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# 生命科学セミナー

(植物生殖遺伝分野担当: 第18回)

(生命科学研究科単位認定セミナー: 2ポイント)

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場所: 生命科学研究科・本館大会議室 (片平・3F)

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## Diversity of epigenetic control in the *FWA* gene within the genus *Arabidopsis*

There is natural variation in epigenetic state both in mammals and plants, but the significance of this variation remains unclear. The *FWA* gene was identified as a late flowering epi-mutant in *Arabidopsis thaliana*. *FWA* is silenced by DNA methylation in vegetative tissue, but it is specifically demethylated in the central cell of the female ovule and continues to be expressed in the endosperm from the maternal copy. A sequence similar to the SINE retroelement found near the transcription start site is conserved in the genus *Arabidopsis* and is the target of DNA methylation in *A. thaliana* (Lippman et al. 2004, Fujimoto et al. 2008). In *A. thaliana*, *FWA* is stably silenced in vegetative tissue, but in the related species, *FWA* expression and DNA methylation levels vary in vegetative tissue. In this study, we examined vegetative *FWA* expression in these species. Variation of vegetative *FWA* expression correlated with differences of methylation at non-CG sites in the region upstream of the transcription start site in the SINE-like region, and we suggest that this region is the critical methylated region for *FWA* silencing. In *A. thaliana*, the *FWA* expression is affected by methylation in regions both upstream and downstream from the transcription start site. The critical methylated region may have spread during evolution by the acquisition of *thaliana*-specific large tandem repeats. Ectopic *thaliana* *FWA* expression causes a late flowering phenotype, but over-expression of *lyrata* *FWA* does not. Stable *FWA* silencing might result from the selection of the large tandem repeats during evolution to inhibit late flowering in *A. thaliana*.

なお、不明な点は、生命科学研究科・植物生殖遺伝分野・渡辺 (nabe@ige.tohoku.ac.jp) までお願いします。  
共催: 特定領域研究「植物ゲノム障壁」、若手研究(S)「アブラナ科自家不和合性」、新農業プロジェクト



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