**Systematic placement of an enigmatic Southeast Asian taxon *Eupetes macrocerus* and implications for the biogeography of a main songbird radiation, the Passerida**

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1. **INTRODUCTION**

The peculiar *Eupetes macrocerus* (Malaysian rail-babbler) is an uncommon bird of the lowland rainforests of the Malay Peninsula, Sumatra and Borneo. It belongs to the forest understorey, foraging on the forest floor among leaf litter and under fallen timber, using a walking gait with the neck extended forward and head jerking like a chicken. By appearance, it mostly resembles the *Ptilorrhoa* spp. (jewel-babblers) of New Guinea and early taxonomic treatments indeed placed them together in the genus *Eupetes* (Sharpe 1883; Temminck 1831). However, Peters (1940) noted some striking differences between *E. macrocerus* and the *Ptilorrhoa* spp. He pointed out several differences in the external morphology, but did not present evidence of a kind that would help placing these taxa in a phylogenetic context. Peters (1940) was the first to suggest that the genus *Eupetes* was monotypic and he proposed the genus name *Ptilorrhoa* (genus novum) for the Papuan birds. However, in his ambitious ‘Birds of the World’ (Peters 1964), he stuck with the name *Ptilorrhoa* to include the New Guinean species as well as the Malayan rail-babbler.

Serle (1952) noted a series of remarkable similarities between *Eupetes* and the West African *Picathartes* (rock-fowl): similar proportions, position of nostrils (different from *Ptilorrhoa*), shape of forehead and tail but did not insist on a relationship. Sibley (1973) considered the resemblance between *Picathartes* and *Eupetes* to be the result of convergence, but Olson (1979) argued that there could well be a relationship between them. He mentioned a series of similarities: morphology, proportions, plumage pattern and behaviour, but failed to identify clear synapomorphies between them. Sibley & Ahlquist (1990) simply ignored the divergence of opinions as they stated that ‘The Cinclosomatinae includes the quail-thrushes (*Cinclosoma*), the three species of Papuan jewel-babblers (*Ptilorrhoa*), the Malaysian rail-babbler (*Eupetes*) and the whipbirds and wedgebills (*Psophodes*). Using molecular sequence data, Barker et al. (2004) and Beresford et al. (2005) associated *Ptilorrhoa* with Pachycephalidae (whistlers), which are placed above the Australian ‘false babblers’ (represented by the genera *Pomatostomus* and *Orthonyx*) in the Corvida phylogeny, but molecular data for *Eupetes* were lacking even in these studies.

It seems highly probable that earlier taxonomists simply looked for similar-looking forms within the same or adjacent geographical areas, thus a priori ruling out relationships between species living far apart. In order to scrutinize alternative possibilities, we used DNA sequence data to assess the systematic affinities of the Malaysian rail-babbler. The mere fact that *E. macrocerus* is distributed in Southeast Asia and that *Ptilorrhoa* is distributed only in New Guinea to the other side of Wallace’s Line and *Picathartes* in West Africa makes the biogeographic history of these birds very intriguing. The most parsimonious explanation would be that they represent a relictual basal group in the Passerida clade established after a long-distance dispersal from the Australo-Papuan region to Africa. Many earlier taxonomic arrangements may have been based on assumptions about relationships with similar-looking forms in the same, or adjacent, biogeographic regions, and revisions with molecular data may uncover such cases of neglect of ancient relictual patterns reflecting past connections between the continents.

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2. **MATERIAL AND METHODS**

We compared the DNA sequences of *Eupetes* with data from 21 taxa representing a broad sampling of the passeriform radiation (as summarized by Jønsson & Fjeldså 2006c). The aligned dataset consists of 1742 bp obtained from three nuclear gene regions, myoglobin intron 2, ornithine decarboxylase (ODC) introns 6–7 and glyceraldehyde-3-phosphate dehydrogenase (G3PDH) intron 11. See the electronic supplementary material for laboratory procedures,

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alignments, selections of models for nucleotide substitutions, parsimony analysis and Bayesian analyses of individual gene regions (table 1).

We also investigated whether Eupetes or Pachycephalopsis possesses the insertion of one codon in exon 3 of the nuclear c-myc gene, which has been proposed to be diagnostic of Passerida (Ericson & Johansson 2003). Laboratory procedures are described in the electronic supplementary material.

An average rate of substitutions in myoglobin intron 2 in passerines has been calculated as 0.145% Myr ago (Fjeldså et al. in press) and this rate was used to estimate the timing of the splits between Eupetes and its closest relatives (electronic supplementary material).

### 3. RESULTS AND DISCUSSION

We were able to sequence all the three gene regions almost completely for all included taxa (Prunella lacks 70 bp in the 3’ end in myoglobin, and in ODC all sequences obtained from study skins lack a 22 bp fragment in exon 7). With the missing base pairs taken into account, the sequences obtained varied in length between 708 and 729 bp for myoglobin intron 2, between 253 and 307 bp for G3PDH intron 11 and between 591 and 621 bp for the ODC region. The combined alignment consists of 1742 bp.

Analysis of three markers all provide strong support that E. macrocerus is nested within the Chaetops/Picathartes clade, its closest relatives being the rock-jumpers, which are endemic to the South African Cape region. A relationship between Chaetops and Picathartes was first suggested (with some hesitation) by Sibley & Ahlquist (1990) as a result of their DNA–DNA hybridizations, and it was later supported by several other studies using DNA sequence data (Barker et al. 2004; Beresford et al. 2005). It was unexpected as they are phenetically rather different: Chaetops resembling Australian grass wrens and inhabiting rocky places in open terrain, and Picathartes being larger and inhabiting rainforest understorey (Fry et al. 2000). Which of these specializations represent the ancestral condition is difficult to tell; on one hand southern Africa lost its forest cover far back in the Tertiary (Axelrod & Raven 1978), but it is also possible that range dynamics driven by climatic instability will gradually push species towards the more productive environments, leading to a general tendency for old lineages to persist in the major rainforest tracts (Storch et al. in press). According to the molecular clock model used (a discussion of the error margins for such clock estimates is trivial and we simply note that our estimates only represent a very rough idea of divergence times), the Picathartes/Chaetops/Eupetes clade diverged from the Australian Petroicidae (represented here by Eopsaltria and Pachycephalopsis) 48 Myr ago, in the Mid-Eocene. According to figure 1, the Picathartes/Chaetops/Eupetes clade is sister to the Australian Petroicidae and these in turn are sister to the Passerida (represented here by Hirundo, Sylvia, Sturnus, Prunella and Saltator). These nodes are poorly supported by our data, but the insertion of one codon in a conserved region of the c-myc gene in the Passerida and the Picathartes/Chaetops/Eupetes clade, as opposed to that in the Petroicidae and all Corvida groups, would seem to suggest that the Australian Petroicidae and Corvida groups are basal to the large Old World radiation of songbirds (Ericson & Johansson 2003).

Biogeographically, it is of great interest to find the Asian E. macrocerus nested together with two African taxa in a terminal position. Fuchs et al. (2006) and Jønsson & Fjeldså (2006b) proposed the idea that an Australian ancestor of the Passerida dispersed directly to Africa across stepping-stones in the southern Indian Ocean during the warm Eocene period (Kennett 1995), and that Passerida originated in Africa and from there radiated and dispersed to Eurasia and then to the
rest of the world. It is of no doubt that the systematic position of *Eupetes* makes the diversification and dispersal patterns even more complex. Since several taxa representing deep branches within the Passerida are African (Beresford et al. 2005), and the Asiatic *Eupetes* and South African *Chaetops* are in a terminal position within their clade having diverged from *Picathartes* ca 44 Myr ago, the most parsimonious interpretation is still a dispersal of an Australian ancestor directly to Africa. The distribution of *Picathartes*, *Chaetops* and *Eupetes* would then be relictual, following a range expansion whereby this clade spread out of Africa. *Eupetes* retreated into the rainforests of the most southeastern part of mainland Asia and the closely associated islands of Sumatra and Borneo. At this time, the distance between Asia (with Greater Sundas) and terranes of Australian origin was too far apart for further range expansion. The other possible—though markedly less parsimonious—interpretation involves a dispersal event from Australia to Asia and then two independent dispersal events onwards to two different parts (and environments) of Africa.

A denser taxon sampling around the transition between Corvida and Passerida (e.g. Petroicidae) is a high priority for future work, as this might give a better idea about the ecological adaptations of the form that made the great leap out of Australia, whether that was via Asia or across the Indian Ocean. However, there is also a broad range of other odd relationships that, if correctly interpreted, would suggest ancient biogeographic connections between regions that are not connected today, such as the rainforests of Africa and the Australasian regions (for details see Olson 1973). Over the last decades, many such cases have been discussed in relation to plate tectonics, while earlier ideas about ancient land bridges were abandoned. However, the idea of transoceanic connections, including radiations within oceanic archipelagos, has recently received renewed attention (De Queiroz 2005; Filardi & Moyle 2005). For an understanding of the relative importance of vicariance driven by plate tectonics, or dispersal by past land bridges or island arcs, or sweepstake long-distance dispersal, it is important to revisit the suggested cases now with molecular data. Such data have revealed several previously neglected cases, where odd-looking species had been compared mainly with other taxa within the same part of the world, and thus were erroneously interpreted as aberrant members of such groups (e.g. Ericson et al. 2002; Fjeldså et al. 2003; Fuchs et al. 2006). A more systematic approach is now needed to compare a broad selection of potential cases of biotic links between ancient land masses.

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Figure 1. The 50% majority rule consensus tree obtained from the Bayesian analysis of the combined dataset (G3PDH intron 11, the myoglobin intron 2 and ODC introns 6–7) with geographical distributions. Posterior probability values are indicated to the right of the nodes.
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