Arsenic (As) is a toxic element and widely distributed not only in the environment but also in some foods. As causes damage to crop quality and productivity in agriculture and carcinogenicity in human health (Azizur et al. 2007). It is well known that As forms various chemical species in soils. Arsenate and arsenite are the inorganic, phytoavailable forms of As in soil solution. Microbes, which can methylate As species in soils, may transform inorganic As species to organic species and vice versa (Meharg et al. 2002). However, the metabolic transformation of As species within the rice plant is still unknown. In addition, it is also unknown about the genetic diversity of As concentration in rice in association with As species. We investigated this point using a rice diversity research set of germplasm produced by Kojima et al. (2005).

A core collection of rice consisting of 69 accessions was grown on a paddy field containing 1.4 mg As kg-1 dry weight as determined by 1 M HCl extraction. After harvest, the grains were ground to a fine powder and a 0.5 g aliquot of the powder was digested in 60 % HNO3 heated at 105 °C, and then the total arsenic concentration was determined by ICP-MS. Another 0.5 g was prepared to As extraction method by Hamano-Nagaoka et al. (2008) for speciation analysis by HPLC-ICP-MS.

A large difference in grain As concentration was found, even though the rice core collection were cultivated on the soil with non-contaminated As. The difference was approximately 3-times at the maximum. The dominant As species in grains was arsenite, followed by DMA and arsenate, irrespective of cultivars. However, the proportions of As species were different among rice cultivars. This difference can be explained by methylation of inorganic As within the plant rather than by uptake of DMA from the soil because DMA was not determined in the soil solution. These results suggest that there is a possibility that As absorption and metabolism in rice could be genetically controlled.

References

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