

A Combinatorial Approach to Map QTL For Grain Size

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Grain size (length, breadth and length/breadth ratio) is important quality attributes of Basmati rice for its high consumer acceptance. Different grain sizes are favoured by different local cultures and cuisines, long and slender grain is generally preferred by the majority of consumers in China, USA and most Asian countries Grain size characteristics, which are immediately obvious to consumers, are major factors defining market value

Detailed knowledge of the genetic and molecular basis of grain size enables breeders to design appropriate genotypes for distinct preferences. Utilization of molecular markers has greatly facilitated the investigation of the genetic basis of complex quantitative traits.

Grain size variation is controlled by a number of biological processes including cell division, cell expansion and division polarity (Li and Li, 2014).

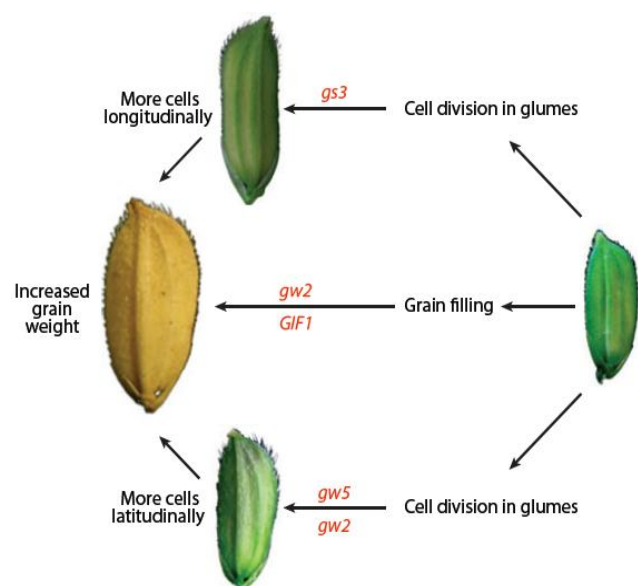


Fig 1. A schematic representation of genes involved in grain size regulation (Xing and Zhang, 2010)

Extensive efforts to determine the genetic basis of grain shape had been made using forward and reverse genetic strategies. Initially, studies focused on characterizing mutants and the expression of major genes associated with grain size, for example, the Lk-f gene, which confers long kernel size (Takeda *et al.*, 1980), or Mi, which confers short kernel size (Takeda *et al.*, 1977).

Quantitative trait locus (QTL) analysis has been widely used for mapping rice grain shape genes.

It is an integration of linkage mapping and traditional statistical and quantitative genetic approaches. QTLs are the loci controlling quantitative traits that are governed by a large number of genes with smaller contributions to the trait resulting in a continuous rather than discrete variables (Liu *et al.*, 2008). Advances in QTL mapping help in the genetic analysis of complex traits, improved selection efficiency with the aid of Marker Assisted Selection, thereby making it possible to enrich and enhance existing germplasm. A number of molecular marker systems such as RFLP, AFLP, SSRs (Microsatellites), SNPs etc. coupled with a number of computer packages such as QTL Cartographer and MAPMAKER (Lander *et al.*, 1994) has made it possible to construct high density maps where in quantitative traits can be associated with markers.

Association mapping, also known as linkage disequilibrium (LD) mapping, is an alternative method of mapping QTLs that takes advantage of historic LD to link phenotypes to genotypes. Rice, a highly selfing species, is also an ideal candidate for association mapping due to the following features: rich resources of germplasm and being genotyped once and repeatedly phenotyped. It is expected that association mapping will detect more genes/QTLs with higher resolution compared to linkage analysis. Compared to linkage analysis, GWAS has not identified many QTLs in rice (Bai *et al.*, 2010).

The plant scientific community can exploit the advantages of both controlled crosses and association mapping to increase statistical power and mapping resolution. (Myles *et al.*, 2009). Converting gene-tagging efforts from traditional QTL mapping to LD-based association studies provides a powerful tool for mapping the genes of interest (Goldstein and Weale, 2001).

Few studies to detect marker-trait association with seed size in rice have been previously reported using association mapping method, although several linkage mapping studies have been conducted to identify some seed size QTLs (Goldstein and Weale, 2001).

For instance, D. A. Deborah *et al.*, 2016 reported the dissection of a QTL region governing grain size traits in Basmati employing association and linkage

mapping approaches. Association mapping using 96 diverse rice germplasm revealed that three markers covering 889 kb in the targeted QTL region were significantly associated with grain size traits. Using linkage mapping in F₂ mapping population of a cross between Basmati370 and Jaya, the targeted QTL region was further delimited to a physical distance of 268 kb comprising 24 annotated genes. The gene expression analysis of parents, revealed 19 genes differentially expressing within the QTL. Of them, 15 genes showed high expression in Basmati370, while four were expressed in Jaya, and whereas five genes did not show any differential expression between parents. Among differentially expressed genes, a highly expressed gene in Basmati370, Os05g0374200 (Cytokinin dehydrogenase 1 precursor) seems to be involved in accumulation of cytokinins, thus affecting the grain size.

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