

Review Article

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A Review on Molecular Marker Analysis for Yield and its Component Traits under Water Stress and Zinc Deficiency Tolerance in Rice

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ABSTRACT

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The Wonder Cereal, Rice (*Oryza sativa* L.) is the heart of our culture and the staple food crop consumed by more than 50 per cent of the world's population. Aerobic rice proves to be a viable technology by reducing water losses through seepage, percolation and evaporation. However, under aerobic condition several essential nutrients, especially zinc became unavailable due to positive soil redox potential. Therefore genetic improvement of rice genotypes for zinc deficiency under aerobic condition is essential to exploit the water saving potential of aerobic condition. Molecular markers augment conventional plant breeding for efficient and precise identification or selection of a trait of interest linked to them.

Introduction

During the last few decades, molecular markers have been immensely used in plant biotechnology and their genetics studies. Microsatellites are tandem repeats of DNA sequences of only a few base pairs (1 - 6 bp) in length, the most abundant being dinucleotide repeats (Morgante and Olivieri, 1993). The completion of rice genome sequence provided an opportunity to identify thousands of new targets for DNA markers, especially SSRs. There were 18,828 SSRs (di-, tri-, tetra-repeats) released after the completion of the Nipponbare genome sequence in 2005. It is estimated that, the

density of SSRs (approx. 51 SSRs per Mb) can provide a considerable map construction and MAS for numerous applications.

Zinc transporters

Zn transporters play a central role in plant acquisition of zinc from soil and its distribution. Many different Zn transporters have been identified and they are distributed throughout the plant system. The maintenance of Zn homeostasis in whole plant relies on a variety of transporters, including the members of zinc-regulated transporter (ZRT) and iron regulated transporter (IRT) like protein (ZIP) which are involved in the cellular uptake of

Zn from soil to root cells at soil root interface (Colangelo and Guerinot, 2006); natural resistance associated macrophage protein (NRAMP) families which regulate the proton driven transport of Zn and other transition metal ions (Thomine *et al.*, 2000). OsZIP1, OsZIP3, OsZIP4, OsZIP5 and OsZIP8 are reported to encode rice plasma membrane Zn transporters and are induced by Zn deficiency (Ramesh *et al.*, 2003; Ishimaru *et al.*, 2005; Yang *et al.*, 2009; Lee *et al.*, 2010a, b and Suzuki *et al.*, 2012). OsZIP1, OsZIP3, and OsZIP4 were expressed in the vascular bundles in shoots and in the vascular bundles and epidermal cells in roots (Ramesh *et al.*, 2003 and Ishimaru *et al.*, 2006).

QTL for yield and its component traits for zinc deficiency tolerance in rice

Yadav *et al.*, 1997 used a DH population of 105 lines derived from a cross between IR64 (irrigated *indica*) and Azucena (upland *japonica*) and identified QTL regions for maximum root length (MRL) and deep root to shoot ratio (DR/SR) on chromosome 1, 2, 5, 6, 7, 8, and 9 using RFLP markers.

Avendano (2000) identified a QTL for zinc deficiency tolerance using mapping (RILs) population of Madhukar and IR26 on chromosome 5 between markers RM164 and RM87 showing a variation 61.9 per cent with a LOD value of 3.45.

Kamoshita *et al.*, (2008) identified QTLs using in the RILs of IR 58821/IR 52561 for root traits. They found 2, 12 and 8 QTLs for shoot biomass, deep root morphology and root thickness respectively with LOD scores ranging from 2.0 to 12.8. Phenotypic variation explained by the QTLs ranged from 6 per cent to 30 per cent. QTLs linked to seminal root length, adventitious root number, lateral root length, lateral root number and the relative parameters under flooding and upland

conditions were located in RI lines developed from IR1552/Azucena (Zheng *et al.*, 2003). A number of quantitative trait loci (QTLs) have been identified in various rice populations for various root traits including basal root thickness (Zheng *et al.*, 2000; Price *et al.*, 2000; Shen *et al.*, 2001; Steele *et al.*, 2006; Gomez *et al.*, 2009; Kanagaraj *et al.*, 2010; Steele *et al.*, 2013).

Gomez *et al.*, (2009) reported QTLs linked to physio-morphological and plant production traits under drought stress using 177 F₆ recombinant inbred (RI) lines of Bala × Azucena. The RI lines showed significant variation for physio-morphological and plant production traits under stress. A total of 24 QTL were identified for various traits under stress, which individually explained 4.6 to 22.3 per cent phenotypic variation. Composite interval mapping detected three markers *viz.*, RM3894, RG409 and G1073 on chromosomes 3 and 8 linked to grain yield under drought stress, respectively explaining 22.3, 17.1 and 10.9 per cent of phenotypic variation. QTL for leaf drying, days to 50 per cent flowering and number of productive tillers under drought stress co-located at certain of these regions. Further, QTL for several root traits overlapped with QTL for grain yield under stress in these RI lines, indicating the pleiotropic effects of root trait QTL on rice performance under stress.

Thanh *et al.*, (2006) mapped QTLs for root traits (maximum root length, root thickness, root weight to shoot and deep root weight to shoot ratios) using AFLP and SSR markers in upland rice using a recombinant inbred (RI) population derived from a cross between Vietnamese upland rice accessions. The QTL on chromosome 12 flanked by SSR marker RM270 and AFLP marker AVM28.17 and QTL on chromosome 2 flanked by markers AVM43.1-RM250 were identified for maximum root length explaining phenotypic

variance of 7.2 and 8.5 per cent respectively. For number of total tillers, the QTL on chromosome 6 flanked by markers RM50-AVM29.2 were identified with the phenotypic variance of 34.70 per cent. For root weight to shoot ratio, QTL was located on chromosome 9 with phenotypic variation of 10.2 per cent flanked by RM242-RM288 markers. In addition to QTLs for root traits, QTL for plant height (PH) on chromosome 1 flanked by markers AVM26.9-AVM26.4 with phenotypic variation of 9.70 per cent was identified.

Wissuwa *et al.*, (2006) using a mapping population of IR64 and Jalmanga reported a QTL *Zmt12* for zinc deficiency induced mortality on chromosome 12 flanked by markers CDO344-1-RG543-1 with adjusted R^2 value of 11.60 and QTL *Zdm3* for shoot dry matter on chromosome 3 flanked by RZ675-P1M9-10 markers with adjusted R^2 value of 18.10. It was considered as a key factor for tolerance to Zn deficiency explaining a major portion of the variation for mortality with a LOD value of 6.40. Stangoulis *et al.*, (2007) detected two QTLs for zinc concentration located on chromosomes 1 and 12, explaining 15 per cent and 13 per cent of the total phenotypic variation with a LOD of 3.4 and 3.1 respectively, using a doubled haploid mapping population between IR64 and Azucena.

Garcia-Olivera *et al.*, (2009) identified two QTLs qZN-8 and qZn-12 for Zn content using backcross populations (85 BILs) obtained by crossing Teqing (*Oryza sativa*) and elite wild rice (*O. rufipogon*) using 179 SSR markers. They found that the QTL near marker RM152 on chromosome 8 accounted for the largest proportion of phenotypic variation (11–19 per cent) for Zn content, whereas the QTL that was located on chromosome 12 accounted for 9 per cent phenotypic variation.

Venuprasad *et al.*, (2009) identified two large effect QTLs DTY3.1 and DTY2.1 for grain yield under water stress in rice using RILs from the cross APO/swarna. Two markers RM234 and RM416 located on chromosome 2 and 3 respectively were shown *via* bulk segregant analysis to be strongly associated with yield under water stress. The QTL linked to RM416 (DTY3.1) had a large effect on yield under severe low land drought stress explaining about 31 per cent of genetic variance of the trait ($P < 0.0001$). It also explained considerable variance for yield under aerobic environment. The QTL linked to RM234 (DTY2.1) had a highly significant effect on grain yield under aerobic environment explaining 16 per cent of genetic variance for the trait.

Ramya *et al.*, (2010) concluded that the region between RM160 – RM215 on chromosome 9, contributing to maximum root depth under both control and drought condition. Primers RM242 and RM296 lying between marker interval RM160 – RM215 on chromosome 9 were reported to be linked with zinc deficiency tolerance indicating maximum root depth plays an important role in zinc deficiency tolerance mechanism.

Vikram *et al.*, (2011) reported a major QTL qDTY1.1 for grain yield under water stress on chromosome 1 flanked by markers RM11943 and RM431 using three mapping populations. In combined analysis over two years qDTY1.1 showed an additive effect of 29.30 per cent, 24.30 per cent and 16.10 per cent of mean yield in N22 and swarna, N22 and IR64 and N22 and MTU100 respectively under water stress.

The major effect QTL for grain yield, qDTY1.1 was identified to show an effect under water stress in several genetic backgrounds. Ghimire *et al.*, (2012) also detected qDTY1.1 in two RIL populations

derived from donor dhagaddesi crossed to swarna and IR64 consistently over two seasons. A large effect QTL associated with grain yield in aerobic environments was identified in three genetic backgrounds. Apo/swarna, Apo/IR72 and vandana/IR72 using bulk segregant analysis (BSA). Two closely linked rice microsatellite markers RM510 and RM19367 located on chromosome 6 were found to be associated with yield under aerobic soil conditions in all three backgrounds. The QTL linked to this marker qDTY6.1 was mapped to a 2.2 cM region between RM19367 and RM3805 at a peak LOD score of 32 in the Apo/swarna population.

Sankar *et al.*, (2013) reported that RM242 and RM296 primers present on chromosome 9 at locus 73.3cM and 20.4cM respectively were also found to be linked with QTL for zinc deficiency tolerance. In his study, according to root scan data obtained from field condition samples showing tolerance had more root length and root volume, which indicated that zinc deficiency tolerance character is directly or indirectly associated with the root length and root volume.

In conclusion, one of the most important uses of QTL mapping is to apply them in marker assisted selection (MAS) for genetic improvement of quantitative traits. Once the tightly linked markers have been identified, the traits can be selected indirectly using MAS. The reported map position of gramene database was used to estimate the QTLs following the inclusive composite interval mapping of additive and dominant (ICIM-ADD) method. The QTL analysis resulted in the identification of many QTLs for zinc deficiency tolerance in rice. Hence these QTLs may be used in Marker Assisted Selection programme (MAS) for zinc deficiency tolerance under aerobic system.

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