## Abstract

During the process of spermatogenesis, histones are replaced by protamines, basic proteins enabling transmission of DNA to the oocyte during fertilization. In mouse sperm, there is only 1% of remaining histones whose N-terminal tails contain post-translationally modified residues. In this study, I was interested in contribution of paternal histone H4 acetylated on lysine K12 residues (H4K12ac) that is present in mature sperm head in remaining nucleosomes. Physiologically, H4K12ac has an important role in transcription factor accumulation and in regulation of gene expression.

The presence and abundance of H4K12ac modification in various pronuclei stages of 1-cell embryo and parthenotes were assessed by imunnoflourescent detection with utilization of anti-H4K12ac antibody. Altogether, the paternal pronucleus exhibits a strong acetylation signal on H4K12 since its formation, while in the maternal one, there is a slow continual increase of H4K12ac getting on the same level as paternal pronucleus till the pronuclei fusion. Simultaneously DNA methylation status in both pronuclei was detected. In paternal pronucleus there is a continual decrease in the DNA methylation detectable as a decrease of 5mC and an increase of 5hmC signal. Meanwhile, the maternal pronucleus stays widely methylated. DNA demethylation and acetylation on lysine K12 histone H4 are genome activating modifications underlying differences in transcription activity of formatting pronuclei.

The significant importance of paternal contribution of H4K12ac during an early embryogenesis was also proven by detection of H4K12ac in parthenogenetically activated oocytes.



Key words: H4K12ac, epigenome, post-translational histone modifications, DNA methylation, 5mC, 5hmC, early embryonic development