

See discussions, stats, and author profiles for this publication at:
<https://www.researchgate.net/publication/273123056>

Dramatic niche shifts and morphological change in two insular bird species

ARTICLE *in* ROYAL SOCIETY OPEN SCIENCE · MARCH 2015

DOI: 10.1098/rsos.140364

READS

188

6 AUTHORS, INCLUDING:



Knud Andreas Jønsson

Natural History Museum of Denmark

50 PUBLICATIONS 1,105 CITATIONS

SEE PROFILE



Jon Fjeldså

University of Copenhagen

188 PUBLICATIONS 5,123 CITATIONS

SEE PROFILE



Anders Odeen

Uppsala University

39 PUBLICATIONS 937 CITATIONS

SEE PROFILE



Per G.P. Ericson

Swedish Museum of Natural History

127 PUBLICATIONS 4,425 CITATIONS

SEE PROFILE



Cite this article: Alström P, Jönsson KA, Fjeldså J, Ödeen A, Ericson PGP, Irestedt M. 2015 Dramatic niche shifts and morphological change in two insular bird species. *R. Soc. open sci.* **2**: 140364. <http://dx.doi.org/10.1098/rsos.140364>

Received: 8 October 2014

Accepted: 9 February 2015

Subject Category:

Biology (whole organism)

Subject Areas:

ecology/evolution/molecular biology

Keywords:

speciation, adaptive change, niche shifts, morphological divergence

Author for correspondence:

Per Alström

e-mail: per.alstrom@slu.se

[†]These authors contributed equally to this study.

Electronic supplementary material is available at <http://dx.doi.org/10.1098/rsos.140364> or via <http://rsos.royalsocietypublishing.org>.

Dramatic niche shifts and morphological change in two insular bird species

Per Alström^{1,2,†}, Knud A. Jönsson^{3,4,5,†}, Jon Fjeldså³, Anders Ödeen⁶, Per G. P. Ericson⁷ and Martin Irestedt^{8,†}

¹Swedish Species Information Centre, Swedish University of Agricultural Sciences, PO Box 7007, Uppsala 75007, Sweden

²Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, 1 Beichen West Road, Chaoyang District, Beijing 100101, People's Republic of China


³Center for Macroecology, Evolution and Climate at the Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark

⁴Department of Life Sciences, Imperial College London, Silwood Park Campus, Ascot SL5 7PY, UK

⁵Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, UK

⁶Department of Animal Ecology, Uppsala University, Norbyvägen 18D, Uppsala 75236, Sweden

⁷Department of Zoology, and ⁸Department of Bioinformatics and Genetics, Swedish Museum of Natural History, PO Box 50007, Stockholm 10405, Sweden

 PA, 0000-0001-7182-2763

1. Summary

Colonizations of islands are often associated with rapid morphological divergence. We present two previously unrecognized cases of dramatic morphological change and niche shifts in connection with colonization of tropical forest-covered islands. These evolutionary changes have concealed the fact that the passerine birds madanga, *Madanga ruficollis*, from Buru, Indonesia, and São Tomé shorttail, *Amaurocichla bocagii*, from São Tomé, Gulf of Guinea, are forest-adapted members of the family Motacillidae (pipits and wagtails). We show that *Madanga* has diverged mainly in plumage, which may be the result of selection for improved camouflage in its new arboreal niche, while selection pressures for other morphological changes have probably been weak owing to preadaptations for the novel niche. By contrast, we suggest that *Amaurocichla*'s niche change has led to divergence in both structure and plumage.

2. Introduction

Colonizations of islands are well-known triggers of speciation [1–4], often involving strong morphological divergence from continental relatives, sometimes resulting in spectacular radiations [5–9]. Such morphological divergence may result in erroneous assumptions about systematics as well as misinterpretations of biogeographical and ecological patterns and processes (cf. [10–16]).

We examine the phylogenetic relationships of two enigmatic forest birds of tropical islands, madanga *Madanga ruficollis* from Buru, Wallacea, Indonesia, and São Tomé shorttail *Amaurocichla bocagii* from São Tomé in the Gulf of Guinea, and demonstrate that both have undergone remarkable morphological change and niche shifts from their continental relatives, completely obscuring their systematic relationships. *Madanga ruficollis* is known from four old museum specimens [17] and a few recent observations [18–20], and has traditionally been placed in a monotypic genus in the family Zosteropidae ('white-eyes') [21,22]. *Amaurocichla bocagii* is placed in a monotypic genus, with presumed sylvioid relationships [23,24], although recent molecular analysis unexpectedly suggested affinities to *Motacilla* [25].

3. Material and methods

3.1. Study group

For a first preliminary molecular analysis of *Madanga*, we used mainly GenBank sequences (electronic supplementary material, table S1), representing a broad array of lineages, including most of the primary lineages within Passerida, as suggested by previous studies (e.g. [25–27]). As we obtained strong support for a close relationship between *Madanga* and Motacillidae, as had previously been suggested also for *Amaurocichla* [25], we expanded the dataset to also include representatives from all genera within Motacillidae and multiple species from the main clades found in earlier studies [28,29]. When preliminary analyses suggested a relationship between *Madanga* and a clade referred to as 'small pipits' by Alström & Mild [30], all the species in that clade were analysed (except *Anthus petrosus*, which has previously been treated as conspecific with *Anthus spinoletta*; cf. [30], as well as the two remaining Asian species with untested relationships, alpine pipit *Anthus gutturalis* and Nilgiri pipit *Anthus nilghiriensis*).

3.2. DNA extraction and sequencing

DNA was obtained from muscle, blood or, in a few cases, feathers or toepads (electronic supplementary material, table S1). Toepads were sampled from two *Madanga* and two *Amaurocichla* specimens. While standard laboratory procedures were used for fresh DNA samples, extractions, amplifications and sequencing procedures from archaic DNA obtained from study skin samples followed the procedures described previously [31,32]. This included extracting DNA in a dedicated 'clean' laboratory, and amplifying short (ca 200 bp), partly overlapping fragments. We sequenced five loci: the main part of the mitochondrial cytochrome *b* gene and part of the flanking tRNA-Thr (combined referred to as *cytb*); the mitochondrial NADH dehydrogenase subunit 2 (*ND2*); the nuclear ornithine decarboxylase (*ODC*) exon 6 (partial), intron 6, exon 7, intron 7 and exon 8 (partial); the entire nuclear myoglobin (*myo*) intron 2 and the Z-linked (*CHD1Z*) intron.

3.3. Phylogenetic analyses

In addition to the sequences obtained specifically for this study, we also used sequences from GenBank (electronic supplementary material, table S1). *Cytb* and *ND2* were analysed for all species and two to three nuclear loci for most species. For *Anthus spragueii* only *Cytb* was available, and for *Anthus brachyurus* only *cytb* and *ND2*. See electronic supplementary material, table S1 for details. All new sequences have been deposited in GenBank (electronic supplementary material, table S1).

Sequences were aligned using Muscle [33] in SEAVIEW v. 4.3.4 [34,35]; some manual adjustment was carried out for the non-coding sequences. For the nuclear loci, heterozygous sites were coded as ambiguous. Trees were estimated by Bayesian inference (BI) using MRBAYES v. 3.2 [36,37] as follows. (i) For the Motacillidae dataset, using *Emberiza* and *Passer* as outgroups, all loci and all sequences, including multiple individuals of the same species when available, were analysed separately (single-locus analyses). (ii) For the same dataset, as well as the one comprising multiple oscine lineages, using the suboscines *Tyrannus* and *Manacus* as outgroups, sequences from one individual per species were

concatenated, partitioned by locus and, for the coding loci, in two codon partitions (1st + 2nd and 3rd). Partitioning schemes and models were selected based on the Bayesian Information Criterion calculated in PARTITIONFINDER v. 1.1.1 [38]: for *cytb* and *ND2* 1st + 2nd codon partitions, the HKY model [39], assuming rate variation across sites according to a discrete gamma distribution with four rate categories (Γ [40]) and an estimated proportion of invariant sites (I [41]); for *cytb* and *ND2* 3rd codon positions, the general time-reversible (GTR) model [42–44] + Γ ; and for the other partitions, HKY + Γ . Rate multipliers were applied to allow different rates for different partitions [37,45]. Ambiguous base pairs and indels were treated as missing data, but indels were plotted on the trees *a posteriori*. Default priors in MRBAYES were used. Four Metropolis-coupled MCMC chains with incremental heating temperature 0.1 or 0.05 were run for 3×10^6 (single-locus analyses) or 5×10^6 (multilocus analyses) generations and sampled every 1000 generations. Convergence to the stationary distribution of the single chains was inspected in TRACER v. 1.5.0 [46] using a minimum threshold for the effective sample size. The joint likelihood and other parameter values reported large effective sample sizes (more than 1000). Good mixing of the MCMC and reproducibility was established by multiple runs from independent starting points. Topological convergence was examined by eye and by the average standard deviation of split frequencies (less than 0.005). The first 25% of generations were discarded as ‘burn-in’, well after stationarity of chain likelihood values had been established, and the posterior probabilities were calculated from the remaining samples (pooled from the two simultaneous runs).

A chronogram was reconstructed for the *cytb* data in BEAST v. 1.7.5 [47,48]. The topology was constrained to match the multilocus tree. XML files were generated in BEAUti v. 1.7.5 [49]. Analyses were run under the GTR + Γ model (cf. [50]), using a ‘birth–death incomplete sampling’ prior, and (i) a fixed clock rate of 2.1%/Myr [50] or (ii) an uncorrelated lognormal relaxed clock [51] with the same mean rate. Other priors were used with default values. For these analyses, 50×10^6 generations were run, sampled every 1000 generations. Every analysis was run twice. The MCMC output was analysed in TRACER v. 1.5.0 [46] to evaluate whether valid estimates of the posterior distribution of the parameters had been obtained. The first 25% of the generations were discarded as ‘burn-in’, well after stationarity of chain likelihood values had been established. Trees were summarized using TREEANNOTATOR v. 1.7.5 [52], choosing ‘Maximum clade credibility tree’ and ‘Mean heights’, and displayed in FIGTREE v. 1.3.1 [53].

The single-locus and concatenated data were also analysed by maximum-likelihood bootstrapping (MLBS). RAXML-HPC v. 7.3.2 [54,55] was run on the Cipres portal [51], 1000 replicates. The data were partitioned by locus, and GTRGAMMA was used both for the bootstrapping phase and for the final tree inference.

3.4. Morphological analyses

We examined all four known specimens of *Madanga* and four specimens of *Amaurocichla* in the American Museum of Natural History, New York (AMNH) and one additional specimen (holotype) of *Amaurocichla* in The Natural History Museum, Tring, UK (NHM). These were compared with large series of pipits (*Anthus*) and wagtails (*Motacilla*) and other relevant species. All the species in clade A (see Results) were measured: wing length (flattened and stretched); tail length (ruler inserted under tail); bill length (to skull); bill depth and width (at distal edges of nostrils); tarsus length (to last complete scutum before toes); hind-claw length (to thin skin at base). Only internally sexed specimens were measured, with the aim to measure 10 of each sex when possible. Measurements were taken in the AMNH, Swedish Museum of Natural History, Stockholm (NRM) and National Zoological Museum of China, Beijing (NZMC). A principal component analysis (PCA) was performed in SPSS STATISTICS v. 20 (IBM Corp.). In addition, X-rays of all four *Madanga* specimens were examined and compared with skeletons of other relevant taxa.

4. Results

4.1. Molecular markers

Madanga was nested within Motacillidae, among the primarily Eurasian ‘small pipits’ *Anthus* (*sensu* [30]) (figure 1, clade A; electronic supplementary material, figures S1–S3). *Madanga* and the New Guinean *A. gutturalis* formed a strongly supported clade (D), sister to another well supported clade (C) comprising the northern Palaearctic breeders *A. trivialis* and *A. hodgsoni* and South Indian *A. nilghiriensis*. *Amaurocichla* was nested within *Motacilla*, as sister to the Afrotropical *M. clara* and *M. capensis*, in a clade (G) also containing the Malagasy *M. flaviventris*; these clades were strongly supported. Clade D was also supported by a unique 19 bp deletion in the ODC alignment (electronic supplementary

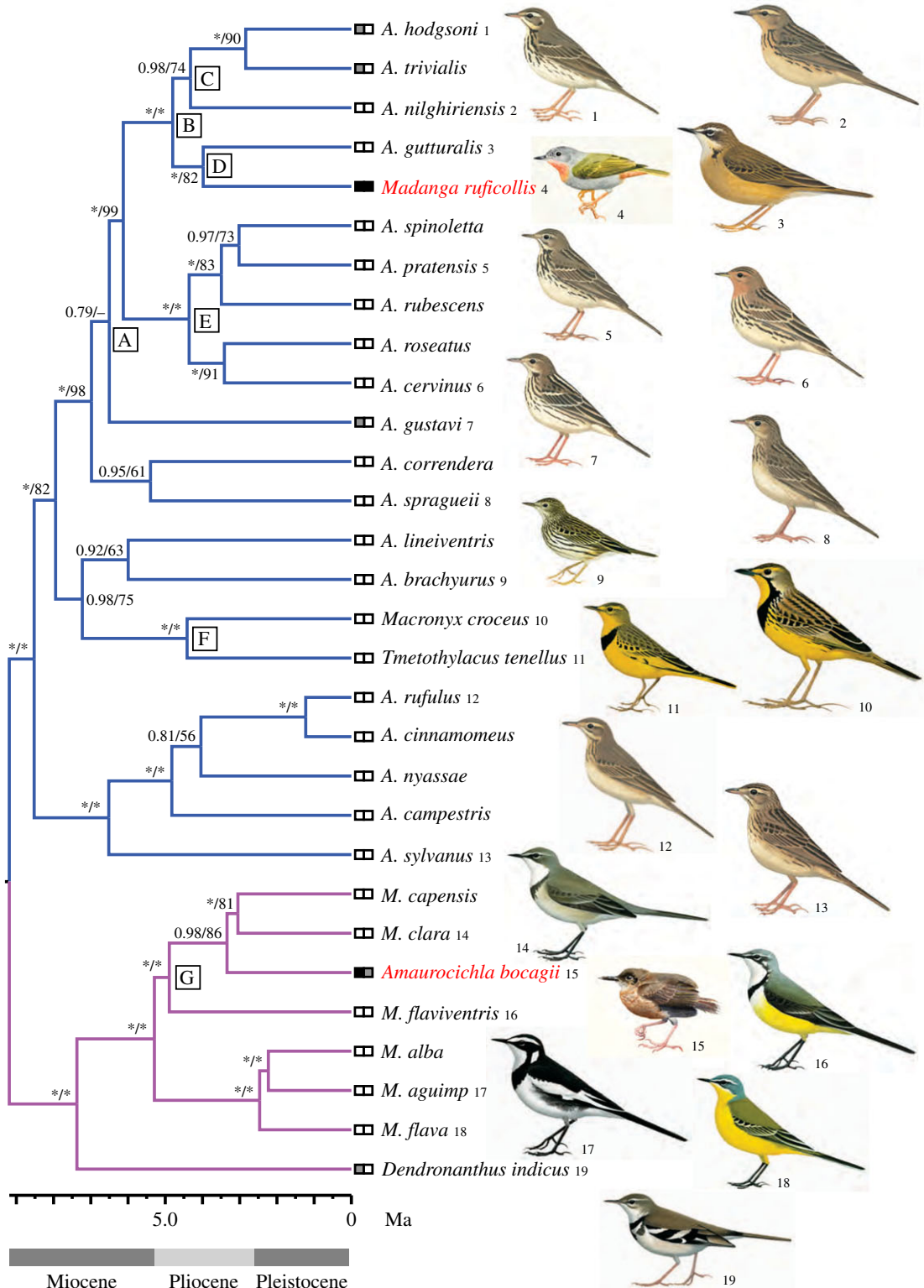


Figure 1. Chronogram of Motacillidae, based on *cytb* and a molecular clock (2.1%/Myr), with the topology constrained to fit the multilocus tree (electronic supplementary material, figure S2). Values at branches are posterior probabilities (PP)/maximum-likelihood bootstrap (MLBS) percentages; * indicates PP 1.00 or MLBS 100%. Letters A–G denote clades discussed in the text. The ‘pipit’ and ‘wagtail’ clades have been highlighted by differently coloured branches; A. — *Anthus*, M. — *Motacilla*. Boxes at tips of branches represent, from left to right, habitat (black—forest; white—open; grey—forest or more open) and foraging niche (black—arboreal; white—terrestrial; grey—terrestrial and arboreal). Illustrations by P.A. (from [30]), Ren Hathway (3, 9–11, 14, 16–19; from [56]) and J.F. (4, 15).

material, figure S2). In the single-locus analyses (electronic supplementary material, figure S3), there was conflict between mitochondrial and nuclear markers regarding the exact position of *Madanga*, with the mitochondrial tree inferring *Madanga* to be sister to the four other species in clade B. There was also some conflict among single-locus analyses regarding the precise position of *Amaurocichla* (electronic supplementary material, figure S3). Although not the focus of this study, *Macronyx croceus* and *Tmetothylacus tenellus* were inferred to be sisters (clade F), deeply nested within *Anthus*, and *Dendronanthus indicus* was found to be sister to *Motacilla*; all these relationships received strong support.

Madanga and *A. gutturalis* were estimated to have diverged from a most recent common ancestor 3.98 (95% HPD 2.65–5.33) million years ago (Ma), *Amaurocichla* and *M. capensis* + *M. clara* 3.34 (95% HPD 2.17–4.64) Ma (figure 1; electronic supplementary material, figure S4).

4.2. Morphology

Madanga shows hardly any plumage similarity with *Anthus* (e.g. completely lacks dark streaking; shows unpatterned head, with no pale supercilium or dark moustachial and malar stripes; rather uniformly green wings without contrastingly pale wing-bars or tertial edgings; vivid green upperparts, and grey head and underparts with a well-demarcated pale rufous throat patch; figure 1). The only decidedly *Anthus*-like plumage trait is the pale markings on the inner webs of the outermost pair of rectrices, although these are less contrasting than in *Anthus*. By contrast, *Madanga* displays typical *Anthus* structure, although it is smaller than any Holarctic/Oriental *Anthus*, with less elongated tertials; on regression factor 1, which reflects overall size, *Madanga* is completely separated from the other ‘small pipits’ (figure 2). It most resembles *A. hodgsoni* and *A. trivialis*, especially in bill and hind-claw structure (figure 2; electronic supplementary material, tables S2–S3). By contrast, *Madanga*’s sister, *A. gutturalis*, is the largest species in clade A, although it resembles *Madanga* in bill and hind-claw structure (figure 2; electronic supplementary material, tables S2–S3).

Madanga differs from all species in Zosteropidae by its rufous throat and in multiple structural aspects (e.g. proportionately longer toes and claws, and the presence of a slight hump on the culmen of the upper mandible over the elliptical nostrils; by contrast, zosteropids have an evenly curved culmen to the upper mandible and slit-like nostrils with more pronounced operculum).

The plumage of *Amaurocichla* bears no resemblance to any *Motacilla*, being uniformly dark brown above and on the wings and tail and paler brown below with slightly paler upper throat and belly (figure 1). Moreover, the blackish bill often has diffusely set-off paler tip, unlike all wagtails. Also the structure is strongly divergent from all wagtails, having proportionately longer bill, much shorter, more rounded wings and much shorter tertials and tail, with 10 rectrices (12 in *Motacilla*) with projecting shafts (figure 1). *Amaurocichla* differs markedly in structure from the ‘warbler’ genus *Macrosphenus*, with which it has been associated [24], by e.g. its vestigial 10th primary, slight hump at the base of the culmen of the upper mandible, no hook at the tip of the upper mandible, less prominent rictal bristles, and proportionately longer and slimmer tarsi, toes and claws, the latter also less strongly decurved.

5. Discussion

5.1. Island colonizations, niche shifts and morphological divergence

We provide evidence that two motacillid species have successfully colonized tropical islands, Buru and São Tomé, although they have diverged so much in morphology, habitat choice and behaviour (cf. figure 1) that their systematic affinities have been gravely misinterpreted. Despite the genus *Anthus*, with more than 40 extant species [22], having existed for some 8–9 Myr (electronic supplementary material, figure S4), the plumage divergence within this genus has been minimal compared to most other similar sized groups of birds, and different pipit species are renowned for being difficult to separate morphologically [30,56,57]. By stark contrast, *Madanga*’s plumage does not resemble that of any other pipit. Likewise, *Amaurocichla bocagii* is very different from other wagtails in plumage and has also diverged dramatically in bill, wing and tail structure.

Colonization of islands requires the capacity to cross open water and may be further facilitated by sociality, which increases the potential for simultaneous arrival of multiple individuals [4]. The family Motacillidae is globally distributed, and includes several long-distance migrants with loose flocking behaviour [28,30,56,58], making them suitable candidates for island colonization. Indeed, endemic pipits are found on several oceanic islands, and one species complex has colonized multiple islands from Sri Lanka to New Zealand [56].

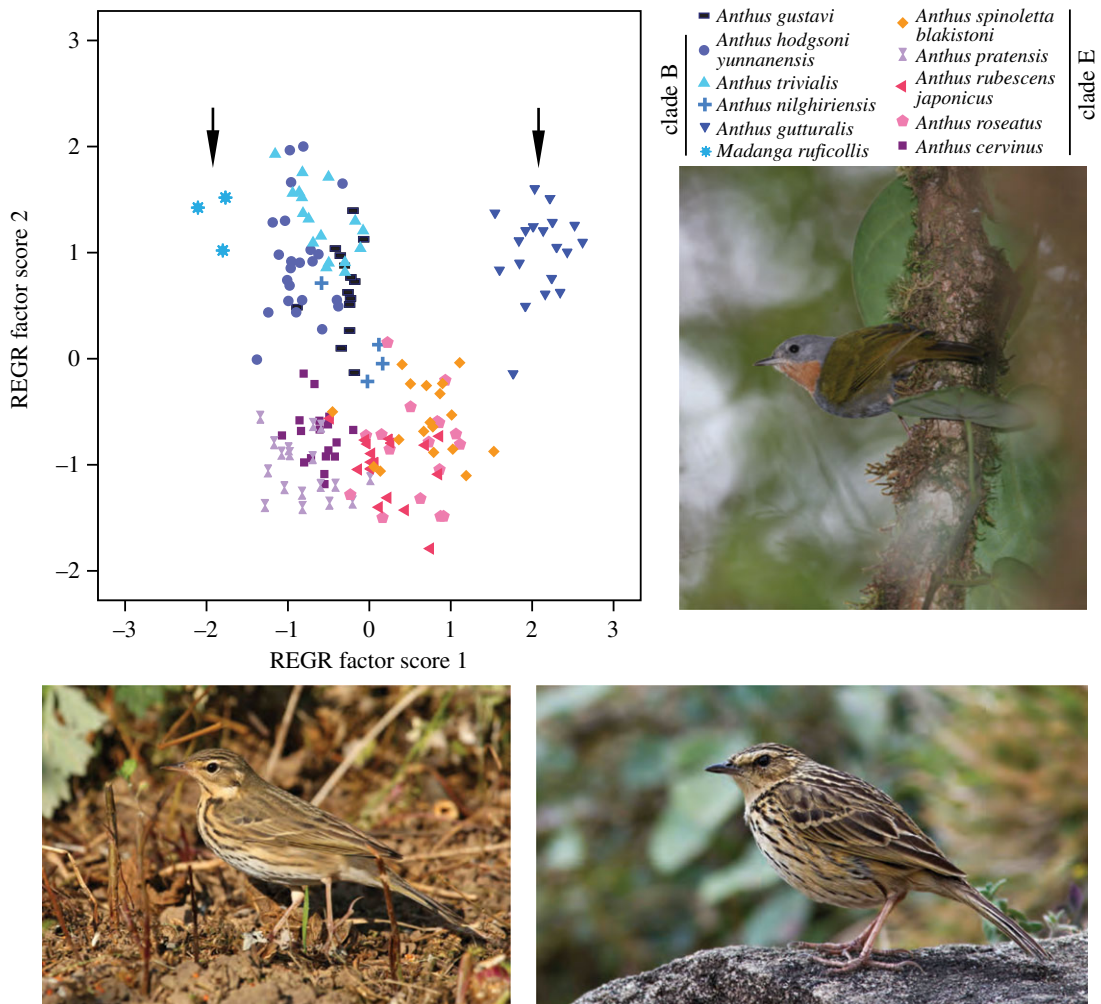


Figure 2. Principal component analysis of seven structural variables of the ‘small pipits’ *sensu lato* [30]. Arrows indicate *Madanga ruficollis* and its sister *Anthus gutturalis*. Photos of *M. ruficollis* (top) and two pipits (*Anthus hodgsoni yunnanensis*, bottom left; *Anthus nilghiriensis*) in their typical habitats. Photos Rob Hutchinson, Aurélien Audevard and Arka Sarkar, respectively.

Madanga occurs in stunted montane forest [19,59], where it has been noted to feed like a nuthatch (*Sitta*) on epiphyte-covered branches and tree trunks, sometimes following mixed-species feeding flocks [59] (R. Hutchinson, F. Rheindt, P.-H. Fabre 2013, personal communication). *Amaurocichla* is found in primary forest, where descriptions in the literature suggest diverse foraging strategies, including feeding on the ground in riparian habitats as well as on tree trunks and branches [24,60,61]. In contrast to both *Madanga* and *Amaurocichla*, nearly all other motacillids occur in open habitats with short grass, such as savannah, steppe, meadows and tundra, and along rivers and lake sides, from sea level to above the tree limit [30,56]. Moreover, unlike *Madanga* and *Amaurocichla*, all other motacillids forage exclusively on the ground [30,56] (the statement that *Dendronanthus indicus* ‘is equally likely to seek food in trees [as on the ground]’ [56] is incorrect [30]; personal observation).

The radical niche shifts in *Madanga* and *Amaurocichla* were most likely instigated by their colonization of tropical islands that, before human settlement, were probably completely forest-covered. In the case of *Madanga*, the conditions for a niche shift were probably favourable, as its ancestor, by chance, settled in an area with strongly epiphyte-covered, i.e. unusually ‘ground-like’, trees (by contrast, its sister species, *A. gutturalis*, colonized an area with open grasslands [56], i.e. a common pipit habitat). We hypothesize that *Madanga*’s niche shift originated by opportunistic feeding in trees used for shelter, and that it was morphologically and behaviourally suitably preadapted for this new niche. For example, short, decurved hind-claws, as in all species in clade B, are typical of arboreal birds (cf. the longer, straighter hind-claws of the species in clade E [30]); two of *Madanga*’s closest relatives, *A. trivialis* and *A. hodgsoni*, are atypical among pipits in breeding mainly in wooded habitats, and in frequently taking cover in trees when

flushed off the ground [30,56], and *Madanga*'s poorly known sister species, *A. gutturalis*, is also said to often fly into bushes and trees when alarmed [56]; the species in clade C, which is sister to the *Madanga*/*A. gutturalis* clade, forage by creeping around in rather dense vegetation of grasses and forbs [30], a habitat rather similar to epiphyte-covered branches; and the species in clade C are all capable of walking rather freely on branches [30]. Novel feeding behaviours leading to niche shifts might spread quickly in a small founder population, first culturally and later obtaining a genetic basis (cf. [4, pp. 128, 133]).

Amaurocichla's niche shift is less marked than in the case of *Madanga*, as it is less arboreal. Its close relative *M. flaviventris* sometimes breeds in forest clearings, open secondary forest and *Eucalyptus* plantations, and the even more closely related *M. clara* occurs along streams and rivers in forested country (although not in closed forest) [56,62].

In general, birds show a strong correlation between morphology and ecology (review [63]). Niche shifts can result in feeding-related morphological differentiation, as in the Hawaiian honeycreepers [8,64], Malagasy vangas [9,65], Darwin's finches (e.g. [6]) and ground tit *Pseudopodoces humilis* [66]. This seems to be true also for *Amaurocichla*, which has diverged markedly in structure from other motacillids, which are all structurally basically similar. *Amaurocichla*'s notable bill elongation is almost certainly feeding-related, whereas the dramatically shortened tail and wings and change in plumage are likely adaptations to its closed forest habitat. Shortening of the tail and wings and cryptic plumage colouration would be advantageous in closed forest, and short tails and wings and mostly brown plumage are common in various distantly related groups of passerines inhabiting dense undergrowth (e.g. many Cettiidae, Pellorneidae, Pnoepygidae, Troglodytidae and Rhinocryptidae) (e.g. [67,68]).

In the case of *Madanga*, surprisingly little divergence has occurred in feeding-related morphology, despite the extraordinary switch in niche and substantial period (*ca* 4 Myr) of independent evolution (cf. *Amaurocichla*, which has been separated from its closest relatives for 3.3 Myr). We suggest that the selection for feeding-related morphological change has been weak because the lineage leading to *Madanga* was suitably preadapted to this new niche (see above). However, the smaller size, which is the main structural difference between *Madanga* and its relatives, might have evolved in response to the niche change, as a smaller, lighter body would be advantageous for feeding on branches and trunks. By contrast, the plumage might have been under strong selection for improved crypsis in its novel niche. At least the plain green upperparts of *Madanga* probably provide better camouflage in trees than the contrastingly marked upperparts of most other pipits, as indicated by the fact that uniformly green upperparts are common in arboreal passerines in many unrelated families (e.g. Pycnonotidae, Phylloscopidae, Zosteropidae, Regulidae, Chloropseidae and Vireonidae). It is possible that *Madanga*'s strong plumage divergence is at least partly the result of changed sexual selection pressures, though the data are not available to test this. A similar example, with strong plumage and niche divergence but comparatively slight structural differentiation, concerns the cinnamon ibon *Hypocryptadius cinnamomeus*, also previously misclassified as an aberrant zosteropid but now identified as a canopy-adapted sparrow [13].

5.2. Taxonomy

A comprehensive taxonomic revision of Motacillidae is required. As a first step, *Madanga* should be synonymized with *Anthus* (type species: *A. pratensis*) and *Amaurocichla* with *Motacilla*. However, we advocate awaiting a more comprehensive sampling before making any further taxonomic recommendations.

5.3. Conclusion

To conclude, we suggest that the strong morphological divergences in the lineages leading to *Madanga ruficollis* and *Amaurocichla bocagii* were triggered by fundamental niche shifts following colonizations of forest-covered tropical islands.

Data accessibility. Supplementary figures and tables, DNA sequence alignments and details of samples, including GenBank numbers (KP671495–KP671599) and photos are deposited in Dryad: <http://dx.doi.org/10.5061/dryad.40s3g>.
Acknowledgements. We thank Peter Capainolo, Joel Cracraft, Paul Sweet, Thomas Trombone and Lydia Garetano at AMNH for photos and X-rays of *Madanga* specimens, DNA samples and access to collections; Town Peterson and Mark Robbins at the University of Kansas Natural History Museum for DNA sample; Aristide Andrianarimisa, Steven Piper and Christer Hemborg for DNA samples; Malcolm Wilson and Staffan Ulfstrand for field assistance; Mats Björklund for support; Marta Vila, Eevi Karvonen, Margareta Hultqvist and Afsaneh Ahmadzadeh for laboratory

support; Ulf Johansson at NRM, and Jun Chen and Peng He at IOZ for access to collections; James Eaton, Pierre-Henri Fabre, Rob Hutchinson, Frank Lambert, Frank Rheindt, Aurélien Audevard and Arka Sarkar for information and/or photos; Josep del Hoyo and Lynx Edicions for permission to use illustrations from Handbook of the Birds of the World; Nigel Redman and A&C Black Publishers for digital copies of P.A.'s illustrations; and Nigel Collar, Lars Larsson, Urban Olsson, Trevor Price, Staffan Ulfstrand and two anonymous reviewers for valuable comments.

Author contributions. K.A.J. and M.I. conceived the idea; P.A. and J.F. collected the museum data; A.Ö. and P.A. collected some DNA samples; K.A.J. carried out initial molecular analyses; P.A. carried out the final molecular and morphological analyses; and M.I., A.Ö. and K.A.J. carried out the laboratory work. All authors contributed to the design of the study and writing of the manuscript, and gave final approval for publication.

Funding statement. Funding provided by the Swedish Research Council (grant no. 621-2010-5321 to P.G.P.E. and B-AA/BU08416-315 to Mats Björklund, to A.Ö.) and Jorvall Foundation (to P.A.); Chinese Academy of Sciences Visiting Professorship for Senior International Scientists (no. 2011T2504; to P.A.); the People Programme (Marie Curie Actions) of the European Union's Seventh Framework Programme (FP7/2007–2013) under REA grant agreement PIEF-GA-2011-300924 (to K.A.J.); and the Danish National Research Foundation (to the Center for Macroecology, Evolution and Climate, to K.A.J. and J.F.).

Conflict of interests. None of the authors have any competing interests.

References

- Darwin C. 1859 *On the origin of species by means of natural selection, or the preservation of favoured races in the struggle for life*. London, UK: John Murray.
- Lack D. 1976 *Island biology, illustrated by the land birds of Jamaica*. Berkeley, CA: University of California Press.
- Coyne JA, Orr HA. 2004 *Speciation*. Sunderland, MA: Sinauer Associates.
- Price T. 2008 *Speciation in birds*. Greenwood Village, CO: Roberts & Company.
- Givnish TJ. 1997 Adaptive radiation and molecular systematics: issues and approaches. In *Molecular evolution and adaptive radiation* (eds TJ Givnish, KJ Sytsma), pp. 1–54. Cambridge, UK: Cambridge University Press.
- Grant PR, Grant BR. 2008 *How and why species multiply. The radiation of Darwin's Finches*. Princeton, NJ: Princeton University Press.
- Losos JB. 2009 *Lizards in an evolutionary tree: ecology and adaptive radiation of anoles*. Berkeley, CA: University of California Press.
- Lerner HR, Meyer M, James HF, Hofreiter M, Fleischer RC. 2011 Multilocus resolution of phylogeny and timescale in the extant adaptive radiation of Hawaiian honeycreepers. *Curr. Biol.* **21**, 1838–1844. (doi:10.1016/j.cub.2011.09.039)
- Jönsson KA *et al.* 2012 Ecological and evolutionary determinants for the adaptive radiation of the Madagascan vangas. *Proc. Natl Acad. Sci. USA* **109**, 6620–6625. (doi:10.1073/pnas.1115835109)
- Fleischer RC, James HF, Olson SL. 2008 Convergent evolution of Hawaiian and Australo-Pacific honeyeaters from distant songbird ancestors. *Curr. Biol.* **18**, 1927–1931. (doi:10.1016/j.cub.2008.10.051)
- Irestedt M, Fuchs J, Jönsson KA, Ohlson JI, Pasquet E, Ericson PGP. 2008 The systematic affinity of the enigmatic *Lamprolia victoriae* (Aves: Passeriformes)—an example of avian dispersal between New Guinea and Fiji over Miocene intermittent land bridges? *Mol. Phylogenet. Evol.* **48**, 1218–1222. (doi:10.1016/j.ympev.2008.05.038)
- Spellman GM, Cibois A, Moyle RG, Winker K, Barker FK. 2008 Clarifying the systematics of an enigmatic avian lineage: what is a bombycillid? *Mol. Phylogenet. Evol.* **49**, 1036–1040. (doi:10.1016/j.ympev.2008.09.006)
- Fjeldså J, Irestedt M, Ericson PGP, Zuccon D. 2010 The cinnamon ibon *Hypocryptadius cinnamomeus* is a forest canopy sparrow. *Ibis* **152**, 747–760. (doi:10.1111/j.1474-919X.2010.01053.x)
- Oliveros CH, Reddy S, Moyle RG. 2012 The phylogenetic position of some Philippine 'babblers' spans the muscicapoid and sylvioid bird radiations. *Mol. Phylogenet. Evol.* **65**, 799–804. (doi:10.1016/j.ympev.2012.07.029)
- Zuccon D, Ericson PGP. 2012 Molecular and morphological evidences place the extinct New Zealand endemic *Turnagra capensis* in the Oriolidae. *Mol. Phylogenet. Evol.* **62**, 414–426. (doi:10.1016/j.ympev.2011.10.013)
- Olsson U, Alström P. 2013 Molecular evidence suggests that the enigmatic Sulawesi endemic *Geomalina heinrichi* belongs in the genus *Zoothera* (Turdidae, Aves). *Chin. Birds* **4**, 155–160. (doi:10.5122/cbirds.2013.0015)
- Rothschild L, Hartert E. 1923 Madanga, *gen. nov.* *Bull. Br. Orn. Club* **43**, 117–118.
- Poulsen MK, Lambert FR. 2000 Altitudinal distribution and habitat preferences of forest birds on Halmahera and Buru, Indonesia: implications for conservation of *Moluccan avifaunas*. *Ibis* **142**, 566–586. (doi:10.1111/j.1474-919X.2000.tb04457.x)
- Rheindt FE, Hutchinson RO. 2007 New island records and new elevational records of birds from South Maluku, Indonesia. *Forktail* **23**, 158–161.
- Reeve AH, Haryoko T, Poulsen MK, Fabre P-H, Jönsson KA. 2014 New ornithological records from Buru and Seram, south Maluku, Indonesia, 1995–2012. *Forktail* **30**, 10–22.
- Mees GF. 1969 A systematic review of the Indo-Australian Zosteropidae (Part III). *Zool. Verhandl.* **102**, 1–390.
- Gill F, Donsker D 2014 (eds) IOC World bird list (v. 4.2). See <http://www.worldbirdnames.org>.
- Dickinson E. 2003 *The Howard and Moore complete checklist of the birds of the world*, 3rd edn. London, UK: Helm.
- Pearson D. 2006 Bocage's Longbill (*Amaurocichla bocagii*). In *Handbook of the birds of the world*, vol. 11 (eds J del Hoyo, A Elliott, DA Christie), p. 643. Barcelona, Spain: Lynx Edicions.
- Johansson US, Fjeldså J, Bowie RCK. 2008 Phylogenetic relationships within Passerida (Aves: Passeriformes): a review and a new molecular phylogeny based on three nuclear intron markers. *Mol. Phylogenet. Evol.* **48**, 858–876. (doi:10.1016/j.ympev.2008.05.029)
- Barker FK, Cibois A, Schikler P, Feinstein J, Cracraft J. 2004 Phylogeny and diversification of the largest avian radiation. *Proc. Natl Acad. Sci. USA* **101**, 11 040–11 045. (doi:10.1073/pnas.0401892101)
- Fregin S, Haase M, Olsson U, Alström P. 2012 New insights into family relationships within the avian superfamily Sylvioidea (Passeriformes) based on seven molecular markers. *BMC Evol. Biol.* **12**, 157. (doi:10.1186/1471-2148-12-157)
- Voelker G. 1999 Dispersal, vicariance and clocks: historical biogeography and speciation in a cosmopolitan passerine genus (*Anthus: Motacillidae*). *Evolution* **53**, 1536–1552. (doi:10.2307/2640899)
- Alström P, Ödeen A. 2002 Incongruence between mitochondrial DNA, nuclear DNA and non-molecular data in the avian genus *Motacilla*: implications for estimates of species phylogenies. In Alström, P. Species limits and systematics in some passerine birds. PhD thesis, Uppsala University, Uppsala, Sweden.
- Alström P, Mild K. 2003 *Pipits and wagtails of Europe, Asia and North America: identification and systematics*. London, UK: Helm/A&C Black.
- Irestedt M, Ohlson JI, Zuccon D, Källersjö M, Ericson PGP. 2006 Nuclear DNA from old collections of avian study skins reveals the evolutionary history of the Old World suboscines (Aves, Passeriformes). *Zool. Scr.* **35**, 567–580. (doi:10.1111/j.1463-6409.2006.00249.x)
- Ohlson JI, Irestedt M, Fjeldså J, Ericson PGP. 2012 Putting an end to a mystery: DNA from a 180 years old study skin reveals the phylogenetic position of the Kinglet *Calyptura calyptura cristata* (Passeriformes: Tyrannidae). *Ibis* **154**, 533–541. (doi:10.1111/j.1474-919X.2012.01243.x)
- Edgar RC. 2004 MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* **32**, 1792–1797. (doi:10.1093/nar/gkh340)
- Gouy M. 2012 Seaview, version 4.3.4. See: <http://pbil.univ-lyon1.fr/software/seaview.html>.

35. Gouy M, Guindon S, Gascuel O. 2010 SeaView version 4: a multiplatform graphical user interface for sequence alignment and phylogenetic tree building. *Mol. Biol. Evol.* **27**, 221–224. (doi:10.1093/molbev/msp259)
36. Huelsenbeck JP, Ronquist F. 2001 MrBayes: Bayesian inference of phylogenetic trees. *Bioinformatics* **17**, 754–755. (doi:10.1093/bioinformatics/17.8.754)
37. Ronquist F, Huelsenbeck JP. 2003 MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19**, 1572–1574. (doi:10.1093/bioinformatics/btg180)
38. Lanfear R, Calcott B, Ho SYW, Guindon S. 2012 PartitionFinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. *Mol. Biol. Evol.* **29**, 1695–1701. (doi:10.1093/molbev/mss020)
39. Hasegawa M, Kishino Y, Yano T. 1985 Dating of the human–ape splitting by a molecular clock of mitochondrial DNA. *J. Mol. Evol.* **22**, 160–174. (doi:10.1007/BF02101694)
40. Yang Z. 1994 Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: approximate methods. *J. Mol. Evol.* **39**, 306–314. (doi:10.1007/BF00160154)
41. Gu X, Fu Y-X, Li W-H. 1995 Maximum likelihood estimation of the heterogeneity of substitution rate among nucleotide sites. *Mol. Biol. Evol.* **12**, 546–557.
42. Lanave C, Preparata C, Saccone C, Serio G. 1984 A new method for calculating evolutionary substitution rates. *J. Mol. Evol.* **20**, 86–93. (doi:10.1007/BF02101990)
43. Rodríguez J, Oliver L, Marín A, Medina R. 1990 The general stochastic model of nucleotide substitution. *J. Theoret. Biol.* **142**, 485–501. (doi:10.1016/S0022-5193(05)80104-3)
44. Tavaré S. 1986 Some probabilistic and statistical problems on the analysis of DNA sequences. *Lect. Math. Life Sci.* **17**, 57–86.
45. Nylander JAA, Ronquist F, Huelsenbeck JP, Nieves-Aldrey JL. 2004 Bayesian phylogenetic analysis of combined data. *Syst. Biol.* **53**, 47–67. (doi:10.1080/10635150490264699)
46. Rambaut A, Drummond AJ. 2009 Tracer, version 1.5. See <http://beast.bio.ed.ac.uk>.
47. Drummond AJ, Rambaut A. 2007 BEAST: Bayesian evolutionary analysis by sampling trees. *BMC Evol. Biol.* **7**, 214. (doi:10.1186/1471-2148-7-214)
48. Drummond AJ, Rambaut A. 2013. *BEAST, version 1.7.5*. See <http://beast.bio.ed.ac.uk>.
49. Rambaut A, Drummond AJ, Xie W. 2013 *BEAUti, version 1.7.5*. See <http://beast.bio.ed.ac.uk>.
50. Weir JT, Schluter D. 2008 Calibrating the avian molecular clock. *Mol. Ecol.* **17**, 2321–2328. (doi:10.1111/j.1365-294X.2008.03742.x)
51. Miller MA, Pfeiffer W, Schwartz T. 2010 Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In *Proc. Gateway Computing Environments Workshop (GCE), 14 November 2010, New Orleans, LA, USA*, pp. 1–8.
52. Rambaut A, Drummond AJ. 2013 *TreeAnnotator, version 1.7.5*. See <http://beast.bio.ed.ac.uk>.
53. Rambaut A. 2009. *FigTree, version 1.3.1*. See <http://tree.bio.ed.ac.uk/software/figtree>.
54. Stamatakis A. 2006 RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* **22**, 2688–2690. (doi:10.1093/bioinformatics/btl446)
55. Stamatakis A, Hoover P, Rougemont J. 2008 A fast bootstrapping algorithm for the RAxML web-servers. *Syst. Biol.* **57**, 758–771. (doi:10.1080/10635150802429642)
56. Tyler S. 2004 Family Motacillidae (pipits and wagtails). In *Handbook of the birds of the world*, vol. 9 (eds J del Hoyo, A Elliott, DA Christie), pp. 686–743. Barcelona, Spain: Lynx Edicions.
57. Hall BP. 1961 The taxonomy and identification of pipits (genus *Anthus*). *Bull. Br. Mus. Nat. Hist.* **7**, 245–289.
58. Voelker G. 2002 Systematics and historical biogeography of wagtails: dispersal versus vicariance revisited. *Condor* **104**, 725–739. (doi:10.1650/0010-5422(2002)104[0725:SAHBOW]2.0.CO;2)
59. BirdLife International. 2001 *Threatened birds of Asia: the BirdLife International Red Data Book*. Cambridge, UK: BirdLife International.
60. Atkinson P, Peet N, Alexander J. 1991 The status and conservation of the endemic bird species of São Tomé and Príncipe, West Africa. *Bird Conserv. Int.* **1**, 255–282. (doi:10.1017/S0959270900000629)
61. de Naurois R. 1994 *Les oiseaux des îles du Golfe de Guinée (Aïão Tomé, Príncipe et Annobon)*. Lisboa, Portugal: Instituto de Investigação Científica Tropical.
62. Hockey PAR, Dean WRJ, Ryan PG. (eds) 2005 *Roberts birds of southern Africa*, 7th edn. Cape Town, South Africa: The Trustees of the John Voelcker Bird Book Fund.
63. Ricklefs RE, Miles DB. 1994 Ecological and evolutionary inferences from morphology: an ecological perspective. In *Ecological morphology: integrative organismal biology* (eds PC Wainwright, SM Reilly), p. 13. Chicago, IL: University of Chicago Press.
64. Pratt HD. 2005 *The Hawaiian honeycreepers*. Oxford, UK: Oxford University Press.
65. Reddy S, Driskell A, Rabosky DL, Hackett SJ, Schulenberg TS. 2012 Diversification and the adaptive radiation of the vangas of Madagascar. *Proc. R. Soc. B* **279**, 2062–2071. (doi:10.1098/rspb.2011.2380)
66. James HF, Ericson PGP, Slikas B, Lei FM, Gill FB, Olson SL. 2003 *Pseudopodoces humilis*, a misclassified terrestrial tit (Paridae) of the Tibetan Plateau: evolutionary consequences of shifting adaptive zones. *Ibis* **145**, 185–202. (doi:10.1046/j.1474-919X.2003.00170.x)
67. Krabbe NK, Schulenberg TS. 2003 In *Handbook of the birds of the world*, vol. 8 (eds J del Hoyo, A Elliott, DA Christie), p. 748. Barcelona, Spain: Lynx Edicions.
68. Collar NJ, Robson C. 2007 Family Timaliidae (babblers). In *Handbook of the birds of the world*, vol. 12 (eds J del Hoyo, A Elliott, DA Christie), pp. 70–133. Barcelona, Spain: Lynx Edicions.