

GEPHE SUMMARY

	Gephebase Gene	GephelD
ALMT gene cluster (https://www.gephebase.org/search-criteria/?and+Gene+Gephebase=^ALMT+gene+cluster)	GP00000079	Main curator
	Entry Status	Martin
Published		

PHENOTYPIC CHANGE

	Trait Category
Physiology (#gephebase-summary-title)	Trait
Metal tolerance (#gephebase-summary-title)	Trait State in Taxon A
Secale cereale (Al-tolerant)	Trait State in Taxon B
Secale cereale (Al-sensitive)	Ancestral State
Data not curated	Taxonomic Status
Domesticated (#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Secale cereale (#gephebase-summary-title)		Secale cereale (#gephebase-summary-title)	
rye	Common Name	rye	Common Name
Secale cereale subsp. cereale; rye; Secale cereale L.; Secale cereal	Synonyms	Secale cereale subsp. cereale; rye; Secale cereale L.; Secale cereal	Synonyms
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Hordeinae; Secale		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Hordeinae; Secale	
	Parent		Parent
Secale () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4549)	NCBI Taxonomy ID	Secale () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4549)	NCBI Taxonomy ID
4550 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4550)		4550 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4550)	
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

ALMT1	Generic Gene Name	UniProtKB Triticum aestivum
ALMT1-1; ALMT1-2	Synonyms	GenebankID or UniProtKB
-	String	ABY52957 (https://www.ncbi.nlm.nih.gov/nucleotide/ABY52957)
Belongs to the aromatic acid exporter (TC 2.A.85) family.	Sequence Similarities	
-	GO - Molecular Function	
GO:0015743 : malate transport (https://www.ebi.ac.uk/QuickGO/term/GO:0015743)	GO - Biological Process	
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)	GO - Cellular Component	
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)		Presumptive Null
No (#gephebase-summary-title)		

Gene Amplification (https://www.gephebase.org/search-criteria?/and+Molecular Type=%27Gene Amplification%27#gephebase-summary-title)	Molecular Type
Indel (https://www.gephebase.org/search-criteria?/and+Aberration Type=%27Indel%27#gephebase-summary-title)	Aberration Type
unknown	Indel Size
Copy number Variant	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%27Linkage Mapping%27#gephebase-summary-title)	Experimental Evidence
An ALMT1 gene cluster controlling aluminum tolerance at the Alt4 locus of rye (<i>Secale cereale</i> L.). (2008) (https://pubmed.ncbi.nlm.nih.gov/18493079)	Main Reference
Collins NC; Shirley NJ; Saeed M; Pallotta M; Gustafson JP	Authors
Aluminum toxicity is a major problem in agriculture worldwide. Among the cultivated Triticeae, rye (<i>Secale cereale</i> L.) is one of the most Al tolerant and represents an important potential source of Al tolerance for improvement of wheat. The Alt4 Al-tolerance locus of rye contains a cluster of genes homologous to the single-copy Al-activated malate transporter (TaALMT1) Al-tolerance gene of wheat. Tolerant (M39A-1-6) and intolerant (M77A-1) rye haplotypes contain five and two genes, respectively, of which two (ScALMT1-M39.1 and ScALMT1-M39.2) and one (ScALMT1-M77.1) are highly expressed in the root tip, typically the main site of plant Al tolerance/susceptibility. All three transcripts are upregulated by exposure to Al. High-resolution genetic mapping identified two resistant lines resulting from recombination within the gene cluster. These recombinants exclude all genes flanking the gene cluster as candidates for controlling Alt4 tolerance, including a homolog of the barley HvMATE Al-tolerance gene. In the recombinants, one hybrid gene containing a chimeric open reading frame and the ScALMT1-M39.1 gene each appeared to be sufficient to provide full tolerance. mRNA splice variation was observed for two of the rye ALMT1 genes and in one case, was correlated with a approximately 400-bp insertion in an intron.	Abstract
	Additional References

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS