

学位論文要旨

Identification and characterization of the loci for the traits associated with lodging resistance in rice, using chromosome segment substitution lines

(染色体断片置換系統群を用いた水稻の倒伏抵抗性に関連する形質の遺伝子座の特定とその作用機作)

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Lodging has been an important constraint on rice production in monsoon Asia. When lodging occurs after a typhoon hits, the canopy structure is destroyed, and the capacities for photosynthesis and dry matter production are sharply reduced. In severe cases, lodging can result in breaking of the stem or pulling out the roots, blocking the transport of water, minerals, and photoassimilates and leading to declines in yield and quality. In cereal crops, stem lodging can be classified into two types: stem-breaking type and stem-bending type. To improve stem-lodging resistance, the strong culm traits of superior lodging-resistant varieties need to be characterized. The identification of quantitative trait loci (QTLs) and the corresponding genes associated with the parameters for bending moment at breaking (M) and flexural rigidity (FR) is expected to enable the efficient development of lodging-resistant varieties. A set of Chromosome Segment Substitution Lines (CSSLs) derived from the cross between Takanari and Koshihikari were used in this study to identify QTLs associated with lodging resistance.

The first part of this thesis was to identify the important traits of bending- and breaking- type lodging resistance between parents that contribute to increasing lodging resistance. Large differences were observed in the parameters of both breaking- and bending-type lodging resistance between Takanari and Koshihikari. The M of Takanari was larger than that of Koshihikari because of the larger section modulus (SM). The large culm diameter of Takanari was responsible for the large SM. In contrast, Takanari had a small bending stress (BS) compared with that of Koshihikari. The FR was larger in Takanari than that in Koshihikari. The large FR in Takanari resulted from a large secondary moment of inertia (SMI). Young's modulus (YM) in Takanari was significantly higher than that in Koshihikari in 2015 but not in the following year. The density of the stem wall material such lignin, holocellulose, hemicellulose and cellulose contributed to culm strength. Takanari

exhibited significantly high densities of holocellulose, lignin, cellulose and hemicellulose densities compared with Koshihikari.

The second part of this thesis was to estimate the QTLs related to breaking- and bending-type lodging resistance on CSSLs in Takanari genetic background. The QTLs for BS were assigned to chromosomes 3, 5, 6, 8, 9, 10, 11, and 12. Koshihikari alleles increased BS in these QTLs. The YM was increased by substitution of the Koshihikari chromosomal segments on chromosomes 2, 10, and 11. Other QTLs mapped to chromosomes 7 and 12, such that the Koshihikari alleles contributed to the decrease of YM. QTLs for cellulose density were assigned to chromosomes 1, 3, and 5, which were replaced by substitutions of Koshihikari segments. Some QTLs for cell wall material densities were detected together with BS on chromosome 5. Moreover, on chromosome 11, QTLs for the densities of holocellulose, hemicellulose, and lignin were detected at the same region with YM. Both regions indicated positive effect of Koshihikari segment on increasing BS and YM. These results suggested that some QTLs for the densities of cell wall materials contribute to increase BS and YM and could be utilized to improve the lodging resistance for both types of breaking and bending in rice varieties.

In the last part of this thesis, the putative QTL region at the long arm region on chromosome 5 was verified using reciprocal CSSLs, furthermore, RNA-seq and real time RT-PCR was conducted to find the candidate genes related to lodging resistance on chromosome 5. QTLs for BS and cellulose density were estimated at the same regions in K-CSSLs and T-CSSLs, respectively. The Koshihikari allele on chromosome 5 had a positive effect on cellulose density, although the Koshihikari accumulated cellulose to a level lower than that in Takanari. These results suggested that the *japonica*-variety Koshihikari has a hidden superior allele on chromosome 5 that contributes to the improved culm stiffness and lodging resistance of *indica* varieties such as Takanari. However, the estimated region in K-CSSLs did not overlap with that in T-CSSLs. Estimating the different regions of QTLs in the reciprocal genetic backgrounds might be explained by the existence of multiple genes with the same function in the segment as a QTL cluster or epistasis with genetic background. The use of strong culm genes in addition to semi dwarf gene is a promising new approach in improving lodging resistance. Some candidate genes associated with cellulose deposition were found by RNAseq.

This study suggested that the lodging resistance of *indica* cultivar could be improved by introduction of genes from *japonica* variety Koshihikari covering high BS through the increase of cellulose density in culm.