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Centromere specific integrations of *copia*-type retrotransposons in *Arabidopsis lyrata*

Retrotransposons are major components of a eukaryotic genome. They may have proliferated in the genome during evolution. In plants, many of retrotransposons show clustered distribution, generating heterochromatin. One possibility for biased distribution is targeted integration of retrotransposons into such region. However, no mobile retrotransposon with targeted integration has been found in plants. We have recently found mobile retrotransposons in *ddm1* (*decrease in DNA methylation 1*) mutant, which shows reduced DNA methylation in genome (1). We have also found that *COPIA93* family LTR (long terminal repeats) retrotransposon, which is one of the mobile retrotransposon families in *ddm1*, showed centromere-specific localization in *A. lyrata* which is a closely related species of *A. thaliana*. Here, we directly show that targeted integration of *COPIA93* family retrotransposon in *A. lyrata*, which we named *Tall* (*Transposon of Arabidopsis lyrata 1*), into centromeric repeats in *A. thaliana* genome. We introduced *Tall* into *A. thaliana* by agrobacterium-mediated transformation. As a result, *Tall* was transcribed and retrotransposed in transgenic plants. Most importantly, *Tall* showed strong preference for integration into 178bp centromeric satellite repeats, suggesting that *Tall* has the ability to target centromeric repeats specifically.

References

(1) Tsukahara, S., Kobayashi, A., Kawabe, A., Miura, A., Mathieu, O., Kakutani, T., Bursts of retrotranspositions reproduced in Arabidopsis. *Nature* (461) 423-427, 2009.

CV

2001 – 2005 Undergraduate studies at the Department of Agriculture, Hokkaido University, Sapporo, Japan
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