GEPHE SUMMARY

Gephebase Gene

Fidgetin-like1 (Fignl1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Fidgetin-like1 (Fignl1)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001668

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

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

Trait

Testis size (testis weight ; spermatogenesis) (https://www.gephebase.org/search-criteria?/and+Trait=^Testis size (testis weight ; spermatogenesis)^#gephebase-summary-title)

Trait State in Taxon A

Mus spretus SEG/PAS strain

Trait State in Taxon B

Mus musculus C57BL6/J strain

Ancestral State

Unknown

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

western wild mouse

Synonyms

Mus musculus spretus; western wild mouse; Algerian mouse

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Parent

Mus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 862507)

NCBI Taxonomy ID

10096 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10096)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Mus spretus SEG/PAS strain

Taxon B

Latin Name

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

Common Name

house mouse

Synonyms

house mouse; mouse; Mus musculus Linnaeus, 1758; mice C57BL/6xCBA/CaJ hybrid

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Parent

Mus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 862507)

NCBI Taxonomy ID

10090 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10090)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Mus musculus C57BL6/J strain

GENOTYPIC CHANGE

Generic Gene Name

Fignl1

Synonyms

-

String

10090.ENSMUSP00000036932 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 10090.ENSMUSP00000036932)

Sequence Similarities

Belongs to the AAA ATPase family.

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0000287 : magnesium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000287)
GO:0016787 : hydrolase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016787)

UniProtKB Mus musculus

Q8BPY9 (http://www.uniprot.org/uniprot/Q8BPY9)

GenebankID or UniProtKB

()

GO:0016887 : ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016887)
GO:0008568 : microtubule-severing ATPase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0008568)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043066)
GO:0001649 : osteoblast differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0001649)
GO:0051726 : regulation of cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0051726)
GO:0046034 : ATP metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0046034)
GO:0071479 : cellular response to ionizing radiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0071479)
GO:0031122 : cytoplasmic microtubule organization
(https://www.ebi.ac.uk/QuickGO/term/GO:0031122)
GO:0007140 : male meiotic nuclear division
(https://www.ebi.ac.uk/QuickGO/term/GO:0007140)
GO:2001243 : negative regulation of intrinsic apoptotic signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:2001243)
GO:0033687 : osteoblast proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0033687)
GO:0010569 : regulation of double-strand break repair via homologous recombination
(https://www.ebi.ac.uk/QuickGO/term/GO:0010569)

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)
GO:0048471 : perinuclear region of cytoplasm
(https://www.ebi.ac.uk/QuickGO/term/GO:0048471)
GO:0000228 : nuclear chromosome (https://www.ebi.ac.uk/QuickGO/term/GO:0000228)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Several non-synonymous SNPs and an alternative splicing encoding a truncated isoform that may act as a competitor of the full length protein in the degradation process

Experimental Evidence

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

Main Reference

Fidgetin-like1 is a strong candidate for a dynamic impairment of male meiosis leading to reduced testis weight in mice. (2011) (https://pubmed.ncbi.nlm.nih.gov/22110678)

Authors

L′HÃ´te D; Vatin M; Auer J; Castille J; Passet B; Montagutelli X; Serres C; Vaiman D

Abstract

In a previous work, using an interspecific recombinant congenic mouse model, we reported a genomic region of 23 Mb on mouse chromosome 11 implicated in testis weight decrease and moderate teratozoospermia (âˆ¼20-30%), a Quantitative Trait Locus (QTL) called Ltw1. The objective of the present study is to identify the gene underlying this phenotype.

In the present study, we refined the QTL position to a 5 Mb fragment encompassing only 11 genes. We showed that the low testis weight phenotype was due to kinetic alterations occurring during the first wave of the spermatogenesis where we could point out to an abnormal lengthening of spermatocyte prophase. We identify Fidgetin-like 1 (Fignl1) as the gene underlying the phenotype, since if fulfilled both the physiological and molecular characteristics required. Indeed, amongst the 11 positional candidates it is the only gene that is expressed during meiosis at the spermatocyte stage, and that presents with non-synonymous coding variations differentiating the two mouse strains at the origin of the cross.

This work prompted us to propose Fignl1 as a novel actor in mammal′s male meiosis dynamics which has fundamental interest. Besides, this gene is a new potential candidate for human infertilities caused by teratozoospermia and blockades of spermatogenesis. In addition this study demonstrates that interspecific models may be useful for understanding complex quantitative traits.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Splicing the causal mutation generating the new splicing is not described