

GEPHE SUMMARY

BCMA (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^BCMA^#gephebase-summary-title)	Gephebase Gene	GP00000136	GephelD
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Trait #1	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	Trait
Glucosinolate content (https://www.gephebase.org/search-criteria?/and+Trait=^Glucosinolate+content^#gephebase-summary-title)	Trait State in Taxon A
Boechera stricta - Colorado	Trait State in Taxon B
Boechera stricta - Montana	

Trait #2	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	Trait
Herbivore resistance (https://www.gephebase.org/search-criteria?/and+Trait=^Herbivore+resistance^#gephebase-summary-title)	Trait State in Taxon A
Boechera stricta - Colorado	Trait State in Taxon B
Boechera stricta - Montana	

Ancestral State			
Taxonomic Status			
Data not curated			
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Boechera stricta (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Boechera+stricta^#gephebase-summary-title)		Boechera stricta (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Boechera+stricta^#gephebase-summary-title)	
-	Common Name	-	Common Name
Arabis drummondii; Boechera drummondii; Arabis drummondii A.Gray; Boechera drummondii (A.Gray) A.Love & D.Love; Boechera stricta (Graham) Al-Shehbaz	Synonyms	Arabis drummondii; Boechera drummondii; Arabis drummondii A.Gray; Boechera drummondii (A.Gray) A.Love & D.Love; Boechera stricta (Graham) Al-Shehbaz	Synonyms
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllphyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Boechereae; Boechera		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllphyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Boechereae; Boechera	
Boechera () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76872)	Parent	Boechera () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76872)	Parent
72658 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 72658)	NCBI Taxonomy ID	72658 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 72658)	NCBI Taxonomy ID
	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
No		No	

GENOTYPIC CHANGE

Generic Gene Name	J9QWI9 (http://www.uniprot.org/uniprot/J9QWI9)	UniProtKB Boechera stricta
Synonyms	JQ337905 (https://www.ncbi.nlm.nih.gov/nuccore/JQ337905)	GenebankID or UniProtKB
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

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

Mutation #1

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%22No%22#gephebase-summary-title>)

Molecular Type

Gene Amplification (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=%22Gene+Amplification%22#gephebase-summary-title>)

Aberration Type

Insertion (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%22Insertion%22#gephebase-summary-title>)

Insertion Size

Duplication of the BCMA3 gene - the BCMA1 gene is present only in the Montana genotype

Molecular Details of the Mutation

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%22Linkage+Mapping%22#gephebase-summary-title>)

Experimental Evidence

A gain-of-function polymorphism controlling complex traits and fitness in nature. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22936775>)

Authors

Prasad KV; Song BH; Olson-Manning C; Anderson JT; Lee CR; Schranz ME; Windsor AJ; Clauss MJ; Manzaneda AJ; Naqvi I; Reichelt M; Gershenson J; Rupasinghe SG; Schuler MA; Mitchell-Olds T

Abstract

Identification of the causal genes that control complex trait variation remains challenging, limiting our appreciation of the evolutionary processes that influence polymorphisms in nature. We cloned a quantitative trait locus that controls plant defensive chemistry, damage by insect herbivores, survival, and reproduction in the natural environments where this polymorphism evolved. These ecological effects are driven by duplications in the BCMA (branched-chain methionine allocation) loci controlling this variation and by two selectively favored amino acid changes in the glucosinolate-biosynthetic cytochrome P450 proteins that they encode. These changes cause a gain of novel enzyme function, modulated by allelic differences in catalytic rate and gene copy number. Ecological interactions in diverse environments likely contribute to the widespread polymorphism of this biochemical function.

Additional References

Mutation #2

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%22No%22#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=%22Coding%22#gephebase-summary-title>)

Aberration Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%22SNP%22#gephebase-summary-title>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Duplication of the BCMA3 gene + coding variation affecting catalytic activity at BCMA1 and BCMA3 - the BCMA3-MT allele produced 3.5-fold higher levels of valine-glucosinolates than the BCMA3-CO allele ($P = 0.0002$) - G134 and P536 in BCMA2 (to BCMA1/3 residues L and K, respectively) cause increased activity towards valine
134GGA (Gly)>TTA (Leu)
536CCA (Pro)>AAA (Lys)

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%22Linkage+Mapping%22#gephebase-summary-title>)

Taxon A	Taxon B	Position	
Codon	GGA	TTA	-
Amino-acid	Gly	Leu	134

Main Reference

A gain-of-function polymorphism controlling complex traits and fitness in nature. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22936775>)

Authors

Prasad KV; Song BH; Olson-Manning C; Anderson JT; Lee CR; Schranz ME; Windsor AJ; Clauss MJ; Manzaneda AJ; Naqvi I; Reichelt M; Gershenson J; Rupasinghe SG; Schuler

Identification of the causal genes that control complex trait variation remains challenging, limiting our appreciation of the evolutionary processes that influence polymorphisms in nature. We cloned a quantitative trait locus that controls plant defensive chemistry, damage by insect herbivores, survival, and reproduction in the natural environments where this polymorphism evolved. These ecological effects are driven by duplications in the BCMA (branched-chain methionine allocation) loci controlling this variation and by two selectively favored amino acid changes in the glucosinolate-biosynthetic cytochrome P450 proteins that they encode. These changes cause a gain of novel enzyme function, modulated by allelic differences in catalytic rate and gene copy number. Ecological interactions in diverse environments likely contribute to the widespread polymorphism of this biochemical function.

Additional References

Mutation #3

No (https://www.gephebase.org/search-criteria/?/and+Presumptive+Null=%No%#gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria/?/and+Molecular+Type=%Coding%#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria/?/and+Aberration+Type=%SNP%#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
Duplication of the BCMA3 gene + coding variation affecting catalytic activity at BCMA1 and BCMA3 - the BCMA3-MT allele produced 3.5-fold higher levels of valine-glucosinolates than the BCMA3-CO allele ($P = 0.0002$) - G134 and P536 in BCMA2 (to BCMA1/3 residues L and K, respectively) cause increased activity towards valine 134GGA (Gly)>TTA (Leu) 536CCA (Pro)>AAA (Lys)	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria/?/and+Experimental+Evidence=%Linkage+Mapping%#gephebase-summary-title)	Experimental Evidence

	Taxon A	Taxon B	Position
Codon	CCA	AAA	-
Amino-acid	Pro	Lys	536

A gain-of-function polymorphism controlling complex traits and fitness in nature. (2012) (https://pubmed.ncbi.nlm.nih.gov/22936775)	Main Reference
Prasad KV; Song BH; Olson-Manning C; Anderson JT; Lee CR; Schranz ME; Windsor AJ; Clauss MJ; Manzaneda AJ; Naqvi I; Reichelt M; Gershenson J; Rupasinghe SG; Schuler MA; Mitchell-Olds T	Authors
Identification of the causal genes that control complex trait variation remains challenging, limiting our appreciation of the evolutionary processes that influence polymorphisms in nature. We cloned a quantitative trait locus that controls plant defensive chemistry, damage by insect herbivores, survival, and reproduction in the natural environments where this polymorphism evolved. These ecological effects are driven by duplications in the BCMA (branched-chain methionine allocation) loci controlling this variation and by two selectively favored amino acid changes in the glucosinolate-biosynthetic cytochrome P450 proteins that they encode. These changes cause a gain of novel enzyme function, modulated by allelic differences in catalytic rate and gene copy number. Ecological interactions in diverse environments likely contribute to the widespread polymorphism of this biochemical function.	Abstract
	Additional References

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

@TwoNucleotideChangesInSameCodon @SeveralMutationsWithEffect

