

GEPHE SUMMARY

	Gephebase Gene		GepheID
Glypican-3 (Gpc3) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="Glypican-3 (Gpc3)"#gephebase-summary-title)		GP00000407	
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology"#gephebase-summary-title)			
	Trait		
Body size (weight) (https://www.gephebase.org/search-criteria?/and+Trait="Body size (weight)"#gephebase-summary-title)			
	Trait State in Taxon A		
Mus musculus			
	Trait State in Taxon B		
Mus musculus			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Domesticated"#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Mus musculus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Mus musculus"#gephebase-summary-title)		Mus musculus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Mus musculus"#gephebase-summary-title)	
	Common Name		Common Name
house mouse		house mouse	
	Synonyms		Synonyms
house mouse; mouse; Mus musculus Linnaeus, 1758; mice C57BL/6xCBA/CaJ hybrid		house mouse; mouse; Mus musculus Linnaeus, 1758; mice C57BL/6xCBA/CaJ hybrid	
	Rank		Rank
species		species	
	Lineage		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		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		Parent
Mus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 862507)		Mus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 862507)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
10090 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10090)		10090 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10090)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Mus musculus
Gpc3		Q8CFZ4 (http://www.uniprot.org/uniprot/Q8CFZ4)	
	Synonyms		GenebankID or UniProtKB
OCI-5		BC036126 (https://www.ncbi.nlm.nih.gov/nucore/BC036126)	
	String		
10090.ENSMUSP00000064131 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000064131)			
	Sequence Similarities		
Belongs to the glypican family.			
	GO - Molecular Function		
GO:0060422 : peptidyl-dipeptidase inhibitor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0060422)			
	GO - Biological Process		
GO:0009617 : response to bacterium (https://www.ebi.ac.uk/QuickGO/term/GO:0009617)			
GO:0090090 : negative regulation of canonical Wnt signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0090090)			
GO:0045807 : positive regulation of endocytosis			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045807>)
 GO:0008285 : negative regulation of cell proliferation
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0008285>)
 GO:0050680 : negative regulation of epithelial cell proliferation
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0050680>)
 GO:0009887 : animal organ morphogenesis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0009887>)
 GO:0030513 : positive regulation of BMP signaling pathway
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030513>)
 GO:0001822 : kidney development (<https://www.ebi.ac.uk/QuickGO/term/GO:0001822>)
 GO:0030324 : lung development (<https://www.ebi.ac.uk/QuickGO/term/GO:0030324>)
 GO:0090263 : positive regulation of canonical Wnt signaling pathway
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0090263>)
 GO:0030282 : bone mineralization (<https://www.ebi.ac.uk/QuickGO/term/GO:0030282>)
 GO:0035116 : embryonic hindlimb morphogenesis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0035116>)
 GO:0009948 : anterior/posterior axis specification
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0009948>)
 GO:0010171 : body morphogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0010171>)
 GO:0001658 : branching involved in ureteric bud morphogenesis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0001658>)
 GO:0042074 : cell migration involved in gastrulation
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0042074>)
 GO:0072111 : cell proliferation involved in kidney development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0072111>)
 GO:0072203 : cell proliferation involved in metanephros development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0072203>)
 GO:0060976 : coronary vasculature development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0060976>)
 GO:0072138 : mesenchymal cell proliferation involved in ureteric bud development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0072138>)
 GO:0072180 : mesonephric duct morphogenesis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0072180>)
 GO:0045926 : negative regulation of growth
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045926>)
 GO:0045879 : negative regulation of smoothened signaling pathway
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045879>)
 GO:0030316 : osteoclast differentiation
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030316>)
 GO:0046326 : positive regulation of glucose import
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0046326>)
 GO:0045732 : positive regulation of protein catabolic process
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045732>)
 GO:0045880 : positive regulation of smoothened signaling pathway
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045880>)
 GO:2000096 : positive regulation of Wnt signaling pathway, planar cell polarity pathway
 (<https://www.ebi.ac.uk/QuickGO/term/GO:2000096>)
 GO:0060828 : regulation of canonical Wnt signaling pathway
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0060828>)
 GO:0040008 : regulation of growth (<https://www.ebi.ac.uk/QuickGO/term/GO:0040008>)
 GO:2000050 : regulation of non-canonical Wnt signaling pathway
 (<https://www.ebi.ac.uk/QuickGO/term/GO:2000050>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
 GO:0005887 : integral component of plasma membrane
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
 GO:0062023 : collagen-containing extracellular matrix
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0062023>)
 GO:0005796 : Golgi lumen (<https://www.ebi.ac.uk/QuickGO/term/GO:0005796>)
 GO:0046658 : anchored component of plasma membrane
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0046658>)
 GO:0005764 : lysosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005764>)

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

unknown; possible 3'UTR variation

Experimental Evidence

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

Main Reference

Regulatory variation at glypican-3 underlies a major growth QTL in mice. (2005) (<https://pubmed.ncbi.nlm.nih.gov/15799711>)

Authors

Oliver F; Christians JK; Liu X; Rhind S; Verma V; Davison C; Brown SD; Denny P; Keightley PD

Abstract

The genetic basis of variation in complex traits remains poorly understood, and few genes underlying variation have been identified. Previous work identified a quantitative trait locus (QTL)

responsible for much of the response to selection on growth in mice, effecting a change in body mass of approximately 20%. By fine-mapping, we have resolved the location of this QTL to a 660-kb region containing only two genes of known function, *Gpc3* and *Gpc4*, and two other putative genes of unknown function. There are no non-synonymous polymorphisms in any of these genes, indicating that the QTL affects gene regulation. Mice carrying the high-growth QTL allele have approximately 15% lower *Gpc3* mRNA expression in kidney and liver, whereas expression differences at *Gpc4* are non-significant. Expression profiles of the two other genes within the region are inconsistent with a factor responsible for a general effect on growth. Polymorphisms in the 3' untranslated region of *Gpc3* are strong candidates for the causal sequence variation. *Gpc3* loss-of-function mutations in humans and mice cause overgrowth and developmental abnormalities. However, no deleterious side-effects were detected in our mice, indicating that genes involved in Mendelian diseases also contribute to complex trait variation. Furthermore, these findings show that small changes in gene expression can have substantial phenotypic effects.

Additional References

RELATED GEPHE

Related Genes

2 (GPR133, Prolactin releasing hormone receptor (PrLhr/GPR10)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^10090^/and+Trait=Body size/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS