GEPHE SUMMARY

Gephebase Gene

Oca2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Oca2^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000747

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

Coloration (eyes; skin, hair) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (eyes; skin, hair)^#gephebase-summary-title)

Trait State in Taxon A

Homo sapiens - Eurasian populations

Trait State in Taxon B

Homo sapiens -Eurasian populations (also; see Cape Verde 2013 study)

Ancestral State

Unknown

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

Oca2

Synonyms

p; D7Nic1; p<cas>; D7H15S12; D7Icr28RN; P

String

10090.ENSMUSP00000032633 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000032633)

Sequence Similarities

Belongs to the CitM (TC 2.A.11) transporter family.

GO - Molecular Function

-

GO - Biological Process

GO:0055085 : transmembrane transport (https://www.ebi.ac.uk/QuickGO/term/GO:0055085)

UniProtKB Mus musculus

Q62052 (http://www.uniprot.org/uniprot/Q62052)

GenebankID or UniProtKB

AAH12097 (https://www.ncbi.nlm.nih.gov/nuccore/AAH12097)

GO:0042438 : melanin biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0042438)
GO:0043473 : pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0043473)
GO:0008283 : cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0008283)
GO:0048066 : developmental pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048066)
GO:0030318 : melanocyte differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030318)
GO:0007286 : spermatid development (https://www.ebi.ac.uk/QuickGO/term/GO:0007286)

GO - Cellular Component

GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0010008 : endosome membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0010008)
GO:0005789 : endoplasmic reticulum membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005789)
GO:0005765 : lysosomal membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005765)
GO:0033162 : melanosome membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0033162)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Causative SNP in enhancer localized in intron of neighbor gene HERC2 : likely rs12913832 within HERC2 which influences on OCA2 expression in eye hair and skin pigmentation

Experimental Evidence

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

Main Reference

Blue eye color in humans may be caused by a perfectly associated founder mutation in a regulatory element located within the HERC2 gene inhibiting OCA2 expression. (2008) (https://pubmed.ncbi.nlm.nih.gov/18172690)

Authors

Eiberg H; Troelsen J; Nielsen M; Mikkelsen A; Mengel-From J; Kjaer KW; Hansen L

Abstract

The human eye color is a quantitative trait displaying multifactorial inheritance. Several studies have shown that the OCA2 locus is the major contributor to the human eye color variation. By linkage analysis of a large Danish family, we finemapped the blue eye color locus to a 166 Kbp region within the HERC2 gene. By association analyses, we identified two SNPs within this region that were perfectly associated with the blue and brown eye colors: rs12913832 and rs1129038. Of these, rs12913832 is located 21.152 bp upstream from the OCA2 promoter in a highly conserved sequence in intron 86 of HERC2. The brown eye color allele of rs12913832 is highly conserved throughout a number of species. As shown by a Luciferase assays in cell cultures, the element significantly reduces the activity of the OCA2 promoter and electrophoretic mobility shift assays demonstrate that the two alleles bind different subsets of nuclear extracts. One single haplotype, represented by six polymorphic SNPs covering half of the 3′ end of the HERC2 gene, was found in 155 blue-eyed individuals from Denmark, and in 5 and 2 blue-eyed individuals from Turkey and Jordan, respectively. Hence, our data suggest a common founder mutation in an OCA2 inhibiting regulatory element as the cause of blue eye color in humans. In addition, an LOD score of Z = 4.21 between hair color and D14S72 was obtained in the large family, indicating that RABGGTA is a candidate gene for hair color.

Additional References

A genome-wide association study identifies novel alleles associated with hair color and skin pigmentation. (2008) (https://pubmed.ncbi.nlm.nih.gov/18483556)
HERC2 rs12913832 modulates human pigmentation by attenuating chromatin-loop formation between a long-range enhancer and the OCA2 promoter. (2012) (https://pubmed.ncbi.nlm.nih.gov/22234890)
Genetic architecture of skin and eye color in an African-European admixed population. (2013) (https://pubmed.ncbi.nlm.nih.gov/23555287)
Loci associated with skin pigmentation identified in African populations. (2017) (https://pubmed.ncbi.nlm.nih.gov/29025994)
Meta-analysis of GWA studies provides new insights on the genetic architecture of skin pigmentation in recently admixed populations. (2019) (https://pubmed.ncbi.nlm.nih.gov/31315583)

RELATED GEPHE

Related Genes

14 (Agouti (ASIP), EGFR, EIF2S2, GSS (glutathione synthetase), IRF4, Kit ligand, MC1R, MFSD12, OPRM1, SLC24A5 (NCKX5), SLC45A2=MATP, TPCN2, tyrosinase (TYR), tyrosinase-related protein 1 (TYRP1)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9606^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Oca2^/and+Taxon ID=^9606^/or+Gene Gephebase=^Oca2^/and+Taxon ID=^9606^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@Parallelism