

10. Mapping quantitative trait loci for yield traits in BC₂F₂ population derived from Swarna x *O. nivara* cross

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Wild progenitors of rice constitute an important gene pool for its improvement and have traditionally been used as sources of disease and pest resistance. *Oryza nivara* is considered the closest progenitor *O. sativa*. An accession of *O. nivara* was the only source of resistance to grassy stunt virus. Molecular mapping has shown that phenotypically poor wild species can contribute genes for improving complex traits such as yield. This has led to a paradigm shift from looking at the phenotype to looking at the genotype. Yield and related QTLs have been identified from wild rice species *O. rufipogon*, *O. grandiglumis* and *O. glumaepatula* (McCouch et al. 2006, Swamy and Sarla, 2008). However, there are no reports of yield QTLs mapped from *O. nivara*. In a previous study QTLs for domestication related traits were mapped from *O. nivara* (Li et al. 2005). The objective of the present study was to map yield enhancing QTLs from *O. nivara*. To select a donor accession for developing a mapping population, genetic diversity was analysed in 22 indigenous *O. nivara* accessions using 14 morphological traits and 22 molecular markers including 6 RAPD, 5 ISSR and 11 SSRs. *Oryza nivara* accession IRGC81832 from Bihar which was quite distant from Swarna was selected as donor parent. 76 F₁ seeds were obtained from Swarna x *O. nivara* cross. Only 44 hybrids survived. The hybrids between *O. sativa* and *O. nivara* are difficult to confirm as true hybrids based on morphology alone. Three RAPD primers OPA 7, OPA 10 and OPB2, two ISSR primers UBC 811 and UBC 834 and one SSR primer RM 490 amplified *O. nivara* specific bands that could help identify true hybrids. These markers can also be used for assessing risk of gene flow from transgenics to *O. nivara*.

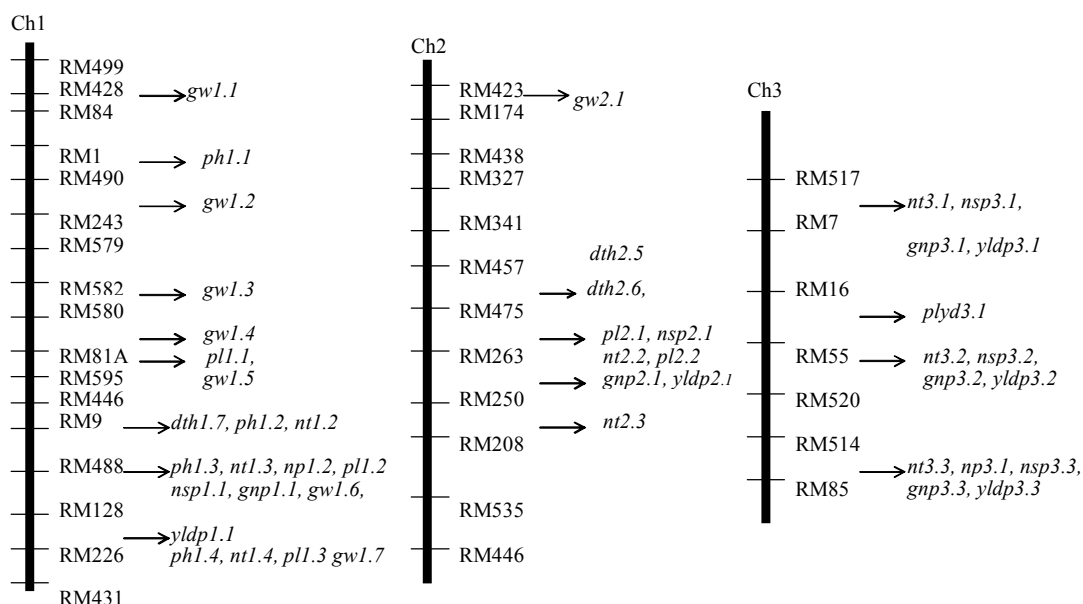
A mapping population of 279 BC₂F₂ families was developed from the cross Swarna x *O. nivara* using advanced backcross method. 245 BC₂F₂ families were grown in two replicates of 3 rows (33 plants) each during Kharif 2005 in DRR field. Swarna was grown as check after every 20 families. Five plants from the centre of middle row of each family were phenotyped for 15 yield traits. Transgressive segregation was observed for most of the yield related traits. 19 families showed >15% increase in yield/plant and 47 families showed >15% increase in grain number/plant over Swarna.

Out of 150 SSR markers surveyed from all chromosomes 108 (43%) were polymorphic between the parents. DNA was extracted as pooled sample from the central 5 plants of each family. Only 75 polymorphic loci were found to segregate in the 245 BC₂F₂ families. 3% families were homozygous for *O. nivara* alleles and 14% were heterozygous. Percent introgression varied from chromosome to chromosome and plant to plant. In the 245 BC₂F₂ families introgression from *O. nivara* ranged from 2.6 % to 38% with overall mean introgression of 16.6%. Some loci from *O. nivara* were introgressed in only 0.4% families (RM499 on chromosome 1), other loci were present in as many as 69% families (RM413 on chromosome 5). Out of 75 marker loci, 18 (24%) were skewed towards Swarna, 33 (44%) were skewed towards *O. nivara* and remaining 24 markers followed Mendelian ratio. The 75 markers grouped into 9 linkage groups corresponding to chromosomes 1, 2, 3, 4, 5, 6, 8, 11 and 12.

In all, 134 QTLs were identified using interval mapping (IM) and composite interval mapping (CIM). It is significant that 88 QTLs out of 134 were trait enhancing and derived from *O. nivara* (Fig. 1). 37 QTLs were identified by both IM and CIM. 17 out of 37 QTLs were major effect QTLs for different yield traits. The maximum QTLs were detected for tiller number (14) followed by plant height (12), grain weight (11) and yield per plant (9). QTL *yldp8.1* explained the highest phenotypic variance (54%) and QTL *ph1.4* was identified at the highest LOD score (32). These two QTLs were identified between the marker interval RM38-RM223 and RM128-RM226 respectively.

Five major effect QTLs (*yldp3.1*, *yldp3.2*, *yldp4.1*, *yldp8.1* and *yldp11.1*) were identified for yield per plant. These are target QTLs for introgression by marker assisted breeding. Significant QTLs were identified from *O. nivara* for plot yield, yield per plant and grain number. For plot yield only one QTL on chromosome 3 derived from *O. nivara* was identified by CIM. For yield per plant nine QTLs were derived from *O. nivara*, seven of these QTLs were identified by both IM and CIM. QTL *yldp8.1* for yield per plant was detected at high LOD (8.76) and identified by both IM and CIM. It increased yield by 5.8g per plant and grain number by 426 grains per plant. Eight *O. nivara* derived QTLs for grain number were significant.

This is the first report of mapping of yield QTLs from *O. nivara* to our knowledge. Mapping of yield enhancing QTLs from another accession of *O. nivara* is in progress. Together our results indicate that there are many *O. nivara* QTL alleles which have the potential to increase yield of Swarna. The introgression lines are also being evaluated for their grain quality traits and their ability to yield under limited water or low soil phosphorus in field conditions.



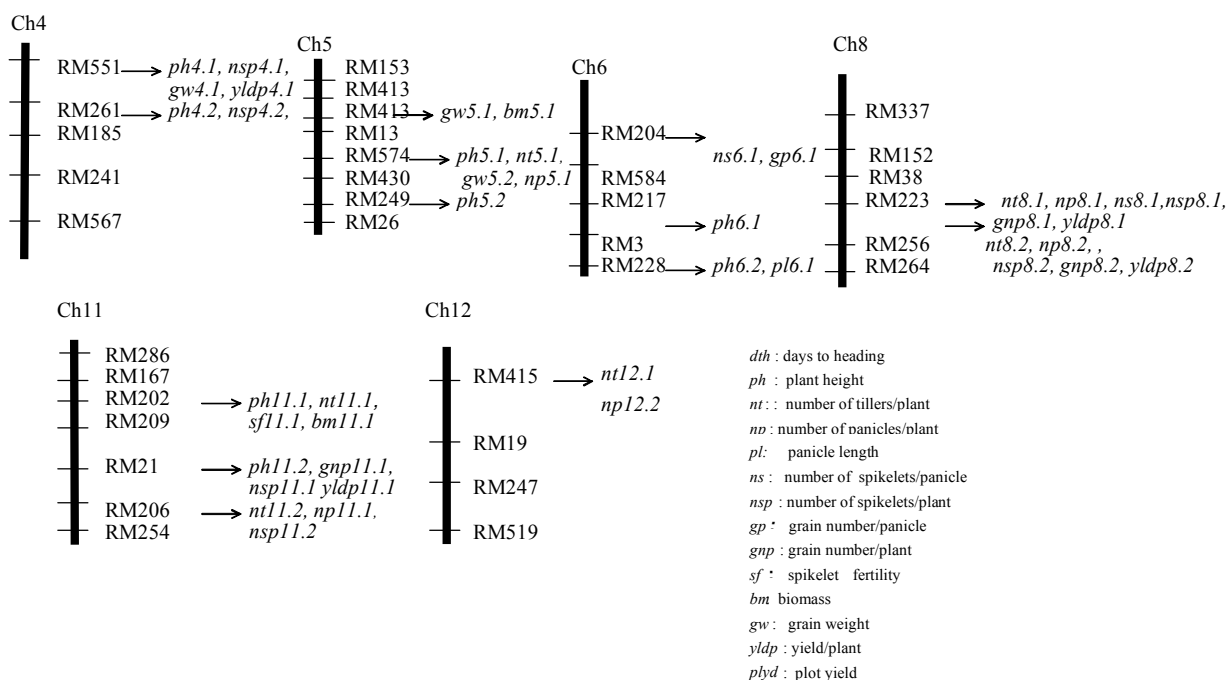


Fig. 1. Linkage map showing location of 88 *O. nivara* derived trait-enhancing QTLs

Acknowledgement

The work was carried out as part of the Network Project on Functional Genomics of Rice funded by the Department of Biotechnology, Govt of India. We thank G. Ashok Reddy for assistance in field work.

References

- Swamy B. P. M. and N. Sarla, 2008. Yield enhancing QTLs from wild species. *Biotechnology Advances* 26, 106-120
- McCouch S. R., M. Sweeney, J. Li, H. Jiang, M. Thomson, E. Septiningsih, J. Edwards, P. Moncada, J. Xiao, A. Garris, T. Tai, C. Martinez, J. Tohme, M. Sugiono, A. McClung, L. P. Yuan and S. N. Ahn, 2007. Through the genetic bottleneck: *O. rufipogon* as a source of trait enhancing alleles for *O. sativa*. <http://www.springerlink.com/content/4177216249321q9m/?p=228b43ba3dfc4eca839034829568559a&pi=0> *Euphytica*, 157: 317 – 339.
- Li C, Zhou A and T. Sang, 2006. Genetic analysis of rice domestication syndrome with the wild annual species, *Oryza nivara*. *New Phytologist*, 170: 185-194.