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Genome-wide association study of rice core set related selenium content

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Abstract

The purpose of this study was to identify the candidate genes involved in selenium content in brown rice. Rice (*Oryza sativa* L.) was important crop including diverse functional substance such as carbohydrate, protein, lysine and tocopherol, mineral. Especially, selenium as nutritionally important minerals, it was known to activate the immune system, antioxidant effect and inhibition of carcinogenesis. Also recommended daily requirements of the United States and the United Kingdom were 55 to 90 ug for selenium. Therefore, selenium content in brown rice of core-set were analyzed by using ICP-MS (Inductively Coupled Plasma Mass Spectrometer) and GWAS (Genome Wide Association Study) was conducted to search for candidate genes in this study. The new natural variants identified through haplotyping analysis would be useful to develop new rice varieties with improved storage ability of the valuable mineral through the future molecular breeding.

Keywords: rice, Genome-Wide Association Studies (GWAS), selenium, core set, ICP-MS

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