GEPHE SUMMARY

Gephebase Gene

BHLHE41 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^BHLHE41^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000144

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Homo sapiens - lowlands

Trait State in Taxon B

Homo sapiens - Ethiopian highlands

Ancestral State

Data not curated

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

human

Synonyms

human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampiens; Homo sapeins; Homo sapian; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Humo sapiens

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; Primates; Haplorrhini; Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo

Parent

Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605)

NCBI Taxonomy ID

9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

human

Synonyms

human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampiens; Homo sapeins; Homo sapian; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Humo sapiens

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; Primates; Haplorrhini; Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo

Parent

Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605)

NCBI Taxonomy ID

9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

BHLHE41

Synonyms

DEC2; hDEC2; BHLHB3; SHARP1

String

9606.ENSP00000242728 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000242728)

Sequence Similarities

-

GO - Molecular Function

GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)
GO:0046982 : protein heterodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046982)

UniProtKB Homo sapiens

Q9C0J9 (http://www.uniprot.org/uniprot/Q9C0J9)

GenebankID or UniProtKB

EF015896 (https://www.ncbi.nlm.nih.gov/nuccore/EF015896)

GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000977)
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
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:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000978)
GO:0043425 : bHLH transcription factor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043425)
GO:0001227 : DNA-binding transcription repressor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001227)
GO:0070888 : E-box binding (https://www.ebi.ac.uk/QuickGO/term/GO:0070888)
GO:0042826 : histone deacetylase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042826)
GO:0043426 : MRF binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043426)
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001078)
GO:0001102 : RNA polymerase II activating transcription factor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0001102)
GO:0000980 : RNA polymerase II distal enhancer sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000980)
GO:1990837 : sequence-specific double-stranded DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:1990837)
GO:0003714 : transcription corepressor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003714)

GO - Biological Process

GO:0050767 : regulation of neurogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0050767)
GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
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:0008283 : cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0008283)
GO:0009887 : animal organ morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0009887)
GO:0032922 : circadian regulation of gene expression (https://www.ebi.ac.uk/QuickGO/term/GO:0032922)
GO:0010832 : negative regulation of myotube differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0010832)
GO:0010944 : negative regulation of transcription by competitive promoter binding (https://www.ebi.ac.uk/QuickGO/term/GO:0010944)
GO:0007219 : Notch signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007219)
GO:0001756 : somitogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0001756)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

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

unknown

Experimental Evidence

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

Main Reference

Genetic signatures reveal high-altitude adaptation in a set of ethiopian populations. (2013) (https://pubmed.ncbi.nlm.nih.gov/23666210)

Authors

Huerta-SÃ¡nchez E; Degiorgio M; Pagani L; Tarekegn A; Ekong R; Antao T; Cardona A; Montgomery HE; Cavalleri GL; Robbins PA; Weale ME; Bradman N; Bekele E; Kivisild T; Tyler-Smith C; Nielsen R

Abstract

The Tibetan and Andean Plateaus and Ethiopian highlands are the largest regions to have long-term high-altitude residents. Such populations are exposed to lower barometric pressures and hence atmospheric partial pressures of oxygen. Such "hypobaric hypoxia" may limit physical functional capacity, reproductive health, and even survival. As such, selection of genetic variants advantageous to hypoxic adaptation is likely to have occurred. Identifying signatures of such selection is likely to help understanding of hypoxic adaptive processes. Here, we seek evidence of such positive selection using five Ethiopian populations, three of which are from high-altitude areas in Ethiopia. As these populations may have been recipients of Eurasian gene flow, we correct for this admixture. Using single-nucleotide polymorphism genotype data from multiple populations, we find the strongest signal of selection in BHLHE41 (also known as DEC2 or SHARP1). Remarkably, a major role of this gene is regulation of the same hypoxia response pathway on which selection has most strikingly been observed in both Tibetan and Andean populations. Because it is also an important player in the circadian rhythm pathway, BHLHE41 might also provide insights into the mechanisms underlying the recognized impacts of hypoxia on the circadian clock. These results support the view that Ethiopian, Andean, and Tibetan populations living at high altitude have adapted to hypoxia differently, with convergent evolution affecting different genes from the same pathway.

Additional References

RELATED GEPHE

Related Genes

4 (EGLN1, EPAS1, PPAR-alpha, hemoglobin; HBA and HBB) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9606^/and+Trait=Hypoxia response/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS