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Expression pattern of *JMJD1C* in oocytes and its impact on early embryonic development

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ABSTRACT. Cell reprogramming mediated by histone methylation and demethylation is crucial for the activation of the embryonic genome in early embryonic development. In this study, we employed quantitative real-time polymerase chain reaction (qRT-PCR) to detect mRNA levels and expression patterns of all known histone demethylases in early germinal vesicle stage and *in vitro*-matured metaphase II (MII) oocytes (which are commonly used as donor cells for nuclear transfer). On screening, the Jumonji domain containing 1C *(JMJD1C)* gene had the highest level of expression and hence was used for subsequent experiments. We also found that *JMJD1C* was primarily expressed in the nucleus and showed relatively high levels of expression at the 2-cell, 4-cell, 8-cell, 16-cell, morula, and blastocyst stages of embryos developed from MII oocytes fertilized *in vitro*. Further, we knocked down the *JMJD1C* gene in MII oocytes using siRNA

and monitored the cleavage of zygotes and development of early embryos after *in vitro* fertilization. The results showed that the zygote cleavage and blastocyst rates of the transfection group were reduced by 57.1 ± 0.07 and 50 ± 0.01% respectively, which were significantly lower than those of the negative control group ($P < 0.05$). These data suggest that *JMJD1C* plays a key role in the normal development of early bovine embryos. Our results also provide a theoretical basis for the investigation of the role and molecular mechanism of histone demethylation in the early development of bovine embryos.

Key words: JMJD1C; Demethylase; Oocyte; Early embryo; Expression pattern

