Resource Summary Report

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UT Genome Browser (Medaka)

RRID:SCR_005857
Type: Tool

Proper Citation

UT Genome Browser (Medaka) (RRID:SCR_005857)

Resource Information

URL: http://medaka.utgenome.org/

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Description: A website containing the complete sequenced genome of the medaka fish. It presents a high-quality draft genome sequence of a small egg-laying freshwater teleost, medaka (Oryzias latipes). Medaka is native to East Asia and an excellent model system for a wide range of biology, including ecotoxicology, carcinogenesis, sex determination4, 5, 6 and developmental genetics7. In the assembled medaka genome (700 megabases), which is less than half of the zebrafish genome, we predicted 20,141 genes, including approx2,900 new genes, using 5’-end serial analysis of gene expression tag information. We found single nucleotide polymorphisms (SNPs) at an average rate of 3.42% between the two inbred strains derived from two regional populations; this is the highest SNP rate seen in any vertebrate species. Analyses based on the dense SNP information show a strict genetic separation of 4 million years (Myr) between the two populations, and suggest that differential selective pressures acted on specific gene categories. Four-way comparisons with the human, pufferfish (Tetraodon), zebrafish and medaka genomes revealed that eight major interchromosomal rearrangements took place in a remarkably short period of approx 50 Myr after the whole-genome duplication event in the teleost ancestor and afterwards, intriguingly, the medaka genome preserved its ancestral karyotype for more than 300 Myr.

Synonyms: UTGB medaka

Resource Type: database, data or information resource

Funding:

Resource Name: UT Genome Browser (Medaka)

Resource ID: SCR_005857

Alternate IDs: nif-0000-03618

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250412T055009+0000

Ratings and Alerts

No rating or validation information has been found for UT Genome Browser (Medaka).

No alerts have been found for UT Genome Browser (Medaka).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Ishikawa T, et al. (2010) High-resolution melting curve analysis for rapid detection of mutations in a Medaka TILLING library. BMC molecular biology, 11, 70.

Sasado T, et al. (2008) Distinct contributions of CXCR4b and CXCR7/RDC1 receptor systems in regulation of PGC migration revealed by medaka mutants kazura and yanagi. Developmental biology, 320(2), 328.

Sugawara H, et al. (2007) DDBJ working on evaluation and classification of bacterial genes in INSDC. Nucleic acids research, 35(Database issue), D13.

Del Bene F, et al. (2007) In vivo validation of a computationally predicted conserved Ath5 target gene set. PLoS genetics, 3(9), 1661.

Soroldoni D, et al. (2007) Dynamic expression pattern of Nodal-related genes during left-right development in medaka. Gene expression patterns : GEP, 7(1-2), 93.

Saito D, et al. (2007) Proliferation of germ cells during gonadal sex differentiation in medaka: Insights from germ cell-depleted mutant zenzai. Developmental biology, 310(2), 280.

Hochmann S, et al. (2007) Expression of marker genes during early ear development in medaka. Gene expression patterns : GEP, 7(3), 355.

Su F, et al. (2007) Radiation hybrid maps of Medaka chromosomes LG 12, 17, and 22. DNA research : an international journal for rapid publication of reports on genes and genomes, 14(3), 135.

Yoshihama M, et al. (2006) Analysis of ribosomal protein gene structures: implications for intron evolution. PLoS genetics, 2(3), e25.