

### 13. Identification of a locus for panicle second branch characteristics in rice

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Grain yield per plant is determined by its three components, panicles per plant, grain weight, and grain numbers per panicle. Among the three components, number of grains per panicle frequently makes the greatest contribution to grain yield (Ashikari M. et al., 2005), and it is mostly determined by the number of the primary and secondary branches and the ratio of filled grains.

A mapping population of 186 F<sub>2</sub> plants, derived from a cross between a modern japonica variety Shennong265 (SN265) and the landrace japonica variety Li-Jiang-Xin-Tuan-Hei-Gu (LTH), was used to detect quantitative trait loci (QTL) for panicle traits. Eight traits of panicle characters, number of primary branches per panicle (NPB), number of secondary branches per panicle (NSB), number of spikelets per panicle (SPP), number of primary branch spikelets per panicle (SPB), number of secondary branch spikelets per panicle (SSB), ratio of filled grains (RG), ratio of primary branch filled grains (RGPB) and ratio of secondary branch filled grains (RGSB) were measured. Significant positive correlations between SPP and other panicle traits such as NPB (0.622 \*\*), NSB (0.973 \*\*), SPB (0.605 \*\*) and SSB (0.968 \*\*) were observed. Fig. 1 shows the relationships among SPP, SPB, SSB, NPB and NSB based on a path analysis. So, the Second Branch Characteristics would contribute more to SPP.

Composite interval mapping was implemented using QGene 4.0 software (Joehanes R. et al., 2008), with a threshold of LOD>2.5. A total of ten putative QTL were detected with percentage of variance explained (PVE) running between 12.3 ~ 52.8%, and LOD of QTL 2.562 ~ 6.002 (Table 1, Fig. 2). We found that an important functional locus RM453 region on chromosome 12 controls three Second Branch Characteristics of Panicle with large PVE such as NSB, SSB and RGSB (Fig. 2). This region also controls SPP, SPB and RG. The orthologous region of RM453 in maize controlling kernel row number and ear diameter the important yield components of maize was identified subsequently through analysis of MaizeGDB ([www.maizegdb.org/](http://www.maizegdb.org/)) (Veldboom L. R. et al., 1994). It suggests that rice Qnsb12 and maize qKR4 originated from the same chromosomal block of ancestral species of grass.

These results will be very useful for further studies on gene map-based cloning and gene function analysis. We have detected a residual heterozygous line (RHL) which contains a heterozygous segment (approximately 10 cM) surrounding RM453 locus but is homozygous in other regions from a recombinant inbred line (RIL) population of same parents. A detailed analysis is underway to confirm the accurate locations of these QTL detected here.

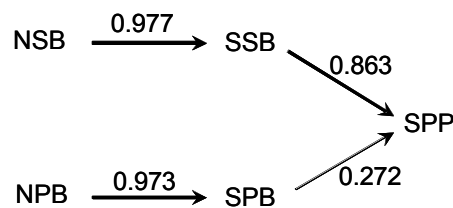


Fig. 1 Path analysis of the panicle traits include number of primary branches per panicle (NPB), number of secondary branches per panicle (NSB), number of spikelets per panicle (SPP), number of primary branch spikelets per panicle (SPB) and number of secondary branch spikelets per panicle (SSB). The values on arrowhead lines are partial  $R^2$  of the dependent variables explained by the independent variables in multiple regression models.

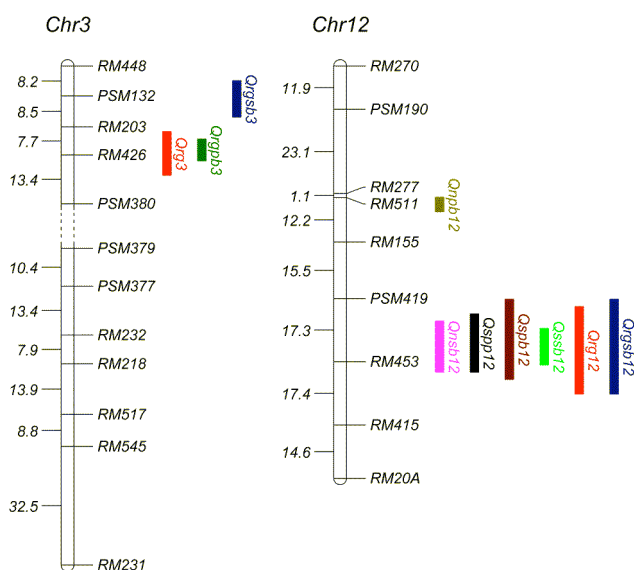


Fig. 2 Chromosomal map of putative QTL detected for panicle traits in F<sub>2</sub> population

Table 1 Quantitative trait loci affecting panicle traits in the F<sub>2</sub> population derived from LTH/SN265

| QTL            | Chromosome | Marker interval | Range(cM) | Position(cM) | LOD score | PEV(%) <sup>a</sup> | Additive effect <sup>b</sup> |
|----------------|------------|-----------------|-----------|--------------|-----------|---------------------|------------------------------|
| <i>Qnpb12</i>  | 12         | RM511-RM155     | 36-40     | 36           | 3.717     | 17.3                | 0.885                        |
| <i>Qnsb12</i>  | 12         | PSM419-RM415    | 70-84     | 78           | 3.358     | 52.8                | -8.813                       |
| <i>Qspp12</i>  | 12         | PSM419-RM415    | 68-84     | 78           | 3.792     | 36.2                | -34.521                      |
| <i>Qspb12</i>  | 12         | PSM419-RM415    | 64-86     | 80           | 3.497     | 21.4                | 6.995                        |
| <i>Qssb12</i>  | 12         | PSM419-RM415    | 72-82     | 78           | 2.993     | 43.2                | -33.852                      |
| <i>Qrg12</i>   | 12         | PSM419-RM415    | 66-90     | 78           | 4.883     | 28.1                | -2.82                        |
| <i>Qrg3</i>    | 3          | RM203-PSM380    | 18-30     | 22           | 3.608     | 16.8                | 1.516                        |
| <i>Qrgpb3</i>  | 3          | RM203-PSM380    | 20-26     | 24           | 2.562     | 12.3                | 3.783                        |
| <i>Qrgsb12</i> | 12         | PSM419-RM415    | 64-90     | 74           | 6.002     | 26.4                | -7.36                        |
| <i>Qrgsb3</i>  | 3          | RM448-RM203     | 4-14      | 10           | 3.441     | 16.1                | 9.504                        |

<sup>a</sup> Percentage of explained phenotypic variation

<sup>b</sup> Negative value indicates effect from SN265

**References**

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