

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

Trait #1	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~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+TraitCategory=~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			
Data not curated		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~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
	Synonyms		Synonyms
Arabis drummondii; Boechera drummondii; Arabis drummondii A.Gray; Boechera drummondii (A.Gray) A.Love & D.Love; Boechera stricta (Graham) Al-Shehbaz		Arabis drummondii; Boechera drummondii; Arabis drummondii A.Gray; Boechera drummondii (A.Gray) A.Love & D.Love; Boechera stricta (Graham) Al-Shehbaz	
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Boechereae; Boechera		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Boechereae; Boechera	
	Parent		Parent
Boechera () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76872)		Boechera () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76872)	
72658	NCBI Taxonomy ID	72658	NCBI Taxonomy ID
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 72658)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 72658)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Boecheria stricta
-		J9QWI9 (http://www.uniprot.org/uniprot/J9QWI9)
	Synonyms	GenebankID or UniProtKB
-		JQ337905 (https://www.ncbi.nlm.nih.gov/nuccore/JQ337905)
	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 #2

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

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

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

Nonsynonymous

Presumptive Null

Molecular Type

Aberration Type

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	GGA	TTA	-
Amino-acid	Gly	Leu	134

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

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

Main Reference

Authors

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 #3

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

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
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Experimental Evidence

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

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

Main Reference

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Authors

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

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Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@TwoNucleotideChangesInSameCodon @SeveralMutationsWithEffect

