

Mini-Symposium on Genome Remodeling

Preface

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After the successful cloning of a sheep in 1997, considerable interest has been focused on the mechanism of genome remodeling in mammalian germ cells, and cloned animals have been produced in a number of species. These cloned animals have been produced by transferring the nuclei from somatic cells into enucleated MII stage oocytes, which indicates that the genome of the differentiated somatic cell is efficiently remodeled into a totipotent genome in the cytoplasm of the enucleated oocyte. Nevertheless, the mechanism of genome remodeling is poorly understood, and genome remodeling per se remains to be fully defined. The rate of successful production of cloned animals is still very low, and this is thought to be due to failures in genome remodeling. Improving this success rate requires advances in our knowledge of genome remodeling. This knowledge is also essential for progress in regenerative medicine. Regeneration requires the efficient differentiation and dedifferentiation of somatic cells and progenitor cells, in which the genomes should be remodeled.

This mini-symposium deals with the mechanism of genome remodeling. Although, as mentioned above, genome remodeling has not yet been defined at the molecular level, several regulatory mechanisms for remodeling have been reported very recently. The authors who have reported those findings are invited to introduce their recent results and/or to review the various problems that have arisen with genome remodeling. In the first paper, Dr. Takahashi reviews

the current state of the production of cloned animals and the associated problems. He also highlights the reprogramming of DNA methylation patterns, since failure of this system is a major cause of failure in the production of cloned animals. The second paper, by Dr. Tanaka and colleagues, focuses on the role of linker histones in genome remodeling. Meiotic chromatins contain the oocyte-specific linker histone, and the replacement of the somatic linker histone with the oocyte-specific histone is an important component in genome remodeling of somatic nuclei that are transplanted into the oocytes. In the third paper, Dr. Kim outlines the roles of histone modifications in genome remodeling, in which the deacetylation of histones is implicated in the erasure of the information on gene expression patterning, and in which the methylation of histones plays a role in retaining information on the parental origin of the chromosomes during the process of genome remodeling in oocytes. In the last paper, by Dr. Tada and co-workers, the important issue of epigenetic reprogramming in genome remodeling is described. The authors review the roles of epigenetic reprogramming in a variety of remodeling processes, i.e., in primordial germ cells, pre-implantation embryos, somatic nuclei that are transplanted into oocytes, and somatic nuclei that are fused with embryonic stem cells. I believe that these reviews will help readers to develop a comprehensive understanding of the mechanism of genome remodeling.