GEPHE SUMMARY

Gephebase Gene

lanosterol c14 demethylase (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^lanosterol c14 demethylase^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001951

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

Cholesterol metabolism (cholesterol biosynthesis) (https://www.gephebase.org/search-criteria?/and+Trait=^Cholesterol metabolism (cholesterol biosynthesis)^#gephebase-summary-title)

Trait State in Taxon A

able to synthesise cholesterol de novo

Trait State in Taxon B

unable to synthesise cholesterol de novo

Ancestral State

Taxon A

Taxonomic Status

Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intergeneric or Higher^#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

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

Common Name

-

Synonyms

roundworm; Rhabditis elegans; Caenorhabditis elegans (Maupas, 1900); Rhabditis elegans Maupas, 1900

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Nematoda; Chromadorea; Rhabditida; Rhabditina; Rhabditomorpha; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis

Parent

Caenorhabditis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6237)

NCBI Taxonomy ID

6239 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6239)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

CYP51A1

Synonyms

CYP51; LDM; CP51; CYPL1; P450L1; P450-14DM

String

9606.ENSP00000003100 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000003100)

Sequence Similarities

Belongs to the cytochrome P450 family.

GO - Molecular Function

GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)
GO:0008398 : sterol 14-demethylase activity

UniProtKB Homo sapiens

Q16850 (http://www.uniprot.org/uniprot/Q16850)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0008398)

GO - Biological Process

GO:0055114 : oxidation-reduction process
(https://www.ebi.ac.uk/QuickGO/term/GO:0055114)
GO:0006695 : cholesterol biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006695)
GO:0016126 : sterol biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0016126)
GO:0016125 : sterol metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0016125)
GO:0006694 : steroid biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006694)
GO:0042177 : negative regulation of protein catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042177)
GO:0045540 : regulation of cholesterol biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0045540)
GO:0033488 : cholesterol biosynthetic process via 24,25-dihydrolanosterol
(https://www.ebi.ac.uk/QuickGO/term/GO:0033488)
GO:1900222 : negative regulation of amyloid-beta clearance
(https://www.ebi.ac.uk/QuickGO/term/GO:1900222)
GO:0050709 : negative regulation of protein secretion
(https://www.ebi.ac.uk/QuickGO/term/GO:0050709)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0005783 : endoplasmic reticulum
(https://www.ebi.ac.uk/QuickGO/term/GO:0005783)
GO:0005789 : endoplasmic reticulum membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005789)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Deletion Size

unknown

Molecular Details of the Mutation

gene absent in the genome

Experimental Evidence

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

Main Reference

Preservation of genes involved in sterol metabolism in cholesterol auxotrophs: facts and hypotheses. (2008) (https://pubmed.ncbi.nlm.nih.gov/18682733)

Authors

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Abstract

It is known that primary sequences of enzymes involved in sterol biosynthesis are well conserved in organisms that produce sterols de novo. However, we provide evidence for a preservation of the corresponding genes in two animals unable to synthesize cholesterol (auxotrophs): Drosophila melanogaster and Caenorhabditis elegans.

We have been able to detect bona fide orthologs of several ERG genes in both organisms using a series of complementary approaches. We have detected strong sequence divergence between the orthologs of the nematode and of the fruitfly; they are also very divergent with respect to the orthologs in organisms able to synthesize sterols de novo (prototrophs). Interestingly, the orthologs in both the nematode and the fruitfly are still under selective pressure. It is possible that these genes, which are not involved in cholesterol synthesis anymore, have been recruited to perform different new functions. We propose a more parsimonious way to explain their accelerated evolution and subsequent stabilization. The products of ERG genes in prototrophs might be involved in several biological roles, in addition to sterol synthesis. In the case of the nematode and the fruitfly, the relevant genes would have lost their ancestral function in cholesterogenesis but would have retained the other function(s), which keep them under pressure.

By exploiting microarray data we have noticed a strong expressional correlation between the orthologs of ERG24 and ERG25 in D. melanogaster and genes encoding factors involved in intracellular protein trafficking and folding and with Start1 involved in ecdysteroid synthesis. These potential functional connections are worth being explored not only in Drosophila, but also in Caenorhabditis as well as in sterol prototrophs.

Additional References

RELATED GEPHE

Related Genes

3 (lanosterol synthase, squalene synthase, sterol C5 desaturase) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9606^/and+Trait=Cholesterol metabolism/or+Taxon ID=^6239^/and+Trait=Cholesterol metabolism/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^lanosterol c14 demethylase^/and+Taxon ID=^9606^/or+Gene Gephebase=^lanosterol c14 demethylase^/and+Taxon ID=^6239^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@ParrallelEvolution in insects