Australasia--Accipitridae: lump the Papuan Harrier, *Circus spilothorax*, as a subspecies of the Swamp Harrier, *Circus approximans*. #76

Drafted by Thane K. Pratt and Leo Joseph, with suggestions by Guy Dutson

Additional AusRAG committee input from Andrew Black, Anna Kearns

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This proposal focusses on two taxa of harriers, *spilothorax* of New Guinea and *approximans* of Australia (species-group epithets used for brevity and simplicity). While confining the discussion mainly to these two taxa, we emphasize they belong to a closely related complex of marsh harriers including three additional taxa outside Australasia. All five taxa following AviList V. 2025 are:

C. maillardi J. Verreaux, 1862 (Reunion Harrier)

C. macrosceles A. Newton, 1863 (Malagasy Harrier)

C. approximans Peale, 1848 (Swamp Harrier)

C. spilonotus Kaup, 1847 (Eastern Marsh Harrier)

C. spilothorax Salvadori and D'Albertis, 1876 (Papuan Harrier)

At the outset, we stress that genetic studies to date have not succeeded in readily distinguishing among the five taxa, so the broader issue that ultimately should be addressed is whether all five might be considered forms of a single species for which the oldest name is *Circus spilonotus* Kaup, 1847. Also notable is that all these harrier taxa except *approximans* show obvious plumage polymorphisms—could it be that *approximans* has lost the pronounced polymorphism?

Main Points.

(1) AviList's treatment of the Papuan Harrier, *Circus spilothorax*, was not investigated for v2025 since IOC, eBird/Clements and BirdLife all treated the two as separate species. IOC (V 13.2) states "*Circus spilothorax* is split from Eastern Marsh Harrier *C. spilonotus* (Simmons 2000; Ferguson-Lees & Christie 2005 [2006?])." The rationale for the split was given by Simmons (2000:32) to be based only on differences in size and plumage and geographical isolation, because at the time "DNA was not available for analysis" (the full text of Simmons's explanation is provided as an appendix to our proposal). DNA is now available and forms the basis for this Australasian RAG proposal to AviList's TaxComm to recognize *spilothorax* as

a subspecies of *approximans* (or alternatively, of *spilonotus*, if related harriers outside Australasia are considered).

(2) For an overview of the taxonomic history of this harrier, Beehler & Pratt 2016: 209 noted:

"Some authorities treat the NG form *spilothorax* as a distinct monotypic species (e.g., Coates & Peckover 2001, del Hoyo & Collar 2014); others treat *spilothorax* as a race of the e Asian *C. spilonotus* (e.g., Dickinson & Remsen 2013); yet others (e.g., Brown & Amadon 1968) treat both *spilothorax* and *spilonotus* as races of the widespread Eurasian C. *aeruginosus*. We follow Christidis & Boles (2008) in treating the Australian and NG populations of marsh-harrier as a single species, *C. approximans*. Unconfirmed reports of *C. melanoleucus* from the highlands of NG (e.g., Crome & Swainson 1974) apparently are field misidentifications of the pied morph males of the race *spilothorax*."

Debus (1994) first treated *spilothorax* as a subspecies of *C. approximans*. Ferguson-Lees & Christie (2001) did too, but in a subsequent edition of their book Ferguson-Lees & Christie (2006) reversed that and split the Papuan taxon out as *C. spilothorax*. At the time of publication of Ferguson-Lees & Christie (2001), they acknowledged the then newly appeared DNA data was revolutionizing [our] thinking "but it will be some years before the picture is complete" (Ferguson-Lees & Christie 2001: 69). They acknowledged that the classification in their book remained "conventional".

(3) The harrier *spilothorax*, endemic to New Guinea, most closely resembles the Swamp Harrier, *Circus approximans*, which breeds in Australia and migrates in part to New Guinea.

The sexes of *C. approximans* share brown, streaked plumage and differ by older males (Marchant and Higgins 1993; Menkhorst et al. 2017; BirdLife Australia 2023) often showing grey dorsally and an unbarred or less clearly barred tail, this variation not being a polymorphism in the strict meaning of the term. What most distinguishes *spilothorax* from *approximans* is the variety of plumage morphs and overall darker plumage of *spilothorax*, as though it were a pied and melanistic version of the more muted pattern of *approximans*. The male's plumage varies in being either "pied" with black hood, shoulders, and back, but showing a range of pattern from one individual to the next, or being all plain black, both morphs with a plain grey tail. Female *spilothorax* can so closely resemble female *approximans* that in some cases they can't be told apart, or she may be all black with a barred tail (see Figure 1 below a reproduction of Pratt & Beehler 2014: Plate 19). Plumage sequence into adulthood is unknown for *spilothorax*. Possibly, these 'morphs' of the adults may be individual variation superimposed on an underlying polymorphism and may also relate to the bird's age, the darker birds being younger as in *approximans*.


1 juv
1 black ♀
1 black ♂
1 pale ♀
1 pied ♂
1 juv
1 black ♂
1 pied ♂
1 pale ♀
1
2♀
2♂
3
2♀
2♂
2 juv

Figure 1. Reproduction of Plate 19 from Pratt & Beehler 2014, Field Guide to Birds of New Guinea, Princeton U. Press. *Circus (approximans) spilothorax* is indicated by (1), *C. approximans approximans* by (2).

(4) Although the status of *approximans* in New Guinea is poorly known given the difficulty of field identification, specimens do exist, and it appears that the marked annual migratory movements of *approximans* during the austral winter (BirdLife Australia 2023) likely reach the geographic range of *spilothorax*, indicating the two forms are not altogether geographically isolated (see discussions in Mees 1982; Beehler and Pratt 2016) . This co-occurrence suggests at least the opportunity for some of the migrant harriers to stay and breed with the residents in New Guinea.

(5) Genetic research has clarified the phylogenetic relationships of *spilothorax* within the genus *Circus*, showing that it and *approximans* are barely, if at all, differentiated sister taxa, and the two are very closely allied with other marsh harriers (Oatley et al. 2015, Knapp et al. 2019). Oatley et al. 2015 explicitly assign the Papuan Harrier as a subspecies of *Circus approximans*.

Oatley et al. 2015 note the following in their abstract (see Figure 2 for relevant tree from their paper): "The monophyly of the raptorial *Circus* genus (harriers) has never been in question, but the specific status of many, often vulnerable island endemic, taxa remains uncertain. Here we utilise one mitochondrial and three nuclear loci from all currently recognised *Circus* taxa (species and subspecies) to infer a robust phylogeny, to estimate the divergence date and to reconstruct the biogeographic origins of the *Circus* group. Our phylogeny supports both the monophyly of *Circus* and polyphyly of the genus *Accipiter*. Depending on the rate of molecular clock used, the emergence of the harrier clade took place between 4.9 and 12.2 mya which coincides with the worldwide formation of open habitats which extant harriers now exploit...Further, the African Marsh *C. ranivorus* and the European Marsh *C. aeruginosus* Harriers emerge as sister species. The remaining marsh harriers exhibit very little genetic diversity, and are all recently diverged taxa that exhibit allopatric distributions. Considering their sister relationship and geographic proximity, we recommend treating *C. approximans* and *C. spilonotus spilothorax* as subspecies of *C. approximans*. For *C. spilonotus spilonotus*, *C. maillardi maillardi* and *C. maillardi macrosceles*, their plumage and morphometric differences, phylogenetic relationship and geographic distributions make lumping of these taxa as a single species complicated. We thus propose to recognise as separate, recently evolved species: *C. spilonotus*, *C. maillardi* and *C. macrosceles*...."

And more specifically, Oatley et al. (2015:159) state:

"The geographic proximity of *C. approximans* and *C. s[pilonotus]. spilothorax*, overall morphometric similarity, their sister relationship coupled with low genetic differentiation, indicate that these two taxa should be treated as subspecies of *C. approximans* Peale 1848: *C. a. approximans* and *C. a. spilothorax*."

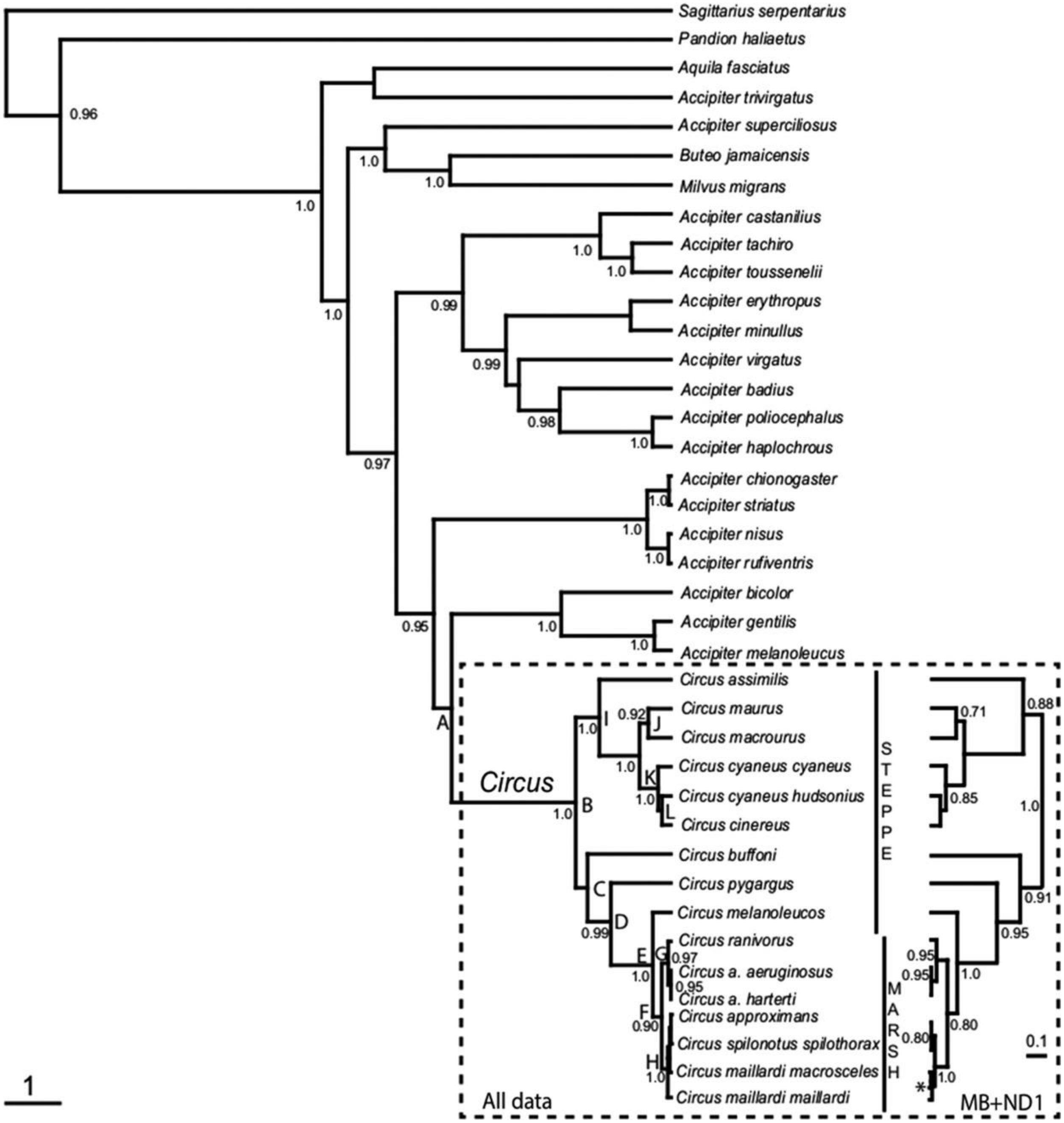

Figure 2. Reproduction of Oatley et al. (2015), their Fig. 2. The figure shows a species tree of *Circus* inferred essentially from one mitochondrial locus (ND1) and three nuclear loci ((MB, FGB and TGFb2). The values on the nodes are the posterior probabilities. Letters on nodes represent timing events and correspond to their Table 1. Also included is the species tree inferred from only ND1

and MB, but which allowed the inclusion of *C. s. spilonotus* (position indicated by*/*). The *Circus* clade is enclosed by a box with dashed borders.

Knapp et al. (2019; see Figure 3) used the mitochondrial ND1 data from Oatley et al. (2015) to generate their own phylogenetic tree (reproduced below). Given that their focus was on taxa other than *Circus*, they did not make taxonomic recommendations for or discuss *spilothorax* (although they assign species rank to all *Circus* taxa on their tree, presumably for simplicity but a little careless). But their phylogenetic tree (essentially inferred from mitochondrial ND1 but including its flanking tRNA-Leu, ND1, tRNA-Ile, and tRNA-Gln regions (1027 bp)) of all *Circus* species shows *spilothorax* in a clade with *approximans* and within that clade branching is shallow and presumably very recent—a flat polytomy of 2 *spilothorax* and 3 *approximans* samples in mixed order, suggesting no phylogenetically significant differentiation between *spilothorax* and *approximans*.

M. Knapp, et al. *Molecular Phylogenetics and Evolution 134 (2019) 122–128*

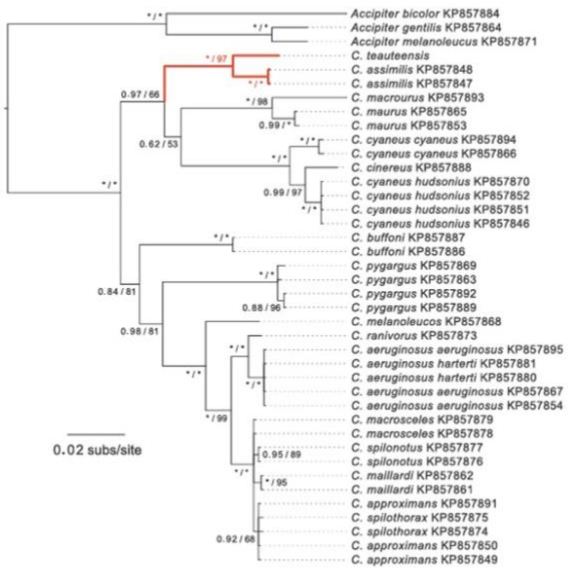

Fig. 1. Bayesian phylogeny of the genus *Circus* inferred from mitochondrial tRNA-Leu, *ND1*, tRNA-Ile, and tRNA-Gln regions (1027 bp). The placement of the root was inferred by treating three species of *Accipiter* as the outgroup. Nodes are labelled with posterior probabilities/ bootstrap support. * represents a posterior probability of 1 and a bootstrap support of 100 respectively. The scale bar represents 0.02 substitutions per site.

Figure 3. Reproduction of Figure 1 from Knapp et al. 2019. Their caption is: “Bayesian phylogeny of the genus Circus inferred from mitochondrial tRNA-Leu,ND1, tRNA-Ile, and tRNA-Gln regions (1027 bp). The placement of the root was inferred by treating three species of *Accipiter* as the outgroup. Nodes are labelled with posterior probabilities/bootstrap support. *represents a posterior Probability of 1 and a bootstrap support of 100 respectively. The scale bar represents 0.02 substitutions per site.”

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(6) Two other, subsequent phylogenetic studies address *Circus*. In the tree published by Mindell et al. 2018 (Figure 4), which for Circus was essentially a synthesis of earlier multilocus analyses of Lerner and Mindell (2005), there is very strong support

that *spilothorax, approximans, macrosceles, maillardi* and *spilonotus* are all each other's closest relatives but none given for relationships within that clade, which therefore were essentially unresolved. With that caveat, *spilothorax* did again appear as sister to *approximans* and they are in turn sister to *macrosceles*, but the branching is so shallow among all three as to essentially be a trichotomy.

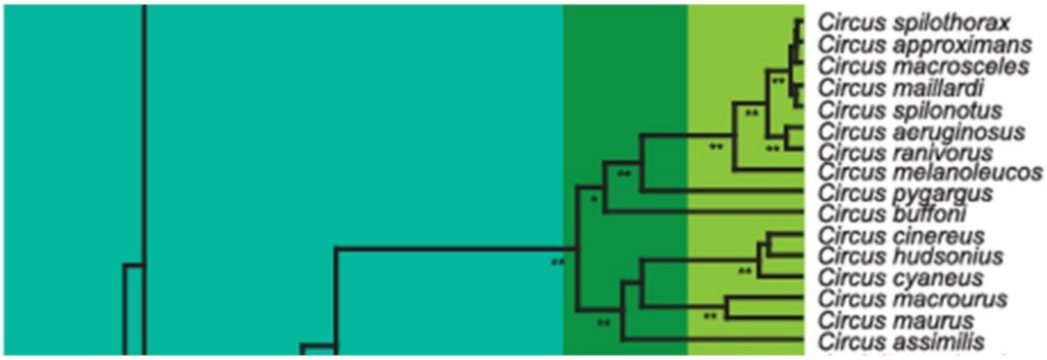

Figure 4. Reproduction of relevant part of Figure 1.2 from Mindell et al. 2018 showing *Circus* taxa. ** designates a posterior probability of 1.0.

(7) Catanach et al 2024 published an analysis based on Ultraconserved Elements (UCEs), which are an increasingly popular tool for phylogenetic analysis. UCEs in general and Catanach et al. (2024) in particular, therefore contributed a data set that was a quantum step up from the mostly uninformative nuclear intron loci that had been used in earlier analyses summarized above and which probably were mostly influenced by the signal in more rapidly evolving mtDNA data in those same analyses. Despite that, it is a key point that the UCE results were much the same as those from the earlier analyses: very little discernible structure across the entire group of five taxa, which are little more than a polytomy with very little diversity. Thus, *spilothorax* is shown as sister to *spilonotus* but with no accompanying support value indicating that this was not a strongly supported arrangement even in UCE data. They together form a trichotomy with (*approximans+maillardi*), which are aligned strongly with 100% support as a pair of sister taxa, and *macrosceles*, but again this is essentially a trichotomy albeit with one strongly supported pair (*approximans+maillardi*) and one poorly supported pair (*spilothorax* and *spilonotus*) each forming two of the three branches. Thus, *spilothorax*, *approximans*, and Asian *spilonotus* together are certainly very closely related, but their phylogenetic

interrelationships aren't clear. These papers make no taxonomic recommendations for *spilothorax*, but they both label it as a species.

(8) The Australasian RAG has reviewed the proposal with a quorum of 5 members supporting it and none opposing. Outside our regional group, there was feedback from Frank Rheindt, Roger Safford, and Callan Cohen urging that this proposal be restricted to only *spilothorax* and *approximans* and not extended to other closely harriers outside the Australasian region, owing to phylogenetic and conservation concerns (see comments on GitHub).

Recommendation:

(1) By this Australasian RAG proposal to TaxComm of AviList, we recommend treating the taxon *spilothorax* as *Circus approximans spilothorax*. Again, we note that a much-needed broader review could result in both *spilothorax* and *approximans* being lumped into an expanded *C. spilonotus*. The recommended English name is Pacific Harrier.

(2) Regardless of whether *spilothorax* is classified as a species or subspecies, its position in the AviList sequence is best changed, based on Oately et al. 2015 and Knapp et al. 2019, so that it follows *C. approximans*.

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Appendix. Explanation for treating *Circus spilonotus* as a species, from Simmons 2000:32:

"A third 'new' species is proposed here although DNA was not available for analysis. As a sedentary island species the Papuan Harrier *C. spilorthoax* on Papua New Guinea [*sic*] has very probably diverged from its nearest geographical neighbour the Eastern Marsh Harrier *C. spilonotus*. The bird is the only truly equatorial harrier and is resident in the central highlands and eastern section of New Guinea (Coates 1985, Beehler et al. 1986). The bird resembles the Eastern Marsh Harrier (*C. spilonotus*) in plumage characters. But whereas the Eastern Marsh Harrier migrates as far south as Borneo, this species is resident on New Guinea (Coates 1985, Fig. 2.3). It is smaller and darker than the Eastern Marsh Harrier and its Latin binomial *spilothorax* suggests it is a "spotted backed" harrier. It is heavily streaked brown on the back and neck (Brown and Amadon 1968). Two forms of males occur: the central highland birds lack the streaked throat of lowland birds and exhibit a well defined black head and pale breast much like the Pied Harrier [TKP: not sure it's true that there is a lowland vs. highland form…]. Because other island harriers prove to be separable at the species level (above), its plumage differs from its nearest neighbour, it is sedentary and it is morphologically smaller and separable from the Eastern Marsh Harrier (Table 2.2), I treat it as a good species."