

GEPHE SUMMARY

<p>GW2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^GW2^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00000425</p> <p>Martin</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)</p> <p>Grain size (https://www.gephebase.org/search-criteria?/and+Trait=^Grain+size^#gephebase-summary-title)</p> <p>Triticum aestivum - Chinese spring</p> <p>Triticum aestivum - Lankaodali</p> <p>Taxon A</p> <p>Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Triticum aestivum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Triticum+aestivum^#gephebase-summary-title)</p> <p>Common Name</p> <p>bread wheat</p> <p>Synonyms</p> <p>Triticum aestivum subsp. aestivum; Triticum vulgare; bread wheat; Canadian hard winter wheat; common wheat; wheat; Triticum aestivum L.; Triticum vulgare L.; Triticum vulgare Vill., nom. illeg.; Tricum aestivum; Triticum aestivum; Triticum aestivum8</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticoidea; Triticeae; Triticinae; Triticum</p> <p>Parent</p> <p>Triticum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4564)</p> <p>NCBI Taxonomy ID</p> <p>4565 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4565)</p> <p>is Taxon A an Intraspecies?</p> <p>Yes</p> <p>Taxon A Description</p> <p>Triticum aestivum - Chinese spring</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Triticum aestivum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Triticum+aestivum^#gephebase-summary-title)</p> <p>Common Name</p> <p>bread wheat</p> <p>Synonyms</p> <p>Triticum aestivum subsp. aestivum; Triticum vulgare; bread wheat; Canadian hard winter wheat; common wheat; wheat; Triticum aestivum L.; Triticum vulgare L.; Triticum vulgare Vill., nom. illeg.; Tricum aestivum; Triticum aestivum; Triticum aestivum8</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticoidea; Triticeae; Triticinae; Triticum</p> <p>Parent</p> <p>Triticum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4564)</p> <p>NCBI Taxonomy ID</p> <p>4565 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4565)</p> <p>is Taxon B an Intraspecies?</p> <p>Yes</p> <p>Taxon B Description</p> <p>Triticum aestivum - Lankaodali</p>
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GENOTYPIC CHANGE

<p>GW2</p> <p>OsL_06523</p> <p>39946.BGIOSGA007870-PA (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39946.BGIOSGA007870-PA)</p> <p>Sequence Similarities</p> <p>-</p> <p>GO - Molecular Function</p> <p>GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)</p> <p>GO:0061630 : ubiquitin protein ligase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0061630)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p>	<p>UniProtKB Oryza sativa subsp. indica</p> <p>A4GWX9 (http://www.uniprot.org/uniprot/A4GWX9)</p> <p>0</p> <p>GenebankID or UniProtKB</p>
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GO - Biological Process

GO:0007275 : multicellular organism development
 (https://www.ebi.ac.uk/QuickGO/term/GO:0007275)
 GO:0016567 : protein ubiquitination (https://www.ebi.ac.uk/QuickGO/term/GO:0016567)
 GO:0080113 : regulation of seed growth
 (https://www.ebi.ac.uk/QuickGO/term/GO:0080113)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Insertion Size

1-9 bp

Molecular Details of the Mutation

1bp insertion resulting in premature stop codon

Experimental Evidence

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

Main Reference

SNP identification and allelic-specific PCR markers development for TaGW2, a gene linked to wheat kernel weight. (2012) (https://pubmed.ncbi.nlm.nih.gov/22643902)

Authors

Yang Z; Bai Z; Li X; Wang P; Wu Q; Yang L; Li L; Li X

Abstract

TaGW2, an orthologous gene of rice OsGW2, has been associated with kernel width and weight of bread wheat (*Triticum aestivum*). Difference in TaGW2 coding sequence was not found among different wheat varieties in previous researches. In this study, we found eight exons and seven introns in TaGW2 with a full-length cDNA sequence of 1,275 bp, which contains a conserved function domain and seven splice sites that shared homology with rice OsGW2. A single T-base insertion in the eighth exon of TaGW2 on chromosome 6A was detected in a large-kernel wheat variety, Lankaodali. This insertion mutation reduces the coding protein sequence from normal 424 amino acids (~47.2 kDa) to 328 amino acids (~37.1 kDa) by truncating 96 amino acids. The result was validated by identifying histidine-tagged TaGW2 proteins encoded by both alleles of the mutant and the wild types in SDS-PAGE. Allele-specific PCR markers were developed based on the single nucleotide polymorphism (SNP) site. The SNP markers were genotyped for an F(2) segregation population from the cross of Lankaodali × Chinese Spring. Seed traits of F(2:3) families were evaluated in three different environments. The association analysis indicated that F(2:3) families with the mutated TaGW2 allele significantly increased kernel width (KW) and thousand-kernel weight (TKW), and slightly improved kernel length (KL). Using the SNP markers, another two varieties harbored the mutated TaGW2 allele were successfully identified from 22 additional wheat varieties, and they both have large KW and TKW. Cloning and sequencing of the gene further confirmed the functions of the mutated allele of TaGW2 in the two large kernel varieties. The results suggested that TaGW2 may negatively regulate kernel size variation, which shares the same function as OsGW2 in rice. The successful development of SNP markers provides a useful tool for improving kernel yield in wheat.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS