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

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

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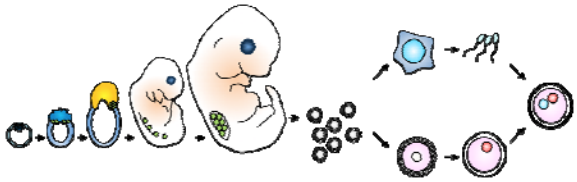
Research Area：Agriculture
Keyword：Germ line cells, Epigenome, Transcriptome, DNA methylation

【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 methlayion status and transcriptome in the germ line cells.



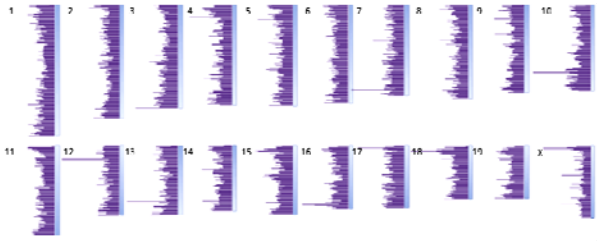
Methylome analysis in mouse germ line

【Research Methods】

DNA samples, which are prepared from germ line cells; PGCs, oocytes, spermprimordial germ cells, progonocyte, and non-growing oocytes etc, are treated with bisulphite to convert non-methylation cytosine to uracil. Using illumina Genome Analyzer, the DNA sequences are determined by high-throughput shotgun bisulphite sequencing method. The sequenced data are mapped to the mouse genome reference to show each CpG methylation status in the whole genome. To evaluate regulation of gene expression, the transcriptome analysis is also conducted in 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 up-loaded on database and open for public, the



information will be extremely valuable.

DNA methylation map in chromosomes

【Publications Relevant to the Project】

- Kobayashi H, Kono T. et al. Identification of the mouse paternally expressed imprinted gene *Zdbf2* on chromosome 1 and its imprinted human homolog ZDBF2 on chromosome 2. Genomics 93. 461-472, 2009.
- Hiura H, Kono T. et al. Oocyte growth-dependent progression of maternal imprinting in mice. Genes to Cells 11. 353-361, 2006.
- Kono T, Obata Y. et al. Birth of parthenogenetic mice that can develop to adulthood. Nature 428. 860-864, 2004.

【Term of Project】 FY2010-2014

【Budget Allocation】 167,400 Thousand Yen

【Homepage Address and Other Contact Information】

http://www.liaison-net.com/ridb/ridb?ucode=189&usno=101221