【Grant-in-Aid for Scientific Research (S)】
Biological Sciences (Biology)

Title of Project: Controlling Mechanism of Epigenome by Silencing and Anti-silencing

Tetsuji Kakutani
(Research Organization of Information and Systems, National Institute of Genetics, Professor)

Research Project Number : 26221105 Researcher Number : 20332174
Research Area : Genetics, chromosome dynamics
Keyword : Epigenetics, DNA methylation, Arabidopsis, chromatin

【Purpose and Background of the Research】

Epigenome dynamics is controlled by silencing and anti-silencing. However, information for the latter (anti-silencing) is limited. We are taking genetic and genomic approaches using mutants of Arabidopsis. By such approaches, we are uncovering novel anti-silencing mechanisms, which affect development and genome dynamics. In this project, we utilize these materials and solve new questions, such as control of development by heterochromatin and molecular mechanisms for the novel DNA demethylating activity.

【Research Methods】

Project1 "control of heterochromatin and its effect on development" In the mutants of a histone demethylase gene *IBM1*, heterochromatin accumulate in gene body, which is associated with diverse developmental defects (Saze et al 2008 Science; Miura 2009 EMBO J; Inagaki et al 2010 EMBO J). The heterochriomatin accumulates progressively over generations, and developmental defects become severer. We screened mutants suppressing the developmental abnormalities of the *ibm1*. Some of the suppressors have mutation in DNA methylase or histone methylase, which disrupt heterochromatin. Some of mutants suppressed the developmental defects without affecting the heterochromatin. Using them, we will try to understand control of heterochromatin and its effect on development.

Project 2 "molecular mechanisms for novel DNA demethylating activity" Through characterization of a DNA transposon, we have identified VANC protein, which has DNA demethylating activity (Fu et al 2013 EMBO J). Expression of VANC induces demethylation of a group of related transposons (Figure).

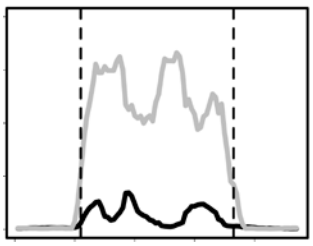

Figure – Transposon demethylation in transgenic line expressing VANC (black). Grey is a control line with methylated transposon

Demethylation induced by VANC is interesting in that entire length of transposon is affected, despite the strong specificity for the affected loci (Figure). To understand the mechanisms, we will examine distribution of VANC on chromosomes, screen proteins interacting VANC, and screen mutants affecting VANC activity.

【Expected Research Achievements and Scientific Significance】

(Project1) We will uncover mechanisms controlling heterochromatin during development. We also understand pathway between heterochromatin accumulation and developmental defects.
(Project2) We will understand mechanism for the novel DNA demethylating activity and identify host factors involved in that.

【Publications Relevant to the Project】

・ 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
・ Inagaki S, Miura-Kamio A, Nakamura Y, Lu F, Cui X, Cao X, Kimura H, Saze H, Kakutani T. (2010) Autocatalytic differentiation of epigenetic modifications within the Arabidopsis genome. ***EMBO J*** 29, 3496-3506.
・ Tsukahara S, Kobayashi A, Kawabe A, Mathieu O, Miura A, and Kakutani T (2009) Bursts of retrotransposition reproduced in Arabidopsis. ***Nature*** 303, 423-426.
・ Saze H, Shiraishi A, Miura A, and Kakutani T (2008) Control of Genic DNA methylation by a jmjC domain-containing protein in Arabidopsis thaliana. ***Science*** 319, 462-465

【Term of Project】

FY2014-2018

【Budget Allocation】

147,600 Thousand Yen

【Homepage Address and Other Contact Information】

http://www.nig.ac.jp/labs/AgrGen/home-j.html