GEPHE SUMMARY

Gephebase Gene

Isocitrate dehydrogenase (NADP) (IDH) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Isocitrate dehydrogenase (NADP) (IDH)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000506

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

Temperature tolerance (temperature range) (https://www.gephebase.org/search-criteria?/and+Trait=^Temperature tolerance (temperature range)^#gephebase-summary-title)

Trait State in Taxon A

Mytilus galloprovincialis (warm adapted)

Trait State in Taxon B

Mytilus trossulus (cold-adapted)

Ancestral State

Data not curated

Taxonomic Status

Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name

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

Common Name

Mediterranean mussel

Synonyms

Mediterranean mussel; Mytilus galloprovincialis Lamarck, 1819

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Lophotrochozoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida; Mytiloidea; Mytilidae; Mytilinae; Mytilus

Parent

Mytilus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6548)

NCBI Taxonomy ID

29158 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 29158)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

common blue mussel

Synonyms

common blue mussel; bay mussel; Mytilus trossulus Gould, 1850

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Lophotrochozoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida; Mytiloidea; Mytilidae; Mytilinae; Mytilus

Parent

Mytilus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6548)

NCBI Taxonomy ID

6551 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6551)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

-

Synonyms

-

String

-

Sequence Similarities

Belongs to the isocitrate and isopropylmalate dehydrogenases family.

GO - Molecular Function

GO:0000287 : magnesium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000287)
GO:0004450 : isocitrate dehydrogenase (NADP+) activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004450)
GO:0051287 : NAD binding (https://www.ebi.ac.uk/QuickGO/term/GO:0051287)

GO - Biological Process

GO:0006102 : isocitrate metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006102)

UniProtKB Mytilus trossulus

I1VYX2 (http://www.uniprot.org/uniprot/I1VYX2)

GenebankID or UniProtKB

JQ429379 (https://www.ncbi.nlm.nih.gov/nuccore/JQ429379)

GO:0006099 : tricarboxylic acid cycle
(https://www.ebi.ac.uk/QuickGO/term/GO:0006099)

GO - Cellular Component

-

Mutation #1

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

Nonsynonymous

Molecular Details of the Mutation

Two a.a. substitutions accounting for Km differences - Site 205 is polymorphic for Asp/Glu in M. trossulus-IDH but fixed for His in M. galloprovincialis-IDH

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	His	-	205

Main Reference

Functional determinants of temperature adaptation in enzymes of cold- versus warm-adapted mussels (Genus Mytilus). (2012) (https://pubmed.ncbi.nlm.nih.gov/22491035)

Authors

Lockwood BL; Somero GN

Abstract

Temperature is a strong selective force on the evolution of proteins due to its effects on higher orders of protein structure and, thereby, on critical protein functions like ligand binding and catalysis. Comparisons among orthologous proteins from differently thermally adapted species show consistent patterns of adaptive variation in function, but few studies have examined functional adaptation among multiple structural families of proteins. Thus, with our present state of knowledge, it is difficult to predict what fraction of the proteome will exhibit adaptive variation in the face of temperature increases of a few to several degrees Celsius, that is, temperature increases of the magnitude predicted by models of global warming. Here, we compared orthologous enzymes of the warm-adapted Mediterranean mussel Mytilus galloprovincialis and the cold-adapted Mytilus trossulus, a native of the North Pacific Ocean, species whose physiologies exhibit significantly different responses to temperature. We measured the effects of temperature on the kinetics (Michaelis-Menten constant-K(m)) of five enzymes that are important for ATP generation and that represent distinct protein structural families. Among phosphoglucomutase (PGM), phosphoglucose isomerase (PGI), pyruvate kinase (PK), phosphoenolpyruvate carboxykinase (GTP) (PEPCK), and isocitrate dehydrogenase (NADP) (IDH), only IDH orthologs showed significantly different thermal responses of K(m) between the two species. The K(m) of isocitrate of M. galloprovincialis-IDH was intrinsically lower and more thermally stable than that of M. trossulus-IDH and thus had higher substrate affinity at high temperatures. Two amino acid substitutions account for the functional differences between IDH orthologs, one of which allows for more hydrogen bonds to form near the mobile region of the active site in M. galloprovincialis-IDH. Taken together, our findings cast light on the targets of adaptive evolution in the context of climate change; only a minority of proteins might adapt to small changes in temperature, and these adaptations may involve only small changes in sequence.

Additional References

Mutation #2

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

Nonsynonymous

Molecular Details of the Mutation

Two a.a. substitutions accounting for Km differences - The substitution at residue 208 differs from the uncharged Asn-208 in M. trossulus-IDH to the negatively charged Asp-208 in M. galloprovincialis-IDH

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Asp	Asn	208

Main Reference

Functional determinants of temperature adaptation in enzymes of cold- versus warm-adapted mussels (Genus Mytilus). (2012) (https://pubmed.ncbi.nlm.nih.gov/22491035)

Authors

Lockwood BL; Somero GN

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect