

# Research on the Molecular Mechanisms of Aluminum Resistance in Rice has progressed

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## Introduction

Aluminum (Al) toxicity in acid soils is a major constraint to grain production around the world, as 13 percent of the world's rice is grown in acid soil with high Al content. Rice is possibly the most Al-resistant cereal, as well as the cereal with the most genetically diverse Al resistance, involving both external detoxification and internal tolerance. Al resistance transcription factor 1 (ART1) and other transcription factors, as well as organic acid transporter genes and metal ion transporter genes, have also been cloned in rice. The recent characterised genes influencing Al tolerance in rice, as well as the interrelationships between Al and other plant nutrients, were summarised in this study. Using a reverse genetics technique, a variety of genes have been well described, vastly improving our understanding of the molecular pathways of rice reaction to Al toxicity.

Interrelationships between Al and other plant nutrients have gotten a lot of coverage recently, and they offer another way to look at the complexities of Al tolerance. We summarised recently identified and characterised genes in this study to provide a quick overview of the progress [1]. To cope with the stress caused by Al toxicity, plants may grow a variety of Al resistance mechanisms. External detoxification and intrinsic immunity are two types of pathways. Roots may exclude Al by secreting organic acids, which is a well-studied plant technique for external detoxification [2]. Over the last few decades, significant progress has been made in discovering the molecular mechanisms of Al resistance in rice. In rice, the transcription factor ART1 is crucial for Al tolerance. Since Al has no effect on ART1 expression or localization, there must be a mechanism for ART1 activation. In the future, it will be important to find ART1-interacting proteins. Just nine of ART1's downstream genes have been identified as functional. The remaining

genes' functional characterization will add to our knowledge of Al tolerance in rice. Several resistant varieties or materials have been screened, and several QTLs regulating Al tolerance have been identified using molecular markers, based on the analysis of Al tolerance at the rice seedling level. However, few studies on fine mapping and cloning of the major QTLs have been conducted [3]. Understanding the genetic function of rice Al resistance is crucial for breeding rice with the trait. As a result, further research into the screening, detection, and functional analysis of the main QTLs for Al tolerance in rice is needed. To classify gene-trait correlations, transcriptome-wide interaction studies (TWAS) combining GWAS and gene expression datasets may be used. For reproduction, marker-assisted selection (MAS) is a better option than transgenic approaches. To boost tolerance, it is also obvious that multiple genes for Al tolerance are needed. It would be more beneficial to introduce several Al-tolerance genes rather than a single gene to enhance Al tolerance and thus increase rice production in acid soils. The presence and status of core plant nutrition have an effect on Al toxicity. Proper application of Mg<sup>2+</sup> fertiliser to rice cultivation in acid soils is a cost-effective and efficient way to increase rice resistance to Al toxicity.

## References

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