GEPHE SUMMARY

Gephebase Gene
CYP6ER1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^CYP6ER1^#gephebase-summary-title)

GepheID
GP00002472

Entry Status
Published

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

Trait State in Taxon A
Nilaparvata lugens - sensitive

Trait State in Taxon B
Nilaparvata lugens - 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
Nilaparvata lugens (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Nilaparvata lugens^#gephebase-summary-title)

Common Name
brown planthopper

Synonyms
brown planthopper; Nilaparvata lugens (Stal, 1854); Nalaparvata lugens

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Paraneoptera; Hemiptera; Auchenorrhyncha; Fulgoromorpha; Fulgoroidea; Delphacidae; Delphacinae; Nilaparvata

Parent
Nilaparvata () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 108930)

NCBI Taxonomy ID
108931 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 108931)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
brown planthopper

Synonyms
brown planthopper; Nilaparvata lugens (Stal, 1854); Nalaparvata lugens

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Paraneoptera; Hemiptera; Auchenorrhyncha; Fulgoromorpha; Fulgoroidea; Delphacidae; Delphacinae; Nilaparvata

Parent
Nilaparvata () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 108930)

NCBI Taxonomy ID
108931 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 108931)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
cyp6er1

Synonyms
-

String
-

Sequence Similarities
Belongs to the cytochrome P450 family.

GO - Molecular Function
GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)
GO:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)
GO:0016705 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (https://www.ebi.ac.uk/QuickGO/term/GO:0016705)

GO - Biological Process
-

UniProtKB Nilaparvata lugens
A0A2I8B6P1 (http://www.uniprot.org/uniprot/A0A2I8B6P1)

GenebankID or UniProtKB Nilaparvata lugens
A0A2I8B6P1 (https://www.ncbi.nlm.nih.gov/nuccore/A0A2I8B6P1)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)

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

T318S substitution results in a marked (20-fold) and significant increase in resistance compared to the wild-type susceptible variant.

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	Thr	Ser	318

Main Reference

Neofunctionalization of Duplicated P450 Genes Drives the Evolution of Insecticide Resistance in the Brown Planthopper. (2018) (https://pubmed.ncbi.nlm.nih.gov/29337073)

Authors

Zimmer CT; Garrood WT; Singh KS; Randall E; Lueke B; Gutbrod O; Matthiesen S; Kohler M; Nauen R; Davies TGE; Bass C

Abstract

Gene duplication is a major source of genetic variation that has been shown to underpin the evolution of a wide range of adaptive traits [1, 2]. For example, duplication or amplification of genes encoding detoxification enzymes has been shown to play an important role in the evolution of insecticide resistance [3-5]. In this context, gene duplication performs an adaptive function as a result of its effects on gene dosage and not as a source of functional novelty [3, 6-8]. Here, we show that duplication and neofunctionalization of a cytochrome P450, CYP6ER1, led to the evolution of insecticide resistance in the brown planthopper. Considerable genetic variation was observed in the coding sequence of CYP6ER1 in populations of brown planthopper collected from across Asia, but just two sequence variants are highly overexpressed in resistant strains and metabolize imidacloprid. Both variants are characterized by profound amino-acid alterations in substrate recognition sites, and the introduction of these mutations into a susceptible P450 sequence is sufficient to confer resistance. CYP6ER1 is duplicated in resistant strains with individuals carrying paralogs with and without the gain-of-function mutations. Despite numerical parity in the genome, the susceptible and mutant copies exhibit marked asymmetry in their expression with the resistant paralogs overexpressed. In the primary resistance-conferring CYP6ER1 variant, this results from an extended region of novel sequence upstream of the gene that provides enhanced expression. Our findings illustrate the versatility of gene duplication in providing opportunities for functional and regulatory innovation during the evolution of an adaptive trait.

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Additional References

RELATED GEPHE

Related Genes

4 (Acetylcholinesterase (Ace-1), CYP6AY1, esterase NI-EST1, GST) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^108931^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

3 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^CYP6ER1^/and+Taxon ID=^108931^/or+Gene Gephebase=^CYP6ER1^/and+Taxon ID=^108931^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@Epistasis. When T318S is combined with P377del (as seen in CYP6ER1vB); an epistatic interaction was observed with the resistance conferred by the double mutation (20-fold) less than the sums of the effects of the component single mutations. In contrast; an additive interaction is observed when T318S is combined with A375del+A376P (as observed in CYP6ER1vA); with this combination exhibiting the highest resistance of all mutant lines (35-fold).