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Rigorous approaches to species delimitation have significant implications for African crocodilian systematics and conservation

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Accurate species delimitation is a central assumption of biology that, in groups such as the Crocodylia, is often hindered by highly conserved morphology and frequent introgression. In Africa, crocodilian systematics has been hampered by complex regional biogeography and confounded taxonomic history. We used rigorous molecular and morphological species delimitation methods to test the hypothesis that the slender-snouted crocodile (*Mecistops cataphractus*) is composed of multiple species corresponding to the Congolian and Guinean biogeographic zones. Speciation probability was assessed by using 11 mitochondrial and nuclear genes, and cranial morphology for over 100 specimens, representing the full geographical extent of the species distribution. Molecular Bayesian and phylogenetic species delimitation showed unanimous support for two *Mecistops* species isolated to the Upper Guinean and Congo (including Lower Guinean) biomes that were supported by 13 cranial characters capable of unambiguously diagnosing each species. Fossil-calibrated phylogenetic reconstruction estimated that the species split $\pm$ 6.5–7.5 Ma, which is congruent with intraspecies divergence within the sympatric crocodile genus *Osteolaemus* and the formation of the Cameroon Volcanic Line. Our results underscore the necessity of comprehensive phylogeographic analyses within currently recognized taxa to detect cryptic species within the Crocodylia. We recommend that the community of crocodilian researchers reconsider the conceptualization of crocodilian species especially in the light of the conservation ramifications for this economically and ecologically important group.

1. Introduction

While numerous concepts have been proposed that emphasize different criteria for delimiting species [1], species themselves may be best conceptualized as population aggregates evolving together as a metapopulation independent of other such aggregates [2–4]. Regardless of definition, accurate species delimitation is critical, because species are a fundamental unit for much of biology [5,6]. Often species delimitation can be relatively trivial owing to allopatry or prezygotic barriers (e.g. different call types in birds and anurans). In reality, species delineation is frequently obfuscated by the presence of cryptic variation [7,8], and the limitations of many species concepts to effectively recognize such [9]. Geographical structuring of lineages resulting from allopatry may be more common in widely distributed taxa subjected to biogeographic or ecogeographic processes at continental or regional scales. As a result, new species are being increasingly detected [10].

The African continent has a long and pronounced geological history of rift formation, volcanic uplift, desertification and ecological heterogeneity, resulting from climatic cycling [11–13]. As many as 30 African biogeographic realms have been recognized [14], three of which are present in sub-Saharan

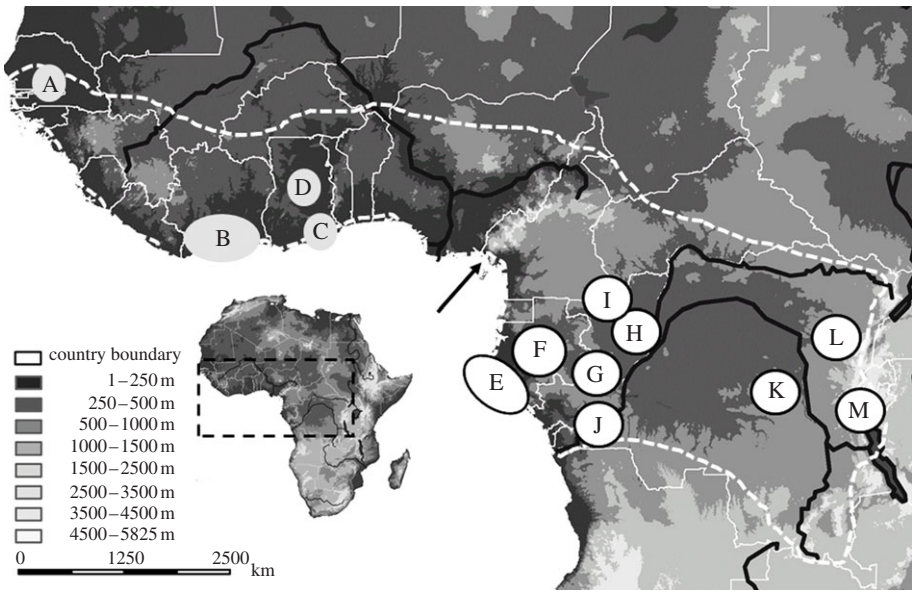

Figure 1. Map of molecular sampling localities. The base map is shaded to reflect topographic and elevation features of the landscape across the sampling distribution. Sample points are colour-coded by corresponding clade (grey, west; white, central), and labels correspond to localities detailed in the electronic supplementary material, table S1. The white, dashed line delimits the distribution of *Mecistops*. The black arrow indicates the Cameroon Volcanic Line. The black, dashed box in the inset map shows the expanded area.

western Africa: the Congolian, Upper Guinean and Lower Guinean (i.e. Cameroon–Gabon) [15]. The slender-snouted crocodile (*Mecistops cataphractus*) has a convoluted systematic history [16–18] emblematic of widely distributed crocodilians globally [19,20] and other African taxa [21,22]. *Mecistops* ranges throughout western Africa (figure 1), largely sympatric with the distribution of the other western African endemic crocodile genus *Osteolaemus*. In the light of recent evidence for speciation in other previously recognized species of African crocodiles [19,20], our goal was to use rigorous, multi-locus coalescent and phylogenetic methods and analysis of cranial morphology to test the hypothesis that western African biogeographic zones have driven cryptic lineage diversification in *Mecistops*.

2. Methods

(a) Taxon and molecular character sampling

We sequenced up to 108 wild-caught slender-snouted crocodiles from throughout its range (figure 1; electronic supplementary material, table S1). We examined sequence variation across 11 gene regions for a total 7768 bp for the *Mecistops* in-group (see electronic supplementary material, table S2)—3768 bp from four partial mitochondrial genes (mtDNA—cytb, 12S, COI, ND4) and 4000 bp from seven nuclear genes (nDNA—LDH-A, rag1 and the flanking regions of five anonymous microsatellites). Primers for mtDNA were designed from a complete *Mecistops* mitogenome (GenBank NC_010639), whereas primers for the nuclear genes were taken from a previously published study [19] or designed from available microsatellite clone sequences [23,24].

(b) Data collection

We used the Qiagen multiplex PCR kit at a volume of 15 µl containing 1.1 µl genomic DNA and primers at 0.2 µM. Cycling conditions for all markers were as follows: 95°C 15 min, 35 cycles of 94°C 30 s/56.5°C (57°C for ND4) 90 s/72°C 105 s, 72°C 10 min final extension. PCR products were exosap-purified, and genes were bidirectionally sequenced (BigDye Terminator v. 3.1, Applied Biosystems, Carlsbad, CA) with the PCR primers. Cycle sequencing conditions for mtDNA markers were 96°C 3 min, 30 cycles of 96°C 30 s/55.7°C 30 s/60°C 1 min; for nuDNA markers 96°C 3 min, 30 cycles of 96°C 30 s/57°C 30 s/60°C 100 s. We assembled contigs and aligned individual marker datasets in CLC v. 3.6.2. Nuclear strands were phased, and microsatellite repeats were removed from the alignment prior to all analyses.

(c) Molecular species delimitation

Coalescent-based Bayesian species delimitation (BSD) may best account for the uncertainty that arises during speciation [25,26]. The method implemented in BP&P v. 2.0 [25,27] uses reversible-jump Markov chain Monte Carlo (rjMCMC) sampling [28] to simultaneously estimate the posterior distribution for different speciation models, mutation-scaled effective population sizes (θ) and divergence times (τ). We established a five-taxon guide tree (figure 2*a*) incorporating two putative *Mecistops* taxa following results from distance- and character-based methods (see below), and three *Osteolaemus* taxa following Eaton *et al.* [19]. We repeated the analysis with three different, fully partitioned multi-locus datasets: (i) six loci—concatenated mtDNA plus the five msat flanking sequences partitioned; (ii) seven loci—all seven nuclear markers partitioned; and (iii) eight loci—concatenated mtDNA plus all seven nuclear markers partitioned. We assessed the impact of ancestral effective population size and time of divergence on species delimitation by testing three different prior distributions for θ and τ_0 [21]: (i) LD—large ancestral populations, deep divergences, $\theta = G(1, 10)$ and $\tau_0 = G(1, 10)$, both with prior mean = 0.1; (ii) SS—small ancestral populations, shallow divergences, $\theta = G(2, 2000)$ and $\tau_0 = G(2, 2000)$, both with prior mean = 0.001; and (iii) LS—large ancestral populations, shallow divergences, $\theta = G(1, 10)$ and $\tau_0 = G(2, 2000)$. We repeated all analyses under both the 0 ($\varepsilon = 15$) and 1 ($\alpha = 3$, $m = 1$) rjMCMC algorithms [25,28]. We ran three independent chains of 500 000 steps, sampling every fifth step, with 10 000 burn-in steps, for each analysis to confirm convergence on posterior optima. We estimated speciation probabilities for each node in the guide tree following Leaché & Fujita [21] and considered values greater than or equal to 0.95 strong support for the inference of distinct species.

For comparison with previous crocodilian systematics studies [19,20], we used similar distance- and character-based methods. Uncorrected *p*-distances were calculated in MEGA5 [29] for each

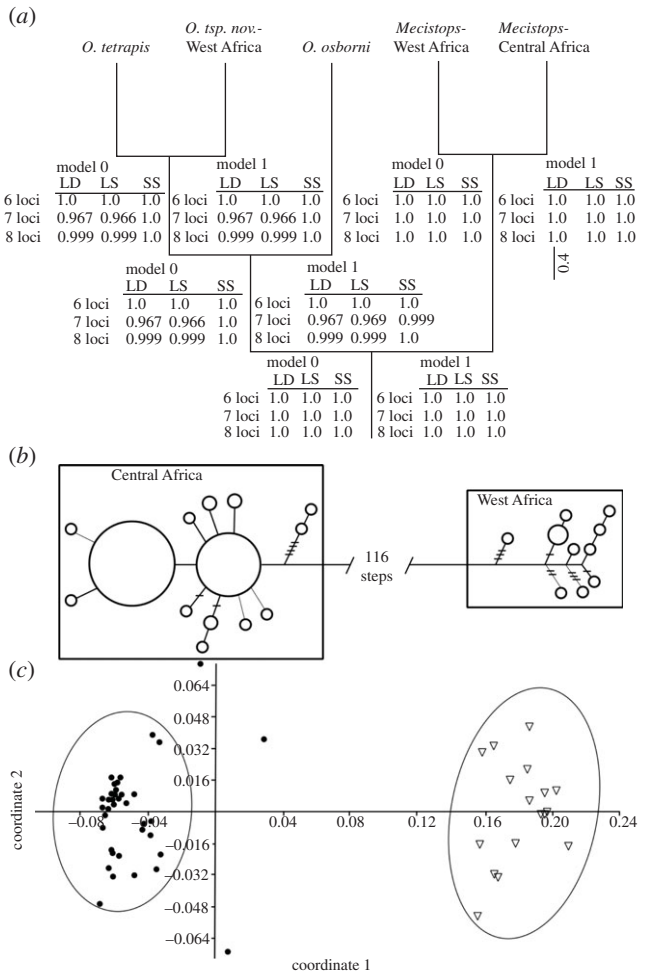

Figure 2. Molecular and morphological species delimitation results. (*a*) Bayesian species delimitation results for *Mecistops* and *Osteolaemus* assuming a resolved, five-species guide tree. The marginal probabilities for speciation are displayed at each node for each of the three datasets (six, seven and eight loci) and each combination of priors for θ and τ_0: LD, prior means 0.1; LS, prior mean $\theta = 0.1$, prior mean $\tau_0 = 0.001$; SS, prior means 0.001. Results from both rjMCMC algorithm 0 (left of node) and 1 (right of node) are displayed. There was high speciation probability (>0.95) for all nodes under all combinations of dataset, priors and rjMCMC algorithm, providing robust support for recognition of two *Mecistops* and three *Osteolaemus* species. (*b*) Haplotype network from CHA analysis of mtDNA. Two distinct haplogroups are evident (boxes), one representing all Central African samples and the other all West African samples, separated by 116 mutational steps. Circle size is representative of the number of individuals with each haplotype. Hash marks on branches represent single base changes; branches without hash marks represent only a single base difference between connected haplotypes. (*c*) NMDS results of multivariate analysis of cranial morphological characters in *Mecistops*. Individuals are colour-coded by group assignment: Central (black) and West (grey). Ellipses represent 95% concentration limits.

marker set individually and by genome, and interindividual distances were manually searched to find the groupings of individuals that minimized intragroup and maximized intergroup distance. We plotted COI distances to determine whether our groups had a barcoding gap of greater than 42%, the proposed COI net distance for identifying species [30,31]. We used population aggregation analysis (PAA) [32] and cladistic haplotype aggregation (CHA) [33] to detect phylogenetic species following [19]. For CHA, we generated unrooted genealogies for the mtDNA dataset using the method of maximum-parsimony implemented in dnapars of the PHYLIP v. 3.69 package [34] with the haplotype network reconstructed from the most parsimonious trees using HAPLOVIEWER [35].

(d) Morphological species delimitation

To test for species diagnostic skeletal characteristics, we compared our molecular species delimitations with geographically verified cranial specimens of slender-snouted crocodile. Two independent observers (M.H.S. and K.A.V.) coded characters from skulls (see electronic supplementary material, table S3) in a double-blind procedure, and consensus decisions were made where characters were coded inconsistently between observers. Ambiguous characters, incomplete specimens (less than 75% of characters coded) and juveniles were omitted. Character fixation was assessed following Wiens & Servedio [6] with a frequency cut-off of 10% ($p = 0.10$). Non-metric multi-dimensional scaling (NMDS) with the Hamming similarity index was used to find discrete clusters of individuals in PAST [36]. Clusters of individuals with non-overlapping 95% occupancy ellipses were considered discrete and strong evidence for unique species. To confirm molecular and morphological congruence, we sequenced the COI fragment for a skull from Cameroon and a skull from Côte d'Ivoire.

(e) Fossil-calibrated divergence dating

Following results of molecular and morphological species delimitation, we used a reduced in-group *Mecistops* dataset (five individuals from each species) combined with outgroup taxa from across the Crocodylia to both provide an updated phylogeny of crown Crocodylia and estimate fossil-calibrated divergence timing between newly diagnosed *Mecistops* taxa and sympatric *Osteolaemus* and African *Crocodylus* (see the electronic supplementary material for details of outgroup sampling). Phylogenetic analysis was conducted in BEAST v. 1.7.5 [37] on both the full (mtDNA + nDNA) and nDNA-only datasets partitioned by gene with the best-fit model of base substitution selected by Bayesian information criterion in JMODELTEST v. 0.1.1 (see electronic supplementary material, table S2) [38]. We applied an uncorrelated lognormal-relaxed clock [39] to each partition. We used a Yule process prior for the tree model of speciation [40] and a uniform prior ($U(0, 5)$) for the uncorrelated lognormal-relaxed clock mean rate with an initial value of 0.005 substitutions per site per Myr [41]. Following previous studies [28], we gave the tree root prior a normal distribution ($N(78, 8)$) placing upper and lower truncations of 68 and 115 million years ago (Ma), respectively [42–45]. We used a gamma prior ($\Gamma(2, 2.9)$) with offset 62 Ma for the divergence between *Alligator* and *Caiman* [44–46]. We additionally added a gamma prior ($\Gamma(3, 5.5)$) with offset 30 Ma for the divergence between *Paleosuchus* and *Caiman*, a gamma prior ($\Gamma(2, 2)$) with offset 18 Ma for the root of the Crocodylinae (i.e. *Mecistops*, *Osteolaemus* and *Crocodylus*), and tested three different gamma priors for the root of *Crocodylus*: ($\Gamma(2, 2.8)$) with offset 10 Ma, and ($\Gamma(2, 3.8)$) and ($\Gamma(3, 3.2)$) both with offset 4 Ma [42,44,45,47]. See the electronic supplementary material for full details of fossil calibration. We ran four independent analyses for 5.0×10^7 generations sampling every 10 000 generations and excluding the first 15% as burn-in. We assessed posterior convergence by examining the likelihood plots through time with TRACER v. 1.5. Bayesian estimates of divergence timing were compared with those estimated by penalized likelihood in R8S (see the electronic supplementary material for details) [48,49].

3. Results

(a) Molecular species delimitation

Bayesian species delimitation resulted in unequivocal support (i.e. speciation probability 1.0) for two *Mecistops*

species and highly robust support (i.e. speciation probability greater than 0.95) for three *Osteolaemus* species (figure 2*a*). The different prior distributions on θ and τ_0, different marker datasets, and different rjMCMC algorithms resulted in nearly identical posterior support for speciation events in these taxa (figure 2*a*). Distance analysis supported the BSD results by revealing two genetic clusters within *Mecistops* corresponding geographically to Central and West Africa. Mean intragroup divergences were estimated to be 0.0–0.0027 ($\pm$0.001), whereas the intergroup distances were 0.0194 ($\pm$0.0046)–0.0789 ($\pm$0.0083) depending on the gene region(s) analysed (see electronic supplementary material, table S4). The COI barcoding gap was 4.9% (see electronic supplementary material, figure S1). PAA offered unambiguous support for phylogenetic divisions between these two geographical regions with no shared haplotypes in nine of the genes and 2–77 segregating sites per gene between regions (see electronic supplementary material, table S2). CHA produced networks that clustered all intraregional samples in contiguous regions of the network separated by a single branch substantially longer than any internal branch (figure 2*b*).

(b) Morphological species delimitation

Comparison of 91 non-juvenile skulls revealed 13 discrete morphological characters distinguishing the two genetically defined West and Central African lineages (figure 3 and the electronic supplementary material provide character descriptions). Of these characters, two showed fixed variation segregating the lineages. Of the remaining characters, one had a fixed state in the Central group (20% frequency in the West group), two had a fixed state in the West group (5–8% frequency in the Central group), eight had the predominantly West trait at a frequency less than 10% in the Central group and six had the predominantly Central trait at a frequency less than 10% in the West group. NMDS detected two discrete clusters of skulls that corresponded to West and Central Africa (figure 2*c*). The NMDS stress value of 0.17 indicated good fit of the data. All individuals of unknown or questionable provenance were grouped within the 95% confidence ellipses of one of the geographical regions with outliers entirely explained by the degree of missing data and not by locality. The COI fragments from the two skulls confirmed molecular and morphological congruence, and matched geographical expectations.

(c) Fossil-calibrated divergence dating

The topologically unconstrained Bayesian analysis of the combined, partitioned by genome and fully partitioned datasets recovered all expected relationships within the Crocodylia at the species, genus and family levels with most nodes receiving 100% posterior probability support (figure 4; electronic supplementary material, S2–S4). Our results supported three distinct *Osteolaemus* species, as well as a sister group relationship of *Osteolaemus* and *Mecistops* to the 'true crocodiles' of *Crocodylus*. Analysis of the partitioned nuDNA-only dataset recovered all family groupings, as well as monophyletic genera, though it placed *Mecistops* as sister to a clade consisting of *Osteolaemus* and *Crocodylus*, and had difficulty resolving interspecies relationships within *Crocodylus* (see electronic supplementary material, figure S4). In all analyses, *Mecistops* consisted of two highly divergent, reciprocally monophyletic

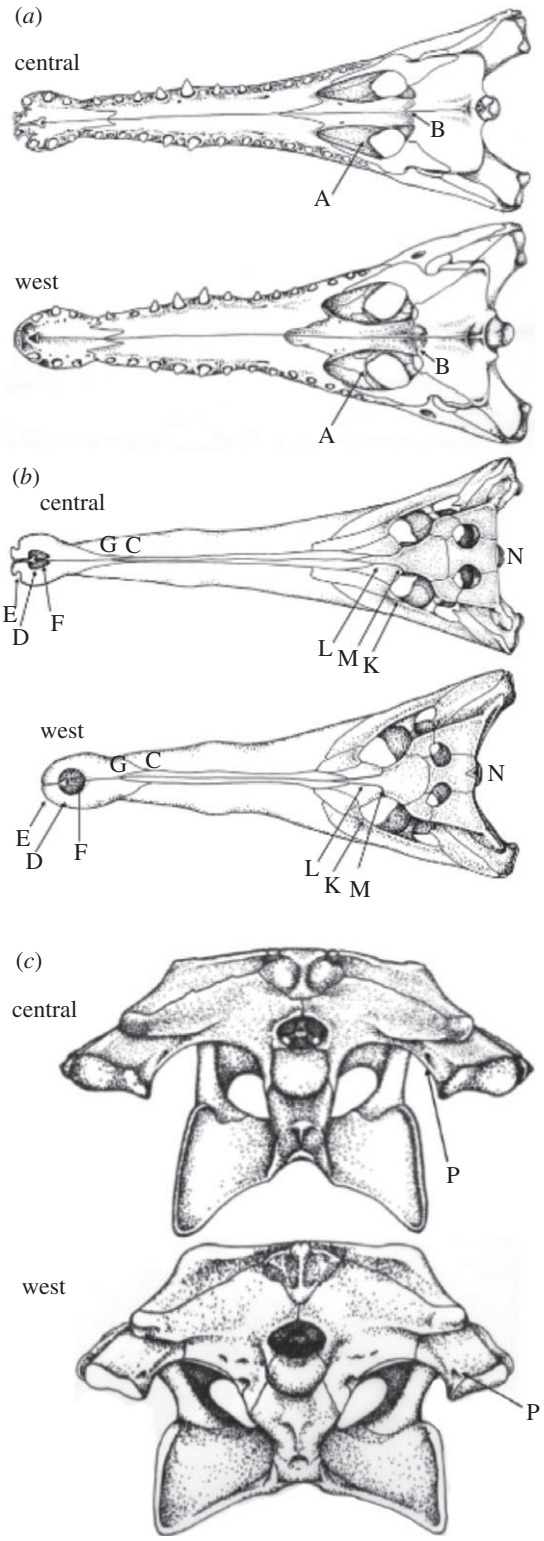

Figure 3. Comparative cranial morphology of *Mecistops* from Central and West Africa: (*a*) dorsal view, (*b*) ventral view, (*c*) occipital view. Labelled characters correspond to character descriptions in the electronic supplementary material.

groups—one composed entirely of individuals from West Africa and the other of individuals from Central Africa.

Estimated divergence times from Bayesian and maximum-likelihood methods were highly congruent as evidenced by the maximum-likelihood estimation falling within the 95% HPD of the Bayesian analyses (see electronic supplementary material, table S5). The different datasets produced slightly different estimates for the MRCA of most clades (electronic supplementary material, table S5), though this is likely to be best explained by the degree of missing outgroup data in the microsatellite

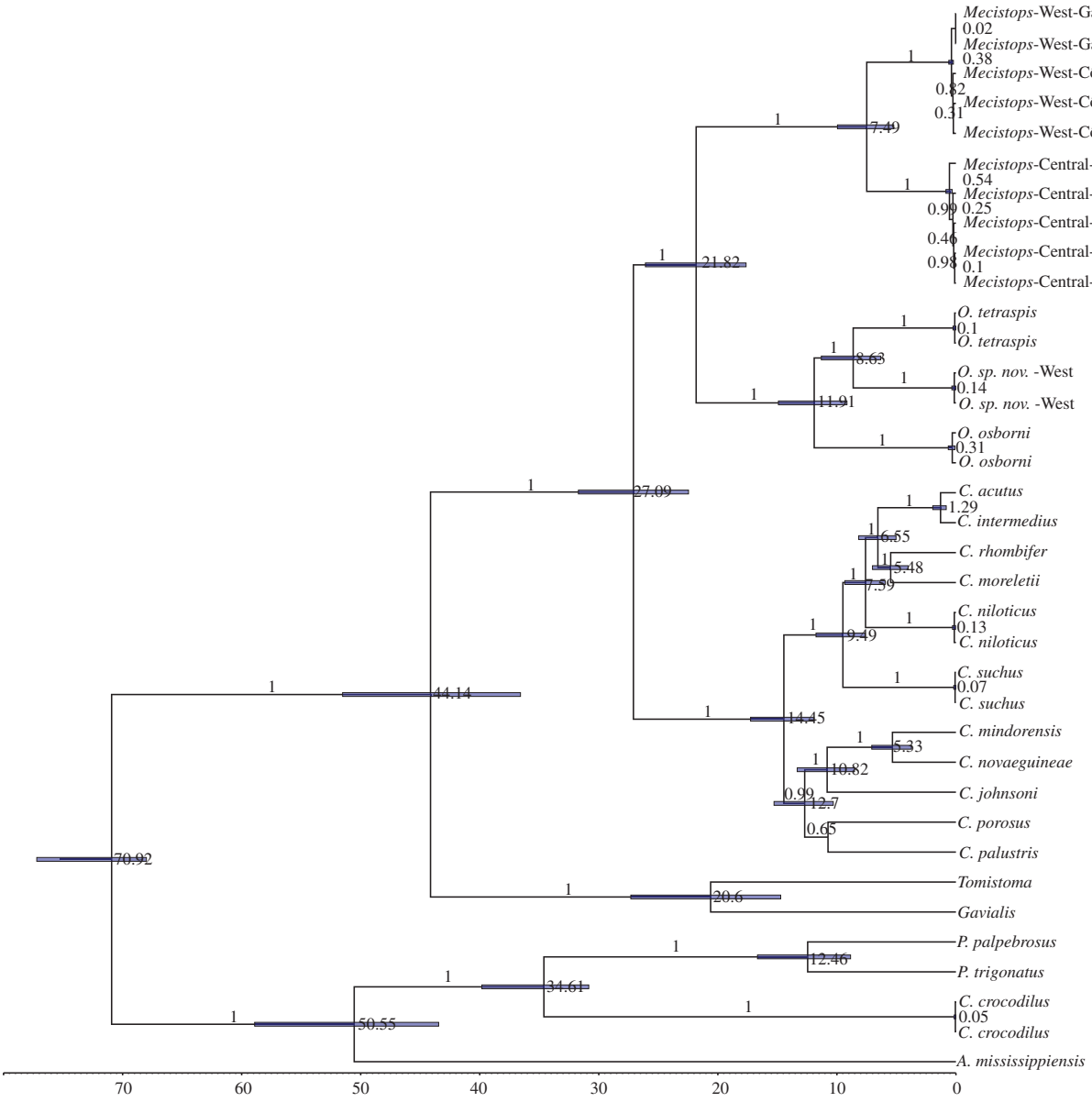

Figure 4. Divergence date estimates within the Crocodylia. This is an updated phylogeny for the crown Crocodylia presenting all seven proposed African species. Median dates are shown as node labels with bars representing the 95% HPD values. Branch labels are Bayesian posterior probability support values for each node following the label. The scale on the bottom is in millions of years before present. This tree topology and displayed dates are from the analysis partitioned by genome. See the electronic supplementary material for all other BEAST results. (Online version in colour.)

flanking sequences. We estimated the MRCA of the *Mecistops* + *Osteolaemus* + *Crocodylus* clade in the Late Oligocene (±26 Ma), the *Osteolaemus* + *Mecistops* sister clade in the Early Miocene (±21 Ma) and the radiation of extant *Crocodylus* species originating in the Mid-Miocene (±14 Ma). The split between the two *Mecistops* lineages was estimated at 6.5–7.5 Ma, slightly after the mean estimate for the split between *O. tetraspis* and *O.* sp. *nov.* cf. *tetraspis* in West Africa (7.5–8.5 Ma), though the 95% HPD values for these two estimates overlapped substantially (figure 4).

4. Discussion

(a) Multiple-criteria species delimitation

It has been recommended that multiple criteria (e.g. genetic, morphological, ecological, biogeographic) are used to delimit species [25,50–52]. In the case of *Mecistops*, we present results from three molecular and two morphological species diagnostic approaches that unambiguously support two highly divergent taxa. Further, our speciation model is well predicted by African biogeography with the two taxa isolated in the Congolian (including Lower Guinean) and Upper Guinean biomes. These combined molecular and morphological findings clarify historic taxonomic uncertainties, and the strength of the evidence presented does not warrant subspecies designation or previously suggested subspecies [18].

The Bayesian species delimitation model of Yang & Rannala [25] uses coalescent theory to predict that increasing θ and decreasing τ_0 will favour fewer species. In the cases of *Mecistops* and *Osteolaemus*, varying the means of the prior distributions by over two orders of magnitude did not impact the speciation inference, and we found unambiguous support for complete isolation and allopatric speciation between the proposed taxa at all θ sizes and τ_0 ages. Aside from prior assumptions on θ and τ_0 [52], the primary limitation of BSD is the use of an inappropriate guide tree [21]. The five-taxon guide tree used in our analyses was not susceptible

to this issue as it was well supported by external evidence (i.e. previous studies [19], African biogeography and results from alternative analyses in this paper), and the seven speciation models explored by the rjMCMC analysis represented all biologically plausible alternative species trees.

BSD results were supported by the more traditional, phylogenetic species delimitation methods. The observed molecular divergence was congruent with that between other recognized pairs of extant crocodilian species (see electronic supplementary material, table S4), and fixed molecular character differences in both genomes can be used to unambiguously diagnose the two *Mecistops* species [32,33,53]. Partitioned phylogenetic analysis resulted in reciprocally monophyletic lineages that shared an MRCA in the Late Miocene. This estimated divergence timing is congruent not only with sympatric *Osteolaemus* crocodiles, but also with expectations derived for other crocodilian sister species pairs globally (see figure 4; electronic supplementary material, table S5 and figures S2–S4).

The standard in morphological taxonomy has traditionally been that a single fixed character difference is necessary to differentiate species [6]. Here, we found 13 characters that segregate Central from West Africa, at least 10 of which show frequencies indicative of no contemporary gene flow [6]. Even though this study is the largest examination of intraspecies discrete cranial morphological variation in a crocodilian species, no other study has found as many morphological characters differentiating lineages previously believed to represent a single species. For example, only up to four cranial characters apparently separate *Osteolaemus osborni* from *O. tetraspis*, which have substantially higher molecular divergence than seen with the two *Mecistops* species [19,54,55]. Two skulls analysed as part of this study presented confounding results, unfortunately both listed with provenance of Nigeria. Further examination of the acquisition data revealed that they were purchased from dealers and it is highly likely that the locality data are inaccurate—a common problem with older museum specimens [56].

The strength of the multiple lines of evidence presented here is threefold [2]. First, the multi-inferential molecular approach to species delimitation overcomes the risk of confounding gene trees with species trees [57]. Second, support from fixed morphological characters should convince those sceptical of strictly molecular taxonomy [58,59]. Third, our geographically thorough in-group and taxonomically comprehensive outgroup sampling ensures that the confounding effects of incomplete taxon sampling are avoided [60]. Existing gaps in the in-group sampling will not impact the inference of distinct species [61]. For example, comparison of inter-individual genetic and geographical distances precludes the possibility of isolation by distance effects despite the molecular sampling gap (see electronic supplementary material, figure S5). Undetected genetic variation will, instead, probably be informative on intraspecies phylogeographic process and fine-scale delimitation of species geographical range limits. For example, COI sequences from zoo *Mecistops* revealed new haplotypes and demonstrated that they all originated exclusively from West Africa (M. H. Shirley 2013, unpublished data). Incidentally, previous studies focusing on the molecular systematics of *Mecistops* [62] or using multiple *Mecistops* individuals in phylogenetic and biogeographic analyses [41] never detected multiple *Mecistops* species because they exclusively sampled zoo individuals.

(b) Divergence timing and the biogeography of *Mecistops* and *Osteolaemus*

Divergence times estimated within the crown Crocodylia generally agree with previous results [20,41] and confirm baseline expectations for the MRCA between crocodilian sister species pairs and intracrocodilian species lineage diversification. Virtually all pairs of extant crocodilian sister species shared MRCAs in the Mid to Late Miocene ($\pm$6–15 Ma). This establishes a timeline of millions of years as a reasonable expectation for crocodilian speciation [63] and suggests that climatic events driving crocodilian mass extinctions in the Miocene [64,65] also served to diversify tenacious crocodilian lineages through allopatric isolation of populations. Slight differences between our estimated divergence dates and those estimated by others are best explained by our additional calibration points closer to the terminal nodes [66,67], different molecular markers and/or prior hyperparameter specification, resulting in, if anything, biased underestimates of divergence time [68]. The incongruent phylogeny hypothesized by the nDNA dataset is best explained by the inconsistent ability to amplify msat flanking sequences in all outgroup species.

This study is the first to estimate divergence time between all pairs of established and putative sister species from the genera *Mecistops* and *Osteolaemus*. Not surprisingly, the estimated divergence timing for *Mecistops* and *Osteolaemus* lineages was highly congruent (see figure 4; electronic supplementary material, table S5 and figures S2–S4), indicating a regional vicariant process, and further this timing is congruent with the earliest fossil appearance of *Mecistops* in Africa, stratigraphically dated to the Late Miocene [62,69,70]. While no samples were available for genetic analysis from Nigeria, our molecular divergence dates and morphological classification of one skull from Nigeria and four skulls from Cameroon to the West and Central species, respectively, and the molecular identification of one Cameroon skull to the Central species, coincide well with the formation of the Cameroon Volcanic Line (CVL) and/or the Benue Trough as the likely biogeographic barrier. Formation of the CVL began in the Late Mesozoic but continued into the Caenozoic, with much of the middle volcanoes and associated highlands (e.g. Mt. Cameroon, Bioko and Bambouto) not arising until the Mid to Late Miocene with final uplifts into the Pleistocene [71,72]. While further molecular sampling may be desired before this biogeography is ultimately accepted, the CVL is a significant geological feature in the region acting as a zoogeographic barrier for many other taxa [20,22,73]. The additional speciation event inferred for *Osteolaemus* relative to *Mecistops* in Central Africa is likely to be the result *Osteolaemus*'s more direct dependence on forest habitat and the cyclical isolation of humid forest cores throughout the Pliocene and Pleistocene.

(c) Implications for crocodilian taxonomy and conservation

Morphological variation thought to characterize a phenotypically diverse species can often be parsed into monomorphic (and even reciprocally monophyletic) groups with the help of DNA evidence and consideration of distribution-wide biogeography and species- or population-level ecology [74]. Despite this, apparent morphological stasis may be a

reasonable expectation even in the face of significant evolutionary change [75]. These ideas are both supported by the divergent genetic diversity and cranial morphologies found in this study and congruent with the prevailing, albeit simplistic, view of crocodiles as morphologically static entities. That we are not the first to find highly divergent, cryptic crocodilian species emphasizes that the crocodile conservation community (and systematists in general) should recognize crocodilians as evolutionarily dynamic species rather than as conveniently binned entities subjected to our limited perception of morphological divergence [76]. Unfortunately, this may not be so straightforward as crocodilian taxonomy often underscores the limitations of many traditional species criteria. For example, *Caiman crocodilus* and *C. yacare* are not easily distinguished molecularly [77] or morphologically [78]. Similarly, *Crocodylus intermedius* and *C. acutus*, despite being readily distinguished morphologically, may not be genetically reciprocally monophyletic [79]. Further, rampant hybridization has been detected between wild *C. acutus* and its sympatric congeners *C. moreletti* [80,81] and *C. rhombifer* [82,83], suggesting that species boundaries between these taxa may yet be porous [26].

Recognizing well-supported, cryptic crocodilian species is not only of theoretical importance but can also have significant implications for species conservation. The slender-snouted crocodile is being evaluated for the 2013 IUCN Red List and may be critically endangered, in recognition of the fact that this species is on the verge of extinction in West Africa and merits considerable efforts to ensure its future [84,85]. By contrast, Central African *Mecistops* has several robust populations, notably in Gabon [85]. Consistent with the age of taxonomic progress [86], the findings discussed here for African and other crocodilians should encourage the crocodilian systematics and, especially, conservation communities to reflect critically on how we are willing to conceptualize species within the Crocodylia.

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Data accessibility. All sequence alignments and the morphological character matrix will be available for download from Dryad six months after the print date of this article or from the corresponding author by request before that time (doi:10.5061/dryad.sh3m0).

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References

1. Wheeler QD, Meier R. 2000 *Species concepts and phylogenetic theory: a debate*. New York, NY: Columbia University Press.
2. de Queiroz K. 2007 Species concepts and species delimitation. *Syst. Biol.* **56**, 879–886. (doi:10.1080/10635150701701083)
3. Simpson GG. 1951 The species concept. *Evolution* **5**, 285–298. (doi:10.2307/2405675)
4. Wiley EO. 1978 The evolutionary species concept reconsidered. *Syst. Zool.* **27**, 17–26. (doi:10.2307/2412809)
5. Agapow P-M, Bininda-Emonds ORP, Crandall KA, Gittleman JL, Mace GM, Marshall JC, Purvis A. 2004 The impact of species concept on biodiversity studies. *Q. Rev. Biol.* **79**, 161–179. (doi:10.1086/383542)
6. Wiens JJ, Servedio MR. 2000 Species delimitation in systematics: inferring diagnostic differences between species. *Proc. R. Soc. Lond. B* **267**, 631–636. (doi:10.1098/rspb.2000.1049)
7. Mayr E, Ashlock PD. 1991 *Principles of systematic zoology*. New York, NY: McGraw-Hill.
8. Knowlton N. 2000 Molecular genetic analyses of species boundaries in the sea. *Hydrobiologia* **420**, 73–90. (doi:10.1023/A:1003933603879)
9. Tattersall I. 2007 Madagascar's lemurs: cryptic diversity or taxonomic inflation. *Evol. Anthropol.* **16**, 12–23. (doi:10.1002/evan.20126)
10. Quattro JM, Stoner DS, Driggers WB, Anderson CA, Priede KA, Hoppmann EC, Campbell NH, Duncan KM, Grady JM. 2005 Genetic evidence of cryptic speciation within hammerhead sharks (Genus *Sphyrna*). *Mar. Biol.* **148**, 1143–1155. (doi:10.1007/s00227-005-0151-x)
11. Coetzee JA. 1993 African flora since the terminal Jurassic. In *Biological relationships between Africa and South America* (ed. P Goldblatt), pp. 37–61. New Haven, CT: Yale University Press.
12. Plana V. 2004 Mechanisms and tempo of evolution in the African Guinea-Congolian rainforest. *Phil. Trans. R. Soc. Lond. B* **359**, 1585–1594. (doi:10.1098/rstb.2004.1535)
13. Livingstone DA. 1993 Evolution of African climate. In *Biological relationships between Africa and South America* (ed. P Goldblatt), pp. 455–472. New Haven, CT: Yale University Press.
14. Udvardy MDF. 1975 *A classification of the biogeographical provinces of the world*. Morges, Switzerland: IUCN.
15. Linder HP, de Klerk HM, Born J, Burgess ND, Fjeldså J, Rahbek C. 2012 The partitioning of Africa: statistically defined biogeographical regions in sub-Saharan Africa. *J. Biogeogr.* **39**, 1189–1205. (doi:10.1111/j.1365-2699.2012.02728.x)
16. Cüvier GL. 1824 *Recherches sur les ossemens fossiles de quadrupedes ou l'on retablit du plusieurs speces d'animaux que les revolutions du globe paroissent avoir detruites*, 3rd edn. Paris: Dufour & d'Ocagne.
17. Bennett ET. 1835 *Crocodilus leptorhynchus*. *Proc. Zool. Soci. Lond.* **3**, 128–132.
18. Fuchs KH, Mertens R, Wermuth H. 1974 Zum status von *Crocodylus cataphractus* und *Osteolaemus tetraspis*. *Stuttgarter Beitraege zuer Naturkunde, Serie A. Biologie* **266**, 1–8.
19. Eaton MJ, Martin A, Thorbjarnarson JB, Amato GD. 2009 Species-level diversification of African dwarf crocodiles (Genus *Osteolaemus*): a geographic and phylogenetic perspective. *Mol. Phylogenet. Evol.* **50**, 496–506. (doi:10.1016/j.ympev.2008.11.009)
20. Hekkala E *et al*. 2011 An ancient icon reveals new mysteries: mummy DNA resurrects a cryptic species within the Nile crocodile. *Mol. Ecol.* **20**, 4195–4215. (doi:10.1111/j.1365-294X.2011.05245.x)

21. Leaché AD, Fujita MK. 2010 Bayesian species delimitation in West African forest geckos (*Hemidactylus fasciatus*). *Proc. R. Soc. B* **277**, 3071–3077. (doi:10.1098/rspb.2010.0662)
22. Marks BD. 2010 Are lowland rainforests really evolutionary museums? Phylogeography of the green hylia (*Hylia prasina*) in the Afrotropics. *Mol. Phylogenet. Evol.* **55**, 178–184. (doi:10.1016/j.ympev.2009.10.027)
23. Miles LG, Isberg SR, Moran C, Hagen C, Glenn TC. 2009 253 Novel polymorphic microsatellites for the saltwater crocodile (*Crocodylus porosus*). *Conserv. Genet.* **10**, 963–980. (doi:10.1007/s10592-008-9600-7)
24. Miles LG, Lance SL, Isberg SR, Moran C, Glenn TC. 2009 Cross-species amplification of microsatellites in crocodilians: assessment and applications for the future. *Conserv. Genet.* **10**, 935–954. (doi:10.1007/s10592-008-9601-6)
25. Yang Z, Rannala B. 2010 Bayesian species delimitation using multilocus sequence data. *Proc. Natl Acad. Sci. USA* **107**, 9264–9269. (doi:10.1073/pnas.0913022107)
26. Knowles LL, Carstens BC. 2007 Delimiting species without monophyletic gene trees. *Syst. Biol.* **56**, 887–895. (doi:10.1080/10635150701701091)
27. Rannala B, Yang Z. 2003 Bayes estimation of species divergence times and ancestral population sizes using DNA sequences from multiple loci. *Genetics* **164**, 1645–1656.
28. Rannala B, Yang Z. 2013 Improved reversible jump algorithms for Bayesian species delimitation. *Genetics* **194**, 245–253. (doi:10.1534/genetics.112.149039)
29. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. 2011 MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol. Biol. Evol.* **28**, 2731–2739. (doi:10.1093/molbev/msr121)
30. Hebert PDN, Ratnasingham S, DeWaard JR. 2003 Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. *Proc. R. Soc. Lond. B* **270**, S96–S99. (doi:10.1098/rsbl.2003.0025)
31. Hebert PDN, Cywinska A, Ball SL, de Waard JR. 2003 Biological identifications through DNA barcodes. *Proc. R. Soc. Lond. B* **270**, 313–321. (doi:10.1098/rspb.2002.2218)
32. Davis JI, Nixon KC. 1992 Populations, genetic variation, and the delimitation of phylogenetic species. *Syst. Biol.* **41**, 421–435. (doi:10.1093/sysbio/41.4.421)
33. Brower AVZ. 1999 Delimitation of phylogenetic species with DNA sequences: a critique of Davis and Nixon's population aggregation analysis. *Syst. Biol.* **48**, 199–213. (doi:10.1080/106351599260535)
34. Felsenstein J. 2005 *PHYLIP* (*phylogeny inference package*) *version 3.6*. Seattle, WA: Department of Genome Sciences, University of Washington.
35. Salzburger W, Ewing GB, Von Haeseler A. 2011 The performance of phylogenetic algorithms in estimating haplotype genealogies with migration. *Mol. Ecol.* **20**, 1952–1963. (doi:10.1111/j.1365-294X.2011.05066.x)
36. Hammer Ø, Harper DAT, Ryan PD. 2001 PAST: paleontological statistics software package for education and data analysis. *Palaeontol. Electron.* **4**, 9.
37. Drummond AJ, Suchard MA, Xie D, Rambaut A. 2012 Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Mol. Biol. Evol.* **29**, 1969–1973. (doi:10.1093/molbev/mss075)
38. Posada D. 2008 jModelTest: phylogenetic model averaging. *Mol. Biol. Evol.* **25**, 1253–1256. (doi:10.1093/molbev/msn083)
39. Drummond AJ, Ho SYW, Phillips MJ, Rambaut A. 2006 Relaxed phylogenetics and dating with confidence. *PLoS Biol.* **4**, e88. (doi:10.1371/journal.pbio.0040088)
40. Gernhard T. 2008 The conditioned reconstructed process. *J. Theor. Biol.* **253**, 769–778. (doi:10.1016/j.jtbi.2008.04.005)
41. Oaks JR. 2011 A time-calibrated species tree of Crocodylia reveals a recent radiation of the true crocodiles. *Evolution* **65**, 3285–3297. (doi:10.5061/dryad.5k9s0)
42. Brochu CA. 2003 Phylogenetic approaches toward Crocodylian history. *Annu. Rev. Earth Planet. Sci.* **31**, 399–427. (doi:10.1146/annurev.earth.31.100901.141308)
43. Salisbury SW, Molnar RE, Frey E, Willis PMA. 2006 The origin of modern crocodyliforms: new evidence from the Cretaceous of Australia. *Proc. R. Soc. B* **273**, 2439–2448. (doi:10.1098/rspb.2006.3613)
44. Brochu CA. 2004 Patterns of calibration age sensitivity with quartet dating methods. *J. Paleontol.* **78**, 7–30. (doi:10.1666/0022-3360(2004)078<0007:POCASW>2.0.CO;2)
45. Brochu CA. 2004 Calibration age and quartet divergence date estimation. *Evolution* **58**, 1375–1382.
46. Muller J, Reisz RR. 2005 Four well-constrained calibration points from the vertebrate fossil record for molecular clock estimates. *BioEssays* **27**, 1069–1075. (doi:10.1002/bies.20286)
47. Brochu CA, Wagner JR, Jouve S, Sumrall CD, Densmore LD. 2009 A correction corrected: consensus over the meaning of Crocodylia and why it matters. *Syst. Biol.* **58**, 537–543. (doi:10.1093/sysbio/syp053)
48. Sanderson MJ. 2003 r8s: inferring absolute rates of molecular evolution and divergence times in the absence of a molecular clock. *Bioinformatics* **19**, 301–302. (doi:10.1093/bioinformatics/19.2.301)
49. Sanderson MJ. 2002 Estimating absolute rates of molecular evolution and divergence times: a penalized likelihood approach. *Mol. Biol. Evol.* **19**, 101–109. (doi:10.1093/oxfordjournals.molbev.a003974)
50. Leaché AD, Koo MS, Spencer CL, Papenfuss TJ, Fisher RN, McGuire JA. 2009 Quantifying ecological, morphological, and genetic variation to delimit species in the coast horned lizard species complex (Phrynosoma). *Proc. Natl Acad. Sci. USA* **106**, 12 418–12 423. (doi:10.1073/pnas.0906380106)
51. Ross KG, Gotzek D, Ascunce MS, Shoemaker DD. 2010 Species delimitation: a case study in a problematic ant taxon. *Syst. Biol.* **59**, 162–184. (doi:10.1093/sysbio/syp089)
52. Zhang C, Zhang D-X, Zhu T, Yang Z. 2011 Evaluation of a Bayesian coalescent method of species delimitation. *Syst. Biol.* **60**, 747–761. (doi:10.1093/sysbio/syr071)
53. Moritz CC. 1994 Defining 'evolutionarily significant units' for conservation. *Trends Ecol. Evol.* **9**, 373–375. (doi:10.1016/0169-5347(94)90057-4)
54. Inger RF. 1948 The systematic status of the crocodile *Osteoblepharon osborni*. *Copeia* **1948**, 15–19. (doi:10.2307/1438784)
55. Brochu CA. 2007 Morphology, relationships, and biogeographical significance of an extinct horned crocodile (Crocodylia, Crocodylidae) from the Quaternary of Madagascar. *Zool. J. Linn. Soc.* **150**, 835–863. (doi:10.1111/j.1096-3642.2007.00315.x)
56. Bauer AM, Watkins-Colwell GJ. 2001 On the origin of the types of *Hypsilurus godefroyii* (Reptilia: Squamata: Agamidae) and early German contributions to the herpetology of Palau. *Micronesia* **34**, 73–84.
57. Rosenberg NA, Nordborg M. 2002 Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. *Nat. Rev. Genet.* **3**, 380–390. (doi:10.1038/nrg795)
58. Uilenberg G, Thiaucourt F, Jongejan F. 2004 On molecular taxonomy: what is in a name? *Exp. Appl. Aracol.* **32**, 301–312. (doi:10.1023/B:APPA.0000023235.23090.a7)
59. DeSalle R, Egan MG, Siddal M. 2005 The unholy trinity: taxonomy, species delimitation and DNA barcoding. *Phil. Trans. R. Soc. B* **360**, 1905–1916. (doi:10.1098/rstb.2005.1722)
60. Zwickl DJ, Hillis DM. 2002 Increased taxon sampling greatly reduces phylogenetic error. *Syst. Biol.* **51**, 588–598. (doi:10.1080/10635150290102339)
61. Rosenberg MS, Kumar S. 2001 Incomplete taxon sampling is not a problem for phylogenetic inference. *Proc. Natl Acad. Sci. USA* **98**, 10 751–10 756. (doi:10.1073/pnas.191248498)
62. McAliley LR, Willis RE, Ray DA, White PS, Brochu CA, Densmore LD. 2006 Are crocodiles really monophyletic? Evidence for subdivisions from sequence and morphological data. *Mol. Phylogenet. Evol.* **39**, 16–32. (doi:10.1016/j.ympev.2006.01.012)
63. Avise JC, Mitchell D. 2007 Time to standardize taxonomies. *Syst. Biol.* **56**, 130–133. (doi:10.1080/10635150601145365)
64. Markwick PJ. 1998 Crocodilian diversity in space and time: the role of climate in paleoecology and its implications for understanding K/T extinctions. *Paleobiology* **24**, 470–497.
65. Markwick PJ. 1998 Fossil crocodilians as indicators of Late Cretaceous and Cenozoic climates: implications for using palaeontological data in reconstructing palaeoclimate. *Palaeogeogr. Palaeoclimatol. Palaeoecol.* **137**, 205–271. (doi:10.1016/S0031-0182(97)00108-9)
66. Linder HP, Hardy CR, Rutschmann F. 2005 Taxon sampling effects in molecular clock dating: an example from the African Restionaceae. *Mol.*

Phylogenet. Evol. **35**, 569–582. (doi:10.1016/j.ympev.2004.12.006)

67. Ho SYW, Phillips MJ. 2009 Accounting for calibration uncertainty in phylogenetic estimation of evolutionary divergence times. *Syst. Biol.* **58**, 367–380. (doi:10.1093/sysbio/syp035)
68. Heath TA. 2012 A hierarchical Bayesian model for calibrating estimates of species divergence times. *Syst. Biol.* **61**, 793–809. (doi:10.1093/sysbio/sys032)
69. Storrs GW. 2003 Late Miocene–Early Pliocene crocodilian fauna of Lothagam, southwest Turkana Basin, Kenya. In *Lothagam: the dawn of humanity in eastern africa* (eds MG Leakey, JM Harris), pp. 137–159. New York, NY: Columbia University Press.
70. Tchernov E. 1986 *Évolution des Crocodiles en Afrique du Nord et de l'Est*. Paris, France: Éditions du Centre National de la Recherche Scientifique.
71. Fitton JG. 1987 The Cameroon Line, West Africa: a comparison between oceanic and continental alkaline volcanism. In *Alkaline igneous rocks* (eds JG Fitton, BCG Upton), pp. 273–291. London, UK: Geological Society of London Special Publication.
72. Fitton JG, Dunlop HM. 1985 The Cameroon Line, West Africa, and its bearing on the origin of oceanic and continental alkali basalt. *Earth Planet. Sci. Lett.* **72**, 23–38. (doi:10.1016/0012-821X(85)90114-1)
73. Fjeldså J, Bowie RCK. 2008 New perspectives on the origin and diversification of Africa's forest avifauna. *Afr. J. Ecol.* **46**, 235–247. (doi:10.1111/j.1365-2028.2008.00992.x)
74. Hebert PDN, Penton EH, Burns JM, Janzen DH, Hallwachs W. 2004 Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astraptes fulgerator*. *Proc. Natl Acad. Sci. USA* **101**, 14 812–14 817. (doi:10.1073/pnas.0406166101)
75. Pfenninger M, Schwenk K. 2007 Cryptic animal species are homogeneously distributed among taxa and biogeographical regions. *BMC Evol. Biol.* **7**, 121. (doi:10.1186/1471-2148-7-121)
76. Cracraft J. 1989 Speciation and its ontology. In *Speciation and its consequences* (eds D Otte, J Endler), pp. 28–59. Sunderland, MA: Sinauer Associates.
77. Hrbek T, Vasconcelos WR, Rebelo G, Farias IP. 2008 Phylogenetic relationships of South American alligatorids and the caiman of Madeira River. *J. Exp. Zool. A, Ecol. Genet. Physiol.* **309**, 588–599. (doi:10.1002/jez.430)
78. Busack SD, Pandya S. 2001 Geographic variation in *Caiman crocodilus* and *Caiman yacare* (Crocodylia: Alligatoridae): systematic and legal implications. *Herpetologica* **57**, 294–312.
79. Venegas-Anaya M, Escobedo A, Sanjur O, Bermingham E. 2008 Cryptic species as a frame on use and conservation of *Crocodylus acutus*. In *Crocodiles: Proc. 19th Working Meeting of the Crocodile Specialist Group of the Species Survival Comission [sic] of IUCN—the World Conservation Union convened at Santa Cruz de la Sierra, Bolivia, 2–6 June 2008*, p. 167. Gland, Switzerland: IUCN. See http://www.iucncsg.org/365_docs/attachments/protarea/19th-06373596.pdf.
80. Rodriguez D, Cedeño-Vásquez JR, Forstner MRJ, Densmore LD. 2008 Hybridization between *Crocodylus acutus* and *Crocodylus moreletii* in the Yucatan Peninsula: II. Evidence from microsatellites. *J. Exp. Zool. A, Ecol. Genet. Physiol.* **309**, 674–686. (doi:10.1002/jez.499)
81. Cedeño-Vásquez JR, Rodriguez D, Calmé S, Ross JP, Densmore LD, Thorbjarnarson JB. 2008 Hybridization between *Crocodylus acutus* and *Crocodylus moreletii* in the Yucatan Peninsula: I. Evidence from mitochondrial DNA and morphology. *J. Exp. Zool. A, Ecol. Genet. Physiol.* **309**, 661–673. (doi:10.1002/jez.473)
82. Weaver JP, Rodriguez D, Venegas-Anaya M, Cedeño-Vásquez JR, Forstner MRJ, Densmore LD. 2008 Genetic characterization of captive Cuban crocodiles (*Crocodylus rhombifer*) and evidence of hybridization with the American crocodile (*Crocodylus acutus*). *J. Exp. Zool. A, Ecol. Genet. Physiol.* **309**, 649–660. (doi:10.1002/jez.471)
83. Milián-García Y *et al*. 2011 Evolutionary history of Cuban crocodiles *Crocodylus rhombifer* and *Crocodylus acutus* inferred from multilocus markers. *J. Exp. Zool. A, Ecol. Genet. Physiol.* **315**, 358–375. (doi:10.1002/jez.683)
84. Shirley MH, Oduro W, Yaokokore-Beibro H. 2009 Conservation status of crocodiles in Ghana and Côte-d'Ivoire, West Africa. *Oryx* **43**, 136–145. (doi:10.1017/S0030605309001586)
85. Shirley MH. 2010 Slender-snouted Crocodile *Crocodylus cataphractus*. In *Crocodiles: status survey and conservation action plan* (eds SC Manolis, C Stevenson), pp. 54–58. Darwin, Australia: Crocodile Specialist Group.
86. Sangster G. 2009 Increasing numbers of bird species result from taxonomic progress, not taxonomic inflation. *Proc. R. Soc. B* **276**, 3185–3191. (doi:10.1098/rspb.2009.0582)