Rice Genetics Newsletter, Vol. 21
Table of Contents

IV. Genetics of disease and insect resistance

V. Gene and genome structure

10.Introgression and mapping of yield enhancing QTLs from *Oryza rufipogon*

M.P. REDDY, N. SARLA*, V.L.N. REDDY and E.A. SIDDIQ

Directorate of Rice Research, Rajendranagar, Hyderabad 500 030
* sarlan@operamail.com

Oryza rufipogon and *O. nivara* are the wild progenitors of *O. sativa*. They constitute an important gene pool for improvement of rice. Recent evidence using molecular marker mapping in rice suggests that, despite their poor phenotype, wild species can contribute genes for improving complex traits such as yield (Septiningsih *et al* 2003). At DRR, wild species (AA genome) are being used to introgress, identify and map quantitative trait loci (QTLs) for enhanced yield (DRR Annual Reports 1999-2003). An accession of *O. rufipogon* (IC 22015) from Kerala was chosen as the donor from 25 accessions as it was genetically moderately distant from the recipient IR 58025A, a widely used cms line. Also IR58025A/ *O. rufipogon* IC 22015 hybrids were vigorous compared to those with 24 other accessions of *O. rufipogon*. The advanced backcross method was followed for mapping. 251 BC_2F_2 families from the cross IR58025A/*O. rufipogon*//KMR3 were phenotyped for 14 yield related traits in two replicates

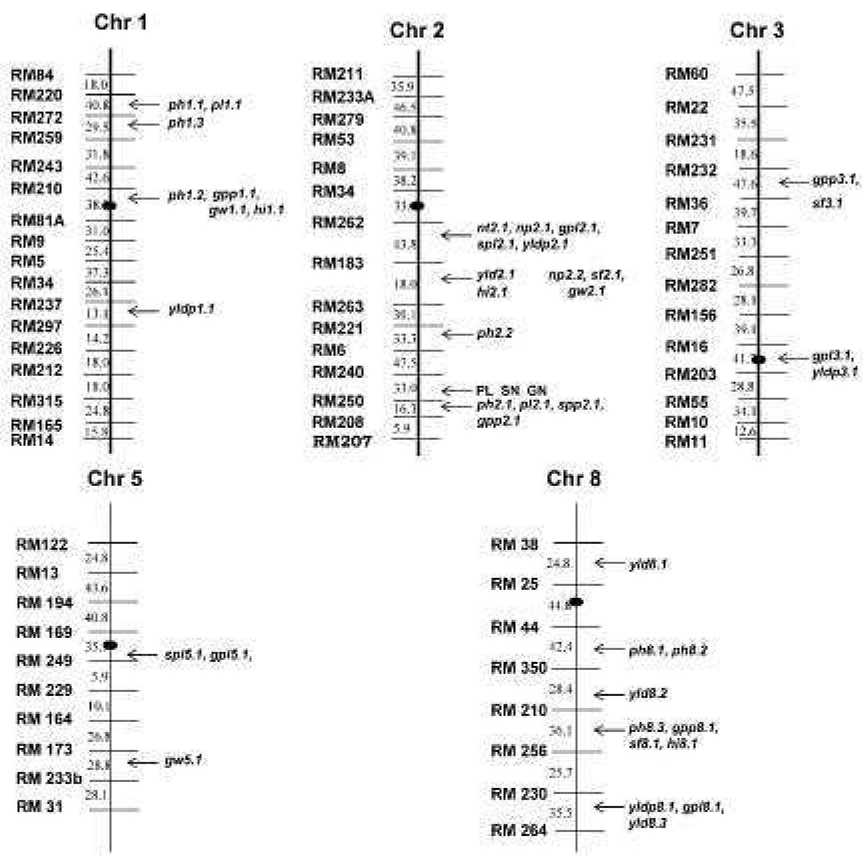

Fig. 1. Distribution of QTLs on the molecular linkage map of five chromosomes. 251 BC_2F_2 families from the cross IR58025A/*O. rufipogon*//KMR3 were used as mapping population. ph: Plant height; pl: Panicle length; gpp: Grain number per panicle; gw: Test grain weight; HI: Harvest index; nt: Number of tillers per plant; yld: Plot yield; sf: Percentage:spikelet fertility; yldp: Yield per plant; np: Number of panicles per plant. spl: Spikelet number per panicle; spp: Spikelet number per plant; gpl:Grain number per plant

and compared with the control (KRH2). The introgressions from the wild species in 39 of these families helped enhance yield of KRH2 by at least 20%. 24 families yielded more than 8 tons/ha and 11 of these yielded at least 9 tons/ha on a one sqm plot basis (40 plants in 4 rows). It is noteworthy that 88 families showed more than 20% increase in spikelet number/panicle and 101 families for grain number per panicle. Two traits spikelet number/plant and grain number/plant were the yielded more than 8 tons/ha and 11 of these yielded at least 9 tons/ha on a one sqm plot basis (40 plants in 4 rows). It is noteworthy that 88 families showed more than 20% increase in spikelet number/panicle and 101 families for grain number per panicle. Two traits spikelet number/plant and grain number/plant were the most influenced both positively and negatively by introgressions from the wild.

Segregation of 81 polymorphic SSR markers was analysed in the population and a linkage map was constructed using Mapmaker3.0. 39% markers showed a skewed segregation, 25% towards IR58025A and 14% towards *O. rufipogon*.

In the linkage map 65 markers grouped into 5 linkage groups corresponding to chromosomes 1, 2, 3, 5 and 8. There were16 markers which did not link with any group. Mapmaker/QTL1.1 was used for both single marker mapping and interval mapping of QTLs.

Single marker analysis using 81 SSR markers revealed presence of 68 QTLs for 13 traits. It is significant that 35 of these QTLs had positive effect on the traits. The percent increase attributed to each QTL ranged from 13% to 73%. Among the QTLs with positive effect, seven showed significantly high positive allele effects. These were gpl 3.1, gpl 8.1, gpl 9.1 for grain number/plant, spp 1.1, spp 8.1 for spikelet number/panicle and yld 2.1, yld 2.2 for yield/plot. Thus chromosome 2, 3, 8 and 9 of *O. rufipogon* have yield enhancing QTL alleles. Four QTLs had most significant effect on the trait. These included two for grain number/ plant (gpl 8.1, gpl 9.1) and two for yield/plot (yld 2.1, yld 2.2).

Interval mapping with a minimum LOD score of 2.0 revealed presence of 41 QTLs for 13 yield related traits on five chromosomes (Fig. 1). 15 of these QTLs were identified in both the replicates. These included 4 each for plant height and plot yield, 2 for harvest index and one each for number of tillers/plant, number of panicles/plant, number of spikelets/plant, number of grains/plant and spikelet fertility. Eight genomic regions showed presence of 2 to 5 yield related QTLs. The peak LOD scores for the QTLs ranged from 2 to 35. Five QTLs mapped to the region flanked by RM 183 and RM 263 on chromosome 2.

Sixteen QTLs were detected by both the methods. 11QTLs were common to the two replicates. RM 263 and RM 183 on Chromosome 2 were associated with 2 yield enhancing QTLs yld 2.1 and yld 2.2. RM16, RM 223 and RM 219 were associated with three QTLs which enhance grain number per plant. RM 297 and RM 223 were associated with high spikelet number per panicle. Many QTLs reported earlier map to the same locations as in this study. Near isogenic lines for significant QTLs will be developed in KMR3 the restorer line for functional genomic studies and marker aided introgression to varieties.

References

Septiningsih, E.M., K.R. Trijatmiko, S. Moeljopawiro and S.R. McCouch, 2003. Identification of quantitative trait loci for yield and yield components in an advanced backcross population derived from the Oryza sativa variety IR64 and the wild relative *O. rufipogon*. Theor. Appl. Genet. **107**: 1419-1432.

Reddy, M.P., 2003. Identification of yield related quantitative trait loci (QTLs) from progenitor wild species of rice *Oryza rufipogon*. PhD thesis. University of Hyderabad.

Vol. 21 >B. Research Notes>II. Genetics of morphological traits