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Analysis of imprinted messenger RNA expression in deceased transgenic cloned goats

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ABSTRACT. Genomic imprinting is an important epigenetic mechanism that has vital effects on fetal growth and development. We observed the differences in four tissues (heart, spleen, liver, and kidney) from dead transgenic cloned goats using hematoxylin and eosin (H&E) staining. Eight imprinted genes in the tissues of dead transgenic cloned and normal goats were analyzed using reverse transcription polymerase chain reaction. H&E staining results from the abortion group indicated the lack of obvious morphological changes in heart and spleen tissues, while inflammatory cell infiltration and glomerular nephritis characteristics were observed in liver and kidney tissues, respectively. Compared to the control group, *CDKN1C*, *H19*, *IGF2R*, and *SNRPN* were significantly ($P < 0.05$) overexpressed in the heart tissue of the abortion group, while *XIST* was significantly reduced. In the liver tissues, *CDKN1C* and *DLK1* expression decreased, while *GNAS*, *H19*, *IGF2R*, *PEG3*, and *XIST* expression increased significantly. In the spleen tissues, *DLK1* expression increased, while *GNAS*, *H19*, *IGF2R*, *PEG3*, *SNRPN*, and *XIST* expression decreased. In the kidney tissues, *CDKN1C*, *DLK1*, *GNAS*, *IGF2R*, and *PEG3* expression increased, while *H19* and *XIST* expression decreased. The overall expression of imprinted genes was abnormal in different tissues of transgenic cloned goats, and the

degree of abnormal genomic imprinting was more severe in the abortion group compared to the death and control groups. These results suggest that abnormal expression of imprinted genes may cause developmental defects in transgenic cloned goats. Moreover, abnormal epigenetic modifications may affect the reprogramming of transgenic donor cells.

Key words: Imprinted gene; Transgenic cloned goat

