



Differential gene expression of epigenetic modifying enzymes between Tibet pig and Yorkshire in high and low altitudes

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Genet. Mol. Res. 14 (2): 3274-3280 (2015)

Received May 9, 2014

Accepted October 7, 2014

Published April 13, 2015

DOI <http://dx.doi.org/10.4238/2015.April.13.6>

ABSTRACT. Epigenetic modifying enzymes play important roles in the adaptation to hypoxia, although no studies have examined their expression levels in Tibet pigs. The lung is an important functional organ in hypoxia adaptation. In this study, we examined the mRNA expression level of 5 enzymes in the lung of Tibet pigs using real-time polymerase chain reaction to determine the epigenetic performance of hypoxia adaptation. We selected four groups of pig as the study object, which were Tibet pig in highland (TH), Yorkshire in highland (YH), Tibet pig in lowland (TL), Yorkshire in lowland (YL). Expression of *Dnmt1* in Tibet pig was higher than that in Yorkshire ($P < 0.01$), although there was no significant difference between different altitudes within each breed. Expression of *Dnmt3a* was higher in Tibet pig than that in Yorkshire ($P < 0.01$), and higher in pigs from highland than that in lowland areas ($P < 0.05$). Expression of *Hdac1* was higher in group TH than in Yorkshire ($P < 0.01$). Expression of *Kdm3a* was higher in group TH than in the rest of the groups ($P < 0.01$). Expression of *Uhrfl* was higher in Tibet pig than in Yorkshire ($P < 0.01$). In conclusion, the expression levels of the 5 epigenetic modifying genes were higher in group TH than in group YH.

Under conditions of oxygen deficiency, breed was the most important factor affecting DNA methylation and gene expression.

Key words: Epigenetic modifying enzyme; Hypoxia adaptation; mRNA expression; Tibet pig