

# Genetic Diversity for Seed Starch and Storage Protein Properties in Vietnam Rice Germplasm and Their Evaluation for Rice Grain Quality Improvement

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<https://hdl.handle.net/2324/1441353>

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出版情報：九州大学, 2013, 博士（農学）, 論文博士  
バージョン：  
権利関係：やむを得ない事由により本文ファイル非公開（3）

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論文題目 : Genetic Diversity for Seed Starch and Storage Protein Properties in Vietnam Rice Germplasm and Their Evaluation for Rice Grain Quality Improvement  
(ベトナムイネにおける胚乳澱粉と貯蔵タンパク質に関する遺伝的多様性と米粒の品質改良に関する評価)

区 分 : 乙

### 論 文 内 容 の 要 旨

Amylose content is one of the important factors influencing the physical and chemical properties of gelatinized starch in rice. Analysis of 352 Vietnamese nonglutinous rice cultivars revealed a wide range of variation in apparent amylose content and the expression level of granule-bound starch synthase. On the basis of single-nucleotide polymorphisms (SNPs) at the splicing donor site of the first intron and in the coding region of the *granule-bound starch synthase I* gene, *Waxy* gene, Vietnamese rice cultivars were classified into seven groups that reflected differences in apparent amylose content. The very low and low apparent amylose content levels were tightly correlated with the SNP in the first intron whereas intermediate and high amylose was associated with the SNP in Ex10. The correlation between the combination of SNPs in the first intron, Ex6, or Ex10 was predominant among low amylose rice varieties. Our analysis confirmed the existence of *Wx<sup>op</sup>* allele in Vietnamese rice germplasm, in addition to its distribution in other Southeast Asian countries. The results suggest that the low amylose content of Vietnamese local rice germplasm is attributable to spontaneous mutations at exons, and not at the splicing donor site.

Twenty one of Vietnamese glutinous rice cultivars were investigated for variation in starch properties and single-nucleotide polymorphism in *starch synthase IIa (SSIIa)* gene. The cultivars were classified into three groups based on chain length distribution of amylopectin. A wide variation of alkali digestibility was also observed with low, intermediate and high. The low alkali digestibility cultivars had peak temperature ( $T_p$ ) ranged from 65.1 °C to 76.2 °C, while the cultivars with intermediate and high alkali digestibility showed  $T_p$  from 59.2 °C to 67.2 °C. Thirteen SNPs and 2 insertion/deletions in the coding region of *SSIIa* gene were found. Five SNPs in the coding region resulted in the substitution of amino acid. The combination of these SNPs was associated to the variation on starch properties.

The diversity of glutelin acidic polypeptides in rice cultivars collected from northern Vietnam was characterized via sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and isoelectric focusing (IEF) electrophoresis. Glutelin acidic subunits were separated into 4 bands by molecular mass, as  $\alpha$ -1 (39 kDa),  $\alpha$ -2 (38 kDa),  $\alpha$ -3 (37.5 or 37 kDa), and  $\alpha$ -4 (34 or 33 kDa). One hundred and eighty-five Vietnamese rice cultivars were divided into 3 types, based on differences in staining intensity and the molecular size of the  $\alpha$ -3 and  $\alpha$ -4 polypeptides derived from SDS-PAGE analysis. Wide variation was also observed in the isoelectric point (pI) of staining intensity, in addition to the absence/presence of pI bands detected via IEF analysis. A total of 16 pI bands, ranging from pI 6.30 to pI 7.52, were identified in the various local rice cultivars. The maximum and minimum of IEF bands detected were 14 and 10, respectively. The genetic variability index ( $H'$ ) ranged from 0.280 to 0.820, which confirms that local rice cultivars from northern Vietnam have the diversity for glutelin.