

W03

Development of the pyramiding lines with strong culm genes derived from crosses among the *SCM* near isogenic lines in rice

Taiichiro Ookawa^{1)*}, Eri Kamahora¹⁾, Takeshi Ebitani²⁾, Takuya Yamaguchi²⁾, Kazumasa Murata²⁾, Yukihide Iyama²⁾, Hidenobu Ozaki²⁾, Shunsuke Adachi¹⁾, Tadashi Hirasawa¹⁾ and Motoki Kanekatsu¹⁾

¹⁾Graduate School of Agriculture, Tokyo University of Agriculture and Technology,

²⁾3-5-8 Saiwai-cho, Fuchu, Tokyo 183-8509, Japan

²⁾Agricultural Research Institute, Toyama Agricultural, Forestry & Fisheries Research Center, 1124-1 Yoshioka, Toyama, Toyama 939-8153, Japan

Abstract

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 *STRONG CULM2* (*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 *STRONG CULM3* (*SCM3*) and *STRONG CULM4* (*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*, a strigolactone signaling associated gene, by performing fine mapping and positional cloning of these genes. 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 or triple combinations derived from step-by-step crosses among NIL-*SCM1* ~ NIL-*SCM4*. Triple pyramiding lines (NIL-*SCM1*+2+3, NIL-*SCM1*+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. *SCM1* mainly contributed to enhance their pyramiding effect. These results in this study suggest the importance of identifying the combinations of superior alleles of strong culm genes among natural variation and pyramiding these genes for improving high-yielding varieties with a superior lodging resistance.

Keywords: lodging resistance, pyramiding line, QTL, rice, strong culm gene

Corresponding author*

Taiichiro Ookawa

Address: Graduate School of Agriculture, Tokyo University of Agriculture and Technology,
3-5-8 Saiwai-cho, Fuchu, Tokyo 183-8509, Japan

Tel and Fax: + 81-42-367-5672

E-mail: ookawa@cc.tuat.ac.jp