

Mitochondrial DNA Part B Resources

ISSN: (Print) (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

The complete mitochondrial genomes of the flapper skate *Dipturus intermedius* and the longnose skate *Dipturus oxyrinchus*

Tanja N. Schwanck, Aurelien N. Delaval, Leslie R. Noble, Peter J. Wright, David W. Donnan & Catherine S. Jones

To cite this article: Tanja N. Schwanck, Aurelien N. Delaval, Leslie R. Noble, Peter J. Wright, David W. Donnan & Catherine S. Jones (2022) The complete mitochondrial genomes of the flapper skate *Dipturus intermedius* and the longnose skate *Dipturus oxyrinchus*, Mitochondrial DNA Part B, 7:5, 897-899, DOI: [10.1080/23802359.2022.2064248](https://doi.org/10.1080/23802359.2022.2064248)

To link to this article: <https://doi.org/10.1080/23802359.2022.2064248>



© 2022 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 26 May 2022.



Submit your article to this journal [↗](#)



Article views: 304



View related articles [↗](#)



View Crossmark data [↗](#)

The complete mitochondrial genomes of the flapper skate *Dipturus intermedius* and the longnose skate *Dipturus oxyrinchus*

Tanja N. Schwanck^a, Aurelien N. Delaval^b, Leslie R. Noble^b, Peter J. Wright^c, David W. Donnan^d and Catherine S. Jones^a

^aSchool of Biological Sciences, University of Aberdeen, Aberdeen, UK; ^bFaculty of Biosciences and Aquaculture, Nord University, Bodø, Norway; ^cMarine Scotland Science, Marine Laboratory, Aberdeen, UK; ^dNatureScot, Perth, UK

ABSTRACT

We describe the complete mitochondrial genomes of the flapper skate *Dipturus intermedius* (Parnell 1837) and the longnose skate *Dipturus oxyrinchus* (Linnaeus 1758), which have been obtained by Sanger sequencing. We report the length of the sequences to be 16,906 and 16,911 bp, respectively. The length and structure of gene regions, containing 13 protein-coding regions, 22 tRNA genes, two rRNA genes, and two non-coding areas, resemble those of related skate species. Despite *D. intermedius* being considered a cryptic species with *D. batis*, the full mitogenomes confirm that *D. intermedius* and *D. oxyrinchus* are more genetically similar. In comparison to other *Dipturus* species, *D. intermedius* is missing a whole codon in its cytochrome oxidase subunit 2 gene. These mitogenomes will be a useful resource furthering investigation of the population genetic differences and evolutionary history of skate species.

ARTICLE HISTORY

Received 17 February 2022
Accepted 2 April 2022

KEYWORDS

Dipturus intermedius;
Dipturus oxyrinchus; flapper skate; common skate;
Dipturus batis; mitogenome

In the Northeast Atlantic, several skate species (family Rajidae) play an important role in fisheries. They make up more than 40% of elasmobranch landings, most from the North Sea and Celtic Sea (Ellis et al. 2008). Though the vulnerability of skate species has been widely recognized, conservation efforts are hindered by reoccurring taxonomic confusion (Dulvy et al. 2000; Iglésias et al. 2010). Recently, the common skate *Dipturus batis* was shown to be two distinct species, now called the blue skate *Dipturus batis* (previously *D. cf. flossada*) and the flapper skate *Dipturus intermedius* (previously *D. batis* and *D. cf. intermedia*) (Griffiths et al. 2010; Last et al. 2016). Phylogenetic analysis based on short mitochondrial markers showed these two species were not the most closely related taxa, instead the longnose skate *Dipturus oxyrinchus* is included in the clade as a sister species to *D. intermedius* (Iglésias et al. 2010).

To contribute to the knowledge of genetic differences between these commonly confused closely related species, we complement the already described mitogenome of the blue skate *D. batis* (Delaval et al. 2020) with full mitochondrial genomes of the flapper skate *D. intermedius* and the longnose skate *D. oxyrinchus*. Fin clips were collected of *D. intermedius*, north coast of Scotland (59° 13' 51.6"N, 3° 29' 49.1994"W) during a Marine Scotland Science survey under UK Home Office License, and of *D. oxyrinchus*, Norway (61° 29' 17.052"N, 5° 16' 23.7174"E) during a University of Bergen research cruise, which are now deposited in the Natural History Museum London (accession numbers

NHMUK014943803 and NHMUK014943802, respectively, contact Jackie Mackenzie-Dodds j.mackenzie-dodds@nhm.ac.uk). No further ethical permissions were required for this study. Species identifications were based on morphological characteristics (Iglésias et al. 2010) and confirmed by genetic barcoding. Genomic DNA was extracted using a phenol–chloroform extraction method (Sambrook et al. 1989). Based on mitochondrial genomes accessible on GenBank (KF318309; KR152643; MF278961), universal primers for the genus *Dipturus* were designed in Geneious V. 11.1.5 (Kearse et al. 2012) using Primer3 V. 2.3.7 to amplify 23 overlapping fragments. PCR products were purified with the QIAquick PCR Purification Kit (Qiagen, Hilden, Germany) and Sanger sequenced (Genewiz, Essex, UK). Resulting sequences were trimmed and mapped against the mitochondrial genome of *D. kwangtungensis* as a reference (KF318309) in Geneious V. 11.1.5 (Kearse et al. 2012). Between 32 and 35 sequences were assembled for full high-quality coverage of each mitogenome and a consensus sequence generated. Regions of the mitochondrial genome were annotated with reference to available mitochondrial genomes.

The assembled products produced a consensus sequence of 16,906 bp in *D. intermedius* (MT890688) and 16,911 bp in *D. oxyrinchus* (MT890691), the mitogenomes resembling those of other *Dipturus* species in size and gene order (Vargas-Caro et al. 2016; Delaval et al. 2020). Like other *Dipturus* relatives, they contain 13 protein-coding regions, 22 tRNA genes, two rRNA genes, and two non-coding areas (control region and

CONTACT Catherine S. Jones  c.s.jones@abdn.ac.uk  School of Biological Sciences, University of Aberdeen, Aberdeen, UK

© 2022 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

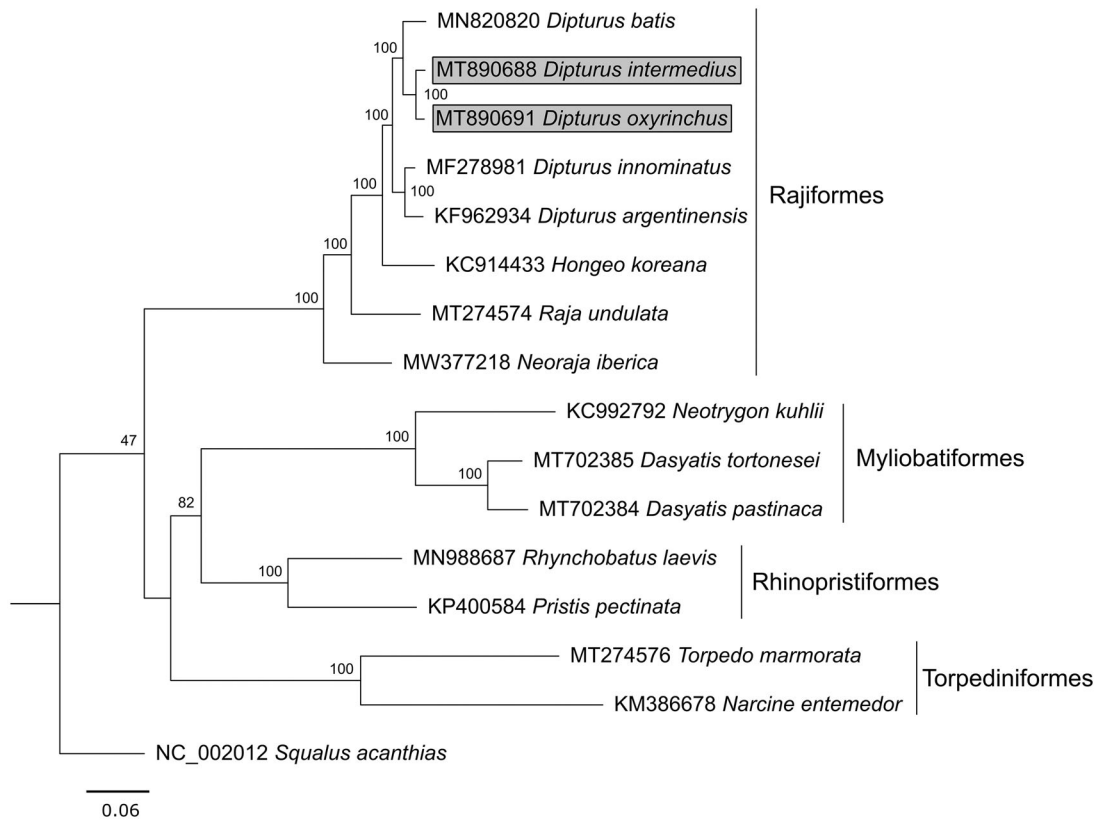


Figure 1. Phylogenetic tree of *Dipturus intermedius* and *D. oxyrinchus* (highlighted with gray background), 13 other batoid species and the spiny dogfish *Squalus acanthias* as outgroup, inferred from complete mitogenomes. Scale bar shows the number of substitutions, node labels display bootstrap support in percent.

the origin of L-strand replication). Nucleotide frequencies in both species were very similar, with the mitogenome of *D. intermedius* consisting of 29.9% A, 26.8% C, 14.4% G, and 28.9% T (G + C composition of 41.2%) and that of *D. oxyrinchus* 29.9% A, 26.9% C, 14.5% G, and 28.8% T (G + C composition of 41.3%). *D. intermedius* has the shortest mitochondrial genome among published sequences of *Dipturus* skates, missing one codon (GAA, glutamic acid) in the cytochrome oxidase subunit 2 gene compared with other species in the genus, while all other genes are of the same length as in other skate species. Phylogenetic reconstruction based on the maximum-likelihood method by RAxML V. 8.2.11 (Stamatakis 2014) in Geneious V. 11.1.5 (Kearse et al. 2012) under the GTR + G + I substitution model with 1000 bootstrap replicates grouped *D. intermedius* and *D. oxyrinchus* as sister taxa (Figure 1), confirming previous phylogenetic analyses based on partial mitochondrial markers (Iglésias et al. 2010; Carugati et al. 2022). Correspondingly, the mitogenome of *D. intermedius* shows a slightly higher pairwise similarity (98.45%) to *D. oxyrinchus* than to *D. batis* (96.39%). These new sequences will complement available mitogenomes of batoid species, furthering investigation of population genetic differences and diversity, taxon identification, and phylogenetics of Rajiformes, thereby supporting their conservation.

Authors contributions

Tanja N. Schwanck, Aurelien N. Delaval, Leslie R. Noble, Peter J. Wright, David W. Donnan, and Catherine S. Jones

contributed to the study conception and design. Primer design, molecular work and analysis were performed by Tanja N. Schwanck under the supervision of Catherine S. Jones. Findings were interpreted and discussed among Tanja N. Schwanck, Aurelien N. Delaval, Leslie R. Noble, Peter J. Wright, David W. Donnan, and Catherine S. Jones. The first draft of the manuscript was written by Tanja N. Schwanck. Aurelien N. Delaval, Leslie R. Noble, Peter J. Wright, David W. Donnan, and Catherine S. Jones commented on previous versions of the manuscript, and together with Tanja N. Schwanck approved the final manuscript and agree to be accountable for all aspects of the work.

Acknowledgements

We thank Martine Solås and Frank Midtøy at the University of Bergen for providing samples, Michelle Frost for genetic identification of the species, and Ceara Hayton and Tanya Gyuleva for assistance in the lab.

Disclosure statement

The authors report no conflict of interest.

Funding

This work was supported by NatureScot.

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI [<https://www.ncbi.nlm.nih.gov>] under the accession numbers MT890688 and MT890691; <https://www.ncbi.nlm.nih.gov/nuccore/MT890688.1/>; <https://www.ncbi.nlm.nih.gov/nuccore/MT890691.1/>

References

- Carugati L, Melis R, Cariani A, Cau A, Crobe V, Ferrari A, Follesa MC, Geraci ML, Iglésias SP, Pesci P, et al. 2022. Combined COI barcode-based methods to avoid mislabelling of threatened species of deep-sea skates. *Anim Conserv*. 25(1):897–52.
- Delaval A, Schwanck T, Kopp MEL, Hoarau G, Jones CS, Noble LR. 2020. The complete mitochondrial genome of the blue skate *Dipturus batis*. *Mitochondrial DNA B Resour*. 5(3):2488–2489.
- Dulvy NK, Metcalfe JD, Glanville J, Pawson MG, Reynolds JD. 2000. Fishery stability, local extinctions, and shifts in community structure in skates. *Conserv Biol*. 14(1):283–293.
- Ellis JR, Clarke MW, Corts E, Heessen HJL, Apostolaki P, Carlson JK, Kulka DW. 2008. Management of elasmobranch fisheries in the North Atlantic. In: Payne A, Cotter J, Potter T, editors. *Advances in fisheries science*. Oxford (UK): Blackwell Publishing Ltd.; p. 184–228.
- Griffiths AM, Sims DW, Cotterell SP, el Nagar A, Ellis JR, Lynghammar A, McHugh M, Neat FC, Pade NG, Queiroz N, et al. 2010. Molecular markers reveal spatially segregated cryptic species in a critically endangered fish, the common skate (*Dipturus batis*). *Proc Biol Sci*. 277(1687):1497–1503.
- Iglésias SP, Toulhoat L, Sellos DY. 2010. Taxonomic confusion and market mislabelling of threatened skates: important consequences for their conservation status. *Aquat Conserv Mar Freshw Ecosyst*. 20(3): 319–333.
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*. 28(12): 1647–1649.
- Last PR, Weigmann S, Yang L. 2016. Changes to the nomenclature of the skates (Chondrichthyes: Rajiformes). In: Last P, Naylor G, Séret B, White W, Stehmann M, de Carvalho M, editors. *Rays of the world: Supplementary information*. Melbourne: CSIRO Publishing, p. 11–34.
- Sambrook J, Fritsch EF, Maniatis T. 1989. Extraction with phenol: chloroform. In: Ford N, Nolan C, Ferguson M, editors. *Molecular cloning: a laboratory manual* 3. 2nd ed. New York: Cold Springs Harbor Press, p. E.3-E.4.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*. 30(9): 1312–1313.
- Vargas-Caro C, Bustamante C, Lamilla J, Bennett MB, Ovenden JR. 2016. The phylogenetic position of the roughskin skate *Dipturus trachyderma* (Krefft & Stehmann, 1975) (Rajiformes, Rajidae) inferred from the mitochondrial genome. *Mitochondrial DNA A DNA Mapp Seq Anal*. 27(4):2965–2966.