Genome announcements

The aim of this new contribution is provide quality descriptions of new complete mitochondrial genome(s) and other large fragments sequence fragments of fish genomes. Multiple genomes from the same genus or species are acceptable.

They should not exceed four printed pages (8,000 characters). Interest of the taxon study and its main characteristics are presented.

The sequence and annotation must be deposited (although they do not need to be released at the time of submission) in the NCBI, DDBJ or EMBL nucleotide database. The authors must provide a Genbank or BOLD accession number and the sequence must be made publicly available in these databases when the paper is published. The sequence(s) and annotation(s) must be sent with the manuscript, as well as the unassembled sequences and list of primers if applicable, and will be provided to the reviewers for control. Results of Blast search and phylogenetic analysis including all closest publicly available sequences must be included for relevant markers (COI and 12S, 16S or cytB for mitochondrial data); a phylogenetic tree for COI must be provided with the manuscript, and briefly described in the manuscript itself.

Specimen vouchers must be kept, with capture location, collection number. Unavailable vouchers or locations must be justified in the letter to the editor, and at least a photograph must be provided for the review and included in the paper. Incomplete mitogenomes might be accepted if there is a valid reason (to discuss in the letter to the editor) preventing the sequencing of a region, and the interest of the new mitogenome is otherwise high.

Please follow the guide below and *Instruction to authors*.

Title : Mitogenome/genome of species name

by

Firstname LASTNAME* (1), Firstname LASTNAME (1) Firstname LASTNAME (1) & Firstname LASTNAME (2)

(1) Address. [Email author] [Email author]

(2) Address. [Email author]

* Corresponding author

1   Characters: XX,XXX; Figs: X; Tabs: X

2

3   **Possible reviewers recommended by the authors**: 3 or 4 names and emails.

4

5   **Running title**

6   *Running title*

7

8   **Abstract**

9   Abstract in English

10

11   **French title**

12   Title in French

13   **French abstract**

14   Abstract in French

15

16   **Key words**

17   In English, 6 max

18

19   Short introduction (text only) of the interest of this new mitogenome (new mitogenome, conservation

20   status, existence of undescribed species, new gene order...)

21

22   **MATERIALS AND METHODS**

23   **Voucher(s)**

24   Collection number. Identification method, identifier.

25   **Brief material and method**

26   NGS or Sanger, long PCRs or shotgun, assembly and cleaning.

27   **Sequence quality**

How many PCRs, overlap of sequences for Sanger. Coverage (min-max-average) for NGS. Problems in the sequences.

RESULTS : SEQUENCE DESCRIPTION

Can be very brief if the gene order is the standard vertebrate order. Must include a picture if the order is different.

DISCUSSION:

Comparison to already available genomes

Phylogenetic tree with the closest relatives available in sequence databases included or at least described. Blast result briefly described for several markers (cytb, COI, 12S and 16S generally have good reference databases).

(other)

(text).

Acknowledgements

REFERENCES

(Should not exceed 8 references)

1   **Figure and Table legends**

2

3   Figure 1. - Legend.

4   Figure 2. - Legend.

5   *Etc.*

6

7   Table I. - Legend.

8   Table II. - Legend.

9   *Etc.*