

Alk / Starch Synthase II (https://www.gephebase.org/search-criteria?/and+Gene)	Gephebase Gene	GP00000078	GepheID
Gephebase="Alk / Starch Synthase II" #gephebase-summary-title			Main curator
Published	Entry Status	Martin	

	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)	

GENOTYPIC CHANGE

SSII-3	Generic Gene Name	UniProtKB <i>Oryza sativa</i> subsp. japonica
ALK; SSS2A; SSII-3; Os06g0229800; LOC_Os06g12450; P0525F01.23	Synonyms	Q0DDE3 (http://www.uniprot.org/uniprot/Q0DDE3)
	String	GenebankID or UniProtKB AF419099 (https://www.ncbi.nlm.nih.gov/nuccore/AF419099)
39947.LOC_Os06g12450.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39947.LOC_Os06g12450.1)	Sequence Similarities	
	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)		
GO:0009011 : starch synthase activity		

GO:0019252 : starch biosynthetic process

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

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

Presumptive Null

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

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	-	-	-
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 IIa (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 IIa 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

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

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	-	-	-
Amino-acid	Gly	Ser	604

Main Reference

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Authors

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>)

Mutation #3

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="+No`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

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

Aberration Type

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

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](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=))

	Taxon A	Taxon B	Position
Codon	-	-	-
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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Mutation #4

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="+No`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

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

Aberration Type

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

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](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=))

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

Main Reference

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Authors

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

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