

GEPHE SUMMARY

AtHKT1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^AtHKT1^#gephebase-summary-title)	Gephebase Gene	GP00000124	GepheID
	Entry Status	Martin	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title)		Trait Category	
Salt tolerance (https://www.gephebase.org/search-criteria?/and+Trait=^Salttolerance^#gephebase-summary-title)		Trait	
Arabidopsis thaliana- Colo		Trait State in Taxon A	
Arabidopsis thaliana- Ts-1		Trait State in Taxon B	
Taxon A		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Intraspecific^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=^Arabidopsisthaliana^#gephebase-summary-title)		Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=^Arabidopsisthaliana^#gephebase-summary-title)	
thale cress		thale cress	
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	
species		species	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
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)	
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)		3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)	
Yes		Yes	
Arabidopsis thaliana- Colo		Arabidopsis thaliana- Ts-1	

GENOTYPIC CHANGE

HKT1		Generic Gene Name		UniProtKB Arabidopsis thaliana
ATHKT1; high-affinity K+ transporter 1; HKT1;1; T9A4.5; At4g10310		Synonyms		GenebankID or UniProtKB
3702.AT4G10310.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT4G10310.1)		String		AY685182 (https://www.ncbi.nlm.nih.gov/nucleotide/AY685182)
Belongs to the TrkH potassium transport family. HKT (TC 2.A.38.3) subfamily.		Sequence Similarities		
GO:0008324 : cation transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008324)		GO - Molecular Function		
GO:0015079 : potassium ion transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015079)				

GO:0015081 : sodium ion transmembrane transporter activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0015081>)

GO - Biological Process

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

GO:0006970 : response to osmotic stress
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006970>)

GO:0009651 : response to salt stress (<https://www.ebi.ac.uk/QuickGO/term/GO:0009651>)

GO:0006814 : sodium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006814>)

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>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title>)

Aberration Type

Deletion (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Deletion~#gephebase-summary-title>)

Deletion Size

100-999 bp

Molecular Details of the Mutation

725bp deletion of part of upstream repeat region

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title>)

Main Reference

Natural variants of AtHKT1 enhance Na⁺ accumulation in two wild populations of Arabidopsis. (2006) (<https://pubmed.ncbi.nlm.nih.gov/17140289>)

Authors

Rus A; Baxter I; Muthukumar B; Gustin J; Lahner B; Yakubova E; Salt DE

Abstract

Plants are sessile and therefore have developed mechanisms to adapt to their environment, including the soil mineral nutrient composition. Ionomics is a developing functional genomic strategy designed to rapidly identify the genes and gene networks involved in regulating how plants acquire and accumulate these mineral nutrients from the soil. Here, we report on the coupling of high-throughput elemental profiling of shoot tissue from various Arabidopsis accessions with DNA microarray-based bulk segregant analysis and reverse genetics, for the rapid identification of genes from wild populations of Arabidopsis that are involved in regulating how plants acquire and accumulate Na⁺ from the soil. Elemental profiling of shoot tissue from 12 different Arabidopsis accessions revealed that two coastal populations of Arabidopsis collected from Tossa del Mar, Spain, and Tsu, Japan (Ts-1 and Tsu-1, respectively), accumulate higher shoot levels of Na⁺ than do Col-0 and other accessions. We identify AtHKT1, known to encode a Na⁺ transporter, as being the causal locus driving elevated shoot Na⁺ in both Ts-1 and Tsu-1. Furthermore, we establish that a deletion in a tandem repeat sequence approximately 5 kb upstream of AtHKT1 is responsible for the reduced root expression of AtHKT1 observed in these accessions. Reciprocal grafting experiments establish that this loss of AtHKT1 expression in roots is responsible for elevated shoot Na⁺. Interestingly, and in contrast to the hkt1-1 null mutant, under NaCl stress conditions, this novel AtHKT1 allele not only does not confer NaCl sensitivity but also cosegregates with elevated NaCl tolerance. We also present all our elemental profiling data in a new open access ionomics database, the Purdue Ionomics Information Management System (PiIMS; <http://www.purdue.edu/dp/ionomics>). Using DNA microarray-based genotyping has allowed us to rapidly identify AtHKT1 as the casual locus driving the natural variation in shoot Na⁺ accumulation we observed in Ts-1 and Tsu-1. Such an approach overcomes the limitations imposed by a lack of established genetic markers in most Arabidopsis accessions and opens up a vast and tractable source of natural variation for the identification of gene function not only in ionomics but also in many other biological processes.

Additional References

A coastal cline in sodium accumulation in Arabidopsis thaliana is driven by natural variation of the sodium transporter AtHKT1;1. (2010) (<https://pubmed.ncbi.nlm.nih.gov/21085628>)

RELATED GEPHE

Related Genes

1 (RAS1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702~/and+Trait=Salt tolerance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

1 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~AtHKT1~/and+Taxon ID=~3702~/or+Gene Gephebase=~AtHKT1~/and+Taxon ID=~3702~#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS