

GEPHE SUMMARY

Inhibitor of DNA binding 3 (id3) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^Inhibitor+of+DNA+binding+3+(id3)^#gephebase-summary-title)	Gephebase Gene	GP00001677	GepheID
Published	Entry Status	Prigent	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)	Trait Category		
Lifespan (https://www.gephebase.org/search-criteria?/and+Trait=^Lifespan^#gephebase-summary-title)	Trait		
Species with captive median lifespan of 12 months	Trait State in Taxon A		
Species with short lifespan of 7.5 months	Trait State in Taxon B		
Taxon A	Ancestral State		
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Interspecific^#gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
Nothobranchius rachovii (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Nothobranchius+rachovii^#gephebase-summary-title)	Latin Name	Nothobranchius pienaari (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Nothobranchius+pienaari^#gephebase-summary-title)	Latin Name
bluefin notho	Common Name	-	Common Name
bluefin notho; Nothobranchius rachovii Ahl, 1926	Synonyms	Nothobranchius pienaari Shidlovskiy, Watters & Wildekamp, 2010	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percomorphaceae; Ovalentaria; Atherinomorpha; Cyprinodontiformes; Aplocheiloidei; Nothobranchiidae; Nothobranchius	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percomorphaceae; Ovalentaria; Atherinomorpha; Cyprinodontiformes; Aplocheiloidei; Nothobranchiidae; Nothobranchius	Lineage
Nothobranchius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=28779)	Parent	Nothobranchius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=28779)	Parent
451742 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=451742)	NCBI Taxonomy ID	704102 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=704102)	NCBI Taxonomy ID
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
N. rachovii with captive median lifespan of 12 months	Taxon A Description	N. pienaari with short lifespan of 7.5 months	Taxon B Description

GENOTYPIC CHANGE

ID3	Generic Gene Name	Q02535 (http://www.uniprot.org/uniprot/Q02535)	UniProtKB Homo sapiens
HEIR-1; bHLHb25; 1R21; BHLHB25; HEIR1	Synonyms	()	GenebankID or UniProtKB
9606.ENSPO0000363689 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPO0000363689)	String		
-	Sequence Similarities		
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)	GO - Molecular Function		
GO:0003700 : DNA-binding transcription factor activity			

(<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; Sahn A; Szafranski K; Taudien S; Groth M; Arisi I; Weise A; Bhatt SS; Sharma V; Kraus JM; Schmid F; Priebe S; Liehr T; GÄ¶rlach M; Than ME; Hiller M; Kestler HA; Volf JN; Scharl M; Cellierino 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- β family growth factor, is the master sex-determining gene in *N.Ä 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.nothobanchius.info/NFINgb>).

Copyright © 2015 Elsevier Inc. All rights reserved.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

Link with phenotype unclear