

GEPHE SUMMARY

	Gephebase Gene		GepheID
ammonium transporter 2;1 (https://www.gephebase.org/search-criteria?/and+Gene)		GP00001431	
Gephebase= [^] ammonium transporter 2;1 [^] #gephebase-summary-title)			Main curator
	Entry Status	Prigent	
Published			

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

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
AMT2		Q9M6N7 (http://www.uniprot.org/uniprot/Q9M6N7)	
	Synonyms		GenebankID or UniProtKB
ammonium transporter 2; AMMONIUM TRANSPORTER 2; AMMONIUM TRANSPORTER 2;1; AMT2;1; ATAMT2; F16M14.22; F16M14_22; At2g38290		()	
	String		
3702.AT2G38290.1			
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT2G38290.1)			
	Sequence Similarities		
Belongs to the ammonia transporter channel (TC 1.A.11.2) family.			
	GO - Molecular Function		
GO:0015398 : high-affinity secondary active ammonium transmembrane transporter activity			
(https://www.ebi.ac.uk/QuickGO/term/GO:0015398)			

GO:0009624 : response to nematode
 (https://www.ebi.ac.uk/QuickGO/term/GO:0009624)

GO:0015696 : ammonium transport (https://www.ebi.ac.uk/QuickGO/term/GO:0015696)
 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)

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)	Aberration Type
seven aa substitutions	Molecular Details of the Mutation
Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title)	Experimental Evidence
Borrowed alleles and convergence in serpentine adaptation. (2016) (https://pubmed.ncbi.nlm.nih.gov/27357660)	Main Reference
Arnold BJ; Lahner B; DaCosta JM; Weisman CM; Hollister JD; Salt DE; Bomblies K; Yant L	Authors
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 <i>Arabidopsis arenosa</i> 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 <i>Arabidopsis lyrata</i> 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 <i>A. arenosa</i> in the context of substantial gene flow from nearby off-serpentine populations of <i>A. arenosa</i> , as well as from <i>A. lyrata</i> . In several cases, quantitative tests of introgression indicate that some alleles exhibiting strong selective sweep signatures appear to have been introgressed from <i>A. lyrata</i> . This finding suggests that migrant alleles may have facilitated adaptation of <i>A. arenosa</i> to this multihazard environment.	Abstract
	Additional References

RELATED GEPHE

9 (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, 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 Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS