

GEPHE SUMMARY

	Gephebase Gene	GephelD
Latexin (Lxn) (https://www.gephebase.org/search-criteria/?and+Gene+Gephebase=%Latexin+(Lxn)%#gephebase-summary-title)	GP00000534	Main curator
Published	Entry Status	Martin

PHENOTYPIC CHANGE

	Trait Category	
Morphology (https://www.gephebase.org/search-criteria/?and+Trait+Category=%Morphology%#gephebase-summary-title)	Trait	
Stem cell number (hematopoietic precursors) (https://www.gephebase.org/search-criteria/?and+Trait=%Stem+cell+number+(hematopoietic+precursors)%#gephebase-summary-title)	Trait State in Taxon A	
Mus musculus C57BL/6 (B6)	Trait State in Taxon B	
Mus musculus DBA/2 (D2)	Ancestral State	
Data not curated	Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic+Status=%Intraspecific%#gephebase-summary-title)		
Taxon A		Taxon B
Mus musculus	Latin Name	Latin Name
(https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Mus+musculus%#gephebase-summary-title)		
house mouse	Common Name	Common Name
house mouse; mouse; Mus musculus Linnaeus, 1758; mice C57BL/6xCBA/CaJ hybrid	Synonyms	Synonyms
	Rank	Rank
species		
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	Lineage	Lineage
Mus () - (Rank: subgenus)	Parent	Parent
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 862507)		
10090	NCBI Taxonomy ID	NCBI Taxonomy ID
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10090)		
Yes	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
Mus musculus C57BL/6 (B6)	Taxon A Description	Taxon B Description

GENOTYPIC CHANGE

Lxn	Generic Gene Name	UniProtKB Mus musculus
-	Synonyms	GenebankID or UniProtKB
10090.ENSMUSP00000060732 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000060732)	String	AK0332170 (https://www.ncbi.nlm.nih.gov/nuccore/AK0332170)
Belongs to the protease inhibitor I47 (latexin) family.	Sequence Similarities	
GO:0008201 : heparin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008201)	GO - Molecular Function	
GO:0008191 : metalloendopeptidase inhibitor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008191)		
		GO - Biological Process

GO:0006954 : inflammatory response

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006954>)

GO:0050965 : detection of temperature stimulus involved in sensory perception of pain

(<https://www.ebi.ac.uk/QuickGO/term/GO:0050965>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Unknown^#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Not identified

Experimental Evidence

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

Main Reference

The quantitative trait gene latexitin influences the size of the hematopoietic stem cell population in mice. (2007) (<https://pubmed.ncbi.nlm.nih.gov/17220891>)

Authors

Liang Y; Jansen M; Aronow B; Geiger H; Van Zant G

Abstract

We mapped quantitative trait loci that accounted for the variation in hematopoietic stem cell (HSC) numbers between young adult C57BL/6 (B6) and DBA/2 (D2) mice. In reciprocal chromosome 3 congenic mice, introgressed D2 alleles increased HSC numbers owing to enhanced proliferation and self-renewal and reduced apoptosis, whereas B6 alleles had the opposite effects. Using oligonucleotide arrays, real-time PCR and protein blots, we identified latexitin (Lxn), a gene whose differential transcription and expression was associated with the allelic differences. Expression was inversely correlated with the number of HSCs; therefore, ectopic expression of Lxn using a retroviral vector decreased stem cell population size. We identified clusters of SNPs upstream of the Lxn transcriptional start site, at least two of which are associated with potential binding sites for transcription factors regulating stem cells. Thus, promoter polymorphisms between the B6 and D2 alleles may affect Lxn gene expression and consequently influence the population size of hematopoietic stem cells.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS