

**Abstract:**

The tribe of the cichlid fishes, Cichlasomatini Kullander, 1998, comprises to date 69 valid species living in South America. This Neotropical assemblage contains genera *Aequidens*, *Cichlasoma* (*sensu stricto*), *Krobia*, *Bujurquina*, *Tahuantinsuyoa*, *Cleithracara*, *Laetacara*, *Nannacara* and *Acaronia* and the '*Aequidens*' species groups at present.

The presented thesis represents the first molecular study dealing with more extensive sampling of species of the tribe Cichlasomatini. Sixty-three representatives of all nine described genera and taxonomically unresolved species group are included. Herein both mitochondrial (16S rRNA, cytochrome b), and nuclear (first intron in S7 ribosomal gene) markers were used for study of the phylogenetic relations.

The methods of Maximum Parsimony, Maximum Likelihood and Bayesian methods of phylogenetic analysis were based on sequences of total length 1542 bp.

The influence of every gene signal to each node of the concatenated tree was explored using the Partitioned Bremer Support. The test of concatenation of genes and the test of other alternative hypothesis was performed by Approximately Unbiased Test.

The method of Molecular Clock was applied to estimate the divergence time within '*Aequidens*' and *Cichlasoma* lineages.