

GEPHE SUMMARY

	Gephebase Gene	GephelD
pericarp color1 (P1) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=%22pericarp+color1+(P1)%22%23gephebase-summary-title)	GP00000859	
Published	Entry Status	Main curator

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=%22Morphology%22%23gephebase-summary-title)	Trait		
Coloration (seed) (https://www.gephebase.org/search-criteria?/and+Trait=%22Coloration+(seed)%22%23gephebase-summary-title)	Trait State in Taxon A		
Zea mays - allele P-RR	Trait State in Taxon B		
Zea mays - allele P-VV	Ancestral State		
Taxon A	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=%22Domesticated%22%23gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%22Zea+mays%22%23gephebase-summary-title)		Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%22Zea+mays%22%23gephebase-summary-title)	
-	Common Name	-	Common Name
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays species	Synonyms	Zea mays var. japonica; maize; Zea mays L.; Zea mays mays species	Synonyms
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	Rank	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	Rank
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)	Lineage	Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)	Lineage
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)	Parent	4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)	Parent
No	NCBI Taxonomy ID	is Taxon A an Infraspecies?	NCBI Taxonomy ID
		No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Zea mays
P1	O24579 (http://www.uniprot.org/uniprot/O24579)	
P; GRMZM2G084799	EF165349 (https://www.ncbi.nlm.nih.gov/nuccore/EF165349)	GenebankID or UniProtKB
	Sequence Similarities	
-		
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)	GO - Molecular Function	
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	GO - Biological Process	
-	GO - Cellular Component	
No (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%22No%22%23gephebase-summary-title)		Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular+Type=%22Cis-regulatory%22%23gephebase-summary-title)		Molecular Type

1-10 kb

Insertion Size

insertion of transposable element Ac within a large intron; affecting transcripts. The five transcripts found in P-RR plants are absent in P-VV. A chimeric transcript containing part of Ac sequence is found.

Molecular Details of the Mutation

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

Experimental Evidence

Isolation and molecular analysis of the maize P locus. (1989) (<https://pubmed.ncbi.nlm.nih.gov/2559311>)

Main Reference

Lechelt C; Peterson T; Laird A; Chen J; Dellaporta SL; Dennis E; Peacock WJ; Starlinger P

Authors

The maize P locus is involved in the synthesis of a red flavonoid pigment in the pericarp, cob and other floral tissues. The tissue-specific pattern of expression of certain P alleles suggests that P may be a complex locus, with more than one functional unit. The P-VV allele, which specifies variegated pericarp and variegated cob, however, shows that insertion and excision of the transposable element Ac affects both pericarp and cob expression as though cob and pericarp pigmentation are controlled by a single gene. Using Ac as a transposon tag, we have isolated 34 kb of genomic DNA from the P-VV and P-RR allele. The cloned DNA contains two 5.8 kb cross-hybridizing regions, in direct orientation relative to each other, separated by 6.6 kb of intervening DNA. A sequence motif of 250 bp is repeated at three locations within the cloned region: once within each of the 5.8 kb repeats, and once outside the 5.8 kb repeats. DNA fragments flanking the Ac element detect five transcripts in RNA from wild type (P-RR) that are absent from mutant (P-VV) tissues. To localize the transcribed sequences, DNA probes spanning the 34 kb of cloned DNA were used in Northern analysis of RNA from mutant and wild-type kernels. The results suggest the presence of a single transcriptional unit located primarily within the DNA between the 5.8 kb repeats. The five RNAs transcribed from this region may be formed by alternative splicing. The size of the P gene derived from the length of the transcribed region seems much smaller than the gene size estimated from Ac-induced P-VV mutations.

Abstract

Additional References

RELATED GEPHE

Related Genes

3 (c1, colored plant 1, r1 colored1) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^4577^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@TE