

GEPHE SUMMARY

Gephebase Gene
Alk / Starch Synthase II

Entry Status
Published

GepheID
GP00000078

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Grain cooking texture

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

Taxon A

Latin Name
Oryza sativa

Common Name
rice

Synonyms
rice; red rice; Oryza sativa L.

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza

Parent
Oryza () - (Rank: genus)

NCBI Taxonomy ID
4530

is Taxon A an Intraspecies?
Yes

Taxon A Description
Oryza sativa indica - Kasalath

Taxon B

Latin Name
Oryza sativa

Common Name
rice

Synonyms
rice; red rice; Oryza sativa L.

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza

Parent
Oryza () - (Rank: genus)

NCBI Taxonomy ID
4530

is Taxon B an Intraspecies?
Yes

Taxon B Description
Oryza sativa japonica - Nipponbare

GENOTYPIC CHANGE

Generic Gene Name
SSII-3

Synonyms
ALK; SSS2A; SSII-3; Os06g0229800; LOC_Os06g12450; P0525F01.23

String
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
GO:0004373 : glycogen (starch) synthase activity
GO:0009011 : starch synthase activity

GO - Biological Process
GO:0019252 : starch biosynthetic process

GO - Cellular Component
GO:0009501 : amyloplast

UniProtKB Oryza sativa subsp. japonica
Q0DDE3

GenebankID or UniProtKB
AF419099

Mutation #1

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

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

	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. \(2002\)](#)

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 $DP_{n=11}$ and depletion in intermediate-size chains of $12 \leq DP_n \leq 24$ 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(t) 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. \(2005\)](#)

[Genome-wide association studies of 14 agronomic traits in rice landraces. \(2010\)](#)

Mutation #2

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

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

	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. \(2002\)](#)

Authors

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the two varieties. The segregation pattern of the profile for amylopectin chain-length, which was distinguished by enrichment in short chains of $DP \leq 11$ and depletion in intermediate-size chains of $12 \leq DP \leq 24$ 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(t) 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.

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Mutation #3

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Val	Met	737

Main Reference

[Mapping of a gene responsible for the difference in amylopectin structure between japonica-type and indica-type rice varieties. \(2002\)](#)

Authors

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

Abstract

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Additional References

[Essential amino acids of starch synthase IIa differentiate amylopectin structure and starch quality between japonica and indica rice varieties. \(2005\)](#)

[Genome-wide association studies of 14 agronomic traits in rice landraces. \(2010\)](#)

Mutation #4

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

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

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

Main Reference

[Mapping of a gene responsible for the difference in amylopectin structure between japonica-type and indica-type rice varieties. \(2002\)](#)

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. \(2005\)](#)

[Genome-wide association studies of 14 agronomic traits in rice landraces. \(2010\)](#)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Epistasis @SeveralMutationsWithEffect