GEPHE SUMMARY

Gephebase Gene
acetyl-CoA carboxylase (ACC) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^acetyl-CoA carboxylase (ACC)^#gephebase-summary-title)

Entry Status
Published

GepheID
GP00002513

Main curator
Courtier

PHENOTYPIC CHANGE

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

Trait
Xenobiotic resistance (insecticide; cyclic ketoenol) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (insecticide; cyclic ketoenol)^#gephebase-summary-title)

Trait State in Taxon A
Bemisia tabaci - sensitive

Trait State in Taxon B
Bemisia tabaci - resistant

Ancestral State
Taxon A

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

Taxon A

Latin Name
Bemisia tabaci
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bemisia tabaci^#gephebase-summary-title)

Common Name
-

Synonyms
Aleyrodes tabaci; sweet potato whitefly; Bemisia tabaci (Gennadius, 1889)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodoidea; Aleyrodidae; Aleyrodinae; Bemisia

Parent
Bemisia () - (Rank: genus)
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7037)

NCBI Taxonomy ID
7038
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7038)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Bemisia tabaci
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bemisia tabaci^#gephebase-summary-title)

Common Name
-

Synonyms
Aleyrodes tabaci; sweet potato whitefly; Bemisia tabaci (Gennadius, 1889)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodoidea; Aleyrodidae; Aleyrodinae; Bemisia

Parent
Bemisia () - (Rank: genus)
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7037)

NCBI Taxonomy ID
7038
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7038)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
ACC

Synonyms
A1Z784_DROME; acc; Acc; ACoT; CG11198; CG8723; dACC; DmACC; Dmel\CG11198; FBgn0043811; Dmel_CG11198

String
-

Sequence Similarities
-

GO - Molecular Function
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0003989 : acetyl-CoA carboxylase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0003989)

GO - Biological Process
GO:0006633 : fatty acid biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006633)

UniProtKB Drosophila melanogaster
Q7JV23 (http://www.uniprot.org/uniprot/Q7JV23)

GenebankID or UniProtKB
()

GO:0019432 : triglyceride biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0019432)
GO:0009744 : response to sucrose (https://www.ebi.ac.uk/QuickGO/term/GO:0009744)
GO:0000902 : cell morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0000902)
GO:0005977 : glycogen metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0005977)
GO:0071329 : cellular response to sucrose stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0071329)
GO:2001295 : malonyl-CoA biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:2001295)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005739 : mitochondrion (https://www.ebi.ac.uk/QuickGO/term/GO:0005739)

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

A2083V

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	Val	2083

Main Reference

Identification and functional characterization of a novel acetyl-CoA carboxylase mutation associated with ketoenol resistance in Bemisia tabaci. (2020) (https://pubmed.ncbi.nlm.nih.gov/32448413)

Authors

Lueke B; Douris V; Hopkinson JE; Maiwald F; Hertlein G; Papapostolou KM; Bielza P; Tsagkarakou A; Van Leeuwen T; Bass C; Vontas J; Nauen R

Abstract

Insecticides of the tetronic/tetramic acid family (cyclic ketoenols) are widely used to control sucking pests such as whiteflies, aphids and mites. They act as inhibitors of acetyl-CoA carboxylase (ACC), a key enzyme for lipid biosynthesis across taxa. While it is well documented that plant ACCs targeted by herbicides have developed resistance associated with mutations at the carboxyltransferase (CT) domain, resistance to ketoenols in invertebrate pests has been previously associated either with metabolic resistance or with non-validated candidate mutations in different ACC domains. A recent study revealed high levels of spiromesifen and spirotetramat resistance in Spanish field populations of the whitefly Bemisia tabaci that was not thought to be associated with metabolic resistance. We confirm the presence of high resistance levels (up to >640-fold) against ketoenol insecticides in both Spanish and Australian B. tabaci strains of the MED and MEAM1 species, respectively. RNAseq analysis revealed the presence of an ACC variant bearing a mutation that results in an amino acid substitution, A2083V, in a highly conserved region of the CT domain. F1 progeny resulting from reciprocal crosses between susceptible and resistant lines are almost fully resistant, suggesting an autosomal dominant mode of inheritance. In order to functionally investigate the contribution of this mutation and other candidate mutations previously reported in resistance phenotypes, we used CRISPR/Cas9 to generate genome modified Drosophila lines. Toxicity bioassays using multiple transgenic fly lines confirmed that A2083V causes high levels of resistance to commercial ketoenols. We therefore developed a pyrosequencing-based diagnostic assay to map the spread of the resistance alleles in field-collected samples from Spain. Our screening confirmed the presence of target-site resistance in numerous field-populations collected in Sevilla, Murcia and Almeria. This emphasizes the importance of implementing appropriate resistance management strategies to prevent or slow the spread of resistance through global whitefly populations.

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Additional References

Next-generation molecular diagnostics (TaqMan qPCR and ddPCR) for monitoring insecticide resistance in Bemisia tabaci. (2022) (https://pubmed.ncbi.nlm.nih.gov/36054028)

RELATED GEPHE

Related Genes

5 (Acetylcholinesterase (Ace-1), Acetylcholinesterase (Ace-2), CYP6CM1, para (kdr), resistance to dieldrin) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7038^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

RNAseq was used to identify candidate genes. CRISPR/Cas9 modified ACC in Drosophila confirmed high levels of resistance. Reciprocal crossing studies suggest an autosomal dominant mode of inheritance.