GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Localization and expression of histone H2A variants during mouse oogenesis and preimplantation embryo development

B.J. Wu[1,2]*, F.L. Dong[1,3]*, X.S. Ma[1], X.G. Wang[1], F. Lin[1] and H.L. Liu[1]

[1]College of Animal Science and Technology, Nanjing Agricultural University, Nanjing, China
[2]Inner Mongolia Saikexing Reproductive Biotechnology Co., Ltd., Helingeer, China
[3]Institutes of Biology and Medical Sciences, Soochow University, Suzhou, China

*These authors contributed equally to this study.
Corresponding author: H.L. Liu
E-mail: liuhonglin@263.net

Genet. Mol. Res. 13 (3): 5929-5939 (2014)
Received September 13, 2013
Accepted February 20, 2014
Published August 7, 2014
DOI http://dx.doi.org/10.4238/2014.August.7.8

ABSTRACT. Epigenetic modifications of the genome, such as histone H2A variants, ensure appropriate gene activation or silencing during oogenesis and preimplantation embryo development. We examined global localization and expression of the histone H2A variants, including H2A.Bbd, H2A.Z and H2A.X, during mouse oogenesis and preimplantation embryo development. Immunocytochemistry with specific antibodies against various histone H2A variants showed their localization and changes during oogenesis and preimplantation development. H2A.Bbd and H2A.Z were almost absent from nuclei of growing oocytes (except 5-day oocyte), whereas H2A.X was deposited in nuclei throughout oogenesis and in preimplantation embryos. In germinal vesicle (GV) oocyte chromatin, H2A.Bbd was detected as a weak signal, whereas no fluorescent signal was detected in GV

breakdown (GVBD) or metaphase II (MII) oocytes; H2A.Z showed intense signals in chromatin of GV, GVBD and MII oocytes. H2A.Bbd showed very weak signals in both pronucleus and 2-cell embryo nuclei, but intense signals were detected in nuclei from 4-cell embryo to blastula. The H2A.Z signal was absent from pronucleus to morula chromatin, whereas a fluorescent signal was detected in blastula nuclei. Our results suggest that histone H2A variants are probably involved in reprogramming of genomes during oocyte meiosis or after fertilization.

Key words: H2A variants; Preimplantation embryo; Oogenesis; Epigenetics; Reprogramming

