

Increasing iron and zinc in rice grains using deep water rices and wild species – identifying genomic segments and candidate genes

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Large genetic variation exists for grain iron and zinc in rice germplasm including wild species and deep water rices. Conventional breeding is an easy and acceptable approach to biofortify rice. Analysis of 126 rice accessions using atomic absorption spectrophotometry showed that Fe concentration in brown rice ranged from 6 ppm in Athira to 72 ppm in *O. nivara* and Zn concentration from 27 ppm in Jyothi to 67 ppm in *O. rufipogon*. Quantitative trait loci (QTL) for high Fe and Zn concentration in grains were mapped from 3 wild progenitors and 2 deep water rices with the aim of gene discovery and also to develop iron/zinc-rich lines of two widely grown, popular rice varieties Swarna (MTU7029) and Samba Mahsuri (BPT5204) through conventional breeding approaches. Three advanced backcross mapping populations were developed using 3 wild accessions: Swarna x *O. nivara* IRGC81832, Swarna x *O. nivara* IRGC81848 and Samba Mahsuri x *O. rufipogon* WR119. In addition, F₇ recombinant inbred lines (RILs) were developed from two crosses: Madhukar x Swarna and Jalmagna x Swarna. Madhukar and Jalmagna are deep-water rice varieties with high grain iron and zinc. Overall, Fe concentration ranged from 0.2 to 224 ppm and Zn concentration from 0.4 to 104 ppm in the 5 mapping populations. QTLs for Fe and Zn concentration in polished rice were mapped from two Swarna x *O. nivara* BC2F3 mapping populations using accession IRGC81848- 227 families, 100 SSR markers and accession IRGC81832- 245 families, 75 SSR markers. *qFe2.1*, *qFe3.1*,

qFe8.1 and *qFe8.2* coincided in the two populations. QTLs for Fe and Zn concentration coincided on chromosomes 2, 3, 8 and 12. Five QTLs for Fe and 3 QTLs for Zn each explained more than 15% phenotypic variance. QTLs were also mapped for Fe and Zn concentration in brown rice from Madhukar x Swarna F₇ RILs using 110 SSR markers including 9 gene specific markers. Seven QTLs for Fe and six QTLs for Zn were identified each explaining >30% phenotypic variance. QTLs for Fe and Zn concentration coincided on chromosomes 7 and 12. Madhukar allele increased Fe in *qFe7.1* and *qFe7.2* and Swarna allele increased Zn in *qZn12.1* and *qZn12.2*. Only two QTL flanking markers RM243 for *qFe1.1* and RM517 for *qZn3.1* were common in the 3 mapping populations. Genotyping of 2 populations is in progress. Candidate genes *OsYSL1*, *OsNAC*, *OsYSL16*, *OsZIP4*, *OsYSL17* and *OsNAAT1* underlie the Fe or Zn QTLs mapped in the Swarna x *O. nivara* mapping population. Likewise, *OsYSL1*, *OsMTP1*, *OsNAS1*, *OsNAS3*, *OsNRAMP1*, *heavy metal ion transporter*, *OsAPRT* underly QTLs for Fe and Zn mapped in the Madhukar x Swarna mapping population. In all, 20 elite lines with >80 ppm iron and >50ppm zinc in brown rice were identified from 5 mapping populations. These non-transgenic rice lines with high iron, high zinc or both are a useful resource for functional genomics and biofortification programmes.

Keywords

rice, biofortification, iron, zinc, quantitative trait loci, candidate genes, non-transgenic.

Reference

- Swamy B.P.M., Kaladhar K., Anuradha K., Batchu A.K., Longvah T., Viraktamath B.C., Sarla N. (2011) Enhancing iron and zinc concentration in rice grains using wild species. ADNAT Convention and International Symposium on Genomics and Biodiversity, CCMB, Hyderabad 23–25 Feb 2011, Abstracts p. 71.
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