GEPHE SUMMARY

Gephebase Gene
dihydroflavonol reductase (DFR) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^dihydroflavonol reductase (DFR)^#gephebase-summary-title)

Entry Status
Published

GepheID
GP00000226

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait
Coloration (tuber skin) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (tuber skin)^#gephebase-summary-title)

Trait State in Taxon A
Solanum tuberosum - red tuber

Trait State in Taxon B
Solanum tuberosum -white tuber

Ancestral State
Data not curated

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

Taxon A

Latin Name
Solanum tuberosum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Solanum tuberosum^#gephebase-summary-title)

Common Name
potato

Synonyms
Solanum tuberosum subsp. tuberosum; potato; potatoes; Solanum tuberosum L.

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae; Solaneae; Solanum

Parent
Solanum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4107)

NCBI Taxonomy ID
4113 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4113)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Solanum tuberosum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Solanum tuberosum^#gephebase-summary-title)

Common Name
potato

Synonyms
Solanum tuberosum subsp. tuberosum; potato; potatoes; Solanum tuberosum L.

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae; Solaneae; Solanum

Parent
Solanum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4107)

NCBI Taxonomy ID
4113 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4113)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
DFRA

Synonyms
dihydroflavonol 4-reductase; DIHYDROFLAVONOL 4-REDUCTASE; DIHYDROKAEMPFEROL 4-REDUCTASE; M318; MJB21.18; MJB21_18; TT3; DFR; At5g42800

String
3702.AT5G42800.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT5G42800.1)

Sequence Similarities
Belongs to the NAD(P)-dependent epimerase/dehydratase family. Dihydroflavonol-4-reductase subfamily.

GO - Molecular Function
GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491)
GO:0050662 : coenzyme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050662)
GO:0016616 : oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (https://www.ebi.ac.uk/QuickGO/term/GO:0016616)

UniProtKB Arabidopsis thaliana
P51102 (http://www.uniprot.org/uniprot/P51102)

GenebankID or UniProtKB
AAZ57436 (https://www.ncbi.nlm.nih.gov/nuccore/AAZ57436)

GO:0045552 : dihydrokaempferol 4-reductase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0045552)
GO:0047890 : flavanone 4-reductase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0047890)

GO - Biological Process

GO:0009718 : anthocyanin-containing compound biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0009718)

GO - Cellular Component

GO:0042406 : extrinsic component of endoplasmic reticulum membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0042406)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)

Molecular Details of the Mutation

unknown; 10 a.a variable positions

Experimental Evidence

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

Main Reference

An allele of dihydroflavonol 4-reductase associated with the ability to produce red anthocyanin pigments in potato (Solanum tuberosum L.). (2003)
(https://pubmed.ncbi.nlm.nih.gov/12955207)

Authors

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Abstract

The potato R locus is necessary for the production of red pelargonidin-based anthocyanin pigments in any tissue of the plant, including tuber skin and flower petals. The production of pelargonidins in plants requires the activity of dihydroflavonol 4-reductase (DFR) to catalyze the reduction of dihydrokaempferol into leucopelargonidin. To test the hypothesis that potato R encodes DFR, portions of both dfr alleles were sequenced from a diploid potato clone known to be heterozygous Rr. Sequence comparison revealed a polymorphic BamHI restriction site. The presence or absence of this site was monitored in three diploid populations that segregated for R, as well as in a wide range of tetraploid breeding clones and cultivars, by amplifying a fragment of dfr and digesting the products with BamHI. An identically sized dfr restriction fragment lacking the BamHI site was present in all potato clones that produced red anthocyanin pigments, while the same fragment was absent in many potato clones with white tuber skin and flowers. An independent RFLP test using DraI to detect sequence polymorphism was performed on a subset of the potato clones. This test also revealed dfr-derived bands that were present in all red-colored potatoes and absent in several white clones. The presence of shared restriction fragments in all red-colored potatoes provides strong evidence that R does indeed code for DFR. The data are also consistent with a 48 year-old hypothesis by Dodds and Long, that R was selected just once during the domestication of potato. A cDNA clone corresponding to the red allele of dfr was sequenced and compared to two other alleles. The red allele is predicted to encode a 382 amino acid protein that differs at ten amino acid positions from the gene products of the two alternative alleles. Several of these differences map in a region known to influence DFR substrate specificity in Gerbera.

Additional References

The potato R locus codes for dihydroflavonol 4-reductase. (2009) (https://pubmed.ncbi.nlm.nih.gov/19588118)

RELATED GEPHE

Related Genes

2 (an2-like (Stan2), flavonoid 3′;5′-hydroxylase (F3′5′H)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4113^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS