Belongs to the PEPCase type 1 family.

GO:0006099: tricarboxylic acid cycle

GO:0008964 : phosphoenolpyruvate carboxylase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008964)

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

GO:0009760 : C4 photosynthesis (https://www.ebi.ac.uk/QuickGO/term/GO:0009760) GO:0015977 : carbon fixation (https://www.ebi.ac.uk/QuickGO/term/GO:0015977)

Gephebase Gene GephelD phosphoenolpyruvate carboxylase (PEPC) (https://www.gephebase.org/search-GP00000867 $criteria?/and + Gene\ Gephebase = ^phosphoenol pyruvate\ carboxylase\ (PEPC) ^ \#gephebase = ^phosphoenol pyruvate\ carboxylase\ (PEPC) ^ #gephebase = ^phosphoenol pyruvate\ carboxylase\ (PEPC) ^ #gephebase\ (PEPC)$ Main curator summary-title) Courtier Entry Status Published PHENOTYPIC CHANGE Trait Category Physiology (https://www.gephebase.org/search-criteria?/and+Trait $Category = ^{Physiology} \#gephebase-summary-title)$ Trait C3-C4 photosynthesis (enzymatic properties) (https://www.gephebase.org/searchcriteria?/and+Trait=^C3-C4 photosynthesis (enzymatic properties)^#gephebase-summary-Trait State in Taxon A Flaveria pringlei : C3 photosynthesis Trait State in Taxon B Flaveria trinervia : C4 photosynthesis Ancestral State Data not curated Taxonomic Status Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=`Interspecific`"#gephebase-summary-title)Taxon A Taxon B Latin Name Latin Name Flaveria pringlei Flaveria trinervia (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Flaveria $(https://www.gephebase.org/search-criteria?/and+Taxon\ and\ Synonyms=^Flaveria.) The continuous continuous and a support of the continuous co$ pringlei^#gephebase-summary-title) trinervia^#gephebase-summary-title) Common Name Common Name Synonyms Synonyms Flaveria pringlei Gand Flaveria australasica; Flaveria australasica Hook.; Flaveria trinervia (Spreng.) C.Mohr Rank Rank species species Lineage Lineage cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Trache ophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangios permae;Trache ophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangios permae;eudicotyledons; Gunneridae; Pentapetalae; asterids; campanulids; Asterales; Asteraceae; eudicotyledons; Gunneridae; Pentapetalae; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae alliance; Tageteae; Flaveria Asteroideae; Heliantheae alliance; Tageteae; Flaveria Parent Parent Flaveria () - (Rank: genus) Flaveria () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4223) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4223) NCBI Taxonomy ID NCBI Taxonomy ID (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4226) $(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4227\,)$ is Taxon A an Infraspecies? is Taxon B an Infraspecies? No Nο **GENOTYPIC CHANGE** Generic Gene Name UniProtKB Flaveria trinervia **PPCA** P30694 (http://www.uniprot.org/uniprot/P30694) GenebankID or UniProtKB Synonyms X61304 (https://www.ncbi.nlm.nih.gov/nuccore/X61304) String

Sequence Similarities

GO - Molecular Function

GO - Biological Process

Mutation #1

Presumptive Null

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

one important amino acid change in region 5: C3 plants: Ala274 and C4 plants: Ser274 - This single amino acid change was introduced by site-directed mutagenesis and shown to alter enzyme kinetics

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	Ala	Ser	274

Main Reference

Evolution of C4 phosphoenolpyruvate carboxylase in Flaveria, a conserved serine residue in the carboxyl-terminal part of the enzyme is a major determinant for C4-specific characteristics. (2000) (https://pubmed.ncbi.nlm.nih.gov/10871630)

Authors

BIäsing OE; Westhoff P; Svensson P

Abstract

C4 phosphoenolpyruvate carboxylases have evolved from ancestral C3 isoforms during the evolution of angiosperms and gained distinct kinetic and regulatory properties compared with the C3 isozymes. To identify amino acid residues and/or domains responsible for these C4-specific properties the C4 phosphoenolpyruvate carboxylase of Flaveria trinervia (C4) was compared with its orthologue in the closely related C3 plant Flaveria pringlei. Reciprocal enzyme chimera were constructed and the kinetic constants, K(0.5) and k(cat), as well as the Hill coefficient, h, were determined for the substrate phosphoenolpyruvate both in the presence and absence of the activator glucose 6-phosphate. By this approach two regions were identified which determined most of the kinetic differences of the C4 and C3 ppcA phosphoenolpyruvate carboxylases with respect to the substrate PEP. In addition, the experiments suggest that the two regions do not act additively but interact with each other. The region between amino acids 296 and 437 is essential for activation by glucose 6-phosphate. The carboxyl-terminal segment between amino acids 645 and 966 contains a C4 conserved serine or a C3 invariant alanine at position 774 in the respective enzyme isoform. Site-directed mutagenesis shows that this position is a key determinant for the kinetic properties of the two isozymes.

Additional References

 $Molecular \ evolution \ of \ C4 \ phosphoenolpy ruvate \ carboxylase \ in \ the \ genus \ Flaveria--a \ gradual \ increase \ from \ C3 \ to \ C4 \ characteristics. \ (2003) \ (https://pubmed.ncbi.nlm.nih.gov/12811556)$

Mutation #2

Presumptive Null

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

several candidate amino acid changes in region 2 - Region 2 between positions 296 and 437 makes a small but significant contribution (according to in vitro analysis of chimeric proteins)

Experimental Evidence

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

	Taxon A	Taxon B	Position
Co	odon -	-	-
Amino	-acid -	-	-

Main Reference

Evolution of C4 phosphoenolpyruvate carboxylase in Flaveria, a conserved serine residue in the carboxyl-terminal part of the enzyme is a major determinant for C4-specific characteristics. (2000) (https://pubmed.ncbi.nlm.nih.gov/10871630)

Authors

 $Bl\tilde{A} x sing \ OE; We sthoff \ P; \ Svensson \ P$

 ${\sf Abstract}$

C4 phosphoenolpyruvate carboxylases have evolved from ancestral C3 isoforms during the evolution of angiosperms and gained distinct kinetic and regulatory properties compared with the C3 isozymes. To identify amino acid residues and/or domains responsible for these C4-specific properties the C4 phosphoenolpyruvate carboxylase of Flaveria trinervia (C4) was compared with its orthologue in the closely related C3 plant Flaveria pringlei. Reciprocal enzyme chimera were constructed and the kinetic constants, K(0.5) and K(cat), as well as the Hill coefficient, K(0.5) in the presence and absence of the activator glucose 6-phosphate. By this approach two regions were identified which determined most of the kinetic differences of the C4 and C3 ppcA phosphoenolpyruvate carboxylases with respect to the substrate PEP. In addition, the

experiments suggest that the two regions do not act additively but interact with each other. The region between amino acids 296 and 437 is essential for activation by glucose 6-phosphate. The carboxyl-terminal segment between amino acids 645 and 966 contains a C4 conserved serine or a C3 invariant alanine at position 774 in the respective enzyme isoform. Site-directed mutagenesis shows that this position is a key determinant for the kinetic properties of the two isozymes.

Additional References

Molecular evolution of C4 phosphoenolpyruvate carboxylase in the genus Flaveria--a gradual increase from C3 to C4 characteristics. (2003) (https://pubmed.ncbi.nlm.nih.gov/12811556)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

 $2 \ (https://www.gephebase.org/search-criteria?/or+Gene \ Gephebase=^phosphoenolpyruvate \ carboxylase \ (PEPC)^/and+Taxon \ ID=^4226^/or+Gene \ Gephebase=^phosphoenolpyruvate \ carboxylase \ (PEPC)^/or+Gene \ Gephebase=^phosphoenolpyruvate \ carboxylase \ (PEPC)^/or+Gene \ Gephebase=^phosphoenolpyruvate \ carboxylase \ (PEPC)^/or+Gene \ Gephebase=^phosphoenolpyruvate \ (PEPC)^/or+Gene \ Gephebase=^phosphoenolpyruvate \ (PEPC)^/or+Gene \ Gephebase=^phosphoenolpyruvate \ (PEPC)^/or+Gene \ Gephebase=^phosphoenolpyruvate \ (PEPC)^/or+Gene \ Gephebase=^phosphoen$

EXTERNAL LINKS

COMMENTS