Agenda Item: SC. 3.5

Crocodile Specialist Group Steering Committee Meeting
Sofitel Royal Bay Hotel, Agadir, Morocco
(12 May 2026)

Taxonomy

The CSG Taxonomy Group continues to monitor advances in the population genetics of species complexes within *Crocodylus* and among caimanines that might, in the near future, prompt the establishment of new species or resurrection of older names previously subsumed into synonymy. The primary focus of the Committee's effort, however, has been the *Osteolaemus* species complex.

Before the turn of the millennium, only one species - *Osteolaemus tetraspis* Cope 1861 - was recognized in West and Central Africa Two subspecies were sometimes accepted - *O. t. tetraspis* in West Africa and *O. t. osborni* in Central Africa. But increasing amounts of morphological and molecular data suggested not only that these should be recognized as separate species, but that more than three or four species might exist (Broch 2007; Eaton *et al*. 2009; Franke *et al*. 2013; Shirley *et al*. 2015; Schmidt *et al*. 2015; Smolensky *et al*. 2015a,b; Gvoždík *et al*. 2024).

Our present consensus is that three species can be regognized: *Osteolaemus osborni* (Schmidt 1919) in the Congo Basin, *O. tetraspis sensu stricto*, and a third species found west of the range of *O. tetraspis*. We have also agreed on the most appropriate existing species name to be applied for this newly-recognized species; although it has appeared sporadically in the literature, it should not be viewed as established until a formal revision of *Osteolaemus* systematics is completed. We anticipate completion and submission for publication this year.

Our primary systematic concerns at present are two-fold - determining the geographic ranges of the West African forms previously lumped as *O. tetraspis*, and establishing morphological criteria by which these species can be consistently differentiated from each other and from *O. osborni.*

Key recent advances

Since the 2024 CSG meeting in Darwin, two papers have been published that might impact conservation and wildlife management *Crocodylus* for species of in the near future.

The first is a study by Avila-Cervantes *et al*. (2025), who used molecular and morphometric data to suggest that populations of *Crocodylus acutus* Cuvier 1807 on Banco Chinchorro and Cozumel Island off the east coast of the Yucatán Peninsula might be isolated species. The distances between the mainland and Cozumel and Banco Chinchorro (about 20 and 35 km, respectively) seem to argue against the presence of genetically isolated populations for a widespread species known to cross marine barriers with regularity. Moreover, geographic sampling was uneven. Samples of *C. acutus* were included from Panama, Cozumel, Banco Chinchorro, and Chiapas, but none from the West Indies, Atlantic coast of Mexico, or any part of Mesoamerica between Mexico and Panama. Nevertheless, these results are intriguing and further work is clearly warranted.

The second is a survey of genetic variation within *Crocodylus porosus* Schneider 1801 and an analysis of crocodylian phylogenetic relationships based on mitogenomic and mitochondrial data (Agne *et al.* 2026). The focus of the paper was genetic structure within *C. porosus* and the identity of the extirpated population of the Seychelles, but the authors also concluded that *Crocodylus halli* Murray *et al*. 2019 should be treated as a junior synonym of *Crocodylus novaeguineae* Schmidt 1928. They based this conclusion on the very low level of molecular divergence between a specimen they referred to *C. halli* and others referred to *C. novaeguineae*.

Crocodylus halli had been split from *C. novaeguineae* based on consistent differences in cranial proportion and postoccipital osteoderm arrangement between New Guinea crocodiles from the northern and southern parts of its range in New Guinea (Murray *et al.* 2019). These differences had been noted before (e.g., Hall, 1989), and mitochondrial and microsatellite data in an unpublished thesis (Gratten 2003) seemed to support some level of distinctiveness between northern and southern samples.

The CSG Taxonomy Committee has generally treated the diagnosability of *C. halli* with skepticism. The split was based entirely on morphometric variation in the skull and scutellation. New molecular data were not presented to support the species-level distinction of the southern New Guinea population, and although the mitochondrial and microsatellite data analyzed by Gratten (2003) showed genetic structure in *C. novaeguineae* distinguishing northern and southern forms, the level of disparity was low and allelic differences did not consistently recover the northern and southern samples as exclusive clades. If the populations had been isolated, Gratten (2003) argued, the isolation had not been a long one.

Although the results reported by Agne *et al*. (2026) do not support species-level status for *C. halli*, there are reasons for caution here as well. Only one specimen referred to *C. halli* was included, and although it was collected in southern New Guinea – "Gulf of Papua, South Papua New Guinea" (Agne *et al*. 2026: Table 1) - it is unclear whether this corresponds with any of the localities from which the specimens studied by Murray *et al*. (2019) were collected. The authors also did not indicate whether the specimen was referred to *C. halli* on morphological criteria or because of its geographic derivation in southern New Guinea.

Agne *et al*. (2026) also argued against the recognition of subspecies within *C. porosus* and *C. palustris* (Lesson 1831). A specimen of *C. palustris* from Sri Lanka was indeed more closely related to an individual from mainland South Asia, but the other two of the four *C. palustris* specimens are of unknown derivation.

It is premature to take action based on either of these papers. In both cases, geographic sampling must be expanded. Samples of *C. acutus* from the Yucatán mainland are needed to test the distinctiveness of the putative insular populations of the species. Indeed, given the direction of prevailing currents in that part of the Atlantic, samples from Belize and further south in Mesoamerica would be relevant, as would samples from the West Indies.

To test the distinctiveness of *C. halli*, future analyses should include samples from throughout southern New Guinea. Ideally, these would include specimens from Lake Murray or the Bnaturi or Aramia Rivers, where the specimens studied by Murray *et al.* (2019) were collected. Indeed, it would be advisable to try to isolate DNA data from one of the skeletal specimens used in that analysis.

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