GEPHE SUMMARY

Gephebase Gene

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)

Entry Status

Published

GepheID

GP00000084

Main curator

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

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

AMPD1

Synonyms

MAD; MADA; MMDD

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)

UniProtKB Homo sapiens

P23109 (http://www.uniprot.org/uniprot/P23109)

GenebankID or UniProtKB

M37920 (https://www.ncbi.nlm.nih.gov/nuccore/M37920)

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

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS