

GEPHE SUMMARY

| | | | |
|--|----------------|------------|--------------|
| | Gephebase Gene | | GepheID |
| Thermo-tolerance 1 (TT1) (https://www.gephebase.org/search-criteria?/and+Gene) | | GP00001566 | |
| Gephebase="Thermo-tolerance 1 (TT1)"#gephebase-summary-title) | | | Main curator |
| Published | Entry Status | Prigent | |

PHENOTYPIC CHANGE

| | | | |
|--|-----------------------------|--|-----------------------------|
| | Trait Category | | |
| Physiology (https://www.gephebase.org/search-criteria?/and+Trait) | | | |
| Category="Physiology"#gephebase-summary-title) | Trait | | |
| Temperature tolerance (https://www.gephebase.org/search-criteria?/and+Trait="Temperature tolerance"#gephebase-summary-title) | | | |
| Asian rice Wuyunjing variety (<i>O. sativa</i> ssp. Japonica) | Trait State in Taxon A | | |
| African rice | Trait State in Taxon B | | |
| Taxon A | Ancestral State | | |
| Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic) | Taxonomic Status | | |
| Status="Interspecific"#gephebase-summary-title) | | | |
| Taxon A | | Taxon B | |
| | Latin Name | | Latin Name |
| <i>Oryza sativa</i> | | <i>Oryza glaberrima</i> | |
| (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Oryza sativa"#gephebase-summary-title) | | (<a glaberrima"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" oryza="">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Oryza glaberrima"#gephebase-summary-title) | |
| | Common Name | | Common Name |
| rice | | African rice | |
| | Synonyms | | Synonyms |
| rice; red rice; <i>Oryza sativa</i> L. | | African rice; <i>Oryza glaberrima</i> Steud. | |
| | Rank | | Rank |
| species | | species | |
| | Lineage | | Lineage |
| cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; <i>Oryza</i> | | cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; <i>Oryza</i> | |
| | Parent | | Parent |
| <i>Oryza</i> () - (Rank: genus) | | <i>Oryza</i> () - (Rank: genus) | |
| (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527) | | (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527) | |
| 4530 | NCBI Taxonomy ID | 4538 | NCBI Taxonomy ID |
| (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530) | | (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4538) | |
| | is Taxon A an Intraspecies? | | is Taxon B an Intraspecies? |
| Yes | | No | |
| | Taxon A Description | | |
| Asian rice Wuyunjing variety (<i>O. sativa</i> ssp. Japonica) | | | |

GENOTYPIC CHANGE

| | | | |
|---|-------------------------|--|---|
| | Generic Gene Name | | UniProtKB <i>Oryza sativa</i> subsp. japonica |
| PAB1 | | Q10KF0 (http://www.uniprot.org/uniprot/Q10KF0) | |
| | Synonyms | | GenebankID or UniProtKB |
| PAB1; OsPAB1; Os03g0387100; LOC_Os03g26970; OsJ_11088; OSJNBb0058G04.11 | | () | |
| | String | | |
| 39947.LOC_Os03g26970.1 | | | |
| (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=39947.LOC_Os03g26970.1) | | | |
| | Sequence Similarities | | |
| Belongs to the peptidase T1A family. | | | |
| | GO - Molecular Function | | |
| GO:0004175 : endopeptidase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004175) | | | |
| GO:0004298 : threonine-type endopeptidase activity | | | |
| (https://www.ebi.ac.uk/QuickGO/term/GO:0004298) | | | |
| | GO - Biological Process | | |
| GO:0043161 : proteasome-mediated ubiquitin-dependent protein catabolic process | | | |

(<https://www.ebi.ac.uk/QuickGO/term/GO:0043161>)
 GO:0010498 : proteasomal protein catabolic process
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0010498>)
 GO:0010499 : proteasomal ubiquitin-independent protein catabolic process
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0010499>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
 GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
 GO:0005839 : proteasome core complex
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0005839>)
 GO:0019773 : proteasome core complex, alpha-subunit complex
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0019773>)

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

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

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

Nonsynonymous SNP Coding Change

p.R99H Molecular Details of the Mutation

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

| | Taxon A | Taxon B | Position |
|------------|---------|---------|----------|
| Codon | - | - | - |
| Amino-acid | - | - | - |

Natural alleles of a proteasome $\hat{1}\pm 2$ subunit gene contribute to thermotolerance and adaptation of African rice. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25985140>) Main Reference

Li XM; Chao DY; Wu Y; Huang X; Chen K; Cui LG; Su L; Ye WW; Chen H; Chen HC; Dong NQ; Guo T; Shi M; Feng Q; Zhang P; Han B; Shan JX; Gao JP; Lin HX Authors

Global warming threatens many aspects of human life, for example, by reducing crop yields. Breeding heat-tolerant crops using genes conferring thermotolerance is a fundamental way to help deal with this challenge. Here we identify a major quantitative trait locus (QTL) for thermotolerance in African rice (*Oryza glaberrima*), Thermo-tolerance 1 (TT1), which encodes an $\hat{1}\pm 2$ subunit of the 26S proteasome involved in the degradation of ubiquitinated proteins. Ubiquitylome analysis indicated that OgTT1 protects cells from heat stress through more efficient elimination of cytotoxic denatured proteins and more effective maintenance of heat-response processes than achieved with OsTT1. Variation in TT1 has been selected for on the basis of climatic temperature and has had an important role in local adaptation during rice evolution. In addition, we found that overexpression of OgTT1 was associated with markedly enhanced thermotolerance in rice, Arabidopsis and Festuca elata. This discovery may lead to an increase in crop security in the face of the ongoing threat of global warming. Abstract

Additional References

RELATED GEPHE

No matches found. Related Genes

No matches found. Related Haplotypes

EXTERNAL LINKS

COMMENTS

Non-null mutation. H99 substitution might have a role in promoting degradation efficiency