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Genetic and Morphometric Support for the Atlantic Pygmy Devil Ray, *Mobula hypostoma* (Bancroft, 1831), in the Eastern Atlantic Ocean

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ABSTRACT

Manta and devil rays are a diverse group of globally endangered elasmobranchs with a complicated taxonomic history. The emergence of genomic techniques has significantly improved our understanding of species units in the group, yet there is one species of devil ray for which uncertainty remains. *Mobula rochebrunei* (Vaillant, 1879), a pygmy devil ray inhabiting tropical waters of the eastern Atlantic, was recently synonymised with *Mobula hypostoma* (Bancroft, 1831), its western Atlantic counterpart. However, since there have been no sightings of the species in West and Central Africa for several decades, the revision was based on limited data, and further investigation was recommended. A dedicated monitoring effort in Cameroon recently led to the rare discovery of three pygmy devil rays, providing a unique opportunity to build on recent work. We use a combination of MinION sequencing and morphometric analysis to provide confirmation that pygmy devil rays on both sides of the Atlantic constitute the same species. Crucially, our work highlights the persistence of pygmy devil rays in West Africa despite concerns of disappearance and emphasises the need for urgent conservation action to avoid local extinction.

1 | Introduction

Manta and devil rays (Mobulidae) are a charismatic yet highly vulnerable group of elasmobranchs (Dulvy et al. 2014; Croll et al. 2016; Lawson et al. 2017). Widespread overexploitation (Ward-Paige, Davis, and Worm 2013; O'Malley et al. 2016) combined with low fecundity and late maturity (Notarbartolo di Sciara 1988; Couturier et al. 2012; Rambahiniarison et al. 2018; Stewart et al. 2018) have led to worrying population declines across the globe (E. R. White et al. 2015; Moazzam 2018; Fernando and Stewart 2021; Carpenter et al. 2023). Furthermore, due to morphological similarities across species, the Mobulidae family has been plagued with taxonomic uncertainties for centuries (Bonnaterre 1788; Walbaum 1792;

Notarbartolo di Sciara 1987; W. T. White et al. 2018; Hosegood et al. 2020). This has hindered the development of effective conservation management, which relies heavily on delineation of meaningful biological units. Fortunately, analytical and technological advances—particularly in DNA sequencing and phylogenomics—have vastly improved species classification pipelines and a suite of recent studies have brought significant clarity to the taxonomic status of devil rays (Adnet et al. 2012; Poortvliet et al. 2015; Hinojosa-Alvarez et al. 2016; W. T. White et al. 2018; Hosegood et al. 2020; Notarbartolo di Sciara, Stevens, and Fernando 2020; Notarbartolo di Sciara, Adnet et al. 2020).

Uncertainty remains around the existence of one species of pygmy devil ray in the eastern Atlantic Ocean. Until recently, the East Atlantic pygmy devil ray (*Mobula rochebrunei*; Vaillant 1879) was considered distinct from the West Atlantic pygmy devil ray (*Mobula hypostoma*; Bancroft, 1831) on the basis of morphometric and dentition differences observed between specimens (Notarbartolo di Sciara 1987). Analysis of genetic data has since brought this into question, with a recent study concluding *M. rochebrunei* should be considered a junior synonym of *M. hypostoma* (W. T. White et al. 2018). Yet, both studies were constrained by small sample sizes and acknowledged the need for further investigation. Moreover, W. T. White et al. (2018) made use of a publicly available *Mobula hypostoma cf. rochebrunei* mitogenome of what had been until then considered *M. rochebrunei*, which originates from a degraded voucher specimen and as a result is only partially assembled (Poortvliet et al. 2015). Attempts to generate additional genetic data based on the same voucher specimen have been unsuccessful (W. T. White et al. 2018; Hosegood et al. 2020).

Further exploration of mobulid diversity in West and Central Africa is therefore recognised as a high research priority to avoid under- or over-estimating perceived extinction risk (Stewart et al. 2018; Hosegood et al. 2020). However, generating new data has been challenging due to a scarcity of *M. hypostoma* sightings in African waters. Elasmobranchs along the coast of West and Central Africa are disproportionately threatened with extinction due to high levels of fishing activity (Dulvy et al. 2021; Seidu et al. 2022; Doherty et al. 2023). Together, this has led to increasing concern that *M. hypostoma* in African waters may be on the verge of local depletion. In response to this conservation need, a collaborative effort by the Manta Trust and the African Marine Mammal Conservation Organisation (AMMCO), through AMMCO's SIREN citizen science network of fishers, recently led to the discovery of three *M. hypostoma* individuals in Cameroon fish markets (Figure 1). These specimens are the first to be collected since the 1960s (Cadenat 1960) and provide a unique opportunity to build on current knowledge. Here, we use a new mitogenome sequence together with morphometric data to investigate the status of *M. hypostoma* in the eastern Atlantic. We discuss our findings in the context of past work and make recommendations for future research and management.

2 | Materials and Methods

2.1 | Specimen Sampling

Between 2019 and 2022, three *M. hypostoma* individuals (Figure 1) were reported in two fish landing sites in Cameroon by fishers of the SIREN citizen science network. SIREN is a mobile application that allows fishers and other users to report opportunistic sightings of marine wildlife. The two landing sites were located in the city of Kribi and included Londji (lat 3.1° N, long 9.9° E) and Boamanga (lat 2.9° N, long 9.9° E).

The individuals were accidentally captured in bottom-set gillnets and brought to the fish markets for sale. Morphometric measurements (see below) and tissue samples were collected from all three individuals. Samples were preserved in vials containing 95% ethanol then shipped to the University of Edinburgh. Samples were collected under research permit 000103/MINRESI/B00/C00/C10/C13 and exported under CITES permit 0923/P/MINFOF/SG/DFAP/SDVEF/SC.

Between 2013 and 2015, 56 *M. hypostoma* individuals were caught in the vicinity of Sarasota Bay, Florida, USA, between north Longboat Key (lat 27.4° N, long −82.7° W) and south Siesta Key (lat 27.2° N, long −82.5° W). Individuals were captured with a nylon seine net for medium to large rays or a cast net for small rays. In-water assistance was provided by one or two snorkellers to transfer them to the vessel's live well where morphometric measurements (see below) were taken prior to release. Dorsal and ventral views of a selection of these rays are presented in Figure 2, while Figure 3 illustrates morphological details of specimens from both Florida and Cameroon. All live animal handling procedures were conducted under Florida Protected Species permits SAL-13-1140-SRP, SAL-14-1140-SRP, SAL-15-1140-SRP, and approved through Mote Marine Laboratory's IACUC permits 13-09-KBH2, 14-09-KBH2 and 15-09-KBH2.

2.2 | DNA Extraction and ONT Library Preparation

Genomic DNA was extracted from the muscle tissue of one Cameroon individual using the Qiagen DNeasy Blood and Tissue Kit following manufacturers' protocols. DNA concentration was determined using a Qubit 3.0 Broad Range Assay. A genomic library was then prepared for genome skimming following ONT's ligation sequencing gDNA protocol (SQL-LSK112) with minor modifications. Briefly, ~1 μg DNA was adjusted to a volume of 48 μL using nuclease-free water. End-repair was then carried out using the NEBNext Companion Module for Oxford Nanopore Technologies Ligation Sequencing (E7180S). For this, 48 μL DNA was combined with 3.5 μL DNA Repair Buffer, 2 μL DNA Repair Mix, 3.5 μL Reaction Buffer and 3 μL Enzyme Mix and incubated at 20°C for 10 min followed by 65°C for 10 min. Next, 108 μL Ampure XP Beads were added for clean-up, and DNA was eluted in 62 μL of nuclease free water, 2 μL of which was used for DNA quantification. We then carried out adaptor ligation by adding 25

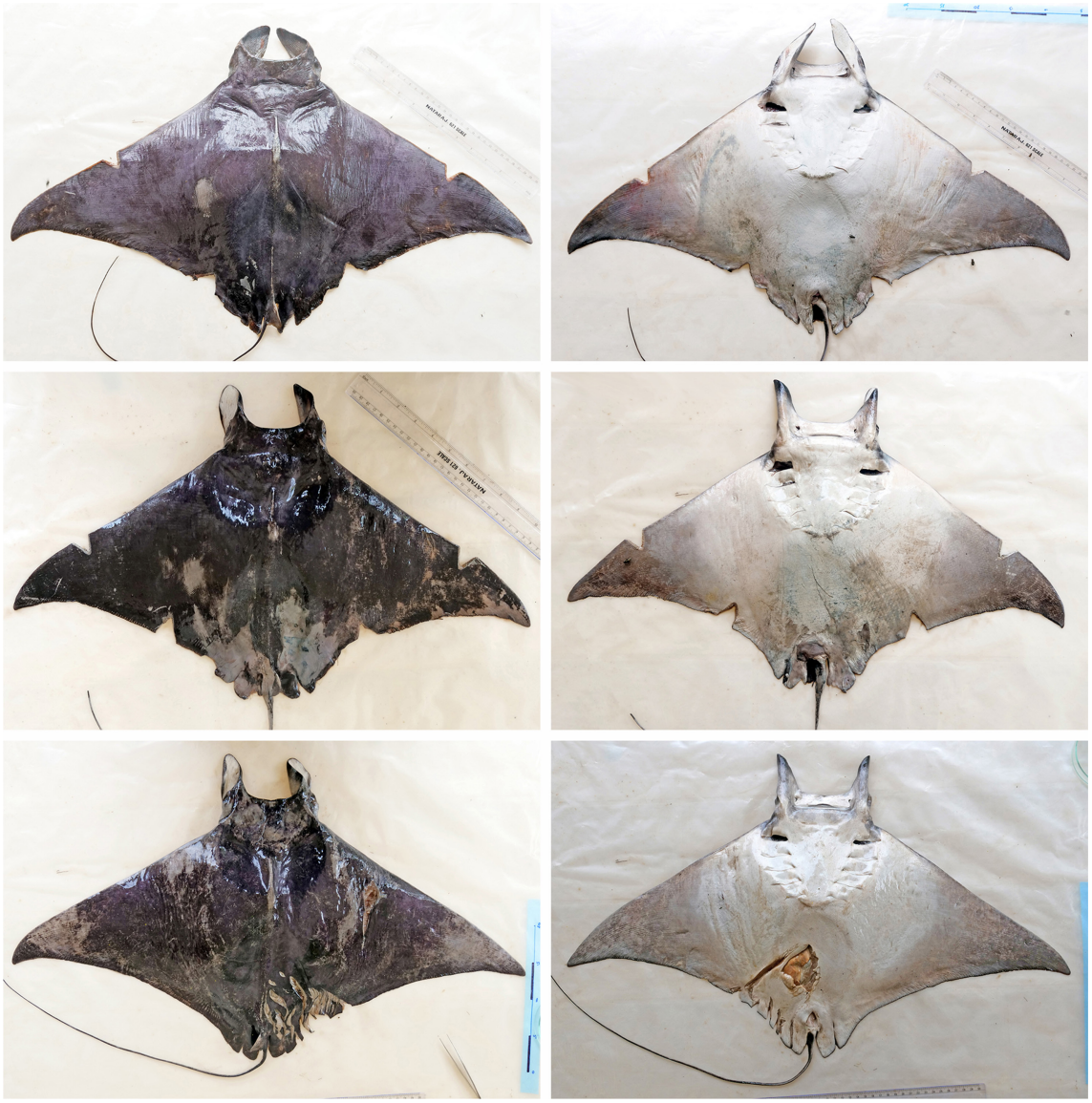

FIGURE 1 | Dorsal and ventral views of the three juvenile *Mobula hypostoma* specimens sampled in Cameroon. Note the darker colouration and the absence of a dorsal head collar compared to the live individuals examined in Florida (Figure 2), which result from post-mortem colouration changes. Photo @ Simon Hilbourne.

μL Ligation Buffer, 10 μL NEBNext Quick T4 DNA Ligase and 5 μL Adapter Mix H before incubation at room temperature for 10 min. Adaptor-ligated DNA was cleaned up by adding 180 μL Ampure XP Beads and washed twice with 250 μL short fragment buffer (SFB). Purified DNA was then resuspended in 16 μL elution buffer (EB), incubated for 20 min at room temperature and then pelleted, retaining 15 μL of eluate.

2.3 | ONT Sequencing and Basecalling

The resulting library was sequenced on one flow cell (FLO-MIN112) using a MinION device. The flow cell was first primed with 800 μL priming mix, followed by a further 200 μL 5 min later. The DNA library (13 μL) was combined with 37.5 μL Sequencing Buffer II (SB11) and 25.5μL Loading Beads II (LBII) and then loaded onto the flow cell via the sample port. Sequencing runtime was set to 18 h, and the resulting data were basecalled using Guppy v6.3.8 in High Accuracy Mode. Quality was assessed using MinIONQC (Lanfear et al. 2019) and ONT adapters removed, and sequences trimmed using Porechop. The resulting data were concatenated for downstream analysis.

2.4 | Mitogenome Assembly and Phylogenetic Analysis

Mitochondrial reads were identified from the sequencing data using mtblaster (Franco-Sierra and Díaz-Nieto 2020) in which the publicly available *Mobula alfredi* mitogenome (GenBank ID: OP562409.1, Whitney, Coleman, and Deakos 2023) was used as a reference. Mitogenome assembly was then performed on the mitochondrial reads using the de novo assembler Flye v2.9.2 (Kolmogorov et al. 2019), specifying a minimum overlap between reads of 1000, an asm coverage of 40 and an estimated genome size of 18 kb. By convention, mitochondrial genomes

FIGURE 2 | Dorsal and ventral views of live, juvenile *Mobula hypostoma* individuals in Sarasota, Florida. Note the lighter colouration and the presence of a dorsal head collar compared to the deceased individuals examined in Cameroon (Figure 1), which displayed post-mortem colouration changes. Photo @ Kim Bassos-Hull.

are reported as linear assemblies starting at the tRNA-phe gene. However, this was not the case for our resulting mitogenome because Flye initiates a random start point. We therefore used MUMmer v3.23 to align our assembly to the *M. alfredi* mitogenome and identify the correct start and end points. We then used samtools v1.9 to split and rearrange the assembly at these locations. The resulting genome was annotated using MITOS (Bernt et al. 2013).

We next downloaded mitogenome sequences for 10 additional devil ray species from GenBank (Table S1) to be included in the phylogenetic analysis. This included the mitogenome derived from the holotype specimen of *M. rochebrunei* (Poortvliet et al. 2015). We also obtained a mitogenome from a bat eagle ray (*Myliobatis californica*) to use as an outgroup. While species misidentification of openly available sequence data can occur (Locatelli et al. 2020), the mitogenomes used here originated from samples collected by experts in ray identification and therefore we can be confident of their species assignment. All 12 mitogenomes were aligned using the MUSCLE v3.8.425 (Edgar 2004) plugin in Geneious Prime. We then identified the protein-coding genes, tRNAs and rRNAs from the alignment using the *M. alfredi* annotation as a reference. These were extracted and concatenated into a separate alignment. We then used PartitionFinder2 to evaluate the best partitioning scheme and the best nucleotide substitution model for each partition (Lanfear et al. 2017). For this, the mitogenome alignment was divided into 63 pre-defined blocks: 13 protein coding genes, each divided into first, second and third codon positions (39 total); 22 tRNAs; and two rRNAs (Table S2). PartitionFinder2 was then run using linked branch lengths, the greedy algorithm, and Bayesian Information Criterion (BIC) for model selection. We then used IQ-TREE (Nguyen et al. 2015) to

FIGURE 3 | Close-up photographs of juvenile *Mobula hypostoma* specimens from Florida (left) and Cameroon (right). Photo @ Kim Bassos-Hull and Simon Hilbourne.

perform maximum likelihood (ML) phylogenetic analysis, implementing the best-fitting model from PartitionFiinder2 for each partition. Ultra-fast bootstrap approximation was used to generate branch support values. The resulting phylogenetic tree was visualised using FigTree.

2.5 | Morphometric Analysis

To complement the genetic analysis, standardised morphometric measurements from the sample of three juvenile specimens from Cameroon were compared with the sample

TABLE 1 | Standardised morphometric measurements of juvenile *Mobula hypostoma* specimens from Cameroon (3) and Florida (56) in thousandths of disc width.

Origin	ID	Sex	Disc width (mm)	Disc length	Cephalic fin length	Cranial width
Cameroon	Mr1	F	680	486.8	123.5	170.6
	Mr2	M	598	501.7	128.8	187.3
	Mr3	F	687	528.4	120.8	173.2
Florida	Mh020	M	770	506.5	119.5	181.8
	Mh021	M	795	503.1	123.3	168.6
	Mh022	M	780	493.6	124.4	179.5
	Mh023	F	825	482.4	117.6	181.8
	Mh024	M	730	534.2	123.3	178.1
	Mh031	F	786	534.4	127.2	188.3
	Mh032	F	790	508.9	126.6	189.9
	Mh033	M	829	499.4	89.3	183.4
	Mh034	F	820	536.6	85.4	207.3
	Mh035	M	800	537.5	100.0	175.0
	Mh036	M	855	502.9	81.9	175.4
	Mh037	M	790	525.3	75.9	183.5
	Mh038	M	658	538.0	121.6	200.6
	Mh039	M	750	533.3	125.3	186.7
	Mh040	M	826	513.3	125.9	181.6
	Mh041	F	728	505.5	96.2	186.8
	Mh042	M	748	534.8	133.7	187.2
	Mh043	F	638	548.6	150.5	203.8
	Mh044	F	692	528.9	115.6	190.8
	Mh045	F	726	523.4	124.0	192.8
	Mh046	F	820	524.4	134.1	175.6
	Mh047	F	724	538.7	132.6	196.1
	Mh048	F	748	508.0	120.3	189.8
	Mh049	M	770	532.5	129.9	194.8
	Mh050	F	751	532.6	133.2	197.1
	Mh051	F	780	525.6	128.2	189.7
	Mh052	M	816	519.6	129.9	203.4
	Mh053	F	790	516.5	124.1	207.6
	Mh054	M	760	505.3	123.7	210.5
	Mh055	F	775	410.3	122.6	206.5
	Mh056	M	818	526.9	124.7	193.2
	Mh057	M	847	517.1	115.7	183.0
	Mh058	M	748	513.4	123.0	207.2
	Mh059	F	762	519.7	127.3	189.0
	Mh061	F	800	520.0	117.5	193.8
	Mh062	F	810	549.4	118.5	204.9

(Continues)

TABLE 1 | (Continued)

Origin	ID	Sex	Disc width (mm)	Disc length	Cephalic fin length	Cranial width
	Mh063	M	741	531.7	126.9	197.0
	Mh064	F	796	522.6	126.9	189.7
	Mh065	F	810	529.6	128.4	202.5
	Mh066	M	773	518.8	122.9	194.0
	Mh067	M	811	504.3	124.5	191.1
	Mh068	M	828	509.7	126.8	193.2
	Mh069	M	846	514.2	126.5	189.1
	Mh070	F	800	522.5	132.5	175.0
	Mh071	F	862	540.6	127.6	178.7
	Mh077	M	884	524.9	122.2	194.6
	Mh079	F	780	525.6	115.4	176.9
	Mh080	F	780	523.1	130.8	192.3
	Mh081	M	736	516.3	135.9	176.6
	Mh082	F	740	527.0	121.6	181.1
	Mh083	M	806	491.3	121.6	188.6
	Mh084	M	760	526.3	128.9	184.2
	Mh085	F	968	533.1	124.0	179.8
	Mh086	F	964	543.6	130.7	190.9
	Mh087	F	758	496.0	121.4	184.7
	Mh088	F	904	513.3	123.9	179.2

of 56 juvenile *M. hypostoma* collected from Florida. Not all measurements were available for the Florida specimens and therefore only the following variates were included in the comparison: disc width (DW), disc length (DL), cranial width (CW) and cephalic fin length (CFL). Following Notarbartolo di Sciara (1987) and to minimise bias based on size and measurement variability across the two samples, we converted raw values into three proportional variates: DL/DW, CW/DW and CFL/DW, where thousandths of DW was used as the denominator (Table 1). The full standardised measurements of the Cameroon specimens are available in the Supporting Information.

We then used two complementary approaches to compare the proportional measurements. First, we ran three linear models to explore the effect of sample origin on morphology with each morphometric measurement as the response variable and sample origin as the predictor variable. Second, using the MASS package in R (Venables and Ripley 2002), we implemented non-metric multidimensional scaling (NMDS) based on a matrix of pairwise Bray–Curtis similarity values to visualise the morphometric data. This dimensionality reduction approach places individual data points into 2D space where individuals that are morphometrically more similar are closer together. Differences between the two samples were compared using non-parametric ANOSIM based on 1000 permutations of the dataset with the R package vegan (Dixon 2003).

3 | Results

3.1 | Mitogenome Sequencing and Analysis

MinION sequencing yielded 7.14 million reads totalling 4.95 Gb of basecalled data with an N50 length of 967 bp and a mean length of 692 bp. Of these, 1927 were identified as originating from the mitochondria and were successfully assembled into a complete mitochondrial genome sequence with a total length of 18,006 bp and a mean coverage of 93X. Annotation with MITOS identified all 37 mitochondrial genes comprising 13 protein coding genes, 22 tRNAs and two rRNAs.

To infer relationships among devil ray species we carried out maximum likelihood phylogenetic analysis. The best-fit partitioning scheme and nucleotide substitution models as determined by PartionFinder2 are provided in Table S3. Recognised species groups all formed well supported clades with a tree topology largely in line with previous work based on nuclear data (Hosegood et al. 2020, W. T. White et al. 2018, Figure 4). The Cameroon sample clusters most closely with *M. hypostoma* where the two mitogenomes share 99.9% sequence similarity across the aligned protein coding region of 15,723 bp. This represents the highest similarity score for any of the pairwise species comparisons (Table S4). Furthermore, at widely used species barcoding genes COI, cyt-B and ND4, there was zero, one and one base pair difference, respectively.

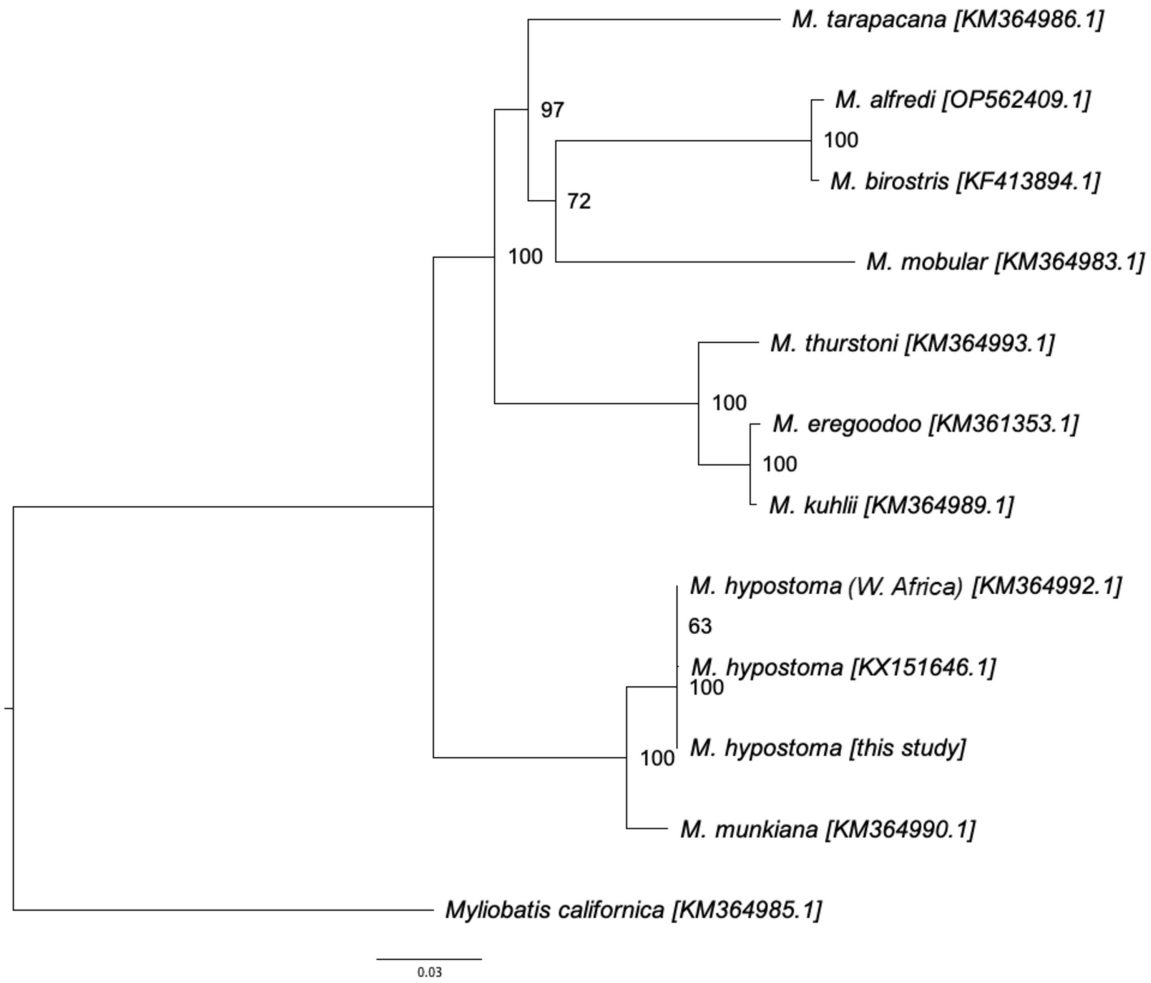

FIGURE 4 | Maximum likelihood tree of devil ray mitogenomes based on a 15,723 bp alignment of mitochondrial genes. Genbank IDs for each mitogenome are provided in square brackets. Node values indicate ultrafast bootstrap percentage support as estimated using IQTREE.

For comparison, recognised sister species *M. alfredi* and *M. birostris* and *M. eregoodoo* and *M. kuhlii* share 99.4% and 99.5% sequence similarity, respectively. Taken together, these findings suggest that the Cameroon sample and *M. hypostoma* are conspecific.

3.2 | Morphometric Analysis

To investigate morphometric differences between samples, we compared three proportional variates across individuals. The average raw DW, DL, CW and CFL measures across all samples were 782.6 mm (min = 598 mm, max = 968 mm), 407.1 mm (min = 300 mm, max = 524 mm), 147.4 mm (min = 112 mm, max = 184 mm) and 95.1 mm (min = 60 mm, max = 126 mm), respectively. Comparison of proportional measurements DL/DW and CFL/DW revealed no significant difference between sample origin (DL/DW: ß = 15.38, 95% CI = −2.42 to 33.2, $p = 0.09$; CFL/DW: ß = −2.75, 95% CI = −18.5 to 13.0, $p = 0.73$, Figure 5A,B). Comparison of CW/DW revealed a weakly significant difference between sample origins (ß = 12.0, 95% CI = 0.41–23.6, $p = 0.04$, Figure 5C). In line with this, NMDS analysis of the associated proportional measurements revealed no clear distinction between the two sample origins, with all samples from Cameroon clustering with those from Florida (Figure 5D) with no significant difference detected between sample origins (ANOSIM: global $R = 0.15$, $p = 0.19$).

4 | Discussion

Genome skimming of a newly acquired pygmy devil ray sample from West Africa provides further confirmation that *M. rochebrunei* should be considered synonymous with *M. hypostoma* on the basis of mitogenome sequence similarity. This result was corroborated by comparison of novel morphometric data, in which no significant differences were observed between specimens from the eastern versus western Atlantic. These findings support recent taxonomic changes (W. T. White et al. 2018; Marshall et al. 2022) and provide a baseline for future work on intraspecific variation in *M. hypostoma*.

The high sequence similarity observed in this study between *M. rochebrunei* and *M. hypostoma* mitogenomes is a similar order of magnitude to that reported by W. T. White et al. 2018. Nonetheless, our findings represent an important contribution since they provide an independent line of evidence based on an alternative sequencing technology and a novel sample. In doing so, they highlight the benefits of MinION sequencing for biodiversity assessment and clarify any ambiguity arising from

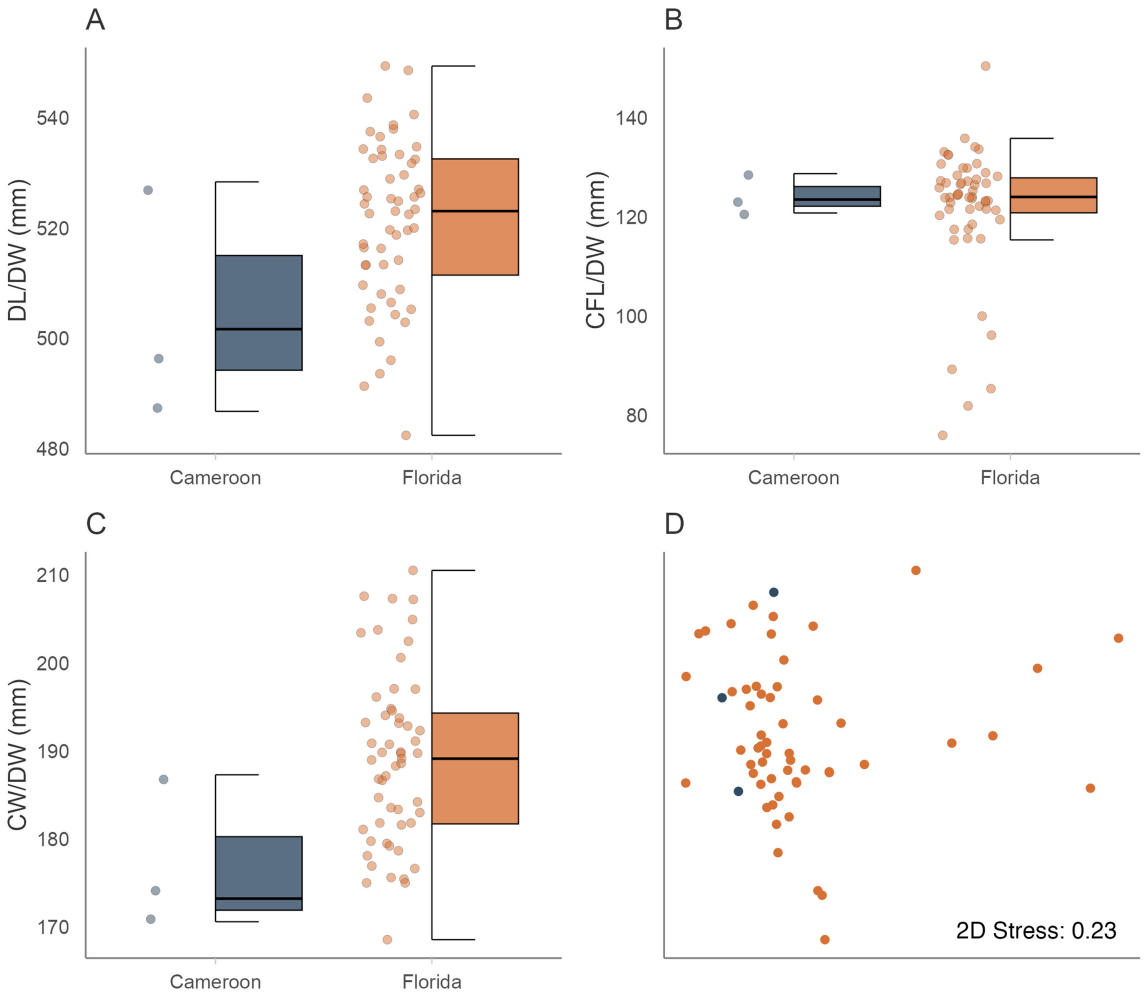

FIGURE 5 | Distribution of proportional measurements (A) Disc Length/Disc Width, (B) Cephalic Fin Length/Disc Width, (C) Cranial Width/Disc Width across sampling origins Cameroon ($n = 3$) and Florida ($n = 56$). Centre lines of boxplots reflect the median, bounds of the boxes extend from the first to the third quartiles and upper and lower whiskers reflect the largest and smallest values but no further than 1.5 * the interquartile range from the hinge. (D) Two-dimensional non-metric multidimensional scaling (NMDS) plot based on proportional measurements DL/DW, CFL/DW and CW/DW from samples originating from Cameroon (blue) and Florida (orange). The closer the samples appear on the plot, the more similar their proportional measurements are.

the original mitogenome sequence being partially complete. However, like with previous studies, we were not able to perform a comparison using nuclear data. Complementary work on two recently synonymised mobulid species *M. mobular* and *M. japanica* (now considered a junior synonym of *M. mobular*) suggest that nuclear data would only strengthen our findings (Bustamente et al. 2016). In particular, sequence similarity between mitogenomes was 99.9%, identical to that observed in our study between *M. rochebrunei* and *M. hypostoma* (Bustamante et al. 2016). Further analysis of nuclear SNPs, exons and NADH2 went on to identify only subtle genetic differences within the limits of that observed in single species (W. T. White et al. 2018; Hosegood et al. 2020). With this in mind, we would expect nuclear data from *M. rochebrunei* to result in the same conclusion: that *M. rochebrunei* and *M. hypostoma* are conspecific.

Previous morphometric assessments concluded that *M. hypostoma* and *M. rochebrunei* were distinct based on a suite of characteristics (Notarbartolo di Sciara 1987). In contrast, the morphometric comparison presented here reveals no distinguishing features between the two groups. While the former study had access to a larger number of measurements, these were obtained several decades ago and by different investigators, which may have introduced inconsistencies and artefacts into the data. For example, historical *M. rochebrunei* measurements included those from both the stuffed holotype and fresh specimens (Cadenat 1960), for which notable variation was apparent (Notarbartolo di Sciara 1987). While we acknowledge that our morphometric analysis remains constrained by a small and unbalanced sample size, we made use of a more comparable set of samples where measurements were taken using standardised procedures. It is possible that a larger dataset would recapture differences between the groups, yet it is worth noting that subtle variation is compatible with intraspecific divergence and local adaptation (e.g. in *M. mobular*: Notarbartolo di Sciara, Stevens, and Fernando 2020). Since it is unlikely for a larger number of eastern Atlantic specimens to become available in the foreseeable future, we believe our results represent the most reliable morphometric evidence to date for one species of pygmy devil ray in the Atlantic.

The presence of a single species on opposite sides of the Atlantic Ocean raises interesting questions about connectivity and population structure. Frequent dispersal between the western and eastern Atlantic is unlikely for a coastal pygmy devil ray which is primarily found over the continental shelf. Instead, sporadic dispersal events may take place via oceanic islands, maintaining a level of gene flow sufficient to preserve the species unit. However, there are few islands within the latitudinal range of the species that could serve as stepping stones, and *M. hypostoma* has not been reported at those where mobulid rays are closely monitored (Sobral and Afonso 2014; Vaske et al. 2005; Beard et al. 2021; Bucair et al. 2024). Alternatively, Eastern and Western populations may in fact be genetically isolated and undergoing incipient speciation. The strength of population differentiation arising from each scenario will depend on several factors including the timing of any population split, ancestral population size and contemporary rates of gene flow. Signals of population structure vary widely across mobulids (Hosegood et al. 2020; Humble et al. 2024) and further analysis using a combination of genome-wide data and satellite tagging will shed important light into the population and evolutionary dynamics of *M. hypostoma*.

Although the presence of pygmy devil rays in the eastern Atlantic was recently documented for the first time in 60 years (Doherty et al. 2023; de Boer, Wieczorek, and Notarbartolo di Sciara 2024), our study is the first in which specimens could be inspected at close quarters, measured, and sampled for genetic analyses. This has important implications for management in a region where illegal, unreported and unregulated fishing pressure is high (Agnew et al. 2009). Although we do not provide evidence for separate populations, we cannot confirm their absence based on mitogenome and morphometric data alone, and therefore strongly recommend the species be considered to comprise two management units. This is due to the incredibly low frequency of sightings in West and Central Africa—indicative of a small and declining population—together with the fact that demographic connectivity between the eastern and western Atlantic seems unlikely. Furthermore, it is possible that the eastern Atlantic population emerged via dispersal of individuals from the West. If this were the case, *M. hypostoma* in West and Central Africa are likely to have lower genetic variation and adaptive potential due to associated founder effects (Le Corre and Kremer 1998). Genomic analysis of nuclear markers will provide the opportunity to explore this hypothesis in detail. In the meantime, our study provides further support for the recent synonymisation of *M. hypostoma* and *M. rochebrunei* and highlights the pressing need for conservation action along the West and Central African coast to prevent local extinction of a unique and highly vulnerable species.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Standardised morphometric measurements of the Cameroon specimens are available in the Supporting Information. The mitogenome sequence has been deposited on NCBI under accession number PQ760241.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section.