

Genetics of Grain Arsenic Content in Two Advanced Rice Breeding Populations

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Introduction

Arsenic species have a well documented toxic effect in humans. Growing rice that meets international standards for total (tAs) and inorganic arsenic (iAs) is key for human food innocuity and access of rice production to international markets. An important proportion of the variation in both tAs and iAs in rice grain is due to genetic factors. Breeding for low As content requires assessing the genetic diversity and developing suitable selection strategies for this trait. There is no previous information on tAs and iAs grain content in INIA's breeding germplasm. Furthermore, standard laboratory methods for quantification of tAs and iAs in rice grain are expensive and time consuming, thus are not suited for selection in breeding. The genetic variability for As content in the breeding germplasm, and the use of new selection strategies such as marked assisted selection (MAS) must be assessed.

Objectives

- Evaluate for the first time the genetic variability of grain tAs and iAs content in Uruguayan rice germplasm.
- Explore the correlation between tAs and iAs in breeding trials.
- Dissect the genetic architecture of grain tAs in INIA's breeding populations
- Assess the usefulness of MAS for grain tAs.

Material and Methods

Two mapping populations (129 indica and 201 tropical japonica) were phenotyped in a field trial with an augmented randomized complete block design in 2018 and their grain tAs content was measured by graphite furnace atomic absorption spectrometry (GF-AAS) and inductively coupled plasma mass spectrometry (ICP-MS) at Laboratorio Tecnológico del Uruguay (LATU) and Trace Element Speciation Laboratory (TESLA, Aberdeen University, UK). A subset of 32 genotypes (17 indica and 15 tropical japonica) representing the genotypic diversity of both populations was grown in a field trial with a randomized complete block design with three replicates in 2019 and assayed for grain iAs and tAs content with HPLC-ICP-MS at LATU.

A genome-wide association study (GWAS) between single nucleotide polymorphism genotyped by sequencing (GBS-SNP, 49K for indica and 27K for tropical japonica) and tAs in the mapping populations was performed with a mixed model accounting for population structure implemented in the R package rBLUP. Quantitative trait loci (QTL) for tAs were defined as >2 SNPs with significant association ($p < 0.0001$) in the same LD block ($r^2 > 0.5$). The significance of all SNPs with the highest $-\log_{10}(p)$ of each QTL was jointly tested in a multi-locus model, removing non-significant SNP with a backwards procedure ($p < 0.05$). Pearson correlation between iAs and tAs was estimated for the 32 lines subset.

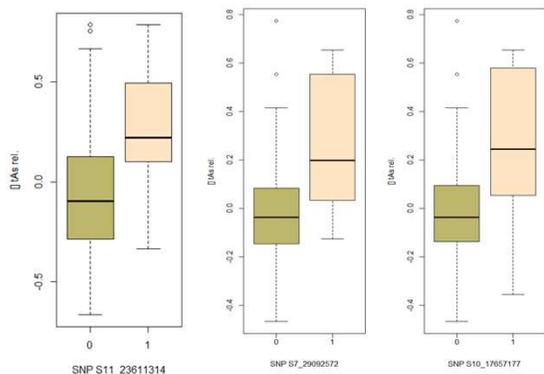


Fig 3. Allelic substitution effects for SNP representing the QTL that were significant in the multi-locus model.

Results

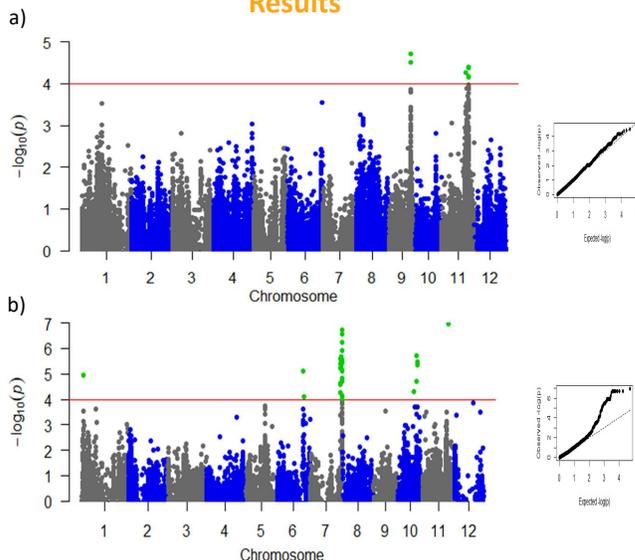


Fig 1. Manhattan and QQ plots with GWAS results for grain tAs in a) indica and b) tropical japonica populations. Significant associations are shown in green.

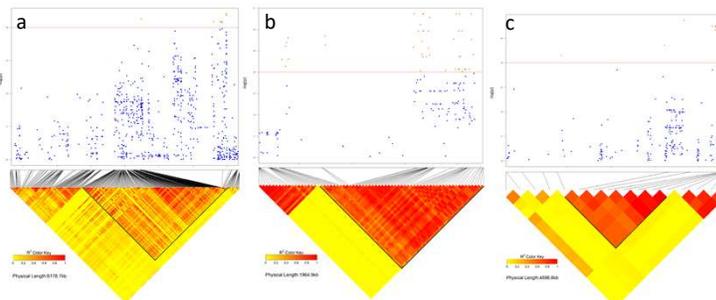


Fig 2. Zoomed-in regions of QTL for grain tAs that were significant in the multi-locus model. a) chromosome 11 (indica), b) chromosome 7 (tropical japonica), c) chromosome 10 (tropical japonica). The lower panel shows LD patterns with linked SNP with LD blocks in red.

The GWAS showed different architectures for indica and tropical japonica. Two QTL in chromosomes 9 and 11 were discovered in the indica population. Only the QTL in chromosome 11 was significant in the multi-locus model, with SNP S11_23611314 explaining 20% of the phenotypic variance. For tropical japonica, QTL in chromosomes 7 and 10 were identified, together explaining 20% of the phenotypic variance in the multi-locus model. The correlation between iAs and tAs in the 15 tropical japonica lines was 0.43, and no significant correlation between iAs and tAs was found for the 17 indica lines.

Conclusions

The genetic variance for tAs and iAs in INIA's advanced germplasm is adequate for breeding new cultivars with improved innocuity. tAs may be used as a proxy for iAs in tropical japonica, but more studies are required for indica. Our preliminary results with one year of field phenotyping suggest a low number of loci determining tAs, and thus a probable usefulness of MAS in both populations. However, more trials and years are required to rule out the magnitude of genotype and QTL by environment interactions.