

## 20. Detection QTLs for deepwater rice ability

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Deepwater rice can survive the flood condition in rainy season by rapid internodal elongation ability. This unique ability was characterized by two factors, that is, starting time of internodal elongation and the ability of internodal elongation along with increasing water depth (Inoue 1987). For elucidating the mechanism of internodal elongation in deepwater rice, cloning genes associated with the deepwater characteristics is necessary. As an initial step of this, we employed the QTL analysis of two characteristics, total internodal length (TIL) and number of elongated internode (NEI), using F<sub>2</sub> population derived from the crosses between an ordinary paddy rice, Taichung 65 (T65), and a deepwater rice cultivated in Bangladesh (N01). Ninety-four F<sub>2</sub> plants were grown at air condition for 2 month, and then they were submerged into water up to 70% of plant height in the 3,000L tanks. Thereafter, the water level was increased 10cm every 3 days for 2 weeks, and TIL and NEI were measured.

The frequency distributions of TIL and NEI indicate that these traits are controlled by several genes (Fig. 1). Genotypes of 94 plants in F<sub>2</sub> each population were determined by 78 SSR markers. The linkage map was constructed using MAPMAKER/EXP v.3.0 (Lander et al. 1987), and QTL analysis was performed by QGene v. 3.06 (Nelson 1997). The result of the QTL analysis is showed in Table 1. Two QTLs at N01 allele for TIL and one QTL at N01 allele for NEI are detected with threshold LOD > 1.50. The QTLs showing the strongest effects for TIL and NEI at N01 allele were detected in common region nearby RM6386 on long arm chromosome 12, indicates that a key QTL for floating ability is located in this region. At T65 allele, on the other hand, only one QTL for TIL was detected on chromosome 7 nearby RM1132. We are going to develop nearly isogenic line of these QTLs for further analysis.

## References

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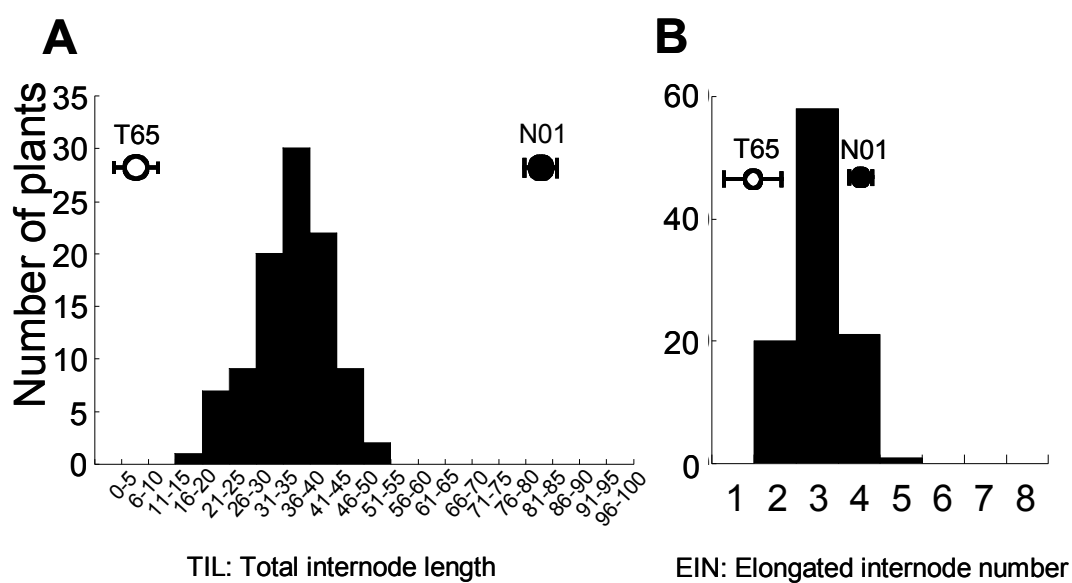


Fig. 1 Frequency distribution of TIL (A) and NEI (B) in  $F_2$  population derived from a cross between T65 and N01.

Table 1 Putative QTLs for Total internode length (TIL) and Elongated internode number (NEI). NML, nearest marker locus of putative QTLs; PVE, phenotypic variation explained by each QTL; LOD, logarithm of odds

trait	QTL name	Chr.	NML	Source	PVE	LOD
TIL	<i>qTIL4</i>	4	RM307	N01	8%	1.63
	<i>qTIL7</i>	7	RM1132	T65	9%	1.81
	<i>qTIL12</i>	12	RM6386	N01	10%	2.04
NEI	<i>qNEI12</i>	12	RM6386	N01	7%	1.50