from John Bates at the Field Museum of Natural History, Chicago, USA, and Markus Unsöld at the Zoologische Staatssammlung München, Munich, Germany.

The starting point for the texts of course was HBW, but the first stop when rechecking basic details for each species account and looking for potential conflicts was Dickinson & Christidis (2014) *Howard and Moore Checklist*, 4th Edition, which rediscusses many of the issues of nomenclature already tackled in HBW, as well as many new ones, and has made many advances in the field of establishing correct publication dates. Also most useful have been certain websites, notably *Zoonomen* (Peterson 2016), *Taxonomy in Flux* (Boyd 2016) and the AOU's South American Classification Committee (Remsen *et al.* 2016), along with the world lists by Clements *et al.* (2016) and Gill & Donsker (2016).

We also offer a particularly hefty thank you with a warm recommendation to Winkler *et al.* (2015) *Bird Families of the World*. This book has provided the entire framework of families for our checklist, and is an excellent source for gaining an idea of how the higher taxonomy of birds has evolved in recent years.

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We also wish to pay tribute to the website Xeno-canto, which has been an extraordinary resource for our research into vocalizations, although we should also mention, with deep appreciation, AVoCet, the Macaulay Library at the Cornell Laboratory of Ornithology and Lynx's own Internet Bird Collection (IBC). Furthermore, the IBC, supplemented by a large number of other websites of different kinds, has been the main source of videos and photographs of live birds, which in this checklist have played a very important role for analysing morphological characteristics, complementing the traditional study of museum skins. Peter Boesman's extensive revision of vocalizations is reflected in there being a separate reference, 393 in total, for each different species (when appropriate). This has proved essential, because he has amassed an enormous amount of material, all of which will be soon available as HBW Alive Ornithological Notes.

The teams that provide us with the French, German and Spanish names have had a busier time than ever, as they have had to revise all of the passerine names to fit with the new taxonomic ideas. We should like to acknowledge our warm appreciation of Normand David and Michel Gosselin for the French names; the "Standing Committee for German Names of the Birds of the World" of the Deutsche Ornithologen-Gesellschaft and IOU, consisting of Peter H. Barthel, Christine Barthel, Einhard Bezzel, Pascal Eckhoff, Renate van den Elzen, Christoph Hinkelmann and Frank Steinheimer, for the German names; and the committee of the Spanish Ornithological Society (SEO/BirdLife), comprising Eduardo de Juana, Josep del Hoyo, Manuel Fernández-Cruz, Xavier Ferrer and Jordi Sargatal, for the Spanish names.

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Issues of nomenclature in the current volume

The relevant contents of papers referred to in this work is commonly commented briefly in the texts, but a notable exception is in alterations of the authors and dates of taxa. To avoid tedious, long drawn-out explanations of very simple modifications, we have merely added the relevant reference number to the author(s) or year when these differ from the version used in HBW.

The nomenclature of *Heliobletus contaminatus* (page 106) has recently suffered considerable upheaval, but the matter is now under control. Nevertheless, at the time of writing, the northern race still lacks a valid name. Vítor de Q. Piacentini (*in litt.*) and Fernando Pacheco are in the process of remedying this situation, but meantime we are in the awkward position of having a well-established and universally recognized subspecies temporarily without a valid name. In these exceptional circumstances, we decided that we had no option but to leave this race in the text but for the present nameless; it is not a simple question of a replacement name, as the authors of the new name will explain in due course. This procedure should not be confused with the numerous cases, some widely known over many years within the ornithological community, of taxa that are undoubtedly valid forms but have not yet been formally described. Such forms have never been included formally in HBW, nor are they in this checklist.

Our treatment of a few names of authors of taxa has evolved with the current volume, in part due to new factors, and in part due to fuller information. For example, the inclusion of an extinct species described by Julian Hume means that we have had to add Allan O. Hume's initials to all of the many accepted taxa he described. Again, up to now the name Bartels received the same treatment as Phelps and Gurney, involving father and son with the same initials. However, we now have a new Bartels (A.), and this means that the father and son now also need their initial, M. Although Max, Sr was M. E. G. Bartels, to date we have not been able to verify the full initials of Max, Jr, but note that they were regularly referred to as Sr and Jr, and so consider it anyway appropriate to maintain this, at any rate until proven wrong; see, e.g. J. H. Becking (2009) *Bull. Brit. Orn. Club* **129(1)**: 18–48. Some years ago we were advised to style the name of a certain taxon describer as R. G. W. Ramsay. However, on revisiting this case recently, we established that the correct form is actually Wardlaw-Ramsay (with a hyphen). It appears that his grandfather, Mr Wardlaw, married a Miss Ramsay, so, if any abbreviated form had been used, he would probably have been more likely to be called Mr Wardlaw than Mr Ramsay. Nonetheless, due to our past treatment of this surname, for clarity we retain the initials for Mr E. P. Ramsay.

Replacement names

As a result of recent studies, mainly genetic, the present volume contains many cases of altered generic limits. Sometimes the work is still in progress and exact divisions between redefined genera have yet to be clarified, leading in a few instances to a provisional lumping together to form outsize genera in order to avoid paraphyly, but at the same time creating a few new cases of homonymy.

In order to resolve these, the following new replacement names are hereby introduced. As all are new replacement names for species-group taxa, they are junior objective synonyms of the taxa they replace. In each case, the type specimen is automatically designated as the same specimen that is the type of the taxon replaced (ICZN Code Art. 72.7). Similarly, in each case the type locality is automatically that of the replaced taxon.

Phylloscopus intermedius zosterops nom. nov. A. Elliott & del Hoyo, 2016

New replacement name for *Abrornis affinis* F. Moore, 1854, in *Phylloscopus* preoccupied by *Motacilla Offinis* [sic] Tickell, 1833 [currently = *Phylloscopus affinis*].
Etymology. From the Greek ζωστηρ, "girdle", and ωψ, "eye", referring to the prominent white eyering of this Himalayan form, and recalling the white-eye genus of the same name. This name is a noun in apposition and is thus invariable.

Phylloscopus montis barisanus nom. nov. Christie & A. Elliott, 2016

New replacement name for *Cryptolopha montis inornata* Robinson & Kloss, 1920, in *Phylloscopus* preoccupied by *Regulus inornatus* Blyth, 1842 [currently = *Phylloscopus inornatus*].
Etymology. An adjectival name based on Bukit Barisan, the mountain range that forms the spinal column of the island of Sumatra and encompasses the range of this taxon.

Tangara episcopus prysjonesi nom. nov. Collar & Kirwan, 2016

New replacement name for *Tanagra Berlepschi* Dalmas, 1900, in *Tangara* preoccupied by *Calliste nigriviridis* [sic] *Berlepschi* Taczanowski, 1884 [currently = *Tangara nigroviridis berlepschi*].
Etymology. Named in honour of Robert Prŷs-Jones, recently retired as Head of the Bird Group at the Natural History Museum (UK), for his unswerving championship of the importance of museum-based ornithology over the past three decades, and his consistently generous assistance to visiting researchers, ourselves included. The name is a noun in the genitive singular, and is invariable.

Tangara episcopus johntoddzimmeri nom. nov. A. Elliott, 2016

New replacement name for *Thraupis episcopus urubambae* J. T. Zimmer, 1944, in *Tangara* preoccupied by *Tangara parzudakii urubambae* J. T. Zimmer, 1943 [currently = *Tangara parzudakii urubambae*].
Etymology. Named in honour of John Todd Zimmer (1889–1957), one of the most prolific contributors to our knowledge of Neotropical birds, late Curator of Birds at the American Museum of Natural History, and describer of both the junior and senior homonyms in this case. The name is a noun in the genitive singular, and is invariable.

Tangara sayaca beniensis nom. nov. A. Elliott, 2016

New replacement name for *Thraupis episcopus boliviana* J. Bond & Meyer de Schauensee, 1941, in *Tangara* preoccupied by *Callospiza boliviana* Bonaparte, 1851 [currently = *Tangara mexicana boliviana*].
Etymology. An adjectival name based on the department of Beni (northern Bolivia), which encompasses much of the range of this taxon, including its type locality of Chatarona.

First Reviser acts

Several cases have been encountered of simultaneously published names vying for precedence, and four of these appear to be unresolved. As no previous valid acts have been located that clearly solve the following cases, A. Elliott hereby acts as First Reviser to establish the precedence of:

(a) *Deconychura longicauda pallida* J. T. Zimmer, 1929 over *Deconychura longicauda connectens* J. T. Zimmer, 1929;
(b) *Anthreptes longmari* [sic] *angolensis* Neumann, 1906 over *Anthreptes longmari* [sic] *nyassae* Neumann, 1906;
(c) *Icterus graduacauda dickeyae* van Rossem, 1938 over *Icterus graduacauda nayaritensis* van Rossem, 1938; and
(d) *Melospiza heermanni* S. F. Baird, 1858a over *Melospiza gouldii* S. F. Baird, 1858a.

Notes on (d)
Also included in this particular synonymy is *Ammodromus samuelis* S. F. Baird, 1858b, which was already placed in the synonymy of *gouldii* by Coues (1872). Subsequently, both Ridgway (1901) and Hellmayr (1938) included *gouldii* in the synonymy of *samuelis*! In his original description of the taxa *heermanni* and *gouldii*, Baird (1858a) already suggested (page 477) that *gouldii* might be merely a variation ("Var. *gouldii*"). In fact, Cooper & Baird (1870) appear maybe to include *gouldii* within *heermanni*, but the text is somewhat unclear, and perhaps not wholly convincing as a First Reviser act, so it has been considered more appropriate to issue a new act here. The precise date of publication of *samuelis* is often reported to be August 1858, but internal evidence indicates that it was certainly no earlier than 25th October 1858; it has been deemed best to treat the two publications as appearing simultaneously, until proven otherwise.

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