GEPHE SUMMARY

Gephebase Gene

growth hormone receptor (GHR) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^growth hormone receptor (GHR)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001475

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#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

Gray wolf of 38 to 66 kg

Trait State in Taxon B

Dog of 6.6 kg on average

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

gray wolf

Synonyms

gray wolf; grey wolf; Canis lupus Linnaeus, 1758

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; Laurasiatheria; Carnivora; Caniformia; Canidae; Canis

Parent

Canis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9611)

NCBI Taxonomy ID

9612 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9612)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

dog

Synonyms

Canis canis; Canis domesticus; Canis familiaris; dog; dogs; Canis familiaris Linnaeus, 1758; Canis lupus familiaris Linnaeus, 1758

Rank

subspecies

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Carnivora; Caniformia; Canidae; Canis; Canis lupus

Parent

Canis lupus (gray wolf) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9612)

NCBI Taxonomy ID

9615 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9615)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

GHR

Synonyms

-

String

9615.ENSCAFP00000037936 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9615.ENSCAFP00000037936)

Sequence Similarities

Belongs to the type I cytokine receptor family. Type 1 subfamily.

GO - Molecular Function

GO:0017046 : peptide hormone binding (https://www.ebi.ac.uk/QuickGO/term/GO:0017046)
GO:0019955 : cytokine binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019955)
GO:0004896 : cytokine receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004896)
GO:0019838 : growth factor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019838)

UniProtKB Canis lupus familiaris

Q9TU69 (http://www.uniprot.org/uniprot/Q9TU69)

GenebankID or UniProtKB

AF133835 (https://www.ncbi.nlm.nih.gov/nuccore/AF133835)

GO:0004903 : growth hormone receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004903)

GO - Biological Process

GO:0050731 : positive regulation of peptidyl-tyrosine phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0050731)
GO:0006897 : endocytosis (https://www.ebi.ac.uk/QuickGO/term/GO:0006897)
GO:0060396 : growth hormone receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0060396)
GO:0046427 : positive regulation of JAK-STAT cascade
(https://www.ebi.ac.uk/QuickGO/term/GO:0046427)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0043235 : receptor complex (https://www.ebi.ac.uk/QuickGO/term/GO:0043235)
GO:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)
GO:0009897 : external side of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0009897)
GO:0070195 : growth hormone receptor complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0070195)

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

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

G>A in exon 5 p.E191K in extracellular domain

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Glu	Lys	191

Main Reference

Derived variants at six genes explain nearly half of size reduction in dog breeds. (2013) (https://pubmed.ncbi.nlm.nih.gov/24026177)

Authors

Rimbault M; Beale HC; Schoenebeck JJ; Hoopes BC; Allen JJ; Kilroy-Glynn P; Wayne RK; Sutter NB; Ostrander EA

Abstract

Selective breeding of dogs by humans has generated extraordinary diversity in body size. A number of multibreed analyses have been undertaken to identify the genetic basis of this diversity. We analyzed four loci discovered in a previous genome-wide association study that used 60,968 SNPs to identify size-associated genomic intervals, which were too large to assign causative roles to genes. First, we performed fine-mapping to define critical intervals that included the candidate genes GHR, HMGA2, SMAD2, and STC2, identifying five highly associated markers at the four loci. We hypothesize that three of the variants are likely to be causative. We then genotyped each marker, together with previously reported size-associated variants in the IGF1 and IGF1R genes, on a panel of 500 domestic dogs from 93 breeds, and identified the ancestral allele by genotyping the same markers on 30 wild canids. We observed that the derived alleles at all markers correlated with reduced body size, and smaller dogs are more likely to carry derived alleles at multiple markers. However, breeds are not generally fixed at all markers; multiple combinations of genotypes are found within most breeds. Finally, we show that 46%-52.5% of the variance in body size of dog breeds can be explained by seven markers in proximity to exceptional candidate genes. Among breeds with standard weights <41 kg (90 lb), the genotypes accounted for 64.3% of variance in weight. This work advances our understanding of mammalian growth by describing genetic contributions to canine size determination in non-giant dog breeds.

Additional References

RELATED GEPHE

Related Genes

5 (HMGA2, Insulin-like growth factor 1 (IGF1), Insulin-like growth factor receptor 1 (IGF1R), SMAD family member 2 (SMAD2), stanniocalcin 2 (STC2))
(https://www.gephebase.org/search-criteria?/or+Taxon ID=^9612^/and+Trait=Body size/or+Taxon ID=^9615^/and+Trait=Body size/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^growth hormone receptor (GHR)^/and+Taxon ID=^9612^/or+Gene Gephebase=^growth hormone receptor (GHR)^/and+Taxon ID=^9615^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

each variant is potentially causal