# Identification of SNPs Associated with Iron Toxicity Tolerance in Rice

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## ABSTRACT

Iron (Fe) toxicity is one of the limiting factors that can lead to the decrease of rice yield in paddy fields. Association studies to identify potential alleles or markers linked to iron toxicity tolerant trait can be carried out using high throughput single nucleotide polymorphisms (SNPs). We conducted an association study for Fe toxicity tolerance characters, using Forty-five double haploid lines derived from reciprocal double-crossing, i.e. IR54 / Parekaligolara // Bio110 / Markuti in high Fe wetland rice field. Genome-wide association study was carried out using 384 SNP-plex markers distributed on 12 rice chromosomes. A total of 77 SNPs were significantly associated with the Fe toxicity tolerance-related traits. Functional annotation allowed us to shortlist four SNP markers associated with Fe toxicity tolerance trait, i.e.: **TBGI204006, TBGI310247, id9006377,** and **id10000498.** The research suggests that association studies followed by functional annotation can effectively detect potential alleles and candidate genes for the trait. The identified QTL and genes provided valuable sources for future genetic improvement of Fe tolerant rice lines..

keyword : Rice, SNPs, Fe Toxicity Tolerance, QTL.