A) Developmental abnormalities induced in DNA hypomethylation mutants: epimutations (heritable perturbation of gene expression) and transposon mobilization.

In an Arabidopsis DNA hypomethylation mutant *ddm1* (*decrease in DNA methylation 1*), a wide variety of developmental abnormalities are induced[1,2]. Through linkage analyses, we have shown that some of them are due to heritable perturbation of transcription[2-5] (Fig 1, 2). For example, a late flowering phenotype was due to ectopic transcription of *FWA* gene, which normally shows imprinted expression in endosperm[2-4]. Another combination of phenotypes, which we named *bonsai*, was due to hypermethylation and silencing of the responsible gene (*BONSAI* gene) [5] (Fig 2)

Another type of the *ddm1*-induced heritable developmental abnormalities was due to transposon insertion (Fig 3) [6,7]. The transposons identified were silent in wild type, but they are mobilized when DNA methylation is lost. We also identified diverse mobile transposons through genome-wide approach using the *ddm1* mutant lines[7]. The transposons we identified by this approach include interesting materials, such as a transposon specifically targeting to centromere[8], and a transposon having anti-silencing activity[9].

Fig 1
Gain-of-function epimutation *FWA*
Wild type (left) and *ddm1*-induced late flowering epimutation (right) (Reference 2-4)

Fig2
Loss-of-function epimutation *bonsai*
(Reference 5)

Fig 3
Insertion mutation induced by a transposon mobilized in *ddm1*
(Reference 7)

References

1. Kakutani T, Jeddeloh J, Flowers S, Munakata K, and Richards E (1996) Developmental abnormalities and epimutations associated with DNA hypomethylation mutants. ***Proc. Natl. Acad. Sci. U.S.A.*** 93, 12406-12411.

2. Kakutani T (1997) Genetic characterization of late-flowering traits induced by DNA hypomethylation mutation in Arabidopsis thaliana. ***Plant J.*** 12, 1447-1451.

3. Soppe W , Jacobsen S, Alonso-Blanco C, Jackson J, Kakutani T, Koornneef M, and Peeters A (2000) The late flowering phenotype of fwa mutants is caused by gain-of-function epigenetic alleles of a homeodomain gene. ***Molecular Cell*** 6, 791-802.

4. Kinoshita T, Miura A, Choi Y, Kinoshita Y, Cao X, Jacobsen SE, Fischer RL, and Kakutani T (2004) One-way control of *FWA* imprinting in *Arabidopsis* endosperm by DNA methylation. ***Science*** 303, 521-523.

5. Saze H, and Kakutani T (2007) Heritable epigenetic mutation of a transposon-flanked gene due to lack of the chromatin-remodeling factor DDM1. ***EMBO J.*** 26, 3641-3652

6. Miura A, Yonebayashi S, Watanabe K, Toyama T, Shimada H and Kakutani T (2001) Mobilization of transposons by a mutation abolishing full DNA methylation in Arabidopsis. ***Nature*** 411, 212-214.

7. Tsukahara S, Kobayashi A, Kawabe A, Mathieu O, Miura A, and Kakutani T (2009) Bursts of retrotransposition reproduced in Arabidopsis. ***Nature*** 303, 423-426.

8. Tsukahara S, Kawabe A, Kobayashi A, Ito T, Aizu T, Shin-i T, Toyoda A, Fujiyama A, Tarutani Y, Kakutani T (2012) Centromere-targeted de novo integration of an LTR retrotransposon of Arabidopdid lyrata. ***Genes Dev*** 26, 705-713

9. Fu Y, Kawabe A, Etcheverry M, Ito T, Toyoda A, Fujiyama A, Colot V, Tarutani Y, Kakutani T (2013) Mobilization of a plant transposon by expression of the transposon-encoded anti-silencing factor. ***EMBO J.*** 32, 2407-2417