

Resource Summary Report

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Tetraodon Genome Browser

RRID:SCR_007079

Type: Tool

Proper Citation

Tetraodon Genome Browser (RRID:SCR_007079)

Resource Information

URL: <http://www.genoscope.cns.fr/externe/tetraodon/>

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Description: The initial objective of Genoscope was to compare the genomic sequences of this fish to that of humans to help in the annotation of human genes and to estimate their number. This strategy is based on the common genetic heritage of the vertebrates: from one species of vertebrate to another, even for those as far apart as a fish and a mammal, the same genes are present for the most part. In the case of the compact genome of Tetraodon, this common complement of genes is contained in a genome eight times smaller than that of humans. Although the length of the exons is similar in these two species, the size of the introns and the intergenic sequences is greatly reduced in this fish. Furthermore, these regions, in contrast to the exons, have diverged completely since the separation of the lineages leading to humans and Tetraodon. The Exofish method, developed at Genoscope, exploits this contrast such that the conserved regions which can be identified by comparing genomic sequences of the two species, correspond only to coding regions. Using preliminary sequencing results of the genome of Tetraodon in the year 2000, Genoscope evaluated the number of human genes at about 30,000, whereas much higher estimations were current. The progress of the annotation of the human genome has since supported the Genoscope hypothesis, with values as low as 22,000 genes and a consensus of around 25,000 genes. The sequencing of the Tetraodon genome at a depth of about 8X, carried out as a collaboration between Genoscope and the Whitehead Institute Center for Genome Research (now the Broad Institute), was finished in 2002, with the production of an assembly covering 90 of the euchromatic region of the genome of the fish. This has permitted the application of Exofish at a larger scale in comparisons with the genome of humans, but also with those of the two other vertebrates sequenced at the time (Takifugu, a fish closely related to Tetraodon, and the mouse). The conserved regions detected in this way have been integrated into the annotation procedure, along with other resources (cDNA sequences from Tetraodon and ab initio predictions). Of the 28,000 genes annotated, some families were examined in detail: selenoproteins, and Type 1 cytokines and their receptors. The comparison of the proteome of Tetraodon with those of mammals has revealed some interesting differences,

such as a major diversification of some hormone systems and of the collagen molecules in the fish. A search for transposable elements in the genomic sequences of Tetraodon has also revealed a high diversity (75 types), which contrasts with their scarcity; the small size of the Tetraodon genome is due to the low abundance of these elements, of which some appear to still be active. Another factor in the compactness of the Tetraodon genome, which has been confirmed by annotation, is the reduction in intron size, which approaches a lower limit of 50-60 bp, and which preferentially affects certain genes. The availability of the sequences from the genomes of humans and mice on one hand, and Takifugu and Tetraodon on the other, provide new opportunities for the study of vertebrate evolution. We have shown that the level of neutral evolution is higher in fish than in mammals. The protein sequences of fish also diverge more quickly than those of mammals. A key mechanism in evolution is gene duplication, which we have studied by taking advantage of the anchoring of the majority of the sequences from the assembly on the chromosomes. The result of this study speaks strongly in favor of a whole genome duplication event, very early in the line of ray-finned fish (Actinopterygians). An even stronger evidence came from synteny studies between the genomes of humans and Tetraodon. Using a high-resolution synteny map, we have reconstituted the genome of the vertebrate which predates this duplication - that is, the last common ancestor to all bony vertebrates (most of the vertebrates apart from cartilaginous fish and agnaths like lamprey). This ancestral karyotype contains 12 chromosomes, and the 21 Tetraodon chromosomes derive from it by the whole genome duplication and a surprisingly small number of interchromosomal rearrangements. On the contrary, exchanges between chromosomes have been much more frequent in the lineage that leads to humans. Sponsors: The project was supported by the Consortium National de Recherche en Genomique and the National Human Genome Research Institute.

Synonyms: TGB

Resource Type: data or information resource, database, portal, topical portal

Keywords: duplication, element, euchromatic, evolution, exon, fish, gene, genetic, actinopterygians, aganth, ancestor, cartilaginous, cdna, chromosome, coding, collagen, cytokine, diversity, genome, genomic, heritage, hormone, human, interchromossomal, intergenic, intron, karyotype, lineage, mammal, molecule, mouse, nigroviridis, protein, proteome, pufferfish, receptor, region, selenoprotein, sequence, size, specie, synteny, system, takifugu, tetraodon, transposable, vertebrate

Resource Name: Tetraodon Genome Browser

Resource ID: SCR_007079

Alternate IDs: nif-0000-20997

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260912T195649+0000

Ratings and Alerts

No rating or validation information has been found for Tetraodon Genome Browser.

No alerts have been found for Tetraodon Genome Browser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Woltering JM, et al. (2014) Conservation and divergence of regulatory strategies at Hox Loci and the origin of tetrapod digits. PLoS biology, 12(1), e1001773.

Kumar A, et al. (2012) Molecular phylogeny of OVOL genes illustrates a conserved C2H2 zinc finger domain coupled by hypervariable unstructured regions. PloS one, 7(6), e39399.

Kumar A, et al. (2011) Spliceosomal intron insertions in genome compacted ray-finned fishes as evident from phylogeny of MC receptors, also supported by a few other GPCRs. PloS one, 6(8), e22046.

Goyal P, et al. (2009) Identifying and characterizing a novel protein kinase STK35L1 and deciphering its orthologs and close-homologs in vertebrates. PloS one, 4(9), e6981.

Korzh V, et al. (2007) Transposons as tools for enhancer trap screens in vertebrates. Genome biology, 8 Suppl 1(Suppl 1), S8.

Liu F, et al. (2006) New perspectives on host-parasite interplay by comparative transcriptomic and proteomic analyses of Schistosoma japonicum. PLoS pathogens, 2(4), e29.

Kumano G, et al. (2006) ADMP2 is essential for primitive blood and heart development in Xenopus. Developmental biology, 299(2), 411.

Dehmelt L, et al. (2005) The MAP2/Tau family of microtubule-associated proteins. Genome biology, 6(1), 204.