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“Bridging the gap between increasing knowledge and decreasing resources”

Genetic Basis of Iron Toxicity Tolerance in Rice (*Oryza sativa* L.)

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Abstract

Iron (Fe^{2+}) toxicity limits rice (*Oryza sativa* L.) growth in paddy fields worldwide, reducing yields up to complete crop failure. Fe^{2+} leads to the formation of reactive oxygen species (ROS) within the plant, followed by bronzing of the leaves. Tolerance varies depending on the genotype, the stress type (pulse vs. chronic stress) and further environmental parameters. Tolerance mechanisms, such as root exclusion, iron compartmentalisation within organs or true tissue tolerance, have been proposed but remain unexplored. We followed several approaches to dissect the genetic basis, including (i) a QTL analysis of a Pokkali/IR29 recombinant inbred population and a Nipponbare/Kasalath/Nipponbare backcross inbred population, yielding seven and three QTLs, respectively. QTLs were found to be co-localised with QTLs previously reported for both pulse and chronic stress treatment. To exploit the genetic diversity of rice, we (ii) conducted a genome wide association study (GWAS), identifying iron tolerance loci in a panel of 329 varieties, representing all subgroups of *O. sativa* from 79 countries. The lines were grown in hydroponic solution for four weeks, then exposed to a pulse stress of 1000 ppm Fe^{2+} for five days. All plants were phenotyped by quantifying leaf damage, growth and shoot iron content. All phenotypic traits yielded genomic loci significantly associated with tolerance to excess iron. *Temperate japonica* and *aromatic* sub-populations proved more tolerant than *tropical japonica*, *indica* and *aus* ($p < 0.001$). (iii) Putative candidate genes such as the metal tolerance protein (OsMTP1) are currently being sequenced and verified in mutant experiments. (iv) A subset of the diversity panel was validated on a known iron-toxic field site in the Philippines, in co-operation with the International Rice Research Institute (IRRI). (v) To bridge different stress types (chronic vs. pulse) and growth conditions (controlled vs. field), contrasting genotypes are currently being grown up to maturity in soil under controlled greenhouse conditions and exposed to both long- and short-term excess iron. This project adds to the genetic understanding of iron uptake, transport and tolerance mechanisms, which is the basis for enhancing yield and producing fortified crops on iron toxic soils.

Keywords: Genetics, genome-wide association study, iron toxicity, rice