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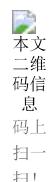
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## 滁州鲫(Carassius auratus)线粒体全基因组序列分析及系统进化

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摘要:

为探讨天然三倍体滁州鲫的系统进化地位,采用直接测序法获得滁州鲫线粒体基因组。其序列全长为16581 bp,碱基组成为31.6% A、26.2% T、16.1% G和26.1% C,包括13个蛋白质基因、22个tRNA基因、2个rRNA基因和1个非编码区,各基因的位置及组成与已公布的鲤科鱼类一致。除tRNA-Ser (AGY)外,其他21个tRNA的二级结构均具有典型的三叶草结构;13个蛋白编码基因中,除CO I起始密码子为GTG外,其余均以ATG为起始密码子;CO II、ND3、ND4和Cyt b基因的终止密码子为不完整的T,其他9个基因均具有完整的终止密码子TAA或TAG。序列分析表明,滁州鲫与其他鲫属鱼类(方正银鲫A系和D系、鲫、淇河鲫、萍乡肉红鲫、黑鲫、日本白鲫和日本银鲫)在线粒体基因组上均具有较高的序列同源性(>94%)。以鲤(Cyprinus carpio haematopterus)为外类群,基于线粒体13个蛋白质基因的核苷酸与氨基酸序列构建上述鲫属鱼类的系统进化树,结果显示,滁州鲫与方正银鲫亲缘关系最近,与黑鲫最远。综合以上研究结果,认为滁州鲫应为银鲫亚种的一个地方种群。

关键词: [滁州鲫](#) [线粒体基因组](#) [系统进化分析](#)DOI: [10.11758/yykx.jz.20150509](https://doi.org/10.11758/yykx.jz.20150509)

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## Sequence and phylogenetic analysis of the complete mitochondrial genome of Chuzhou Crucian Carp (Carassius auratus)

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**Abstract:**

Chuzhou Crucian Carp (Carassius auratus in Chuzhou) is one of the natural gynogenetic crucian carp originated from Anhui Province in China. It belongs to the genus of Carassius within the family of Cyprinidae. To investigate the species status of this fish, we performed the direct DNA sequencing on the PCR products of the complete mitochondrial DNA (mtDNA). The total length of the mtDNA was 16581 bp, including 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and a non-coding control region. The composition and location of genes in the mitochondrial genome of Chuzhou Crucian Carp were consistent with those of Cyprinidae fishes published in GenBank. The tRNA genes formed typical secondary structures except for tRNA-Ser (AGY). The CO I gene had GTG as its initiation codon, and the other 12 protein-coding genes had ATG as the initiation codon. Among the 13 protein-coding genes, 9 had complete stop codons but CO II, ND3, ND4 and Cyt b had an incomplete T as the stop codon. Sequence analysis showed that there was high similarity between the mtDNA sequences of Chuzhou Crucian Carp and other species in genus Carassius recorded in GenBank (>94%). The nucleotide composition of Chuzhou Crucian Carp was 31.6% (A), 26.2% (T), 16.1% (G) and 26.2% (C). We conducted the phylogenetic analysis of the mitochondrial genomes of 9 Carassius fishes and 1 Cyprinus carpio, based on their nucleotide and amino acid sequences of all protein-coding genes. The results indicated that the phylogenetic relationship between C. auratus gibelio in Chuzhou and in Fangzheng was the closest while C. auratus gibelio in Chuzhou and Carassius carassius was the farthest. Our study may provide basic data and contribute to the classification of Carassius and Cyprinidae fishes.

Key words: [Chuzhou Crucian Carp \(Carassius auratus\)](#) [Mitochondrial genome](#)

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