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Detection of the genetic region associated with the high-yielding ability of Japanese soybean variety, 'Fukuibuki'

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Soybean [*Glycine max* (L.) Merr.] is one of the important food crops in Japan, however, its yields have been lower compared to the other countries. Therefore, high yield varieties are expected to be developed continuously and utilized in farm field. A variety, 'Fukuibuki', is newly released and characterized with high yield in the Tohoku region (Northeast of Japan), but it has not been used widely because of its quality problem. In this study, the genetic analyses were performed to detect genetic regions associated with the high-yielding ability of 'Fukuibuki'.

Six breeding lines selected by conventional breeding methods and a recombinant inbred lines (RILs) population composed of 155 lines were used. The six breeding lines and RILs were derived from a same cross combination between 'Tohoku156' and 'Fukuibuki'. A seed parent, 'Tohoku156', is ranked normal yield in the Tohoku region. The six breeding lines were selected based on agricultural traits such as maturity, plant lodging and seed size, as well as seed yield. It was hypothesized that their genomic structures were biased for seed yield.

Genotypes of the six breeding lines were analyzed using 129 single sequence repeat (SSR) markers, and detected 11 genetic regions biased to 'Fukuibuki'-allele. Then, the effects of the biased SSR markers for seed yield were validated by using 155 RILs. Two years' experiments for 155 RILs showed that a genetic region near the SSR marker, 'Sat_219', on chromosome 20 was associated with seed yield. 'Fukuibuki'-allele on this region increased around 20% of seed yield compared to 'Tohoku156'-allele. 'Fukuibuki'-allele also extended post-flowering period and increased seed size, but decreased seed protein content. The results would be useful to develop new varieties with high yield, although additional studies are necessary.