

GEPHE SUMMARY

	Gephebase Gene	GepheID
Starch branching enzyme (SBEI) = rugosus (R) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^Starch+branching+enzyme+(SBEI)+=+rugosus+(R)^#gephebase-summary-title)	GP00001078	Main curator
	Entry Status	
Published		

PHENOTYPIC CHANGE

Trait #1	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)	
	Trait
Starch structure (https://www.gephebase.org/search-criteria?/and+Trait=^Starch+structure^#gephebase-summary-title)	
	Trait State in Taxon A
Pisum sativum smooth	
	Trait State in Taxon B
Pisum sativum wrinkled	

Trait #2	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)	
	Trait
Seed aspect (https://www.gephebase.org/search-criteria?/and+Trait=^Seed+aspect^#gephebase-summary-title)	
	Trait State in Taxon A
-	
	Trait State in Taxon B
-	

	Ancestral State
Taxon A	
	Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)	

Taxon A	
	Latin Name
Pisum sativum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Pisum+sativum^#gephebase-summary-title)	
	Common Name
pea	
	Synonyms
pea; garden pea; peas; Pisum sativum L.	
	Rank
species	
	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	
	Parent
Pisum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3887)	
	NCBI Taxonomy ID
3888 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3888)	
	is Taxon A an Intraspecies?
No	

Taxon B	
	Latin Name
Pisum sativum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Pisum+sativum^#gephebase-summary-title)	
	Common Name
pea	
	Synonyms
pea; garden pea; peas; Pisum sativum L.	
	Rank
species	
	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	
	Parent
Pisum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3887)	
	NCBI Taxonomy ID
3888 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3888)	
	is Taxon B an Intraspecies?
No	

GENOTYPIC CHANGE

SBEI	Generic Gene Name	Q41058 (http://www.uniprot.org/uniprot/Q41058)	UniProtKB Pisum sativum
-	Synonyms	X80009 (https://www.ncbi.nlm.nih.gov/nucore/X80009)	GenebankID or UniProtKB
-	String		
	Sequence Similarities		
Belongs to the glycosyl hydrolase 13 family. GlgB subfamily.			
	GO - Molecular Function		
GO:0043169 : cation binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043169)			
GO:0004553 : hydrolase activity, hydrolyzing O-glycosyl compounds (https://www.ebi.ac.uk/QuickGO/term/GO:0004553)			
GO:0003844 : 1,4-alpha-glucan branching enzyme activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003844)			
GO:0102752 : 1,4-alpha-glucan branching enzyme activity (using a glucosylated glycogenin as primer for glycogen synthesis) (https://www.ebi.ac.uk/QuickGO/term/GO:0102752)			
	GO - Biological Process		
GO:0019252 : starch biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0019252)			
GO:0005978 : glycogen biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0005978)			
GO:0009793 : embryo development ending in seed dormancy (https://www.ebi.ac.uk/QuickGO/term/GO:0009793)			
	GO - Cellular Component		
GO:0009501 : amyloplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009501)			
GO:0009507 : chloroplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009507)			
Yes (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes^#gephebase-summary-title)			Presumptive Null
Coding (https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding^#gephebase-summary-title)			Molecular Type
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Insertion^#gephebase-summary-title)			Aberration Type
100-999 bp			Insertion Size
800 bp TE insertion; probably disrupts the last 61 amino acids of the SBEI protein			Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping^#gephebase-summary-title)			Experimental Evidence
The wrinkled-seed character of pea described by Mendel is caused by a transposon-like insertion in a gene encoding starch-branching enzyme. (1990) (https://pubmed.ncbi.nlm.nih.gov/2153053)			Main Reference
Bhattacharyya MK; Smith AM; Ellis TH; Hedley C; Martin C			Authors
We describe the cloning of the r (rugosus) locus of pea (Pisum sativum L.), which determines whether the seed is round or wrinkled. Wrinkled (rr) seeds lack one isoform of starch-branching enzyme (SBEI), present in round (RR or Rr) seeds. A major polymorphism in the SBEI gene between near-isogenic RR and rr lines shows 100% cosegregation with the r locus, establishing that the SBEI gene is at the r locus. An aberrant transcript for SBEI is produced in rr embryos. In rr lines the SBEI gene is interrupted by a 0.8 kb insertion that is very similar to the Ac/Ds family of transposable elements from maize. Failure to produce SBEI has complex metabolic consequences on starch, lipid, and protein biosynthesis in the seed.			Abstract
			Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

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