

GEPHE SUMMARY

	Gephebase Gene		GepheID
MLO1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MLO1^#gephebase-summary-title)		GP00000673	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)		Trait	
Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=~Pathogenresistance^#gephebase-summary-title)			
	Trait State in Taxon A		
Pisum sativum		Trait State in Taxon B	
Pisum sativum			
	Ancestral State		
Data not curated		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Pisum sativum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Pisumsativum^#gephebase-summary-title)		Pisum sativum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Pisumsativum^#gephebase-summary-title)	
	Common Name		Common Name
pea		pea	
	Synonyms		Synonyms
pea; garden pea; peas; Pisum sativum L.		pea; garden pea; peas; Pisum sativum L.	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; Hologalegina; IRL clade; Fabeae; Pisum		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; Hologalegina; IRL clade; Fabeae; Pisum	
	Parent		Parent
Pisum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3887)		Pisum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3887)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
3888 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3888)		3888 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3888)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Hordeum vulgare
MLO		P93766 (http://www.uniprot.org/uniprot/P93766)	
	Synonyms		GenebankID or UniProtKB
-		ACO07297 (https://www.ncbi.nlm.nih.gov/nuccore/ACO07297)	
	String		
-			
	Sequence Similarities		
Belongs to the MLO family.			
	GO - Molecular Function		
GO:0005516 : calmodulin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005516)			
	GO - Biological Process		
GO:0006952 : defense response (https://www.ebi.ac.uk/QuickGO/term/GO:0006952)			
GO:0009607 : response to biotic stimulus (https://www.ebi.ac.uk/QuickGO/term/GO:0009607)			
	GO - Cellular Component		
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)			

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes~#gephebase-summary-title))

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

Nonsense

1bp substitution resulting in premature stop codon

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

Presumptive Null

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

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

Pea powdery mildew er1 resistance is associated to loss-of-function mutations at a MLO homologous locus. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21850477>)

Pavan S; Schiavulli A; Appiano M; Marcotrigiano AR; Cillo F; Visser RG; Bai Y; Lotti C; Ricciardi L

The powdery mildew disease affects several crop species and is also one of the major threats for pea (*Pisum sativum* L.) cultivation all over the world. The recessive gene er1, first described over 60 years ago, is well known in pea breeding, as it still maintains its efficiency as a powdery mildew resistance source. Genetic and phytopathological features of er1 resistance are similar to those of barley, Arabidopsis, and tomato mlo powdery mildew resistance, which is caused by the loss of function of specific members of the MLO gene family. Here, we describe the obtainment of a novel er1 resistant line by experimental mutagenesis with the alkylating agent diethyl sulfate. This line was found to carry a single nucleotide polymorphism in the PsMLO1 gene sequence, predicted to result in premature termination of translation and a non-functional protein. A cleaved amplified polymorphic sequence (CAPS) marker was developed on the mutation site and shown to be fully co-segregating with resistance in F(2) individuals. Sequencing of PsMLO1 from three powdery mildew resistant cultivars also revealed the presence of loss-of-function mutations. Taken together, results reported in this study strongly indicate the identity between er1 and mlo resistances and are expected to be of great breeding importance for the development of resistant cultivars via marker-assisted selection.

Main Reference

Authors

Abstract

Additional References

RELATED GEPHE

No matches found.

No matches found.

Related Genes

Related Haplotypes

EXTERNAL LINKS

COMMENTS