GEPHE SUMMARY

Gephebase Gene

early responsive to dehydration stress protein 4 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^early responsive to dehydration stress protein 4^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001434

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

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

Trait

Xenobiotic resistance (soil contamination; serpentine) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (soil contamination; serpentine)^#gephebase-summary-title)

Trait State in Taxon A

Arabidopsis arenosa Hochlantsch & Kasperstein populations not adapted to serpentine

Trait State in Taxon B

Arabidopsis arenosa Gulsen population adapted to serpentine

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

Arabidopsis arenosa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis arenosa^#gephebase-summary-title)

Common Name

-

Synonyms

Arabis arenosa; Cardaminopsis arenosa; Arabidopsis arenosa (L.) Lawalree; Arabis arenosa (L.) Scop.; Cardaminopsis arenosa (L.) Hayek.

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent

Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

38785 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 38785)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Arabidopsis arenosa Hochlantsch & Kasperstein populations not adapted to serpentine

Taxon B

Latin Name

Arabidopsis arenosa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis arenosa^#gephebase-summary-title)

Common Name

-

Synonyms

Arabis arenosa; Cardaminopsis arenosa; Arabidopsis arenosa (L.) Lawalree; Arabis arenosa (L.) Scop.; Cardaminopsis arenosa (L.) Hayek.

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent

Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

38785 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 38785)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Arabidopsis arenosa Gulsen population adapted to serpentine

GENOTYPIC CHANGE

Generic Gene Name

ERD4

Synonyms

early-responsive to dehydration 4; T4K22.4; T4K22_4; At1g30360

String

3702.AT1G30360.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G30360.1)

Sequence Similarities

Belongs to the CSC1 (TC 1.A.17) family.

GO - Molecular Function

GO:0005227 : calcium activated cation channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005227)

UniProtKB Arabidopsis thaliana

Q9C8G5 (http://www.uniprot.org/uniprot/Q9C8G5)

GenebankID or UniProtKB

()

GO - Biological Process

-

GO - Cellular Component

GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0009506 : plasmodesma (https://www.ebi.ac.uk/QuickGO/term/GO:0009506)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0005774 : vacuolar membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005774)
GO:0009507 : chloroplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009507)
GO:0005773 : vacuole (https://www.ebi.ac.uk/QuickGO/term/GO:0005773)
GO:0009941 : chloroplast envelope (https://www.ebi.ac.uk/QuickGO/term/GO:0009941)

Presumptive Null

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

Molecular Type

Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#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

Experimental Evidence

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

Main Reference

Borrowed alleles and convergence in serpentine adaptation. (2016) (https://pubmed.ncbi.nlm.nih.gov/27357660)

Authors

Arnold BJ; Lahner B; DaCosta JM; Weisman CM; Hollister JD; Salt DE; Bomblies K; Yant L

Abstract

Serpentine barrens represent extreme hazards for plant colonists. These sites are characterized by high porosity leading to drought, lack of essential mineral nutrients, and phytotoxic levels of metals. Nevertheless, nature forged populations adapted to these challenges. Here, we use a population-based evolutionary genomic approach coupled with elemental profiling to assess how autotetraploid Arabidopsis arenosa adapted to a multichallenge serpentine habitat in the Austrian Alps. We first demonstrate that serpentine-adapted plants exhibit dramatically altered elemental accumulation levels in common conditions, and then resequence 24 autotetraploid individuals from three populations to perform a genome scan. We find evidence for highly localized selective sweeps that point to a polygenic, multitrait basis for serpentine adaptation. Comparing our results to a previous study of independent serpentine colonizations in the closely related diploid Arabidopsis lyrata in the United Kingdom and United States, we find the highest levels of differentiation in 11 of the same loci, providing candidate alleles for mediating convergent evolution. This overlap between independent colonizations in different species suggests that a limited number of evolutionary strategies are suited to overcome the multiple challenges of serpentine adaptation. Interestingly, we detect footprints of selection in A. arenosa in the context of substantial gene flow from nearby off-serpentine populations of A. arenosa, as well as from A. lyrata In several cases, quantitative tests of introgression indicate that some alleles exhibiting strong selective sweep signatures appear to have been introgressed from A. lyrata This finding suggests that migrant alleles may have facilitated adaptation of A. arenosa to this multihazard environment.

Additional References

RELATED GEPHE

Related Genes

9 (ammonium transporter 2;1, calmodulin binding hydrolase, Casparian strip membrane domain protein 1, Ferroportin 2, high expression of osmotically responsive genes 2, K+ uptake permease 9, LACCASE 8, sulfate transporter 1;1, two pore channel) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^38785^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS