

Category	: International Rice Research Conference
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Keyword 1	: Breeding Strategy
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Title of Entry	: Improvement of lodging resistance in rice by pyramiding four strong culm genes identified from superior lodging resistant varieties
Presenting author	: Taiichiro Ookawa
Presenting author email	: ookawa@cc.tuat.ac.jp
Co author 1	: Eri Kamahora
Co author 2	: Makoto Matusoka
Co author 3	: Kenzi Yano
Co author 4	: Ko Hirano
Co author 5	: Shunsuke Adachi
Co author 6	: Yukihide Iyama
Co author 7	: Takuya Yamaguchi
Co author 8	: Kazumasa Murata
Co author 9	:
Co author 10	:
Co author 11	:
Co author 12	:
Co author 13	:
Co author 14	:
Affiliation presenting author	: Graduate School of Agriculture, Tokyo University of Agriculture and Technology
Affiliation 1	: Bioscience and Biotechnology Center, Nagoya University

Affiliation 2	: Center for Advanced Intelligence Project, Institute of Physical and Chemical Research
Affiliation 3	: Agricultural Research Institute, Toyama Agricultural, Forestry & Fisheries Research Center
Affiliation 4	:
Affiliation 5	:
Affiliation 6	:
Affiliation 7	:
Affiliation 8	:
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Select only one type of presentation	: 15 minute oral presentation
Abstract	<p>: Severe lodging has recurrently occurred at strong typhoon's hitting in recent climate change. The identification of quantitative trait loci (QTLs) and their responsible genes associated with a strong culm and their pyramiding are important for developing high-yielding varieties with a superior lodging resistance. To identify QTLs for lodging resistance, the tropical japonica line, Chugoku 117 and the improved indica variety, Habataki were selected as the donor parent, as these had thick and strong culms compared with the temperate japonica varieties in Japan such as Koshihikari. By using chromosome segment substitution lines (CSSLs) in which chromosome segments from the japonica variety were replaced to them from Habataki, we identified the QTLs for strong culm on chrs. 1 and 6, which were designated as STRONG CULM1 (SCM1) and SCM2, respectively. By using recombinant inbred lines (BILs) derived from a cross between Chugoku 117 and Koshihikari and introgression lines, we also identified the other QTLs for strong culm on chrs. 3 and 2, which were designated as SCM3 and SCM4, respectively. Candidate region of SCM1 includes Gn1 related to grain number. SCM2 was identical to APO1, a gene related to the control of panicle branch number, and SCM3 was identical to FC1. To evaluate the effects of SCM1~SCM4 on lodging resistance, the Koshihiakri near isogenic line (NIL) with the introgressed SCM1 or SCM2 locus of Habataki (NIL-SCM1, NIL-SCM2) and the another Koshihikari NIL with the introgressed SCM3 or SCM4 locus of Chugoku 117 (NIL-SCM3, NIL-SCM4) were developed. Then, we developed the pyramiding lines with double, triple and quadruple combinations derived from step-by-step crosses among NIL-SCM1~NIL-SCM4. Quadruple pyramiding lines (NIL-SCM1+2+3+4) showed the largest culm diameter and the highest culm strength among the combinations and increased spikelet number due to the pleiotropic effects of these genes. Pyramiding of strong culm genes resulted in much increased culm thickness, culm strength and spikelet number due to their additive effect. These results suggest the importance of identifying the superior alleles for strong culm among natural variation and pyramiding these genes for improving high-yielding varieties with a superior lodging resistance. Keywords: Lodging resistance, Pyramiding, QTL, Rice, Strong culm gene</p>

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