GEPHE SUMMARY

Gephebase Gene
DDB1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^DDB1^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00001363
Main curator
Prigent

PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)
Trait
Resistance to UV irradiation (sun exposure to skin) (https://www.gephebase.org/search-criteria?/and+Trait=^Resistance to UV irradiation (sun exposure to skin)^#gephebase-summary-title)
Trait State in Taxon A
DNA repair in darker skin tones in various populations
Trait State in Taxon B
DNA repair associated with lighter skin tones in Eurasia
Ancestral State
Taxon A
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
DDB1
Synonyms
XPE; DDBA; XAP1; XPCE; XPE-BF; UV-DDB1
String
9606.ENSP00000301764
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000301764)
Sequence Similarities
Belongs to the DDB1 family.
GO - Molecular Function
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)
GO:0044877 : protein-containing complex binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0044877)

UniProtKB Homo sapiens
Q16531 (http://www.uniprot.org/uniprot/Q16531)
GenebankID or UniProtKB
()

GO:0030674 : protein binding, bridging
(https://www.ebi.ac.uk/QuickGO/term/GO:0030674)
GO:0003684 : damaged DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0003684)
GO:0097602 : cullin family protein binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0097602)
GO:0071987 : WD40-repeat domain binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0071987)

GO - Biological Process

GO:0016567 : protein ubiquitination (https://www.ebi.ac.uk/QuickGO/term/GO:0016567)
GO:0043066 : negative regulation of apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043066)
GO:0006511 : ubiquitin-dependent protein catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006511)
GO:0043687 : post-translational protein modification
(https://www.ebi.ac.uk/QuickGO/term/GO:0043687)
GO:0042752 : regulation of circadian rhythm
(https://www.ebi.ac.uk/QuickGO/term/GO:0042752)
GO:0045732 : positive regulation of protein catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0045732)
GO:0043161 : proteasome-mediated ubiquitin-dependent protein catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043161)
GO:0042769 : DNA damage response, detection of DNA damage
(https://www.ebi.ac.uk/QuickGO/term/GO:0042769)
GO:0016032 : viral process (https://www.ebi.ac.uk/QuickGO/term/GO:0016032)
GO:0070914 : UV-damage excision repair
(https://www.ebi.ac.uk/QuickGO/term/GO:0070914)
GO:0016055 : Wnt signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0016055)
GO:0006974 : cellular response to DNA damage stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0006974)
GO:0006281 : DNA repair (https://www.ebi.ac.uk/QuickGO/term/GO:0006281)
GO:0045722 : positive regulation of gluconeogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0045722)
GO:0048511 : rhythmic process (https://www.ebi.ac.uk/QuickGO/term/GO:0048511)
GO:0010498 : proteasomal protein catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0010498)
GO:0070911 : global genome nucleotide-excision repair
(https://www.ebi.ac.uk/QuickGO/term/GO:0070911)
GO:0035518 : histone H2A monoubiquitination
(https://www.ebi.ac.uk/QuickGO/term/GO:0035518)
GO:0051702 : interaction with symbiont
(https://www.ebi.ac.uk/QuickGO/term/GO:0051702)
GO:0006289 : nucleotide-excision repair
(https://www.ebi.ac.uk/QuickGO/term/GO:0006289)
GO:0000715 : nucleotide-excision repair, DNA damage recognition
(https://www.ebi.ac.uk/QuickGO/term/GO:0000715)
GO:0000717 : nucleotide-excision repair, DNA duplex unwinding
(https://www.ebi.ac.uk/QuickGO/term/GO:0000717)
GO:0033683 : nucleotide-excision repair, DNA incision
(https://www.ebi.ac.uk/QuickGO/term/GO:0033683)
GO:0006295 : nucleotide-excision repair, DNA incision, 3′-to lesion
(https://www.ebi.ac.uk/QuickGO/term/GO:0006295)
GO:0006296 : nucleotide-excision repair, DNA incision, 5′-to lesion
(https://www.ebi.ac.uk/QuickGO/term/GO:0006296)
GO:0006294 : nucleotide-excision repair, preincision complex assembly
(https://www.ebi.ac.uk/QuickGO/term/GO:0006294)
GO:0006293 : nucleotide-excision repair, preincision complex stabilization
(https://www.ebi.ac.uk/QuickGO/term/GO:0006293)
GO:0046726 : positive regulation by virus of viral protein levels in host cell
(https://www.ebi.ac.uk/QuickGO/term/GO:0046726)
GO:0045070 : positive regulation of viral genome replication
(https://www.ebi.ac.uk/QuickGO/term/GO:0045070)
GO:1902188 : positive regulation of viral release from host cell
(https://www.ebi.ac.uk/QuickGO/term/GO:1902188)
GO:1901990 : regulation of mitotic cell cycle phase transition
(https://www.ebi.ac.uk/QuickGO/term/GO:1901990)
GO:0006283 : transcription-coupled nucleotide-excision repair
(https://www.ebi.ac.uk/QuickGO/term/GO:0006283)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005654 : nucleoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005654)
GO:0070062 : extracellular exosome (https://www.ebi.ac.uk/QuickGO/term/GO:0070062)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0032991 : protein-containing complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0032991)
GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)
GO:0000784 : nuclear chromosome, telomeric region

(https://www.ebi.ac.uk/QuickGO/term/GO:0000784)
GO:0080008 : Cul4-RING E3 ubiquitin ligase complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0080008)
GO:0031464 : Cul4A-RING E3 ubiquitin ligase complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0031464)
GO:0031465 : Cul4B-RING E3 ubiquitin ligase complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0031465)
GO:0031461 : cullin-RING ubiquitin ligase complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0031461)

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

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

Molecular Details of the Mutation

most strongly associated SNPs are located in a region conserved across vertebrates flanked by TMEM138 and TMEM216 ~36 to 44 kb upstream of DDB1 and in high LD ; includes rs7948623 located 172 bp downstream of TMEM138 which shows enhancer activity in melanoma cells and interacts with the promoters of DDB1

Experimental Evidence

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

Main Reference

Loci associated with skin pigmentation identified in African populations. (2017) (https://pubmed.ncbi.nlm.nih.gov/29025994)

Authors

Crawford NG; Kelly DE; Hansen MEB; Beltrame MH; Fan S; Bowman SL; Jewett E; Ranciaro A; Thompson S; Lo Y; Pfeifer SP; Jensen JD; Campbell MC; Beggs W; Hormozdiari F; Mpoloka SW; Mokone GG; Nyambo T; Meskel DW; Belay G; Haut J; ; Rothschild H; Zon L; Zhou Y; Kovacs MA; Xu M; Zhang T; Bishop K; Sinclair J; Rivas C; Elliot E; Choi J; Li SA; Hicks B; Burgess S; Abnet C; Watkins-Chow DE; Oceana E; Song YS; Eskin E; Brown KM; Marks MS; Loftus SK; Pavan WJ; Yeager M; Chanock S; Tishkoff SA

Abstract

Despite the wide range of skin pigmentation in humans, little is known about its genetic basis in global populations. Examining ethnically diverse African genomes, we identify variants in or near SLC24A5, MFSD12, DDB1, TMEM138, OCA2, and HERC2 that are significantly associated with skin pigmentation. Genetic evidence indicates that the light pigmentation variant at SLC24A5 was introduced into East Africa by gene flow from non-Africans. At all other loci, variants associated with dark pigmentation in Africans are identical by descent in South Asian and Australo-Melanesian populations. Functional analyses indicate that MFSD12 encodes a lysosomal protein that affects melanogenesis in zebrafish and mice, and that mutations in melanocyte-specific regulatory regions near DDB1/TMEM138 correlate with expression of ultraviolet response genes under selection in Eurasians.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

possible selective sweep with high levels of homozygosity extending ~350 to 550 kb in Europeans and Asians