

GEPHE SUMMARY

calmodulin binding hydrolase (<https://www.gephebase.org/search-criteria?/and+Gene>
 Gephebase=[^]calmodulin binding hydrolase[^]#gephebase-summary-title) Gephebase Gene GP00001438 GepheID
 Entry Status Prigent Main curator
 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) (<a href="https://www.gephebase.org/search-criteria?/and+Trait=<sup>^</sup>Xenobiotic resistance (soil contamination; serpentine)<sup>^</sup>#gephebase-summary-title">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 (<a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Arabidopsis arenosa<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=[^]Arabidopsis arenosa[^]#gephebase-summary-title) | | Arabidopsis arenosa (<a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Arabidopsis arenosa<sup>^</sup>#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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701) | | Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701) | | |
| | NCBI Taxonomy ID | | NCBI Taxonomy ID | |
| 38785 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 38785) | | 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 |
| - | | Q9FHQ0 (http://www.uniprot.org/uniprot/Q9FHQ0) | |
| | Synonyms | | GenebankID or UniProtKB |
| - | | 0 | |
| | String | | |
| - | | | |
| | Sequence Similarities | | |
| - | | | |
| | GO - Molecular Function | | |
| GO:0016787 : hydrolase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016787) | | | |
| | GO - Biological Process | | |
| GO:0016042 : lipid catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0016042) | | | |
| | GO - Cellular Component | | |
| - | | | |

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

unknown

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 *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.

Abstract

Additional References

RELATED GEPHE

9 (ammonium transporter 2;1, 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

@Introgression convergence with *A. lyrata*