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Genotypic differences in shoot silicon content and the impact on grain arsenic accumulation in rice

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Genotypic differences in shoot silicon content and the impact on grain arsenic accumulation in rice

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Genotypic differences in shoot silicon content and the impact on grain arsenic accumulation in rice

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Abstract:
Silicon in rice has been demonstrated to be involved in resistance to lodging, tolerance to both drought and salinity, and also enhances resistance to pests and diseases. The aim of this study was to determine the range of silicon content in a set of rice (Oryza sativa L.) accessions, and to determine if the natural variation of shoot silicon is linked to the previously identified silicon transporters (Lsi genes). Silicon content was determined in 50 field-grown accessions, representing all sub-populations of rice, with all accessions being genotyped with 700K SNPs. SNPs within 10 kb of the Lsi genes were examined to determine if any were significantly linked with the phenotypic variation. An XRF method of silicon determination compared favourably with digestion and colorimetric analysis. There were significant genotypic differences in shoot silicon ranging from 16.5 – 42.4 mg g⁻¹ of plant dry weight, there was no significant difference between the rice sub-populations. Plants with different alleles for SNPs representing Lsi2 and Lsi3 were significantly different for shoot silicon content. Shoot silicon correlated negatively with grain arsenic in the tropical and temperate japonica sub-population, suggesting that accessions with high shoot silicon have
reduced grain arsenic. This study indicates that alleles for *Lsi* genes are excellent candidate
genes for further study to explain the natural variation of shoot silicon in rice.

Key words: arsenic, natural variation, rice, silicon, XRF
1 Introduction

Global rice (*Oryza sativa* L.) production needs to increase continuously to ensure the world’s food security (*Hibberd et al.*, 2008). As a beneficial element, silicon alleviates biotic and abiotic stresses in rice which helps to maintain yield (*Ma and Takahashi*, 2002; *Detmann et al.*, 2012; *Meharg and Meharg*, 2015). Silicon is mainly available as monosilicic acid ranging from 0.1 to 0.6 mM in the soil solution (*Epstein*, 1994; *Ma and Takahashi*, 2002). Previous studies have demonstrated that monosilicic acid is taken up by rice roots as an undissociated molecule and translocated into the shoots through the transpiration stream (*Takahashi and Hino*, 1978; *Mitani-Ueno et al.*, 2005). It then polymerises on the surface of cells in the shoot in the form of a silica-cellulose double layer and silica-cuticle double layer. This silica-base layer improves resistance to lodging, salinity tolerance, drought tolerance, and enhances resistance to pests and diseases (*Takahashi and Hino*, 1978; *Mitani-Ueno et al.*, 2005, *Chen et al.*, 2011; *Han et al.*, 2015).

Genetically rice can be classified into two major sub-species, *Japonica* and *Indica* (*Chang*, 2003) and these have been further classified into 5 sub-populations; *indica, aus*, (both *Indica* sub-species) *tropical japonica, temperate japonica*, and *aromatic* (all three *Japonica* sub-species) (*Garris et al.*, 2005; *Zhao et al.*, 2011). Several previous studies indicate that there are differences in shoot silicon content between the *Indica* and *Japonica* sub-species of rice. *Deren et al.*, (1992) showed that *Japonica* sub-species usually have a higher silicon content than *Indica* rice varieties, based on screening 10 accessions in the greenhouse and 18 under field conditions. A study conducted by *Winslow* (1992) revealed that African upland *Japonica* rice accessions had 50 to 100% higher silicon content in mature flag leaves than Asian upland *Indica* accessions. In addition to the differences at the subspecies level several studies have looked at genotypic differences in silicon content, showing ranges of 41 to 60 mg g\(^{-1}\) (*Deren*, 2001) and 28 to 61 mg g\(^{-1}\) (*Norton et al.*, 2010a). *Ma et al.*, (2007a) also
observed that silicon uptake by the root and the concentration silicon present in the shoot are both higher in *Japonica* than *Indica* rice accessions, which they attributed to differences in the expression of silicon transporter genes.

Two types of silicon transporters have been identified in rice to date. A gene (LOC_Os02g51110) identified for silicic acid influx in rice is classified as an aquaporin (Low silicon 1 or *Lsi1*) which is a member of the nodulin 26-like intrinsic protein (OsNIP2; 1) group of aquaporins (*Ma* et al., 2006; *Ma* et al., 2008). A homologue of *Lsi1*, known as *Lsi6* (LOC_Os06g12310; OsNIP2; 2), responsible for shoot and husk silicon distribution in rice is also classified as an aquaporin (*Yamaji* et al., 2008). The efflux of silicic acid through the plasma membrane protein known as low silicon 2 (*Lsi2*; LOC_Os03g01700) is an energy dependent process in rice (*Ma* et al., 2007b). A homologue of *Lsi2*, known as *Lsi3* (LOC_Os10g39980), is also an energy dependent active transporter involved in regulating shoot silicon accumulation in rice (*Yamaji* et al., 2015).

It has been shown that arsenic, classified as a class one carcinogen, can be transported through silicon transporters in rice (*Ma* et al., 2008; *Zhao* et al., 2010; *Mitani-Ueno* et al., 2011). There are two different forms of arsenic present in rice: organic arsenic and inorganic arsenic (*Williams* et al., 2005). Organic arsenic is found in rice in two main types of molecular species dimethylarsinic acid (DMA), and monomethylarsonic acid (MMA) as well as tetramethylarsonium (*Williams* et al., 2005; *Hansen* et al., 2011). Inorganic arsenic is found in rice as two molecular species; arsenate and arsenite (*Abedin* et al., 2002; *Williams* et al., 2005). Arsenate is an analogue of phosphate and is taken up via phosphate transporters while arsenite is taken up by silicic acid transporters in rice (*Abedin* et al., 2002; *Ma* et al., 2008). It has been shown that the silicon transporters *Lsi1*, *Lsi2* and *Lsi6* are also arsenic transporters, using a combination of mutants and transgenic lines (*Ma* et al., 2008; *Zhao* et al., 2010; *Mitani-Ueno* et al., 2011). Several studies indicate that anaerobic rice cultivation
leads to increased mobilisation of soil arsenic in the form of arsenite, which causes anaerobically-grown rice to accumulate more arsenic through silicon transporters (Ma et al., 2008; Xu et al., 2008; Carey et al., 2010). Silicon fertilisation has also been shown to decrease shoot and grain arsenic indicating that silicon could play an important role in decreasing total arsenic uptake in rice (Li et al., 2009; Seyfferth and Ferdorf, 2012).

This study was designed to address four questions all related to the process of silicon and arsenic accumulation in rice: How does the cultivation method affect silicon distribution in different organs of rice plants? Are there significant genotypic differences in shoot silicon concentration across a diverse panel of rice related to the 5 different sub-populations of rice? Is there a relationship between natural variation in shoot silicon and arsenic content in rice? Can natural variation in shoot silicon be linked to known silicon transporters in rice? The results provide a deeper understanding of the natural variation in silicon content across rice accessions and its relationship to arsenic accumulation in rice grains.
2 Materials and Methods

2.1 Silicon content in different organs of rice (*Oryza sativa* L.) grown in flooded and non-flooded conditions

An experiment was conducted in a greenhouse at the University of Aberdeen, UK under both flooded and non-flooded conditions with four replicates for each treatment. One litre plastic pots were filled with soil (~530 g soil described in *Norton et al.*, 2013). For the flooded condition, a plastic liner was used to line the pots and hold the water within the pot whereas the non-flooded pots were kept without a liner to allow drainage of water through the pot.

Five Italica Carolina (*temperate japonica*) seeds were sown in each pot, then thinned to one plant in each pot after two weeks. To maintain the flooded condition, tap water from the greenhouse was used to flood the pots to 2 cm above the soil surface when plants were 3 weeks old. Every two weeks during the first four weeks of growth 100 mL of half strength Yoshida’s nutrient solution was added (*Yoshida et al.*, 1976). The dose of Yoshida’s nutrient solution was increased up to 100 mL of full strength solution every week after four weeks and continued until the filled grains had matured when samples were harvested.

At harvest, samples were collected from different parts of the mature plants: root, 3rd sheath, 3rd node, 3rd leaf, 2nd sheath, 2nd node, 2nd leaf, flag sheath, 1st node, flag leaf, husk and unpolished grains. The sheath, node and leaves were taken from the main tiller, with the most recent leaf prior to the flag leaf designated 2nd leaf. Root samples were washed thoroughly with tap water followed by deionised water and confirmed to be free of soil particles by examining the roots under a microscope (Leica MZ8, 10445932, 16×/14B, PLAN 1.0X).

Samples were dried at 80°C for 5 days until a constant weight was achieved. All samples were mixed and subsampled prior to being ball-milled. The silicon content was determined by Flow Injection Analyser (FIA) after alkali digestion.
2.2 Genotypic differences in shoot silicon content of rice

Seeds were obtained from the Rice Diversity Panel 1 (RDP1) ([http://ricediversity.org/](http://ricediversity.org/)) ([Ali et al., 2011; Eizenga et al., 2014](http://ricediversity.org/)). The classification of Zhao et al., (2011) was used for the sub-population classification of rice accessions. In 2009 a total of 312 accessions were cultivated at the experimental site in Bangladesh. Seedlings were transplanted by hand in a single 2m row of 10 hills, each hill (one seedling) 20 cm apart and each row 20 cm apart in a randomised complete block design with four replicates of each accession. The experimental site was kept flooded until the grains were filled. Plant material from the central six plants was harvested and used for chemical analysis. Detailed information about the experimental site and experimental methods are described in Norton et al., (2012). For shoot silicon analysis, fifty accessions (10 accessions from each rice sub-population) were randomly selected based on the initial sub-population assignment using single sequence repeat (SSR) markers (Ali et al., 2011) (Supplementary Table 1). Subsequently, after selection and silicon analysis, these accessions have been assigned to sub-populations based on the 700K SNP data (McCouch et al., 2016), these sub-population assignments are used for classification of the accessions in this study.

2.3 Analysis of rice shoot silicon by FIA

Plant material and certified reference material (CRM) were prepared for silicon analysis as described by Carneiro et al., (2007). A total of 1.5 g shoot material from each sample was sub-sampled at random and powderised using a ball mill (Retsch, MM200, Germany). From the powderised plant material, a sub-sample of 20 mg was weighed into a 50 mL polyethylene centrifuge tube (Corning®, NY). To digest the sample, 0.6 mL of hydrogen peroxide (H$_2$O$_2$, > 30% W/V, Fisher Scientific) and 1.5 mL of sodium hydroxide (NaOH, solutions 50%, Fluka) were added and the samples were then vortexed (mixed using a vortex mixer). The samples were heated for 1 hour at 90°C in a water bath, then vortexed again and
left overnight. The tubes were vortexed again after overnight extraction, then heated at 123°C under a pressure of 0.15 MPa for 1 h. Samples were kept at room temperature for 2 h then vortexed, followed by addition of 18.5 mL of ddH$_2$O. Prior to analysis, samples were diluted 1:5 with Milli-Q water. Silicon content was measured using an FIA spectrophotometer (Tecator FIAstar 5010) a wavelength of 410 nm (Carneiro et al., 2007; Norton et al., 2010a; Norton et al., 2010b).

2.4 Analysis of rice shoot silicon by P-XRF

A total of 1.5 g of dried shoot material for each rice accession was sub-sampled at random and powdered using a ball mill (Retsch, MM200, Germany). To perform the analysis of shoot silicon by P-XRF, 19 accessions were selected at random from the 50 accessions for which shoot silicon had been determined by FIA. For P-XRF analysis, 0.7 g of homogeneous powder sample was compressed into 13 mm diameter pellets using a manual hydraulic press with a 13mm die at a pressure of 10 tons (Specac, Orpington, United Kingdom). Shoot silicon content (% of silicon dry shoot weight) was measured using a commercial P-XRF instrument (Niton XL3t900 GOLDD analyzer: Thermo Scientific Winchester, UK), calibrated using Si-spiked synthetic methyl cellulose and validated using Certified Reference Materials of NCS DC73349 ‘Bush branches and leaves’ obtained from the China National Analysis Center for Iron and Steel, as described in Reidinger et al., (2012). The mean value of samples for each accession was used for correlation analysis between P-XRF and FIA measurements.

2.5 Relationship between silicon and arsenic content in rice

The plant material used in this study was previously examined for grain arsenic content (Norton et al., 2012) which provided an opportunity to examine the relationship between shoot silicon and grain arsenic in rice. The relationship between shoot silicon (log
transformed) and grain arsenic (log transformed) was investigated for the 50 rice accessions based on accession means.

2.6 Single Marker Analysis

The accessions used in this study have been genotyped using a high-density SNP chip (McCouch et al., 2016). SNPs for the accessions were extracted using PLINK (Purcell et al., 2007). SNPs were extracted from 10 kb upstream of the start codon to 10 kb downstream of the stop codon of the Lsi1, Lsi2, Lsi3, and Lsi6 loci. SNPs were excluded from the analysis if they were invariant or if minor alleles were present in less than 5% of the accessions. The RDP1 population has a high degree of stratification by rice sub-population (Zhao et al., 2011; McCouch et al., 2016). To overcome this stratification, sub-population assignment was used (based on the 700 K SNP data; McCouch et al., 2016) as a factor in a two-way ANOVA, with SNP base call as the other factor. The two-way ANOVA was used to determine if the phenotype for the accession was significantly different for each SNP tested.

2.7 Sequence alignments

Based on the result achieved from the single-marker analysis the sequence diversity of Lsi2 and Lsi3 were investigated for 5 cultivars using BAM files produced after aligning sequence reads against Nipponbare version 7 reference genome. The genome sequences of the cultivars used in this study have been previously published (Kawahara et al., 2013; Cardoso et al., 2014; Schatz et al., 2014). The accessions were from the following sub-populations; 2 indica accessions (IR64 and Bala), 1 aus accession (DJ123) and 2 tropical japonica accessions (Azucena and Nipponbare). The genomic DNA sequence was visualised using the IGV (https://www.broadinstitute.org/igv) to identify the difference of genomic DNA sequence within Lsi2 and Lsi3 in 5 cultivars (Thorvaldsdóttir et al., 2013; Robinson et al., 2011). Using
Clustal Omega the DNA sequences of 5 cultivars were aligned for *Lsi2* and *Lsi3* separately and showed in supplementary figure 3 and 4 respectively (Sievers et al., 2011).

### 2.8 Statistical analysis

Statistical significance was set at $P < 0.05$ for all analyses, which were performed using Minitab 16. The normality of distribution and homogeneity of variance of the data were tested prior to one or two-way analysis of variance (ANOVA), as appropriate. Pearson correlation analysis was used to investigate the relationship between measurements of shoot silicon and grain arsenic.
3 Results

3.1 Shoot silicon content in different organs of rice plants

Flooding increased plant silicon content in the flag sheath, 1st node, flag leaf and husk compared to plants grown under non-flooded conditions (Fig. 1). The content of silicon in grain and root tissues were significantly lower than any in other organs of plants grown under either condition. There was a significant difference ($P < 0.001$, $F = 27.40$, $R^2 = 78.20\%$) of silicon content between different organs of the plant in non-flooded conditions: The highest mean content was in the husks (46.8 mg g$^{-1}$), while the lowest was in the grain (3.5 mg g$^{-1}$). For plants grown under flooded conditions: The highest silicon content was observed in the flag leaf (67.3 mg g$^{-1}$) and the lowest was in the grains (4.4 mg g$^{-1}$).

3.2 Genotypic difference in shoot silicon content of rice

Fifty diverse rice accessions were examined by FIA to determine the difference in shoot silicon content of rice. There was a significant genotypic difference in shoot silicon content among the 50 accessions, where genotype explained 55% of the variation ($P < 0.001; F = 5.80; R^2 = 55.30\%; df = 49$). The mean shoot silicon content of the 50 accessions was 28.1 mg g$^{-1}$, and the lowest mean shoot silicon was observed in Dhala Shita (16.5 mg g$^{-1}$) The highest mean shoot silicon was observed in Bala (42.4 mg g$^{-1}$) (Fig. 2). There was no significant difference for shoot silicon content of the 5-major rice sub-populations (Fig. 3).

Nineteen rice accessions were selected at random from the 50 accessions analysed by FIA, for measurement of shoot silicon content by P-XRF. The silicon content of four individual field grown replicates of each accession were measured separately by P-XRF and FIA and the mean value of each accession was used for correlation analysis. Using both methods, genotypic differences were observed between the accessions ($P < 0.001; F = 9.90; df = 18$ for P-XRF; $P < 0.001; F = 7.30; df = 18$ for FIA). Correlation analysis indicated that there was a
significant and large positive correlation between the two methods ($r = 0.95; P < 0.001; \text{df} = 18$) (Fig 4).

### 3.3 Correlation between shoot silicon and grain arsenic in rice

No significant correlation was observed between mean shoot silicon and mean shoot arsenic for all of the 50 accessions (supplementary Figure 1), or for within each of the 5 sub-populations. There was a weak negative correlation ($r = -0.31; P = 0.028; \text{df} = 49$) (supplementary Figure 2) between shoot silicon and grain arsenic content for all 50 accessions. When correlation analysis was conducted separately for shoot silicon and grain arsenic on each of the sub-populations, significant negative correlations were found for the temperate japonica ($r = -0.78; P = 0.007; \text{df} = 9$) and tropical japonica ($r = -0.84; P = 0.002; \text{df} = 9$) accessions (Fig. 5). No significant correlations were observed for the other 3 major rice sub-populations (indica, aus and aromatic).

### 3.4 Testing accessions with different alleles of SNPs around and within Lsi genes for variation in shoot silicon concentration

A total of 10 SNPs from the SNP database are within 10 kb upstream and downstream of the \text{Lsi2} gene (selected SNPs for the rice accessions are presented in supplementary Table 2).

Shoot silicon concentration for accessions with the different alleles for two of these SNPs was significantly different. SNP-3.434426 is located 2551 bp before the start codon, and revealed a significant difference between the C and T polymorphism ($P = 0.006$), where the mean silicon content of accessions with the C allele was 29.3 mg g$^{-1}$ while the mean silicon content of the accessions with the T allele was 23.1 mg g$^{-1}$. SNP-3.438416 is located 6541 bp before the start codon and revealed a significant difference between the A and C polymorphism ($P = 0.008$), where the mean silicon content of the accessions with the A allele was 29.6 mg g$^{-1}$ while the silicon content of the accessions with the G allele had a mean of...
23.1 mg g\(^{-1}\). Both SNPs group the accessions in a similar way, the only difference was more missing SNP information for SNP-3.438416 (Fig. 6).

A total of 20 SNPs from the SNP database are within 10 kb upstream and downstream of the \(Lsi3\) gene (selected SNPs for the rice accessions are presented in supplementary Table 3). Shoot silicon concentration for accessions with the different alleles for one of these SNPs was significantly different. SNP-10.21340470 is located 5299 bp prior to the start codon, and revealed a significant difference between the G and A polymorphism \((P = 0.016)\), where the mean silicon content of accessions with the G allele was 28.4 mg g\(^{-1}\) while the mean silicon content of the accessions with the A allele was 35.6 mg g\(^{-1}\) (Fig. 6).

There were 20 SNPs and 19 SNPs observed within 10 kb of \(Lsi1\) and \(Lsi6\) respectively. However, at each of these SNPs the different alleles were not significantly different for shoot silicon concentration.

To explore further, the sequence alignments of \(Lsi2\) and \(Lsi3\) were performed using available high-quality genome sequences. The accessions used were Nipponbare, Azucena, IR64, Bala, and DJ123 which are from the \textit{tropical japonica}, \textit{tropical japonica}, \textit{indica}, \textit{indica} and \textit{aus} rice subgroups respectively. From the sequence analyses of \(Lsi2\) and \(Lsi3\) a number of polymorphisms within the genes were identified. For \(Lsi2\), there was a synonymous SNP substitution within the first exon, where DJ123 has “C” allele while the other 4 accessions have “T” allele (Supplementary Figure 3). For \(Lsi3\), 4 SNPs were detected in exons and 6 SNPs in introns (Supplementary Figure 4). There was only one non-synonymous SNP observed in the first exon of \(Lsi3\) where DJ123 and Bala have “T” allele and other accessions have “A” allele. The available 3000 rice genome sequence data indicates that this polymorphism between “A” and “T” in \(Lsi3\) is associated with the \textit{aus} sub-population in rice where 15 accessions have “A” allele and 184 accessions have “T” allele (Alexandrov et al., 2013).
This non-synonymous polymorphism between “A” and “T” in Lsi3 with the “T” allele is very rarely observed in indica and japonica subpopulations of rice in 3000 rice genome sequence data (Alexandrov et al., 2015).
4 Discussion

In this study, genotypic differences in shoot silicon content were identified from field grown rice cultivars. However, no differences in shoot silicon were observed across the 5 different sub-populations of rice. Additionally, SNPs detected in the accessions were significantly linked to known silicon transporter genes in rice, which indicates that these genes are potentially involved in natural variation of silicon accumulation in rice.

Flooded conditions increased silicon content in the upper part of the plant (flag sheath, 1\textsuperscript{st} node, flag leaf and husk) compared to the non-flooded conditions, which suggests that the uptake or translocation of shoot silicon into these plant organs might be controlled by different processes (compared to those determining silicon uptake in other tissues) which differ between aerobic and anaerobic conditions. It has been shown that silicon dissolution and bio-availability plays a significant role in the variation of silicon content in grasses (Quigley et al., 2017). Therefore, the difference in dissolved silicon in flooded and non-flooded conditions might affect the accumulation of silicon in the rice plants used in this study. It was also notable that there was no significant difference in silicon content in different tissues between the internodes (e.g. flag leaf, 2\textsuperscript{nd} leaf) in non-flooded conditions but there was a significant difference between the silicon content of internodes under flooded conditions (Fig. 1). Previous studies have shown that transpiration is one of the most important factors responsible for higher silicification in plants and that transpirational flow is higher in anaerobic conditions than in aerobic ones (Mitani-Ueno et al., 2005; Kato and Okami, 2011; Kumar et al., 2017; McLarnon et al., 2017). Therefore, one potential explanation for increased silicon accumulation in the upper organs or developing organs of rice plants (e.g. flag sheath, 1\textsuperscript{st} node, flag leaf and husk) grown in flooded soils is a higher transpirational flow in these plants. Importantly, the data presented in figure 1 shows that tissue silicon content is reasonably evenly distributed across tissues with only that from
flooded plants in tissue associated with flowering and seed production significantly higher than the rest. Since this reproductive tissue was removed from the field samples used in this study we can be reassured that a mean value obtained from straw will be a good estimate of the tissue concentration of the majority of rice plant.

Fifty accessions from 5 different sub-populations (10 accessions from each sub-population) were selected at random to examine the difference of shoot silicon content in rice and this revealed highly significant differences of shoot silicon content. A genotypic difference in shoot silicon content across a wide group of accessions has been observed previously (Deren, 2001; Norton et al., 2010a). The 2.6-fold difference of shoot silicon content in this study is similar to the previous 2.2 fold range detected for genotypic differences of shoot silicon content in rice (Norton et al., 2010a). However, the maximum value observed in our study is slightly lower than that detected previously (42.4 mg g\(^{-1}\) in this study, 60 mg g\(^{-1}\) (Deren, 2001), 61 mg g\(^{-1}\) (Norton et al., 2010a).

The plant material used for determination of shoot silicon content in the 50 rice accessions was grown in flooded, irrigated conditions (Norton et al., 2012). Previous studies estimated that 27% - 44% of the silicon taken up by rice plants is supplied by irrigation, while the remaining percentage must be supplied by soil constituents (Desplanques et al., 2006; Klotzbücher et al., 2015). All the accessions tested in this study had a silicon content below 50 mg g\(^{-1}\) which, according to Dobermann and Fairhurst (2000), is below the critical level of mineral deficiency for rice production. The low shoot silicon content (16.5 mg g\(^{-1}\) to 42.4 mg g\(^{-1}\)) observed in this study may be due to removal of rice straw from the paddy field, which is common practice in Bangladesh, and has been shown to contribute to lower shoot silicon in the subsequent rice crop (Seyfferth et al., 2013). Future work should focus on linking the flooded and non-flooded pot based experiment and the removal of straw at the field scale to
establish the importance of water management and field management on silicon accumulation in field grown rice.

Several studies have demonstrated that the *Japonica* sub-species of rice have higher shoot silicon than *Indicas* (Winslow, 1992; Winslow et al., 1997; Ma et al., 2007a). These studies may have been limited by the number of accessions that were screened. For example, Ma et al., (2007b) only screened two rice accessions to examine the genotypic difference in silicon uptake of rice. To improve the current understanding of silicon biology in rice, we investigated field grown shoot samples of 50 rice accessions across 5 sub-populations. Within the material tested in this study the data suggests that the natural variation observed in shoot silicon is not governed by genetic differences between rice sub-populations, but rather is largely due to the genetic differences within individual sub-groups.

Data on more than 50 accessions would have opened the opportunity to conduct genome-wide association (GWA) mapping where 200 accessions is considered a lower limit. However, the FIA colorimetric method for the determination of silicon in rice shoots proved not to be high throughput. However, in addition to the FIA method, a sub-set of samples were also analysed by P-XRF. The two different methods were strongly correlated, but not perfectly, and indicated that values for silicon content in samples measured by FIA were slightly higher than those measured by P-XRF. The observation that both methods provide comparable results highlights the conclusion that P-XRF can be used for silicon analysis to detect and measure genotypic differences across populations, instead of the more laborious and time-consuming alkali digestion method. Furthermore, a second advantage of P-XRF is that it is a non-destructive method. This would make it much more suitable for future GWA mapping studies.

The plant material used in this study was previously used to examine the variation of shoot and grain arsenic (Norton et al., 2012). The comparison of shoot silicon and grain arsenic in
this study is in agreement with previous studies where, in general, plants that had high shoot
silicon also had lower grain arsenic (Seyfferth and Ferdorf, 2012; Norton et al., 2012; Norton
et al., 2013). However, this study also adds more insight by taking into consideration the sub-
population structure of rice cultivars. The correlation between shoot silicon and grain arsenic
was sub-population specific. A strong relationship in between shoot silicon and grain arsenic
was observed in temperate japonica and a weaker one in tropical japonica, but was not
observed in indica, aus or aromatic. This important observation suggests that the genetic
regulation of arsenic content in rice grain is different in temperate and tropical japonicas
compared to the other rice sub-populations, implying that the silicon-transport-linked
pathway implicated for arsenic accumulation (Ma et al., 2007b; Norton et al., 2012) may be
less relevant in the other sub-populations.

The accessions used in the study have been genotyped using a 700K SNP chip (McCouch et
al., 2016). Single-marker analysis was used to test the candidacy of the known transporters of
silica in rice. The study indicated that two SNPs within 10 kb of Lsi2 and one within 10 kb
of Lsi3 were involved in contributing to the natural variation of shoot silicon accumulation in
rice (Fig. 6). The Lsi2 gene has been shown to be pivotal for transport of silicon and
inorganic arsenic in studies conducted with mutants and transgenic plants (Ma et al., 2006;
Ma et al., 2007b; Yamaji et al., 2008; Mitani-Ueno et al., 2011; Yamaji et al., 2015). The
identification of differences in shoot silicon and the link with three SNPs close to the genes
further suggest that Lsi2 and Lsi3 are excellent candidate genes to explain the natural
variation observed in shoot silicon content of rice. When looking at the sequencing variation
of a number of diverse cultivars (which have been sequenced to a high depth) it is evident
that there is only a small number of polymorphisms within the genes (Supplementary figures
3 and 4). The highly conserved sequence for Lsi2 may be due to its importance function for
silicon accumulation in rice. However, the accessions screened in this study are likely to have
greater sequence variation than the cultivars for which high quality sequence is available, and
therefore there may be greater sequence variation for Lsi2 (and the other Lsi genes) than that
is represented in the 5 accessions reported here. A focus for future study will be to expand
sequence information to more accessions to more fully explore sequence variation associated
with the polymorphic SNPs presented in figure 6.

5 Conclusion

This study has demonstrated strong genotypic differences in shoot silicon in a diverse
collection of rice cultivars, showing that there is potential to breed rice with increased silicon
content that could improve resistance to both biotic and abiotic stresses in rice, which would
help to maintain crop yields. The identification of significant SNPs linked with the shoot
silicon phenotype within 10 kb of known silicon transporters warrants further study to
investigate the impact of different alleles of these genes on silicon and arsenic accumulation
in rice. Furthermore, the XRF method of silicon determination could be applied to GWA
mapping studies that might reveal further candidate genes for silicon content in rice.
Acknowledgements: We acknowledge the financial support of School of Biological Sciences (SBS), University of Aberdeen (UoA) for the analysis of silicon using FIA. We also acknowledge the support provided by the SBS member of staffs (Annette Raffan, Michael Mcgibbon, and David Galloway) for the analysis of silicon using FIA.

References


**Figure 1:** Silicon in different organs of rice (bars are the mean of four replicates and error bars represent standard error of the mean). Letters above the columns (upper-case = anaerobic and lower case = aerobic) indicate statistically significant differences in silicon content of different plant organs using Tukey’s test in two conditions. *denotes a significant difference between the two treatments for that plant organ.

**Figure 2:** Mean shoot silicon (mg g$^{-1}$) of 50 rice accessions determined by FIA. Different symbols refer to the accessions belonging to the different sub-populations; circle = *aus*, square = *indica*, cross = *aromatic*, triangle = *tropical japonica*, upside down triangle = *temperate japonica*. Error bars indicate the standard error of the mean (n = 4).

**Figure 3:** Shoot silicon (mg g$^{-1}$) content of 50 accessions in 5 different sub-populations of rice. ARO = *aromatic*, AUS = *aus*, IND = *indica*, TEJ = *temperate japonica* and TRJ = *tropical japonica*. The edges of each box show the upper and lower quantile and the bold line in the box shows the median value and the dotted line the mean value. The whiskers are the 10th and 90th percentiles.

**Figure 4:** Correlation of mean shoot silicon in 19 rice accessions determined by FIA and P-XRF. Error bars indicate the standard error of the mean (n = 4). Dotted line is the 1:1 line.

**Figure 5:** Correlation between shoot silicon (mg g$^{-1}$) and grain arsenic (µg kg$^{-1}$) in ARO= *aromatic*, AUS = *aus*, IND = *indica*, TEJ = *temperate japonica* and TRJ = *tropical japonica* subpopulations.

**Figure 6:** Variation in shoot silicon (mg g$^{-1}$) between different SNPs within 10 kb of *Lsi2* and *Lsi3*.
Figure 1
Figure 2

Shoot silicon content (mg g\(^{-1}\))

Genotypes

- DHALA SHAITTA
- DAM
- DULAR
- LD 24
- AZUCENA
- BASMATI 217
- DAWEBYAN
- DJIMORON
- N12
- DOURADO AGULHA
- TA MAO TSAO
- NIRA
- BYAKKOKU Y 5006 SELN
- GHARIB
- ARC 10177
- KITRANA 508
- KHAO GAEW
- PAUNG MALAUNG
- DZ78
- PADI KASALLE
- NPE 844
- TCHAMPA
- GHATI KAMMA NANGARHAR
- CA 902 B 2 1
- SAB INI
- FIROOZ
- SADRI BELYI
- MIRITI
- BLACK GORA
- P 737
- KU115
- KOSHIHIKARI
- RAZZA 77
- IR 36
- MARATELLI
- DOM ZARD
- TAICHUNG NATIVE 1
- GERDEH
- LUSITANO
- ARC 10352
- TOPLOEA 70 76
- BICO BRANCO
- KON SUITO
- KALUBALA VEE
- AZERBAIDJANICA
- LEMONT
- MOROBEREKAN
- NORIN 20
- BALA
- MIRITI
- ARC 10177
- KITRANA 508
- KHAO GAEW
- PAUNG MALAUNG
- DZ78
- PADI KASALLE
- NPE 844
- TCHAMPA
- GHATI KAMMA NANGARHAR
- CA 902 B 2 1
- SAB INI
- FIROOZ
- SADRI BELYI
- MIRITI
- BLACK GORA
- P 737
- KU115
- KOSHIHIKARI
- RAZZA 77
- IR 36
- MARATELLI
Figure 3

Shoot silicon content (mg g⁻¹)

Rice subpopulation

ARO AUS IND TEJ TRJ
Figure 4

Shoot silicon content measured by FIA (mg g\(^{-1}\)) vs. Shoot silicon content determined by XRF (mg g\(^{-1}\)).
Figure 5
Figure 6
Supplementary Table 1: Selected genotype from RDP1 for shoot silicon analysis

Supplementary Table 2: SNPs with 10 kb (upstream and downstream) of Lsi2. SNPs data taken from the High-density rice array (HDRA, 700k SNPs data) available at http://ricediversity.org/data/index.cfm. After each SNP name (in brackets) is the location of that SNP aligned to the Rice Genome Annotation Project – release 7 sequence available at http://rice.plantbiology.msu.edu/

Supplementary Table 3: SNPs with 10 kb (upstream and downstream) of Lsi3. SNPs data taken from the High-density rice array (HDRA, 700k SNPs data) available at http://ricediversity.org/data/index.cfm. After each SNP name (in brackets) is the location of that SNP aligned to the Rice Genome Annotation Project – release 7 sequence available at http://rice.plantbiology.msu.edu/
**Supplementary figure 1:** Correlation between shoot silicon (mg g\(^{-1}\)) and shoot arsenic (µg kg\(^{-1}\)) within 50 accessions of RDP1.
Supplementary figure 2: Correlation between shoot silicon (mg g$^{-1}$) and grain arsenic (µg kg$^{-1}$) within 50 accessions of RDP1.

$r = -0.323, P<0.022$
Bala
ATGGTGGGCTCACAATGCTGGAGCCGCACACACAGCGGTGCGCTGCTGTCGTC

IR64
ATGGTGGGCTCACAATGCTGGAGCCGCACACACAGCGGTGCGCTGCTGTCGTC

DJ123
ATGGTGGGCTCACAATGCTGGAGCCGCACACACAGCGGTGCGCTGCTGTCGTC

Nipponbare
ATGGTGGGCTCACAATGCTGGAGCCGCACACACAGCGGTGCGCTGCTGTCGTC

Azucena
ATGGTGGGCTCACAATGCTGGAGCCGCACACACAGCGGTGCGCTGCTGTCGTC

Bala
GACTTCCGACCGCCAGGCCAGCGTGCCCTGGAACGCTGCTTACTGCTGCTTGCTGCT

IR64
GACTTCCGACCGCCAGGCCAGCGTGCCCTGGAACGCTGCTTACTGCTGCTTGCTGCT

DJ123
GACTTCCGACCGCCAGGCCAGCGTGCCCTGGAACGCTGCTTACTGCTGCTTGCTGCT

Nipponbare
GACTTCCGACCGCCAGGCCAGCGTGCCCTGGAACGCTGCTTACTGCTGCTTGCTGCT

Azucena
GACTTCCGACCGCCAGGCCAGCGTGCCCTGGAACGCTGCTTACTGCTGCTTGCTGCT

Bala
TCCGGGATGTACACCTACCGCTACCGCTTCCAAACAGACGCGCTCCCGGAGCATTCTTG

IR64
TCCGGGATGTACACCTACCGCTACCGCTTCCAAACAGACGCGCTCCCGGAGCATTCTTG

DJ123
TCCGGGATGTACACCTACCGCTACCGCTTCCAAACAGACGCGCTCCCGGAGCATTCTTG

Nipponbare
TCCGGGATGTACACCTACCGCTACCGCTTCCAAACAGACGCGCTCCCGGAGCATTCTTG

Azucena
TCCGGGATGTACACCTACCGCTACCGCTTCCAAACAGACGCGCTCCCGGAGCATTCTTG

Bala
ATCTACTCTCTCTCTCTCTACCTCCTACCTACTACCTATACACACGTCCAAACAGGGT

IR64
ATCTACTCTCTCTCTCTCTACCTCCTACCTACTACCTATACACACGTCCAAACAGGGT

DJ123
ATCTACTCTCTCTCTCTCTACCTCCTACCTACTACCTATACACACGTCCAAACAGGGT

Nipponbare
ATCTACTCTCTCTCTCTCTACCTCCTACCTACTACCTATACACACGTCCAAACAGGGT

Azucena
ATCTACTCTCTCTCTCTCTACCTCCTACCTACTACCTATACACACGTCCAAACAGGGT

Bala
TAATCCGAAATATACATTACACTTACACTTACATATAGTATATAACTAACATACAAAATAT

IR64
TAATCCGAAATATACATTACACTTACACTTACATATAGTATATAACTAACATACAAAATAT

DJ123
TAATCCGAAATATACATTACACTTACACTTACATATAGTATATAACTAACATACAAAATAT

Nipponbare
TAATCCGAAATATACATTACACTTACACTTACATATAGTATATAACTAACATACAAAATAT

Azucena
TAATCCGAAATATACATTACACTTACACTTACATATAGTATATAACTAACATACAAAATAT

Bala
ATATGCCTGATCTGCTAGGCCTGAGGCTGAGGCACAGGCGGCGGCGCGGCGGCGGCGG

IR64
ATATGCCTGATCTGCTAGGCCTGAGGCTGAGGCACAGGCGGCGGCGGCGGCGGCGGCGG

DJ123
ATATGCCTGATCTGCTAGGCCTGAGGCTGAGGCACAGGCGGCGGCGGCGGCGGCGGCGG

Nipponbare
ATATGCCTGATCTGCTAGGCCTGAGGCTGAGGCACAGGCGGCGGCGGCGGCGGCGGCGG

Azucena
ATATGCCTGATCTGCTAGGCCTGAGGCTGAGGCACAGGCGGCGGCGGCGGCGGCGGCGG

Bala
TATCAGGCAGGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG

IR64
TATCAGGCAGGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG

DJ123
TATCAGGCAGGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG

Nipponbare
TATCAGGCAGGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG

Azucena
TATCAGGCAGGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG

Bala
GGACACTGCACCTGCTCTGCGAGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGG

IR64
GGACACTGCACCTGCTCTGCGAGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGG

DJ123
GGACACTGCACCTGCTCTGCGAGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGG

Nipponbare
GGACACTGCACCTGCTCTGCGAGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGG

Azucena
GGACACTGCACCTGCTCTGCGAGCTGAGGCTGAGGCGGACAGGCGGCGGCGGCGGCGG
Genomic sequence alignment of \textit{Lsi2}. Regions highlighted in bold are predicted exon regions based on the Rice Genome Annotation Project – release 7 sequence available at \url{http://rice.plantbiology.msu.edu/}.
Lsi3 (LOC_Os10g39980)

**Bala**
ACTCTCATGCCACCACCACCTCCCCACTCCAAGAGCTAGTCTGATTGATGGAGAGA

**IR64**
ACTCTCACGCACCACCACCTCCCCACTCCAAGAGCTAGTCTGATTGATGGAGAGA

**DJ123**
ACTCTCATGCCACCACCACCTCCCCACTCCAAGAGCTAGTCTGATTGATGGAGAGA

**Nipponbare**
ACTCTCATGCCACCACCACCTCCCCACTCCAAGAGCTAGTCTGATTGATGGAGAGA

**Azucena**
ACTCTCATGCCACCACCACCTCCCCACTCCAAGAGCTAGTCTGATTGATGGAGAGA

**Bala**
GAGGCGCGCATGCGGCTGCTGCAGTCGAGATGATGGATGGAGAGA

**IR64**
GAGGCGCGCATGCGGCTGCTGCAGTCGAGATGATGGATGGAGAGA

**DJ123**
GAGGCGCGCATGCGGCTGCTGCAGTCGAGATGATGGATGGAGAGA

**Nipponbare**
GAGGCGCGCATGCGGCTGCTGCAGTCGAGATGATGGATGGAGAGA

**Azucena**
GAGGCGCGCATGCGGCTGCTGCAGTCGAGATGATGGATGGAGAGA

**Bala**
GTCTGGCTGGATCTGGGATGATCCGCTGACAGGATGATGGATGGAGAGA

**IR64**
GTCTGGCTGGATCTGGGATGATCCGCTGACAGGATGATGGATGGAGAGA

**DJ123**
GTCTGGCTGGATCTGGGATGATCCGCTGACAGGATGATGGATGGAGAGA

**Nipponbare**
GTCTGGCTGGATCTGGGATGATCCGCTGACAGGATGATGGATGGAGAGA

**Azucena**
GTCTGGCTGGATCTGGGATGATCCGCTGACAGGATGATGGATGGAGAGA

**Bala**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**IR64**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**DJ123**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**Nipponbare**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**Azucena**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**Bala**
TAGGCCCTCCATGCCACCTCCCCCTGCGCTGACAGGATGATGGATGGAGAGA

**IR64**
TAGGCCCTCCATGCCACCTCCCCCTGCGCTGACAGGATGATGGATGGAGAGA

**DJ123**
TAGGCCCTCCATGCCACCTCCCCCTGCGCTGACAGGATGATGGATGGAGAGA

**Nipponbare**
TAGGCCCTCCATGCCACCTCCCCCTGCGCTGACAGGATGATGGATGGAGAGA

**Azucena**
TAGGCCCTCCATGCCACCTCCCCCTGCGCTGACAGGATGATGGATGGAGAGA

**Bala**
TAATCTCAAGAACCGCGCATGCTCCGAGCAGGATGATGGATGGAGAGA

**IR64**
TAATCTCAAGAACCGCGCATGCTCCGAGCAGGATGATGGATGGAGAGA

**DJ123**
TAATCTCAAGAACCGCGCATGCTCCGAGCAGGATGATGGATGGAGAGA

**Nipponbare**
TAATCTCAAGAACCGCGCATGCTCCGAGCAGGATGATGGATGGAGAGA

**Azucena**
TAATCTCAAGAACCGCGCATGCTCCGAGCAGGATGATGGATGGAGAGA

**Bala**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**IR64**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**DJ123**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**Nipponbare**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**Azucena**
GGGGGCGCTGCCGCAGTGGATAGTGCAGGATGATGGATGGAGAGA

**Bala**
ACCAAGCACCTCTGGCTGCTGCACCGGAGTGTGCTGACTGGCGTGGCAGGCAGGC

**IR64**
ACCAAGCACCTCTGGCTGCTGCACCGGAGTGTGCTGACTGGCGTGGCAGGCAGGC

**DJ123**
ACCAAGCACCTCTGGCTGCTGCACCGGAGTGTGCTGACTGGCGTGGCAGGCAGGC

**Nipponbare**
ACCAAGCACCTCTGGCTGCTGCACCGGAGTGTGCTGACTGGCGTGGCAGGCAGGC

**Azucena**
ACCAAGCACCTCTGGCTGCTGCACCGGAGTGTGCTGACTGGCGTGGCAGGCAGGC
Genomic sequence alignment of *Lsi3*. Regions highlighted in bold are predicted exon regions based on the Rice Genome Annotation Project – release 7 sequence available at [http://rice.plantbiology.msu.edu/](http://rice.plantbiology.msu.edu/).