e-ISSN:2320-0189
p-ISSN:2347-2308

Research & Reviews: Journal of Botanical Sciences

Arsenic in Rice: A Recent Update

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Editorial

Received date: 01/09/2015
Accepted date: 07/09/2015
Published date: 09/09/2015

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INTRODUCTION

Arsenic (As) exposure, in human has been associated with an increased risk of malignant arsenical skin lesions, and carcinomas [1]. Rice is the major crop in areas where severe as contamination occurs and has been reported to accumulate up to 2 mg Kg^{-1} As in grains and up to 92 mg Kg^{-1} in straw [2]. The population consume as polluted rice are under the threat from As contamination, which may pose a significant health risk [3-5]. Paddy rice is relatively efficient in As accumulation due to (a) higher arsenite [As (III)] mobilization as a consequence of anaerobic condition and (b) its transport via high efficient Si transport pathway [6,7]. Both inorganic forms of As [Arsenate {As(v)} and arsenite {As(III)] are highly toxic because they hamper the various metabolic pathways in cells such as the interaction with the sulfhydryl groups of proteins and the replacement of phosphate in ATP for energy [8]. Plant growth and crop yield is compromised as a result of as toxicity [9]. Arsenic like other heavy metals, stimulate the formation of free radicals and reactive oxygen species leading to oxidative stress. As a detoxification mechanism, after uptake, As(V) is rapidly reduced to As(III) which is then sequestered in the vacuoles with the help of phytochelatins (PCs) [8] **(Figure 1)**.

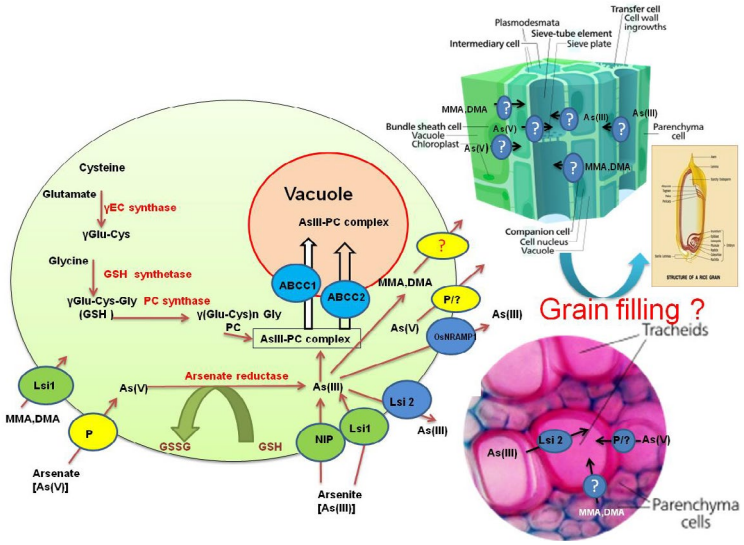

Figure 1. As metabolism, transport and defence mechanism in plants GSH reduced glutathione, GSSG oxidised glutathione, As(V) arsenate, As(III) arsenite, MMA monomethylarssonic acid, DMA Dimethylarsenic acid, P phosphate, PC phytochelatin, *PCsynthase Phytochelatin synthase*, NIP Noduline26 like intinsic protein Os NRAMP Natural resistance associated macrophage protein of rice, *ABCC1 and ABCC2 ABC transporter for AS(III)*-PC complex in vacuole,? Unknown transporters.

Understanding the molecular mechanisms of As transport and accumulation in rice may provide promising solutions to the problem. To characterize the As-responsive genes, analysis of the genome-wide expression of the rice transcriptome was carried out by different groups [10-13]. Most of the genes that are involved in glutathione synthesis, metabolism, and transport such as glutathione S-transferases (GSTs), multidrug resistance proteins, genes of sulphate metabolizing proteins, metallothionines, sulphate transporters, multidrug and toxic compound extrusion transporter (MATE), glutathione conjugated transporters [10-13]. MicroRNAs (miRNAs) are a novel class of short, endogenous, non-coding small RNA molecules involved in a wide variety of biological processes such as organ polarity, morphogenesis, floral transition, hormone signalling and adaptation to environment [14]. A study carried out by Sharma et al., clearly demonstrated the involvement of miRNA such as miR528, miR1861, miR2102 and miR395, miR529 and few more in response to As in rice [14].

Considerable variation in response to As exposure, in terms of its uptake, metabolism and accumulation in grains as well as other tissues of different rice genotypes has been observed even if grown with consistent soil As concentration [15,16]. Several QTLs for variations in the As accumulation in different rice tissues have been already mapped in rice genome [17,18]. Though, these QTLs could not elucidate the mechanism responsible for variation in As accumulation among different rice genotypes [15,18]. A comparative transcriptome analysis of rice cultivars contrasting in As uptake led to the identification of specific genotype-dependent genes responsible for As accumulation/tolerance in six different rice genotypes and this study suggested the need for development of genotype dependent strategy instead of common strategy [13].

Transcriptional analysis has a number of their own limitation [19]. Thus, gaining information at proteomic levels can offer deeper insights into the responses. Ahsan et al., and Liu et al., performed proteomic analysis to get a clear picture of mechanisms responsible for as metabolism [20-22]. On the basis of differential level of proteins, the role of GSH in protecting the plants against as stress due to synchronous function of S-adenosylmethionine synthetase, GSTs, cysteine synthase and glutathione reductase was suggested. Ahsan et al., also reported the first proteome map of rice leaves in response to as stress [21]. There was down regulation of chloroplast proteins and this modulation was correlated with decreased photosynthetic efficiency. All the studies carried out clearly demonstrate that sulphate assimilation pathway [17,22,23] and glutathione metabolism together with antioxidant system is the backbone of detoxification of As in rice and support the results of Shri et al., which clearly indicated thiols (GSH and Cys) mediated protection against as [24].

Levels of small metabolites such as MDA, ascorbate, glutathione also respond to environmental changes. Amino acid profiling of different rice cultivars on the basis of as accumulation was carried out by Dwivedi et al., [25]. This study concluded that most of the essential amino acids (EAAs) metabolites such as valine, metheionine, leucine, alanine, and nonessential amino acids (NEAAs) viz. histidine, alanine, proline, glutamic acid, and cysteine increased in most of the rice genotypes during As (V) exposure. Among stress responsive amino acids, proline is a much studied molecules and can function as an osmolyte, free radical scavenger and also protects the cell membrane against damage. The level of proline has also been observed to be elevated in O. sativa during As (III) stress [26]. MDA a marker of lipid peroxidation has also been reported during As strss in rice [27]. As (V) exposure caused an increase in the ratio of AsA/DAsA indicating the significant role of ascorbate for as induced stress amelioration. Nitric oxide, a signaling molecule was also found to be induced during As (V) stress condition in O. sativa [17].

Breeding (conventional and molecular), transgenic and agronomical approaches can be used to minimise as accumulation in rice which further reduces food chain contamination. As accumulation in straw and grain correlated negatively with root porosity and the rate of radial O_2 release among rice cultivars, presumably through the effect of O_2 release on Fe plaque formation, arsenite oxidation and subsequent arsenate retention on the Fe plaque [25,28]. Breeding for rice cultivars with stronger O_2 release characteristic may have the potential for decreasing as accumulation. In an attempt to minimise as accumulation in grains various genes has been introduced in rice [29-32] **Table 1.** Transgenic approach has their own limitation in field. So agronomic practices such as cultivation of aerobic rice and utilization of silicon fertilizers for farming practices may further decrease as accumulation in rice.

Table 1. Transgenic rice plants developed for modulated As accumulation in grain.

S.No.	Source	Gene name	Consequence	Reference
1	*Rhodopseudomonas palustris*	As(III)-S-adenosyl methyl transferase (arsM)	Decreased As in rice grain	[29]
2	*O. sativa*	Phosphate transporter (Pht1;8) Phosphate Starvation Response 2 (PHR2)	Increased phosphate and As(V) uptake and translocation	[30]
3	*S. cerevisiae*	Arsenate reductase (ACR3)	Increased As(III) efflux. Decreased As accumulation in rice grain.	[31]
4	*C. demersum*	Phytochelatin synthase (CdPCS1)	Increased As accumulation in roots and decreased accumulation in grain	[32]

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