GEPHE SUMMARY

Gephebase Gene

Inhibitor of DNA binding 3 (id3) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Inhibitor of DNA binding 3 (id3)^#gephebase-summary-title)

GepheID

GP00001677

Entry Status

Published

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Lifespan (https://www.gephebase.org/search-criteria?/and+Trait=^Lifespan^#gephebase-summary-title)

Trait State in Taxon A

Species with captive median lifespan of 12 months

Trait State in Taxon B

Species with short lifespan of 7.5 months

Ancestral State

Taxon A

Taxonomic Status

Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name

Nothobranchius rachovii (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Nothobranchius rachovii^#gephebase-summary-title)

Common Name

bluefin notho

Synonyms

bluefin notho; Nothobranchius rachovii Ahl, 1926

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Atherinomorphae; Cyprinodontiformes; Aplocheiloidei; Nothobranchiidae; Nothobranchius

Parent

Nothobranchius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 28779)

NCBI Taxonomy ID

451742 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 451742)

is Taxon A an Infraspecies?

Yes

Taxon A Description

N. rachovii with captive median lifespan of 12 months

Taxon B

Latin Name

Nothobranchius pienaari (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Nothobranchius pienaari^#gephebase-summary-title)

Common Name

-

Synonyms

Nothobranchius pienaari Shidlovskiy, Watters & Wildekamp, 2010

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Atherinomorphae; Cyprinodontiformes; Aplocheiloidei; Nothobranchiidae; Nothobranchius

Parent

Nothobranchius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 28779)

NCBI Taxonomy ID

704102 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 704102)

is Taxon B an Infraspecies?

Yes

Taxon B Description

N. pienaari with short lifespan of 7.5 months

GENOTYPIC CHANGE

Generic Gene Name

ID3

Synonyms

HEIR-1; bHLHb25; 1R21; BHLHB25; HEIR1

String

9606.ENSP00000363689 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000363689)

Sequence Similarities

-

GO - Molecular Function

GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)
GO:0003700 : DNA-binding transcription factor activity

UniProtKB Homo sapiens

Q02535 (http://www.uniprot.org/uniprot/Q02535)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0008134 : transcription factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0008134)
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific
(https://www.ebi.ac.uk/QuickGO/term/GO:0000981)
GO:0001085 : RNA polymerase II transcription factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0001085)
GO:0003714 : transcription corepressor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0003714)
GO:0019904 : protein domain specific binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0019904)
GO:1901707 : leptomycin B binding (https://www.ebi.ac.uk/QuickGO/term/GO:1901707)

GO - Biological Process

GO:0007275 : multicellular organism development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007275)
GO:0007417 : central nervous system development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007417)
GO:0030182 : neuron differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030182)
GO:0007507 : heart development (https://www.ebi.ac.uk/QuickGO/term/GO:0007507)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0045892 : negative regulation of transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0045892)
GO:0006351 : transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0006351)
GO:0030903 : notochord development
(https://www.ebi.ac.uk/QuickGO/term/GO:0030903)
GO:0007623 : circadian rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0007623)
GO:0009611 : response to wounding (https://www.ebi.ac.uk/QuickGO/term/GO:0009611)
GO:0043433 : negative regulation of DNA-binding transcription factor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0043433)
GO:0045665 : negative regulation of neuron differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045665)
GO:0030855 : epithelial cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0030855)
GO:0042476 : odontogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0042476)
GO:0043065 : positive regulation of apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043065)
GO:0051726 : regulation of cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0051726)
GO:0043392 : negative regulation of DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0043392)
GO:0007517 : muscle organ development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007517)
GO:0045662 : negative regulation of myoblast differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045662)
GO:0045668 : negative regulation of osteoblast differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045668)
GO:0006275 : regulation of DNA replication
(https://www.ebi.ac.uk/QuickGO/term/GO:0006275)
GO:0072750 : cellular response to leptomycin B
(https://www.ebi.ac.uk/QuickGO/term/GO:0072750)
GO:0001656 : metanephros development
(https://www.ebi.ac.uk/QuickGO/term/GO:0001656)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)

Deletion Size

1-9 bp

Molecular Details of the Mutation

One evolutionarily conserved aa (E) is deleted in id3 C-terminus

Experimental Evidence

Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title)

Main Reference

Insights into Sex Chromosome Evolution and Aging from the Genome of a Short-Lived Fish. (2015) (https://pubmed.ncbi.nlm.nih.gov/26638077)

Authors

Reichwald K; Petzold A; Koch P; Downie BR; Hartmann N; Pietsch S; Baumgart M; Chalopin D; Felder M; Bens M; Sahm A; Szafranski K; Taudien S; Groth M; Arisi I; Weise A; Bhatt SS; Sharma V; Kraus JM; Schmid F; Priebe S; Liehr T; GÃ¶rlach M; Than ME; Hiller M; Kestler HA; Volff JN; Schartl M; Cellerino A; Englert C; Platzer M

Abstract

The killifish Nothobranchius furzeri is the shortest-lived vertebrate that can be bred in the laboratory. Its rapid growth, early sexual maturation, fast aging, and arrested embryonic development (diapause) make it an attractive model organism in biomedical research. Here, we report a draft sequence of its genome that allowed us to uncover an intra-species Y chromosome polymorphism representing-in real time-different stages of sex chromosome formation that display features of early mammalian XY evolution "in action." Our data suggest that gdf6Y, encoding a TGF-Î² family growth factor, is the master sex-determining gene in N.Â furzeri. Moreover, we observed genomic clustering of aging-related genes, identified genes under positive

selection, and revealed significant similarities of gene expression profiles between diapause and aging, particularly for genes controlling cell cycle and translation. The annotated genome sequence is provided as an online resource (http://www.nothobranchius.info/NFINgb).

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Link with phenotype unclear