Title of Project: Analysis of epigenome marks and transcriptome in the germ line by the next generation sequencer

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Research Area: Agriculture
Keyword: Germ line cells, Epigenome, Transcriptome, DNA methylation

Purpose and Background of the Research
To explore mechanisms underlying function of the germ cells is an important research theme in animal reproduction, reproductive medicine, and developmental biology. Genome-wide dynamic changes of DNA methylation occur throughout gametogenesis in mammals. Acquisition of the epigenome marks including the DNA methylation is particularly indispensable for functions of oocytes and sperm genomes. In this study, to gain better understanding of re-programming of the epigenome marks in mouse germ line, we conduct analysis of the genome-wide DNA methylation status and transcriptome in the germ line cells.

Expected Research Achievements and Scientific Significance
This project provides the first extensive and high-resolution DNA methylome maps in mouse germ line cells. Using these data, we can look over the whole reprogramming of epigenome marks. This would contribute to progress of further understanding in various research fields such as animal production, cell differentiation and growth, stem cells function, gamete biology, and reproductive medicine, etc. Furthermore, if the obtained enormous data are uploaded on database and open for public, the information will be extremely valuable.

Publications Relevant to the Project

Term of Project
FY2010-2014

Budget Allocation
167,400 Thousand Yen

Homepage Address and Other Contact Information