

Complete mitochondrial genome of golden conure (*Guaruba guarouba*)

Adam Dawid Urantówka^a, Tomasz Strzała^a and Paweł Mackiewicz^b

^aDepartment of Genetics, Wrocław University of Environmental and Life Sciences, Wrocław, Poland; ^bDepartment of Genomics, Faculty of Biotechnology, Wrocław University, Wrocław, Poland

ABSTRACT

Arini tribe with 19 genera is the most diversified tribe of neotropical parrots. Six of them are classified as macaws and nine as conures. The presence of bare facial area distinguishes macaws from conures and other members of this tribe. However, such morphological division seems to be disputable as the smallest macaw (monotypic *Diopsittaca* genus) turned out to be more closely related to three monotypic conures genera (*Guaruba*, *Leptosittaca*, *Thectocercus*) than to other macaws. We sequenced the complete mitochondrial genome of *Guaruba guarouba* to enrich the resource of molecular markers for examination of phylogenetic relationships between macaws and conures.

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Subfamily *Arinae* (the New World parrots) is the most species-rich group within the order *Psittaciformes* (Schweizer et al. 2014). It is divided into four tribes (Schodde et al. 2013) from which the *Arini* tribe is the most taxon-rich. The majority of nineteen extant genera recognized within this tribe are divided into two morphologically diverse groups. Six of them (*Anodorhynchus*, *Ara*, *Cyanopsitta*, *Diopsittaca*, *Orthopsittaca* and *Primolius*) are classified as macaws (Forshaw 2010) based on the presence of bare facial area, which distinguishes them from other members of the tribe. Another nine genera (*Aratinga*, *Enicognathus*, *Eupsittula*, *Guaruba*, *Leptosittaca*, *Ognorhynchus*, *Psittacara*, *Pyrrhura* and *Thectocercus*) belong to conures (Remsen et al. 2016).

Recent molecular studies showed that a conure *Aratinga acuticaudata* should be shifted to a new genus *Thectocercus acuticaudatus* because it is more closely related to three monotypic genera (*Diopsittaca*, *Guaruba* and *Leptosittaca*) than to any member of the previously broadly defined genus *Aratinga* (Remsen et al. 2013; Urantowka et al. 2013). The correctness of macaws morphological classification was further undermined by the significant separation of the smallest macaw (*Diopsittaca nobilis*) from other members of this groups and its close relationship to conures – *Guaruba*, *Leptosittaca* and *Thectocercus*.

Many phylogenetic relationships within conures and macaws are still unsolved. Therefore, more molecular data are required to reconstruct precise their phylogenies. It was shown that complete mitochondrial genomes can provide useful information for evolutionary studies of many taxa (Nabholz et al. 2013). So far, complete mitogenomes of only

three representative macaws (*Ara*, *Orthopsittaca* and *Primolius*) and four conures (*Eupsittula*, *Psittacara*, *Pyrrhura* and *Thectocercus*) are available (Pacheco et al. 2011; Urantowka et al. 2013; Urantowka et al. 2014; Urantowka 2016a,b,c; Urantowka et al. 2016). Therefore, we sequenced *Guaruba guarouba* mitogenome with the length of 17,008 bp (GeneBank accession number JQ782217) to gain appropriate molecular data for future examination of evolutionary diversification of macaws and conures.

Although morphology of the analyzed specimen (Polish captive bird with CITES document no. 1281/2009 issued on 15.07.2009 in Hannover) was absolutely typical for *Guaruba guarouba* individuals, we aligned its control region sequence with all available other such sequences of the species as well as selected macaws and conures, to prove its species belonging. The obtained tree (Figure 1) revealed that the analyzed *G. guarouba* individual grouped significantly with two other representatives of this species. The clade *Guaruba* was sister to the group of *Thectocercus* and *Diopsittaca*. Three macaws (*Ara*, *Orthopsittaca* and *Primolius*) formed a monophyletic group but were clearly separated from the smallest macaw (*Diopsittaca nobilis*).

Gene order found in *G. guarouba* mitogenome was the same as in *Thectocercus acuticaudatus* mitogenome, so far, the only fully sequenced member of the clade *Guaruba/Leptosittaca/Thectocercus/Diopsittaca*. The sequence identity of both genomes was 93.9% and base composition of their H-strand was nearly the same. The start and stop codons usage was also consistent for both species with the exception to the *atp6* gene. In *Guaruba guarouba*, this gene had a

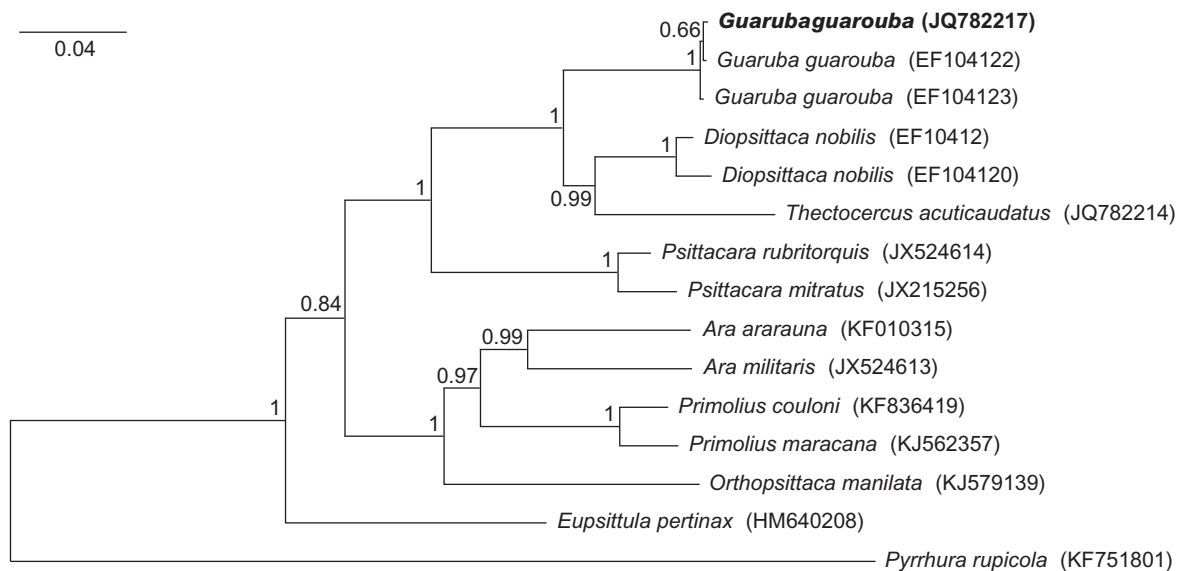


Figure 1. The phylogenetic tree obtained in MrBayes for control region sequences indicating that the studied individual (bolded) belongs to *Guaruba guarouba* species. The tree was generated with Bayesian method in MrBayes 3.2.5 (Ronquist et al. 2012) using the model GTR + I + G as suggested by jModelTest 2.1.7 (Guindon & Gascuel 2003; Durraba et al. 2012). 10,000,000 MCMC repetitions with burn-in of 25% was assumed. Tree was rooted with *Pyrrhura rupicola* sequence. Genbank accession numbers are shown in parenthesis. Bayesian posterior probabilities are shown at nodes.

truncated (TA_) stop codon, but in *Thectocercus* it ended with TAA codon.

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This work is dedicated to the memory of beloved parrot named Guccio.

Disclosure statement

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

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