

## GEPHE SUMMARY

	Gephebase Gene	GephelD
RCR3 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase="RCR3">#gephebase-summary-title)	GP00000963	Main curator
Published	Entry Status	Courtier

## PHENOTYPIC CHANGE

	Trait Category	
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category="Physiology">#gephebase-summary-title)	Trait	
Pathogen resistance ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen">https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen</a> resistance "#gephebase-summary-title)	Trait State in Taxon A	
Solanum peruvianum	Trait State in Taxon B	
Solanum peruvianum	Ancestral State	
Data not curated	Taxonomic Status	
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status="Intraspecific">#gephebase-summary-title)		
Taxon A	Latin Name	Taxon B
Solanum peruvianum ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Solanum+peruvianum">#gephebase-summary-title)</a> )	Solanum peruvianum ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Solanum+peruvianum">#gephebase-summary-title)</a> )	Solanum peruvianum ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Solanum+peruvianum">#gephebase-summary-title)</a> )
-	-	-
Lycopersicon peruvianum; Solanum peruvianum var. dentatum; Peruvian tomato; Lycopersicon peruvianum (L.) Mill.; Solanum peruvianum L.	Synonyms	Synonyms
-	-	-
species	Rank	Rank
cellular organisms; Eukaryota; Viridiplanteae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae; Solaneae; Solanum; Lycopersicon	Lineage	Lineage
Lycopersicon () - (Rank: subgenus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=49274">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=49274</a> )	Parent	Parent
4082 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4082">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4082</a> )	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

## GENOTYPIC CHANGE

Rcr3	Generic Gene Name	UniProtKB Solanum lycopersicum
101251145	Synonyms	GenebankID or UniProtKB
4081.Solyc02g076980.2.1 ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4081.Solyc02g076980.2.1">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4081.Solyc02g076980.2.1</a> )	String	AFP73362 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/AFP73362">https://www.ncbi.nlm.nih.gov/nuccore/AFP73362</a> )
Belongs to the peptidase C1 family.	Sequence Similarities	
GO:0004197 : cysteine-type endopeptidase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0004197">https://www.ebi.ac.uk/QuickGO/term/GO:0004197</a> )	GO - Molecular Function	
GO:0051603 : proteolysis involved in cellular protein catabolic process ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0051603">https://www.ebi.ac.uk/QuickGO/term/GO:0051603</a> )	GO - Biological Process	
		GO - Cellular Component

GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO.0005615>)

GO:0005764 : lysosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005764>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=%22No%22#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive%20Null=%22No%22#gephebase-summary-title))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type=%22Coding%22#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%22Coding%22#gephebase-summary-title))

Aberration Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%22SNP%22#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%22SNP%22#gephebase-summary-title))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Candidate amino acid changes are I206K and/or Q222E and/or S330A

Experimental Evidence

Candidate Gene ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%22Candidate Gene%22#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%22Candidate%20Gene%22#gephebase-summary-title))

Taxon A	Taxon B	Position
Codon	-	-
Amino-acid	-	-

Balancing selection at the tomato RCR3 Guardee gene family maintains variation in strength of pathogen defense. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22829777/>)

Main Reference

HÄger AC; Ilyas M; Stephan W; Tellier A; van der Hoorn RA; Rose LE

Authors

Coevolution between hosts and pathogens is thought to occur between interacting molecules of both species. This results in the maintenance of genetic diversity at pathogen antigens (or so-called effectors) and host resistance genes such as the major histocompatibility complex (MHC) in mammals or resistance (R) genes in plants. In plant-pathogen interactions, the current paradigm posits that a specific defense response is activated upon recognition of pathogen effectors via interaction with their corresponding R proteins. According to the "Guard-Hypothesis," R proteins (the "guards") can sense modification of target molecules in the host (the "guardees") by pathogen effectors and subsequently trigger the defense response. Multiple studies have reported high genetic diversity at R genes maintained by balancing selection. In contrast, little is known about the evolutionary mechanisms shaping the guardee, which may be subject to contrasting evolutionary forces. Here we show that the evolution of the guardee RCR3 is characterized by gene duplication, frequent gene conversion, and balancing selection in the wild tomato species Solanum peruvianum. Investigating the functional characteristics of 54 natural variants through *in vitro* and *in planta* assays, we detected differences in recognition of the pathogen effector through interaction with the guardee, as well as substantial variation in the strength of the defense response. This variation is maintained by balancing selection at each copy of the RCR3 gene. Our analyses pinpoint three amino acid polymorphisms with key functional consequences for the coevolution between the guardee (RCR3) and its guard (Cf-2). We conclude that, in addition to coevolution at the "guardee-effector" interface for pathogen recognition, natural selection acts on the "guard-guardee" interface. Guardee evolution may be governed by a counterbalance between improved activation in the presence and prevention of auto-immune responses in the absence of the corresponding pathogen.

Additional References

## RELATED GEPHE

Related Genes

1 (Mi1.2) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=%224082%22/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%224082%22/and+Trait=Pathogen%20resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@BalancingSelection