

Title of Project : Elucidation of genetic systems conducting an early development of plant germ cells

Ken-Ichi Nonomura

(National Institute of Genetics, Experimental Farm, Associate Professor)

Research Area : Biological science, Agricultural sciences, Agriculture, Breeding Science

Keyword : Plant breeding/Plant genetics, Gene/Protein, Developmental genetics, Reproduction

[Purpose and Background of the Research]

Reproduction is the foundation of genetic events for all organisms, and an indispensable process for the seed production in flowering plants. However, the genetic system to regulate an early development of plant germ cells have been remained unclear. This project will genetically dissect the mechanism conducting the processes during which plant germ cells initiate and differentiate to undergo meiosis, by means of using reproduction-related mutants.

We previously identified the rice *MEL1* gene, which encoded an Argonaute (AGO) family protein expressed specifically in an early germ-cell development. The AGO binds to target RNAs guided by small RNAs and functions in gene silencing and chromatin modification. Reprogramming of chromatin modification has been reported in plants, and meiotic plant chromosomes form a specific composition to recognize a homologous pair, as same in animals. Thus it would be expected that a dynamic alteration in the chromatin structure takes place during an early development of plant germ cells.

This project aims to elucidate a regulatory system to promote an early development of plant germ cells by functional analyses of reproduction-related and chromatin-related genes.

[Research Methods] In addition to the MEL1, we succeeded to identify a novel rice protein MEL2 which was essential for the transition to meiosis (unpublished). First, we will try to identify RNA- and/or protein-interactors with the MELs by the immuno-coprecipitation. It has been known that several chromatin-related genes were downregulated in *mel1* mutants (Fig. 1). Thus we also plan to investigate the relationship between the MEL1 function and these chromatin-related genes. Application of the laser microdissection technique for developing plant germ cells will help to reveal expression profile chromatin the and modification of these genes. All candidate genes targeted by MEL proteins from the above analyses, other than chromatin-related genes,

will also be investigated.

[Expected Research Achievements and

Scientific Significance] (1) An elucidation of the MEL1 AGO pathway will lead to a better understanding of the genetic system required for an early development of plant germ cells. (2) A molecular mechanism to promote the transition to meiosis will be revealed. (3) A dynamic alteration of chromatin modifications during the germ-cell development will be partly elucidated. (4) The results should be extended to give some hints to solve the problems in the applied breeding, such as overcoming the reproductive barrier and the seed sterility by environmental stresses.



Fig. 1. In the wild-type rice meiocyte (left), the pericentromeric (red) histone H3K9s were dimethylated (green). In the *mel1* mutant (right), the H3K9s were hypo-methylated. Chromosomes were stained in blue.

[Publications Relevant to the Project]

• Nonomura, K.I., et al. A germ cell-specific gene of the *ARGONAUTE* family is essential for the progression of premeiotic mitosis and meiosis during sporogenesis in rice. *Plant Cell* 19: 2583-2594 (2007)

• Nonomura, K.I., Kurata, N., et al. PAIR2 is essential for homologous chromosome synapsis in rice meiosis I. *J. Cell Sci.* 119, 217-225 (2006)

[Term of Project]	FY2009 - 2013
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[Budget Allocation] 65,500 Thousand Yen

[Homepage Address and Other Contact Information]

http://www.nig.ac.jp/labs/ExpFarm/jweb/jto p/jlab.html