

GEPHE SUMMARY

K+ uptake permease 9 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^K+ uptake permease 9^#gephebase-summary-title)	Gephebase Gene	GP00001430	GephelD
Published	Entry Status	Prigent	Main curator

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria/?and+Trait Category=^Physiology^#gephebase-summary-title)
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	Taxon B	Latin Name
Arabidopsis arenosa (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Arabidopsis+arenosa^#gephebase-summary-title)		Arabidopsis arenosa (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Arabidopsis+arenosa^#gephebase-summary-title)	
-	Common Name	-	Common Name
Arabis arenosa; Cardaminopsis arenosa; Arabidopsis arenosa (L.) Lawalree; Arabis arenosa (L.) Scop.; Cardaminopsis arenosa (L.) Hayek.	Synonyms	Arabis arenosa; Cardaminopsis arenosa; Arabidopsis arenosa (L.) Lawalree; Arabis arenosa (L.) Scop.; Cardaminopsis arenosa (L.) Hayek.	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis	Lineage
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)	Parent	Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)	Parent
38785 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 38785)	NCBI Taxonomy ID	38785 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 38785)	NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Arabidopsis arenosa Hochlantsch & Kasperstein populations not adapted to serpentine	Taxon A Description	Arabidopsis arenosa Gulsen population adapted to serpentine	Taxon B Description

GENOTYPIC CHANGE

POT9	Generic Gene Name	UniProtKB Arabidopsis thaliana
ATKUP9; F18F4_60; F18F4_60; HAK9; K+ uptake permease 9; KT9; KUP9; At4g19960	Synonyms	GenebankID or UniProtKB
3702.AT4G19960.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT4G19960.1)	String	0
Belongs to the HAK/KUP transporter (TC 2.A.72.3) family.	Sequence Similarities	
GO:0015079 : potassium ion transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015079)	GO - Molecular Function	
		GO - Biological Process

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, multtrait 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, Caspary 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*