

GEPHE SUMMARY

MCO (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MCO~#gephebase-summary-title)	Gephebase Gene	GP00001814	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)	Trait Category		
Metal tolerance (copper) (https://www.gephebase.org/search-criteria?/and+Trait=~Metal tolerance (copper)~#gephebase-summary-title)	Trait		
sensitive	Trait State in Taxon A		
tolerant	Trait State in Taxon B		
Taxon A	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific~#gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
Erythranthe guttata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Erythranthe guttata~#gephebase-summary-title)	Latin Name	Erythranthe guttata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Erythranthe guttata~#gephebase-summary-title)	Latin Name
spotted monkey flower	Common Name	spotted monkey flower	Common Name
Mimulus guttatus; Mimulus guttatus subsp. guttatus; spotted monkey flower; common monkey flower; yellow monkey flower; Erythranthe guttata (Fisch. ex DC.) G.L.Nesom; Mimulus guttatus Fisch. ex DC.; Erythranthe guttatus	Synonyms	Mimulus guttatus; Mimulus guttatus subsp. guttatus; spotted monkey flower; common monkey flower; yellow monkey flower; Erythranthe guttata (Fisch. ex DC.) G.L.Nesom; Mimulus guttatus Fisch. ex DC.; Erythranthe guttatus	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Lamiales; Phrymaceae; Erythranthe	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Lamiales; Phrymaceae; Erythranthe	Lineage
Erythranthe () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1502711)	Parent	Erythranthe () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1502711)	Parent
4155 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4155)	NCBI Taxonomy ID	4155 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4155)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
		population present in Copperopolis copper mine in California	Taxon B Description

GENOTYPIC CHANGE

LPR2	Generic Gene Name	Q949X9 (http://www.uniprot.org/uniprot/Q949X9)	UniProtKB Arabidopsis thaliana
F23N20.3; F23N20_3; Low Phosphate Root2; At1g71040	Synonyms		GenebankID or UniProtKB
3702.AT1G71040.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT1G71040.1)	String	()	
Belongs to the multicopper oxidase family.	Sequence Similarities		
GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491)	GO - Molecular Function		
GO:0005507 : copper ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005507)	GO - Biological Process		

GO:0016036 : cellular response to phosphate starvation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016036>)
GO:0010073 : meristem maintenance
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010073>)

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)
GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)
GO:0005789 : endoplasmic reticulum membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)
GO:0005618 : cell wall (<https://www.ebi.ac.uk/QuickGO/term/GO:0005618>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

-

Molecular Details of the Mutation

several recent tandem duplications of this gene are responsible for the 12x increase in expression observed in copper tolerant lines - 6X fold enrichment of aligned reads at MCO

Experimental Evidence

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

Main Reference

Indirect evolution of hybrid lethality due to linkage with selected locus in *Mimulus guttatus*. (2013) (<https://pubmed.ncbi.nlm.nih.gov/23468595>)

Authors

Wright KM; Lloyd D; Lowry DB; Macnair MR; Willis JH

Abstract

Most species are superbly and intricately adapted to the environments in which they live. Adaptive evolution by natural selection is the primary force shaping biological diversity. Differences between closely related species in ecologically selected characters such as habitat preference, reproductive timing, courtship behavior, or pollinator attraction may prevent interbreeding in nature, causing reproductive isolation. But does ecological adaptation cause reproductive incompatibilities such as hybrid sterility or lethality? Although several genes causing hybrid incompatibilities have been identified, there is intense debate over whether the genes that contribute to ecological adaptations also cause hybrid incompatibilities. Thirty years ago, a genetic study of local adaptation to copper mine soils in the wildflower *Mimulus guttatus* identified a locus that appeared to cause copper tolerance and hybrid lethality in crosses to other populations. But do copper tolerance and hybrid lethality have the same molecular genetic basis? Here we show, using high-resolution genome mapping, that copper tolerance and hybrid lethality are not caused by the same gene but are in fact separately controlled by two tightly linked loci. We further show that selection on the copper tolerance locus indirectly caused the hybrid incompatibility allele to go to high frequency in the copper mine population because of hitchhiking. Our results provide a new twist on Darwin's original supposition that hybrid incompatibilities evolve as an incidental by-product of ordinary adaptation to the environment.

Additional References

Adaptation to heavy-metal contaminated environments proceeds via selection on pre-existing genetic variation . (2015) (<https://pubmed.ncbi.nlm.nih.gov/00000000.000006>)

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

large differences in expression of MCO between tolerant and nontolerant lines - other loci are involved in the tolerance - Not sure the *Arabidopsis* multicopper oxidase gene is the exact ortholog of the gene identified in *Mimulus*. The gene identified in *Mimulus* is not in UniProtKB.