

GEPHE SUMMARY

<p>MDR1 (<a +mdr1+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+MDR1+"#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001858</p> <p>Courtier</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)</p> <p>Xenobiotic resistance (<a +xenobiotic+resistance+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Xenobiotic+resistance+"#gephebase-summary-title)</p> <p>sensitive</p> <p>resistant</p> <p>Taxon A</p> <p>Intraspecific (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Homo sapiens (<a +homo+sapiens+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Homo+sapiens+"#gephebase-summary-title)</p> <p>Common Name</p> <p>human</p> <p>Synonyms</p> <p>human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampiens; Homo sapeins; Homo sapien; Homo sapiens; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Humo sapiens</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>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</p> <p>Parent</p> <p>Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9605)</p> <p>NCBI Taxonomy ID</p> <p>9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9606)</p> <p>is Taxon A an Intraspecies?</p> <p>No</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Homo sapiens (<a +homo+sapiens+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Homo+sapiens+"#gephebase-summary-title)</p> <p>Common Name</p> <p>human</p> <p>Synonyms</p> <p>human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampiens; Homo sapeins; Homo sapien; Homo sapiens; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Humo sapiens</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>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</p> <p>Parent</p> <p>Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9605)</p> <p>NCBI Taxonomy ID</p> <p>9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9606)</p> <p>is Taxon B an Intraspecies?</p> <p>No</p>
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GENOTYPIC CHANGE

<p>ABCB1</p> <p>MDR1; CLCS; P-GP; PGY1; ABC20; CD243; GP170</p> <p>9606.ENSPO0000478255 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSPO0000478255)</p> <p>Sequence Similarities</p> <p>Belongs to the ABC transporter superfamily. ABCB family. Multidrug resistance exporter (TC 3.A.1.201) subfamily.</p> <p>GO - Molecular Function</p> <p>GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)</p> <p>GO:0042626 : ATPase activity, coupled to transmembrane movement of substances (https://www.ebi.ac.uk/QuickGO/term/GO:0042626)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p>	<p>P08183 (http://www.uniprot.org/uniprot/P08183)</p> <p>0</p>	<p>UniProtKB Homo sapiens</p> <p>GenebankID or UniProtKB</p>
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GO:0090554 : phosphatidylcholine-translocating ATPase activity
 (https://www.ebi.ac.uk/QuickGO/term/GO:0090554)
 GO:0005215 : transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005215)
 GO:0099038 : ceramide-translocating ATPase activity
 (https://www.ebi.ac.uk/QuickGO/term/GO:0099038)
 GO:0090555 : phosphatidylethanolamine-translocating ATPase activity
 (https://www.ebi.ac.uk/QuickGO/term/GO:0090555)

GO - Biological Process

GO:0045332 : phospholipid translocation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0045332)
 GO:0055085 : transmembrane transport
 (https://www.ebi.ac.uk/QuickGO/term/GO:0055085)
 GO:0042493 : response to drug (https://www.ebi.ac.uk/QuickGO/term/GO:0042493)
 GO:0000086 : G2/M transition of mitotic cell cycle
 (https://www.ebi.ac.uk/QuickGO/term/GO:0000086)
 GO:0099040 : ceramide translocation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0099040)
 GO:1901529 : positive regulation of anion channel activity
 (https://www.ebi.ac.uk/QuickGO/term/GO:1901529)
 GO:2001225 : regulation of chloride transport
 (https://www.ebi.ac.uk/QuickGO/term/GO:2001225)
 GO:0047484 : regulation of response to osmotic stress
 (https://www.ebi.ac.uk/QuickGO/term/GO:0047484)
 GO:0072089 : stem cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0072089)

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:0016324 : apical plasma membrane
 (https://www.ebi.ac.uk/QuickGO/term/GO:0016324)
 GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
 GO:0070062 : extracellular exosome (https://www.ebi.ac.uk/QuickGO/term/GO:0070062)
 GO:0009986 : cell surface (https://www.ebi.ac.uk/QuickGO/term/GO:0009986)

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

Synonymous

Molecular Details of the Mutation

C3435T - synonymous mutation Ile - The SNP at position 26/3435 that changes the codon from ATC to ATT (Ile) reduces the codon usage from 47% to 35% (RSCU values change from 20.9 to 15.8). Leads to similar mRNA and protein levels but altered conformation of the protein.

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	ATC	ATT	-
Amino-acid	Ile	Ile	-

Main Reference

A "silent" polymorphism in the MDR1 gene changes substrate specificity. (2007) (https://pubmed.ncbi.nlm.nih.gov/17185560)

Authors

Kimchi-Sarfaty C; Oh JM; Kim IW; Sauna ZE; Calcagno AM; Ambudkar SV; Gottesman MM

Abstract

Synonymous single-nucleotide polymorphisms (SNPs) do not produce altered coding sequences, and therefore they are not expected to change the function of the protein in which they occur. We report that a synonymous SNP in the Multidrug Resistance 1 (MDR1) gene, part of a haplotype previously linked to altered function of the MDR1 gene product P-glycoprotein (P-gp), nonetheless results in P-gp with altered drug and inhibitor interactions. Similar mRNA and protein levels, but altered conformations, were found for wild-type and polymorphic P-gp. We hypothesize that the presence of a rare codon, marked by the synonymous polymorphism, affects the timing of cotranslational folding and insertion of P-gp into the membrane, thereby altering the structure of substrate and inhibitor interaction sites.

Additional References

RELATED GEPHE

Related Genes

4 (alcohol dehydrogenase (ADH1B), CYP2C9, CYP4F2, Vkorc1) (https://www.gephebase.org/search-criteria?/or+Taxon ID="9606"/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Synonymous mutation