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Consensus QTLs for drought tolerance and agronomic traits in rice

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For association mapping, identification of candidate QTL regions is valuable for focusing the genotyping of a collection of accessions.

Map construction

A database containing flanking markers for 1678 QTLs for components of drought tolerance and agronomical traits in rice from 42 publications (Fig. 1) was constructed. These QTLs corresponded to 40 traits that included morphophysiological traits related to drought tolerance such as osmotic adjustment, carbon isotope discrimination, leaf drying, and leaf rolling, yield, yield components, root traits and plant height and phenology, which were detected among a wide range of environments (99 in total), and 29 mapping populations from 39 parent lines. We located the flanking markers in the rice genome (Gramene Annotated Nipponbare Sequence 2006, www.gramene.org) searching them in the feature name database. For those markers that could not be located, the genebank sequence was analyzed by BLAST using the rice genomic sequence, and the location of the most homologous sequence was recorded. When more than one sequence was found or the marker sequence was not available (i.e. AFLP), we used the closest marker in the map of origin and followed the same steps described above. If no marker was close enough in the original map, the (www.gramene.org/db/cmap/viewer) CMap tool was used to compare the original map to either the Cornell SSR 2001 (Temnykh *et al*., 2001) map or the JRGP RFLP 2000 (Harushima *et al*., 1998) to find other markers in the same region that could be located in the rice sequence. Genomepixelizer was used to visualize the QTL map.

Results and discussion

From the 1678 QTLs, 1314 have been successfully located in the rice genome sequence. The QTLs were spread around the whole genome, being the number of QTLs 254, 129, 185, 132, 91, 83, 101, 98, 62, 47, 90, 42 in each chromosome, from 1 to 12, respectively (Fig. 1) and the average QTL size was 3.90 Mbp.

An accumulation of QTLs for all traits was observed on the distal long arm of chromosomes 1 probably due to the presence of the *sd1* gene in this region, a defective gibberellin 20-oxidase gene (Spielmeyer *et al*., 2002).

There is also a region with high density of QTLs for yield components, mainly grain weight and number of spikelets per spike, which co-locates with QTLs for root traits on the long arm of chromosome 4. This might indicate the linkage of genes controling both traits or that differences in root architecture may have an effect on the number of spikelets per spike and grain weight through a sequence of causally related events. ABA has an important role on stress signalling and plant development and it has been related to root architecture (Lebreton *et al*., 1995). Giuliani *et al*. (Giuliani *et al*., 2005) showed that root architecture may have an effect on ABA content.

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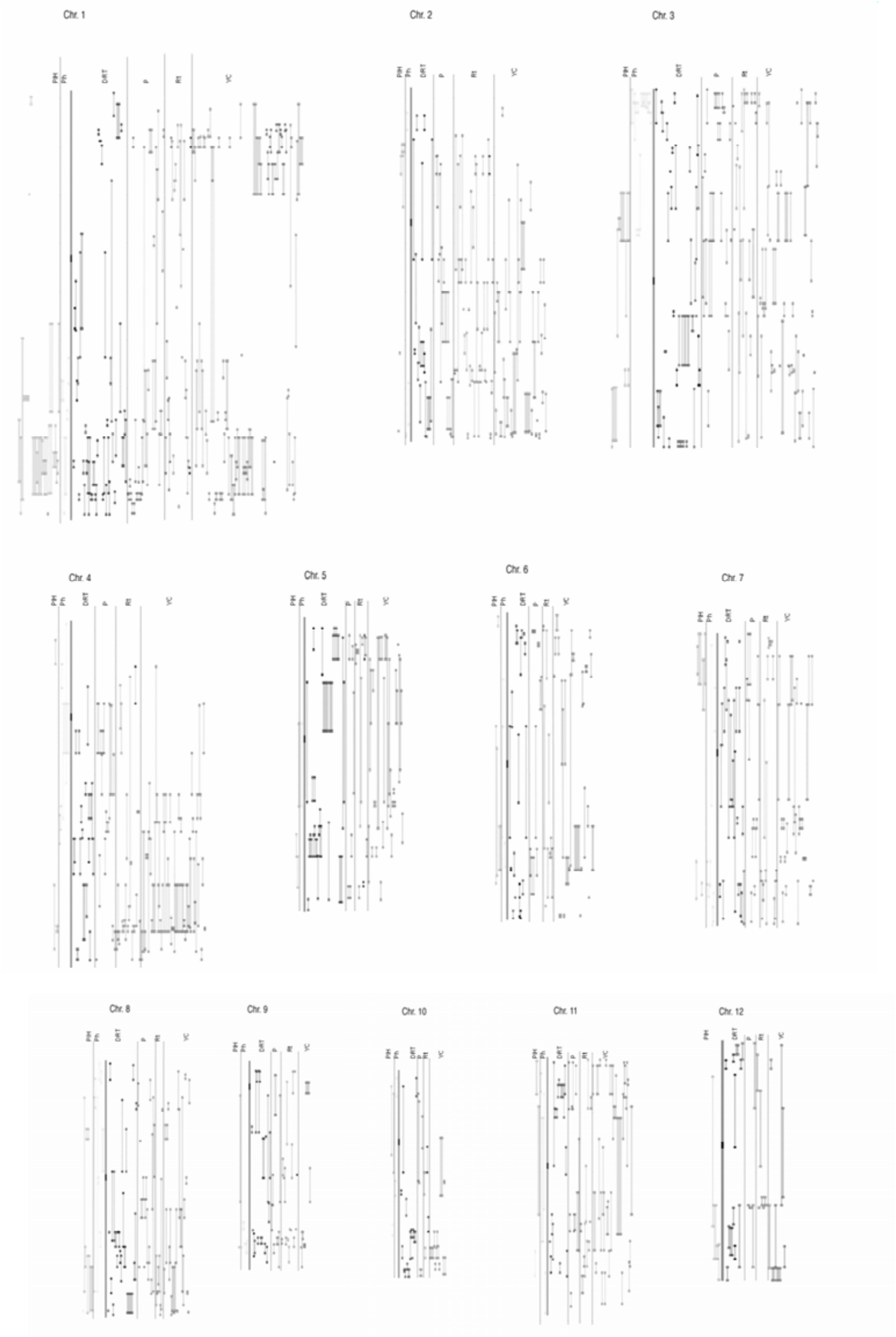

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Fig. 1. QTL location on the Nipponbare rice sequence. Grey thick bars are rice chromosomes. Black boxes, centromeres. On the left side of each chromosome, QTLs for plant height (PlH) and phenology (Ph). On the right side, QTLs for drought related traits (DRT), productivity (P), root traits (RT), and yield components (YC).

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