

# RECENT 'SPLITS' FOR WESTERN AUSTRALIAN BIRDS

The widely-cited IOC World Bird List (Gill and Donsker 2015) has recently recognised four new 'splits' affecting Western Australian bird species, and bringing some new English names for our local birds. These taxonomic changes will all be adopted in the next update of the official Western Australian Checklist maintained by the Western Australian Museum (Ron Johnstone, *pers. comm.*).

The Silver-backed Butcherbird (*Cracticus argenteus*) of the Kimberley and Northern Territory was split from Grey Butcherbird in IOC v. 4.3 (July 2014). This form has always been recognised as fairly distinct, with an obviously silvery back, whiter underparts, and lack of white in the lores. However, supporting genetic evidence was rather muddy in early studies (Kearns *et al.* 2013), which found the Northern Territory (*colletti*) and Kimberley (*argenteus*) clades are widely separated in their mitochondrial genes (mtDNA), making the proposed species paraphyletic. However this puzzle was rather elegantly solved in a follow-up paper by Kearns *et al.* (2014), which showed that expanding aridity during the Last Glacial Maximum (c. 21 000 years ago) brought the eastern form of Grey Butcherbird into contact with NT birds, introducing mitochondrial genes through low-level hybridization which 'captured' the Top End but not the Kimberley birds. However, analysis of nuclear genes suggests that the Silver-backed Butcherbird forms a good species, and from the sum of this evidence must actually be more closely related to Black-backed Butcherbird *Cracticus mentalis*, than it is to Grey Butcherbird.

The split of Western Whistler *Pachycephala occidentalis* from Golden Whistler in IOC v. 5.1 (Jan 2015) was rather a surprise, since south-western birds were previously not even recognised as a subspecies, but rather lumped with the South Australian subspecies *fuliginosa* which shares similarly buff-bellied females. The split was only revealed in a series of genetic studies of the whole 'Golden Whistler' complex (Jønsson *et al.* 2008; Andersen *et al.* 2014) and formalised by Joseph *et al.* (2014), who showed that Western Whistler is probably less closely related to eastern forms of Golden Whistler, than it is to Mangrove Golden Whistler (~2.5% mtDNA divergence from both). This is a 'cryptic species', only separated from the most similar form of Golden Whistler *fuliginosa* by a slightly paler back and breast, greyer tail with less black in males, and even-toned neutral grey dorsum in females and immatures. The English name is a direct translation of *occidentalis* (Latin for 'western'), and mirrors an older name 'Western Thick-head'. However, it is not strictly-speaking a new WA endemic, since its range extends along the south-western edge of the Nullarbor to include a few records just across the Western Australian-South Australian border — thus separated from the eastern species by only about 200 km. (see photo, front cover)

The Naretha Bluebonnet (or Blue Bonnet) *Northiella narethae* has been re-elevated to species rank in IOC v. 5.2 (April 2015), resolving decades of debate about the status of this distinct and isolated form. Unique plumage features (e.g. two-tone blue on face), smaller size and other differences (e.g. greater sexual dimorphism) have

always made this stand out as the most distinctive form of Blue Bonnet. A wide-ranging genetic study of southern Australian birds recently published in Emu (Dolman and Joseph 2015) recommended its separation on the basis of substantial mtDNA divergence (2.16% on ND2 genes) from the now Eastern Bluebonnet and notes the unusual role of a minor biogeographic barrier, the Yellabinna Region or Barton Sandhills, in the evolution of this species.

The Copperback Quail-thrush *Cinclosoma clarum* was recently split (IOC v. 5.2) after the same Dolman and Joseph (2015) paper revealed a big surprise hidden in the genes of Chestnut Quail-thrush — a huge (4.38%) mtDNA divergence across the Eyrean Barrier, the ancient arid basin stretching from South Australia's Spencer Gulf to Lake Eyre. Birds west of this barrier were long known to have a bigger and brighter dorsal chestnut band (hence appropriation of the old colloquial 'Copperback'), but given the extent of regional and clinal plumage variation including what look like hybrid zones (e.g. eastern Eyre Peninsula), the presence of such a large and abrupt genetic gap was rather surprising. This split raises interesting questions about the south-western form *fordianum*, which has a rather small (but bright) dorsal chestnut band and lacks chestnut scapulars, and shows obvious sexual dimorphism — the reduction of which was cited as a defining character of *clarum* in Dolman and Joseph (2015). The similarity between *fordianum* and some eastern Chestnut Quail-thrush hints this may be a relict form of the original east-west separation — though it is also clear that plumage variation does not necessarily match genetic variation in this superspecies complex.

There may be more surprises in store for WA birds. The Dolman and Joseph (2015) Emu paper also found species-level mtDNA divergence (2.79%) for south-western samples of Scarlet Robin, which comprise most of the subspecies *Petroica boodang campbelli*. Better sampling will be needed to resolve this, particularly how to treat robins on SA's Eyre Peninsula, which are morphologically included in subspecies *campbelli*, but genetically align with other eastern birds from the single sample included in the recent study. White-eared Honeyeaters also showed an extremely cryptic but possibly species-level genetic split (2.23%) across the Eyrean Barrier, demonstrating again how powerful this ancient barrier has been in southern Australian bird evolution.

## References

- Andersen, M.J., Nyári, A.S., Mason, I., Joseph, L., Dumbacher, J.P., Filardi, C.E. and Moyle, R.G. (2014). Molecular systematics of the world's most polytypic bird: the *Pachycephala pectoralis/melanura* (Aves: Pachycephalidae) species complex. *Zoological Journal of the Linnean Society* **170**, 566-588.
- Dolman, G., and Joseph, L. (2015). Evolutionary history of birds across southern Australia: structure, history and taxonomic implications of mitochondrial DNA