GEPHE SUMMARY Gephebase Gene GephelD  $Alk\ /\ Starch\ Synthase\ II\ (https://www.gephebase.org/search-criteria?/and+Genebase.org/search-criteria.$ GP00000078 Gephebase=^Alk / Starch Synthase II^#gephebase-summary-title) Main curator Entry Status Martin **Published** PHENOTYPIC CHANGE Trait Category Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title) Trait Grain cooking texture (https://www.gephebase.org/search-criteria?/and+Trait=^Grain cooking texture^#gephebase-summary-title) Trait State in Taxon A Oryza sativa indica - Kasalath Trait State in Taxon B Oryza sativa japonica - Nipponbare Ancestral State Taxon A Taxonomic Status Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title) Taxon A Taxon B Latin Name Latin Name Orvza sativa Orvza sativa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Oryza (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Oryza sativa^#gephebase-summary-title) sativa^#gephebase-summary-title) Common Name Common Name rice rice Synonyms Synonyms rice; red rice; Oryza sativa L. rice; red rice; Oryza sativa L. Rank Rank species species Lineage Lineage cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza Oryzinae; Oryza Parent Parent Oryza () - (Rank: genus) Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527 )  $(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527\,)\\$ NCBI Taxonomy ID NCBI Taxonomy ID (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530 )  $(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530\ )$ is Taxon A an Infraspecies? is Taxon B an Infraspecies? Yes Yes Taxon A Description Taxon B Description Oryza sativa indica - Kasalath Oryza sativa japonica - Nipponbare

## **GENOTYPIC CHANGE**

GO:0009011: starch synthase activity

Generic Gene Name SSII-3 Synonyms ALK; SSS2A; SSII-3; Os06g0229800; LOC\_Os06g12450; P0525F01.23 String 39947.LOC\_Os06g12450.1 (http://string-db.org/newstring\_cgi/show\_network\_section.pl?identifier= 39947.LOC\_Os06g12450.1) Sequence Similarities Belongs to the glycosyltransferase 1 family. Bacterial/plant glycogen synthase subfamily.

GO - Molecular Function GO:0033201 : alpha-1,4-glucan synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0033201) GO:0004373: glycogen (starch) synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004373)

UniProtKB Oryza sativa subsp. japonica

Q0DDE3 (http://www.uniprot.org/uniprot/Q0DDE3)

GenebankID or UniProtKB

AF419099 (https://www.ncbi.nlm.nih.gov/nuccore/AF419099)

GO - Biological Process

GO:0019252 : starch biosynthetic process

(https://www.ebi.ac.uk/QuickGO/term/GO:0019252)

GO - Cellular Component

 $GO:0009501: amyloplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009501) \\ GO:0009507: chloroplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009507) \\$ 

Mutation #1

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

Molecular Type

Presumptive Null

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

4 epistatic amino-acid substitutions - Glu-88 and Gly-604 in SSIla of indica-cultivars IR36 and Kasalath versus Asp-88 and Ser-604 in japonica cultivars Nipponbare and Kinmaze SSIla - Val-737 and Leu-781 in indica SSIla versus Met-737 in cv. Nipponbare and Phe-781 in cv. Kinmaze SSIla.

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Glu	Asp	88

Main Reference

Mapping of a gene responsible for the difference in amylopectin structure between japonica-type and indica-type rice varieties. (2002) (https://pubmed.ncbi.nlm.nih.gov/12579422)

Authors

Umemoto T; Yano M; Satoh H; Shomura A; Nakamura Y

Abstract

The present investigation revealed that the alk and gel(t) genes, which cause the differences between a japonica rice variety Nipponbare and an indica rice variety Kasalath in terms of the disintegration of endosperm starch granules in alkali solution and their gelatinisation in a 4 M urea solution, respectively, cosegregated in backcross inbred lines derived from a cross between the two varieties. The segregation pattern of the profile for amylopectin chain-length, which was distinguished by enrichment in short chains of DP<==11 and depletion in intermediate-size chains of 12<==DP<==24 in japonica as compared with indica, was exactly the same as those of the above physico-chemical properties of starch granules, and the gene was designated as acl(t). Gene-mapping analysis showed that the starch synthase Ila (SSIIa) gene is located at the alk locus on chromosome 6 in the rice genome. These results lead us to the possibility that different alleles of the SSIIa gene are responsible for differences in amylopectin structure between the two varieties, in that SSIIa plays a distinct role in the elongation of short chains within clusters (A+B(1) chains) of amylopectin. It is proposed that the activity of SSIIa in japonica rice is reduced in amount or functional capacity relative to the activity of this enzyme in indica rice. This, in turn, would explain why starch from japonica rice has a lower gelatinisation temperature than starch from indica rice and is more susceptible to disintegration in alkali or urea. The evidence for this hypothesis is that the alk(t), gel(t), acl(t) and SSIIa genes all map to the same locus.

Additional References

Essential amino acids of starch synthase Ila differentiate amylopectin structure and starch quality between japonica and indica rice varieties. (2005) (https://pubmed.ncbi.nlm.nih.gov/16027975)

Genome-wide association studies of 14 agronomic traits in rice landraces. (2010) (https://pubmed.ncbi.nlm.nih.gov/20972439)

Mutation #2

Presumptive Null

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Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

4 epistatic amino-acid substitutions - Glu-88 and Gly-604 in SSIIa of indica-cultivars IR36 and Kasalath versus Asp-88 and Ser-604 in japonica cultivars Nipponbare and Kinmaze SSIIa - Val-737 and Leu-781 in indica SSIIa versus Met-737 in cv. Nipponbare and Phe-781 in cv. Kinmaze SSIIa.

 ${\sf Experimental\ Evidence}$ 

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Gly	Ser	604

Main Reference

Mapping of a gene responsible for the difference in amylopectin structure between japonica-type and indica-type rice varieties. (2002) (https://pubmed.ncbi.nlm.nih.gov/12579422)

Authors

The present investigation revealed that the alk and gel(t) genes, which cause the differences between a japonica rice variety Nipponbare and an indica rice variety Kasalath in terms of the disintegration of endosperm starch granules in alkali solution and their gelatinisation in a 4 M urea solution, respectively, cosegregated in backcross inbred lines derived from a cross between the two varieties. The segregation pattern of the profile for amylopectin chain-length, which was distinguished by enrichment in short chains of DP<=11 and depletion in intermediate-size chains of 12<=2DP<=24 in japonica as compared with indica, was exactly the same as those of the above physico-chemical properties of starch granules, and the gene was designated as acl(t). Gene-mapping analysis showed that the starch synthase Ila (SSIIa) gene is located at the alk locus on chromosome 6 in the rice genome. These results lead us to the possibility that different alleles of the SSIIa gene are responsible for differences in amylopectin structure between the two varieties, in that SSIIa plays a distinct role in the elongation of short chains within clusters (A+B(1) chains) of amylopectin. It is proposed that the activity of SSIIa in japonica rice is reduced in amount or functional capacity relative to the activity of this enzyme in indica rice. This, in turn, would explain why starch from japonica rice has a lower gelatinisation temperature than starch from indica rice and is more susceptible to disintegration in alkali or urea. The evidence for this hypothesis is that the alk(t), gel(t), acl(t) and SSIIa genes all map to the same locus.

Additional References

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Genome-wide association studies of 14 agronomic traits in rice landraces. (2010) (https://pubmed.ncbi.nlm.nih.gov/20972439)

Mutation #3

Presumptive Null

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Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

4 epistatic amino-acid substitutions - Glu-88 and Gly-604 in SSIIa of indica-cultivars IR36 and Kasalath versus Asp-88 and Ser-604 in japonica cultivars Nipponbare and Kinmaze SSIIa - Val-737 and Leu-781 in indica SSIIa versus Met-737 in cv. Nipponbare and Phe-781 in cv. Kinmaze SSIIa.

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	<del>-</del>	-
Amino-acid	Val	Met	737

Main Reference

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Authors

Umemoto T; Yano M; Satoh H; Shomura A; Nakamura Y

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Additional References

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 $Genome-wide \ association \ studies \ of \ 14 \ agronomic \ traits \ in \ rice \ landraces. \ (2010) \ (https://pubmed.ncbi.nlm.nih.gov/20972439)$ 

Mutation #4

Presumptive Null

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Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

 ${\sf Molecular\ Details\ of\ the\ Mutation}$ 

4 epistatic amino-acid substitutions - Glu-88 and Gly-604 in SSIla of indica-cultivars IR36 and Kasalath versus Asp-88 and Ser-604 in japonica cultivars Nipponbare and Kinmaze SSIla - Val-737 and Leu-781 in indica SSIla versus Met-737 in cv. Nipponbare and Phe-781 in cv. Kinmaze SSIla.

Experimental Evidence

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

	Taxon A	Taxon B	Position	
Codon	-	-	-	
Amino-acid	Leu	Phe	781	

Main Reference

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Umemoto T; Yano M; Satoh H; Shomura A; Nakamura Y

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Genome-wide association studies of 14 agronomic traits in rice landraces. (2010) (https://pubmed.ncbi.nlm.nih.gov/20972439)

## **RELATED GEPHE**

Related Genes

No matches found.

Related Haplotypes

No matches found.

## **EXTERNAL LINKS**

## COMMENTS

 $@Epistasis \ @Several Mutations With Effect\\$