

GEPHE SUMMARY

	Gephebase Gene	GepheID
AMPD1 [clinical; candidate gene study; added for insights on fly-human parallelism] (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^AMPD1 [clinical; candidate gene study; added for insights on fly-human parallelism]^#gephebase-summary-title)	GP00000084	
	Entry Status	Main curator
Published		Martin

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	Trait	
Drug resistance (https://www.gephebase.org/search-criteria?/and+Trait=^Drug resistance^#gephebase-summary-title)	Trait State in Taxon A	
Homo sapiens	Trait State in Taxon B	
Homo sapiens	Ancestral State	
Data not curated	Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)		
	Taxon A	Taxon B
	Latin Name	Latin Name
Homo sapiens (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Homo sapiens^#gephebase-summary-title)	Homo sapiens (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Homo sapiens^#gephebase-summary-title)	Homo sapiens (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Homo sapiens^#gephebase-summary-title)
	Common Name	Common Name
human	human	human
	Synonyms	Synonyms
human; man; Homo sapiens Linnaeus, 1758; Homo sapiens; Homo sampaens; Homo sapien; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Homo sapiens	human; man; Homo sapiens Linnaeus, 1758; Homo sapiens; Homo sampaens; Homo sapien; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Homo sapiens	human; man; Homo sapiens Linnaeus, 1758; Homo sapiens; Homo sampaens; Homo sapien; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Homo sapiens
	Rank	Rank
species	species	species
	Lineage	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	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	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	Parent
Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605)	Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605)	Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605)
9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)	9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)	9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name		
AMPD1	P23109 (http://www.uniprot.org/uniprot/P23109)		UniProtKB Homo sapiens
	Synonyms		
MAD; MADA; MMDD	M37920 (https://www.ncbi.nlm.nih.gov/nuccore/M37920)		GenebankID or UniProtKB
	String		
9606.ENSP00000430075 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000430075)			
	Sequence Similarities		
Belongs to the metallo-dependent hydrolases superfamily. Adenosine and AMP deaminases family.			
	GO - Molecular Function		
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)			

GO:0003876 : AMP deaminase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003876>)
GO:0032036 : myosin heavy chain binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032036>)

GO - Biological Process

GO:0032264 : IMP salvage (<https://www.ebi.ac.uk/QuickGO/term/GO:0032264>)
GO:0043101 : purine-containing compound salvage
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043101>)
GO:0010033 : response to organic substance
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010033>)

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)

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

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

Main Reference

A clinical pharmacogenetic model to predict the efficacy of methotrexate monotherapy in recent-onset rheumatoid arthritis. (2007) (<https://pubmed.ncbi.nlm.nih.gov/17530705>)

Authors

Wessels JA; van der Kooij SM; le Cessie S; Kievit W; Barerra P; Allaart CF; Huizinga TW; Guchelaar HJ;

Abstract

To develop a clinical pharmacogenetic model to predict the efficacy of methotrexate (MTX) in rheumatoid arthritis (RA).

Two hundred five patients with newly diagnosed RA and active disease were treated with MTX (initiated at a dosage of 7.5 mg/week and increased to 15 mg/week after 4 weeks) and folic acid (1 mg/day). If the Disease Activity Score (DAS) was >2.4 at 3 months, the dosage of MTX was increased up to 25 mg/week. Twenty-four baseline variables possibly influencing disease state and drug response were selected. In addition, 17 polymorphisms in 13 genes related to the MTX mechanism of action, purine and pyrimidine synthesis, were determined. Factors were compared between responders (defined as patients with a DAS < or = 2.4 at 6 months) and nonresponders. In case of differences, a stepwise selection procedure identified the predictors for response. A clinical score was designed by simplifying regression coefficients of the independent variables. Cutoff levels were chosen based on the clinical score, and positive and negative response rates were calculated. An evaluation of the model was performed in a second group of patients.

The model for MTX efficacy consisted of sex, rheumatoid factor and smoking status, the DAS, and 4 polymorphisms in the AMPD1, ATIC, ITPA, and MTHFD1 genes. This prediction model was transformed into a scoring system ranging from 0 to 11.5. Scores of < or = 3.5 had a true positive response rate of 95%. Scores of > or = 6 had a true negative response rate of 86%. Sixty percent of the patients were categorized as either responders or nonresponders, whereas 32% of the patients were categorized using a nongenetic model. Evaluation of the model in 38 additional patients with RA supported the results.

This study established a model for predicting the efficacy of MTX in patients with RA. This pharmacogenetic model may lead to better-tailored initial treatment decisions in patients with RA.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS