MITOCHONDRIAL DNA PART B: RESOURCES, 2016
VOL. 1, NO. 1, 338–340
http://dx.doi.org/10.1080/23802359.2016.1172053

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MITOGENOME ANNOUNCEMENT

OPEN ACCESS

# The complete mitochondrial genome of *Anomaloglossus baeobatrachus* (Amphibia: Anura: Aromobatidae)

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**ABSTRACT**

The complete mitogenome of the rocket frog *Anomaloglossus baeobatrachus* was sequenced using a shotgun approach on an Illumina HiSeq 2500 platform (Illumina Inc., San Diego, CA), providing the first mitogenome for this genus. The genome was 17,572 bp long and presents the typical organization found in other neobatrachian anurans. A phylogenetic analysis including *A. baeobatrachus* and all other available mitogenomes of Hyloidea provided relationships in accordance with previous phylogenetic studies.

**ARTICLE HISTORY**
Received 23 March 2016
Accepted 25 March 2016

**KEYWORDS**
Amphibia; Aromobatidae; Guiana Shield; mitochondrial genome

*Anomaloglossus baeobatrachus* (Boistel & Massary, 1999) is a species of frog endemic to the eastern part of the Guiana Shield. It is currently known to occur in French Guiana, Suriname and the State of Amapá (Fouquet et al. 2012), and the State of Pará (Avila-Pires et al. 2010). The taxonomy of the genus *Anomaloglossus* is not well resolved, as several mitochondrial lineages currently associated with nominal species might in fact represent undescribed species (Fouquet et al. 2007, 2012; Kok et al. 2012). This is the case of *A. baeobatrachus* for which four distinct mitochondrial lineages have been identified (Fouquet et al. 2012). Molecular data can significantly contribute in resolving the systematics and species boundaries within this genus but available genomic data are still scarce. Here, we describe the complete mitochondrial genome of *Anomaloglossus baeobatrachus*.

A calling male of *A. baeobatrachus* was collected at Saint-Eugène, French Guiana (4°49′17.2″N; 53°04′03.4″W), the *terra typica* of the species (Boistel & Massary, personal communication). DNA was isolated from liver tissue using the Wizard Genomic extraction protocol (Promega Inc., Madison, WI). We then used 200 ng of DNA to create a DNA sequencing library at the Genopole of Toulouse (France). The library was hybridized and sequenced on a 1/24th of lane of an Illumina HiSeq 2500 flow cell (Illumina Inc., San Diego, CA). Over 24 million paired-end read of 150 bp were obtained. The mitochondrial genome was assembled using an iterative mapping strategy (Besnard et al. 2014). We obtained a circular sequence of 17,572 bp in length. The overall base composition was as follows: A (28.5%), C (27.4%), G (13.9%) and T (30.3). We annotated the mitogenome with the MITOS webserver (Bernt et al. 2013). We validated the coding regions using Geneious version 9.0.5 (Kearse et al. 2012). The annotated sequence was submitted to NCBI (accession no. KU958559).

We then used MAFFT v.7 (Katoh & Standley 2013) to align the mitogenome of *A. baeobatrachus* with all available mitochondrial genomes of Hyloidea (Nobleobatrachia), a superfamily of Neobatrachia. The gene order was fully conserved in this clade, and we conducted a maximum-likelihood phylogenetic analysis on this alignment with RAxML v. 8.2.4. (Stamatakis 2014) excluding the control region. The resulting phylogenetic tree (Figure 1) shows that *A. baeobatrachus* and *Mannophryne trinitatis*, which belong to the family Aromobatidae, form a strongly supported clade. This clade is the sister group of Dendrobatidae, which is in accordance with previous studies (Grant et al. 2006). Given several species within this genus might face decline or might already have gone extinct (Courtois et al. 2015; Fouquet et al. 2015), resolving taxonomic uncertainties is crucial to assess conservation priorities. These data, which represent the first mitogenome for the genus and the second for Aromobatidae, will serve as a reference for further studies on the taxonomy and evolution of this group of amphibians.

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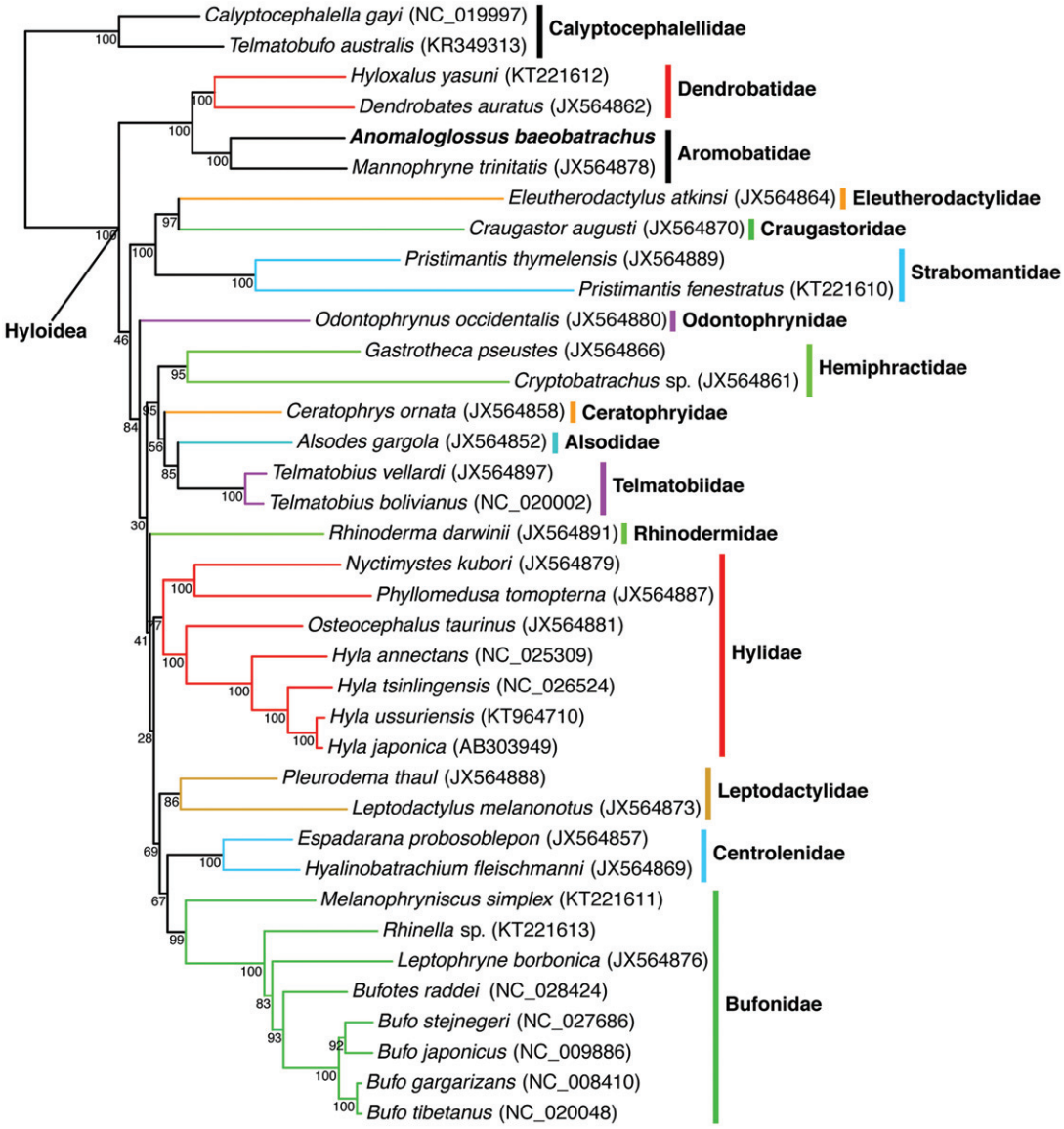


**Figure 1.** Maximum-likelihood phylogeny of Hyloidea inferred with a GTR + G + I model from all available mitochondrial genomes in this clade. Calyptocephalellidae was used to root the tree. The new sequence is represented in bold. The Bootstrap values (based on 1000 iterations and 100 independent maximum-likelihood searches) are indicated for each internal node.

## Acknowledgements

The authors would like to thank Benoît Villette, Jean-François Szpigel and Sébastien Cally for their help in the field, and Guillaume Besnard for his advices on genome assembling and suggestions to improve the manuscript.

## Disclosure statement

The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

## Funding information

This work has benefited from an "Investissement d'Avenir" grant managed by *Agence Nationale de la Recherche* (CEBA, ref.ANR-10-LABX-25-01), France.

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