GEPHE SUMMARY

Gephebase Gene
K+ uptake permease 9 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^K+ uptake permease 9^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00001430
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
POT9
Synonyms
ATKUP9; F18F4.60; F18F4_60; HAK9; K+ uptake permease 9; KT9; KUP9; At4g19960
String
3702.AT4G19960.1
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT4G19960.1)
Sequence Similarities
Belongs to the HAK/KUP transporter (TC 2.A.72.3) family.
GO - Molecular Function
GO:0015079 : potassium ion transmembrane transporter activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0015079)
GO - Biological Process

UniProtKB Arabidopsis thaliana
O49423 (http://www.uniprot.org/uniprot/O49423)
GenebankID or UniProtKB
()

GO:0006813 : potassium ion transport (https://www.ebi.ac.uk/QuickGO/term/GO:0006813)

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:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)

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, early responsive to dehydration stress protein 4, Ferroportin 2, high expression of osmotically responsive genes 2, 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

@Introgression convergence with A lyrata