

Category	: International Rice Research Conference
Select Theme	: Pathways to health and nutrition
Endorsement email	:
Keyword 1	: Low-arsenic and low-cadmium rice
Keyword 2	: Biofortification
Keyword 3	: Food safety
Title of Entry	: Genes and Physiological Factors Associated With Natural Variation in Rice Arsenic Concentrations
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Select only one type of presentation	: 15 minute oral presentation
Abstract	<p>: Previous study of 1763 diverse accessions (the USDA Rice Core), found a 200-fold difference in concentration of total arsenic (tAs) in unmilled rice grains, indicating large genetic variance that could be exploited by breeders to produce varieties with low grain-As. This study identified subsets of rice accessions with high grain-tAs concentrations (a.k.a. “grain-tAs Accumulators”) and others with low grain-tAs concentrations (a.k.a. “Excluders”). Interestingly, all the modern USA rice varieties (released since 1980) included in that study were Excluders. This data prompted a series of studies to identify the genes and physiological mechanisms underlying the low grain-tAs found in modern US varieties so that they could be utilized in breeding efforts in the USA and internationally. Several grain-tAs Accumulators were crossed with Excluders. Among 15 segregating F2 populations, five showed Mendelian segregation patterns (i.e. 1:2:1 or 3:1) for grain-tAs, indicative of single major-gene control. Four F2 populations have been selectively genotyped to date. Marker-trait associations observed in two populations indicate a grain-tAs locus on the short arm of chromosome 11; data from the third population points to the long arm of chromosome 10; and the fourth population points to chromosomes 2 and 8. When subsets of Accumulator and Excluder accessions were compared for As concentration and metabolism in leaves and roots, data suggested that the lower grain-tAs of Excluders might be in part due to more efficient sequestration of As in leaf vacuoles. It is thus notable that glutathione S-transferase genes (involved in As chelation and sequestration) are near the associated markers on chromosomes 10 and 11. A likely candidate gene on chromosome 2 is Lsi1, a membrane transporter protein known to affect root uptake of both silica and As. Reduced As uptake or enhanced As detoxification and sequestration would be expected to improve both grain-As and resistance to As-induced plant stress (e.g., straighthead disease). However, association mapping for these seemingly-related traits in the USDA Rice Minicore (subset of the USDA Rice Core) using 3.3 million SNPs detected no overlapping QTLs, suggesting that the wide variation in grain-tAs and straighthead observed within the Minicore are regulated by different genes and mechanisms.</p>

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