

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

	Trait Category		
	Trait		
	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+Taxonomic Status="Domesticated">#gephebase-summary-title)			
	Taxon A	Taxon B	
	Latin Name	Latin Name	
Pisum sativum (#gephebase-summary-title)	Pisum sativum (#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; Papilioideae; 50 kb inversion clade; NPAAA clade; Hologlegina; IRL clade; Fabeae; Pisum	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilioideae; 50 kb inversion clade; NPAAA clade; Hologlegina; 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)		
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)		
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?	

GENOTYPIC CHANGE

	Generic Gene Name		
MLO	P93766 (http://www.uniprot.org/uniprot/P93766)		UniProtKB Hordeum vulgare
	Synonyms		
-			GenebankID or UniProtKB
	String		
-			ACO07297 (https://www.ncbi.nlm.nih.gov/nuccore/ACO07297)
	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 (#gephebase-summary-title)	Presumptive Null
Coding (#gephebase-summary-title)	Molecular Type
SNP (#gephebase-summary-title)	Aberration Type
Nonsense	SNP Coding Change
1bp substitution resulting in premature stop codon	Molecular Details of the Mutation
Linkage Mapping (#gephebase-summary-title)	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)	Main Reference
Pavan S; Schiavulli A; Appiano M; Marcotrigiano AR; Cillo F; Visser RG; Bai Y; Lotti C; Ricciardi L	Authors

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 60Å 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.

Additional References

RELATED GEPHE

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

EXTERNAL LINKS

COMMENTS