

## MITOGENOME ANNOUNCEMENT

# Complete mitochondrial genome of the speckled dace *Rhinichthys osculus*, a widely distributed cyprinid minnow of western North America

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### Abstract

The speckled dace *Rhinichthys osculus* (order Cypriniformes), also known as the carpita pinta, is a small cyprinid minnow native to western North America. Here, we report the sequencing of the full mitochondrial genome (mitogenome) of *R. osculus* from a male fish collected from the Amargosa River Canyon in eastern California, USA. The assembled mitogenome is 16 658 base pair (bp) nucleotides, and encodes 13 protein-coding genes, and includes both a 12S and a 16S rRNA, 22 tRNAs, and a 985 bp D-loop control region. Mitogenome synteny reflects that of other Ostariophysian fishes with the majority of genes and RNAs encoded on the heavy strand (H-strand) except *nd6*, *tRNA<sup>Gln</sup>*, *tRNA<sup>Ala</sup>*, *tRNA<sup>Asn</sup>*, *tRNA<sup>Cys</sup>*, *tRNA<sup>Tyr</sup>*, *tRNA<sup>Ser</sup>*, *tRNA<sup>Glu</sup>*, and *tRNA<sup>Pro</sup>*. The availability of this *R. osculus* mitochondrial genome – the first complete mitogenome within the lineage of *Rhinichthys* riffle daces – provides a foundation for resolving evolutionary relationships among morphologically differentiated populations of *R. osculus*.

### Keywords

Cyprinidae, Cypriniformes, Leuciscinae, mitogenome, mtDNA

The speckled dace *Rhinichthys osculus* (Girard, 1856) is a small fish within the Leuciscinae subfamily of true minnows (Cyprinidae, Cypriniformes). The native range for *R. osculus* extends from the Columbia River basin of southwestern Canada, through the western United States of America (USA), and into the Sonora region of northern Mexico (La Rivers, 1962; Minckley, 1973; Moyle, 2002; Scott & Crossman, 1998). *Rhinichthys osculus* occurs in ecologically diverse habitats from groundwater-fed springs to rivers, and populations can vary extensively in morphological traits (Oakley et al., 2004; Sada et al., 1995; Woodman, 1992). *Rhinichthys osculus* was originally described across its range as at least 18 distinct species (e.g., Cope, 1874; Girard, 1856; Hubbs & Kühne, 1937; Jordan & Evermann, 1896), although it is now considered a single species comprised of morphologically distinct subspecies and populations.

Here, we describe the first complete mitochondrial genome of *R. osculus*. An adult male *R. osculus* (Amargosa Canyon spp.; Deacon & Williams, 1984) measuring 68.20 mm SL and 5.17 g body mass was collected on 27 June 2015 from the Amargosa River near Tecopa, CA, USA (N 35°50.976'N 116°13.851'W). DNA was extracted from skeletal muscle tissue (DNeasy Blood

and Tissue Kit; Qiagen, Valencia, CA) and amplified (GoTaq® Long PCR Master Mix, Promega Corp., Madison, WI) using primers designed to available partial mtDNA regions of *R. osculus* (GenBank accession nos. AF081863, EU780582, EU158227, KF421812, HQ579004, DQ990249, DQ990314, AY366299, and FJ748866). The resulting PCR products were Sanger sequenced (Molecular Cloning Laboratory, South San Francisco, CA) and assembled (Sequencher v5, Gene Codes Corp., Ann Arbor, MI).

The complete mitogenome of *R. osculus* (KT424924) is 16 658 bp nucleotides in length with a composition of 13 protein coding genes, 22 tRNAs, and 2 rRNAs, as has been observed in other teleost fish mitogenomes. Nucleotide composition of the H-strand of the full *R. osculus* mitogenome is 28.43% A, 18.18% G, 26.84% T, and 26.55% C, with a combined G+C content of 44.73%. Phylogenetic analysis confirmed *R. osculus* belongs to what is referred by Simons et al. (2003) as the Open Posterior Myodome (OPM) clade of the Leuciscinae subfamily of 'true minnows' within the Cyprinidae (Figure 1) (Imoto et al., 2013; Mayden et al., 2009).

One described subspecies of *R. osculus* is extinct (*R. o. reliquus*; Burkhead, 2012; Miller et al., 1989), five subspecies have legally imperiled status (Gould & Kaya, 1991; Williams & Sada, 1985), and other populations appear distinct morphologically, but do not yet have a subspecies trinomen (Deacon & Williams, 1984; Sada et al., 1995). There is also evidence that at least one habitat may support genetically-isolated sympatric populations of *R. osculus* (Pfreder et al., 2004). This complete mitogenome for *R. osculus* will enable future genetic studies into whether such populations are indeed distinct evolutionary lineages.

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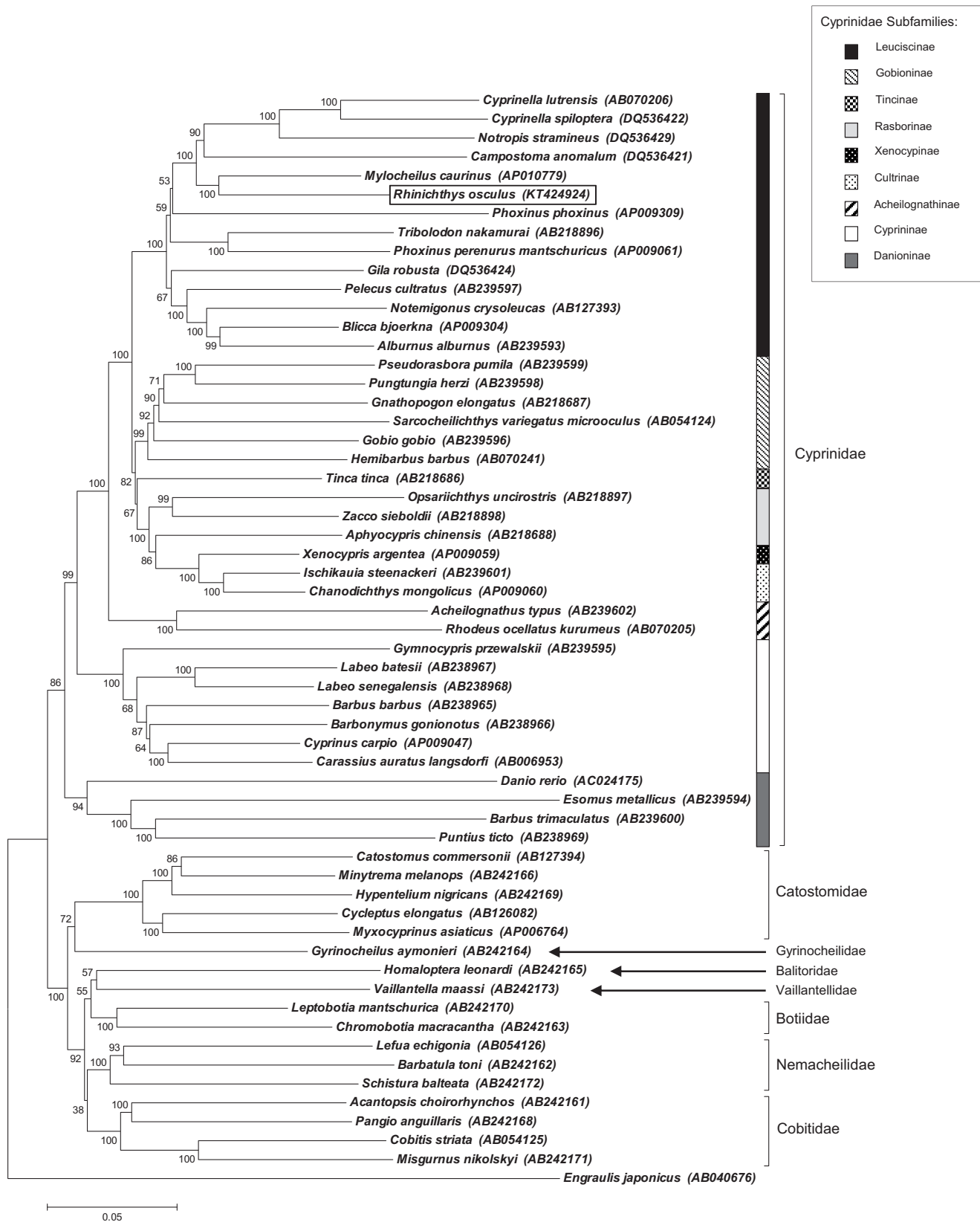


Figure 1. Neighbor-joining phylogenetic tree of the complete mitogenome of *R. osculus* (GenBank accession no. KT424924) and other Cypriniform fishes. Complete nucleotide sequences for each species were aligned using Clustal X software, and the tree was constructed using all nucleotide sites with a maximum likelihood model and pairwise gap deletion using MEGA v5.1 (Tamura et al., 2011). The *R. osculus* mitogenome is indicated by enclosure within the box. Japanese anchovy (*Engraulis japonicus*, Order Clupeiformes) was used as the outgroup. Bootstrap values (1000 replicates) are shown for each node, and GenBank accession numbers are provided in parentheses accompanying each species name. Families within the order Cypriniformes are indicated by brackets, and subfamily designations within the family Cyprinidae are demarcated by the color and pattern categories. Based on this phylogenetic analysis, *R. osculus* belongs to the Leuciscinae subfamily of 'true minnows' within the Cyprinidae.

## Declaration of interest

This research was supported by the CSU Program for Education and Research in Biotechnology (CSUPERB) and by the Cal Poly Frost Scholar program. The authors report that they have no conflicts of interest and are solely responsible for the content and writing of this manuscript.

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