Red-tailed black cockatoos

I have a confession to make – I love Australia's black cockatoos. Whenever I see them careen and roll above me, I get a frisson of joy. They seem to move effortlessly on gently pounding wings, calling to other members of their flock in sonorous delight. Their feeding can quickly produce a carpet of discarded gum nuts and other debris that have been torn apart in search of tiny seeds that they ingest. It's not often that I become lyrical about nature, but these birds are wonderful and I feel privileged to witness their antics.

Apart from the very different palm cockatoo, the five species of black cockatoos are placed in the genus *Calyptorhynchus*, but three species, the yellow-tailed black cockatoo in eastern Australia and two others, Baudin's cockatoo and Carnaby's cockatoo, which occur only in south-western Australia, are sometimes placed in the genus *Zanda*. Eastern Australia's glossy black cockatoo is *C. lathami*.

However, the most widespread species is the red-tailed black cockatoo (*C. banksii*), which ranges over much of Australia although it is largely absent from wetter south-eastern Australia and Tasmania. Due to differences in size and morphology (particularly in the shades and patterning of colour in females), it has been divided into five subspecies: *C. b. banksii* and *C. b. macrorhynchus* in northern Australia, *C. b. graptogyne* in south-eastern Australia, *C. b. naso* in south-western Australia, and *C. b. samueli* in arid Australia.

A recent study has been published by Dr Kyle Ewart from the Australian Museum and the University of Sydney, and his co-authors in the journal *Heredity*, used single-nucleotide polymorphisms (SNPs or 'snips') and mitochondrial DNA from over 100 birds across Australia. These techniques are remarkably powerful for discerning population structure and provide insights into how these populations have evolved over time, much like tracing the genealogy of a family tree. Detailed analysis of the sequence data found some surprising results.

Notably, the two northern subspecies, *C. b. banksii* and *C. b. macrorhynchus*, could not be distinguished from each other, having remarkably similar SNP and DNA profiles.

The western population of the widespread arid Australian subspecies, *C. b. samueli*, was found to be genetically disparate from isolated populations in inland eastern, central and western parts of Australia. The authors suggest that these differences are sufficient to regard the western population as a distinct evolutionary unit, which they describe as a new subspecies, *C. b. escondidus*.

The name that they have chosen is derived from a Spanish and Portuguese word meaning 'hidden' and refers to this subspecies having been 'hidden in plain sight'. Indeed, the inclusion of the western population in *C. b. samueli* reflects convergence where different evolutionary units have evolved similar morphological traits, and only the use of molecular data finally resolved the puzzle.

Populations of the new subspecies are known from the Pilbara, Murchison and Wheatbelt districts. The removal of these populations from *C. b. samueli* thus drastically reduces the known range of *C. b. samueli*, which occurs in the southern Northern Territory, and inland Queensland and New South Wales.

The discovery of a distinct subspecies in Western Australia raises significant conservation considerations due to land clearing impacting their food plants, including the double-gee widespread noxious weed that is regularly removed by landholders.

The research undertaken by Dr Ewart and his colleagues demonstrates the unique power of molecular data to unravel the evolutionary relationships of our precious biota. The discovery of a unique evolutionary lineage of cockatoos in mid-western Australia continues to shed light on the fauna of a fascinating region. Let's hope that they continue to careen and wheel in the sky, delighting all who see them.

Above Red-tailed black cockatoos bask in the warm glow as morning breaks in the Central Wheatbelt.
Photo – Adrian Chesson/DBCA