

GEPHE SUMMARY

Gephebase Gene
opaque2 (O2)

Entry Status
Published

GepheID
GP00000754

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Lysine content (endosperm)

Trait State in Taxon A
Zea mays - hard translucent endosperm

Trait State in Taxon B
Zea mays - soft opaque endosperm with lysine contents - allele o2-m_____

Ancestral State
Taxon A

Taxonomic Status
Domesticated

Taxon A

Latin Name
Zea mays

Common Name
-

Synonyms
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea

Parent
Zea () - (Rank: genus)

NCBI Taxonomy ID
4577

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Zea mays

Common Name
-

Synonyms
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea

Parent
Zea () - (Rank: genus)

NCBI Taxonomy ID
4577

is Taxon B an Intraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
O2

Synonyms
-

String
4577.GRMZM2G015534_P01

Sequence Similarities
Belongs to the bZIP family.

GO - Molecular Function
GO:0003700 : DNA-binding transcription factor activity
GO:0003677 : DNA binding

GO - Biological Process
-

GO - Cellular Component
GO:0005634 : nucleus

Presumptive Null
No

UniProtKB Zea mays
P12959

GenebankID or UniProtKB
X16618

Molecular Type

Cis-regulatory

Aberration Type

Insertion

Insertion Size

1-10 kb

Molecular Details of the Mutation

insertion of a non-autonomous rbg transposable element in the untranslated leader sequence of the O2 gene

Experimental Evidence

Linkage Mapping

Main Reference

Transposon tagging and molecular analysis of the maize regulatory locus opaque-2. (1987)

Authors

Schmidt RJ; Burr FA; Burr B

Abstract

Genetic analyses suggested that the opaque-2 (o2) locus in maize acts as a positive, transacting, transcriptional activator of the zein seed storage-protein genes. Because isolation of the gene is requisite to understanding the molecular details of this regulation, transposon mutagenesis with the transposable element suppressor-mutator (Spm) was carried out, and three mutable o2 alleles were obtained. One of these alleles contained an 8.3-kilobase autonomous Spm, another a 6.8-kilobase nonautonomous Spm, and the third an unidentified transposon that is unrelated to Spm. A DNA sequence flanking the autonomous Spm insertion was verified to be o2-specific and provided a probe to clone a wild-type allele. Northern blots indicated that the gene is expressed in wild-type endosperm but not in leaf tissues or in endosperms homozygous for a mutant allele of the O2 gene. A transcript was detected in endosperms homozygous for mutations at opaque-7 and floury-2, an indication that O2 expression is independent of these two other putative regulators of zein synthesis.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

1

COMMENTS

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