



Short Communication

Differential expression analysis of porcine *MDH1*, *MDH2* and *ME1* genes in adipose tissues

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ABSTRACT. Malate dehydrogenases 1 and 2 (*MDH1* and *MDH2*), and malic enzyme 1 (*ME1*) play important roles in the Krebs cycle for energy metabolism. The mRNA abundance changes of *MDH1*, *MDH2* and *ME1* genes were measured across six different adipose tissues from the leaner Landrace and fatty Rongchang pig breeds using quantitative real-time PCR. The mRNA of *MDH1*, *MDH2* and *ME1* was more abundant in fatty Rongchang pigs than in leaner Landrace pigs. In both breeds, females exhibited higher adipocyte volume and mRNA abundance of *MDH1*, *MDH2* and *ME1* compared with males. These values were higher in the subcutaneous adipose tissue compared with visceral adipose tissue. Furthermore, mRNA abundance changes of *MDH1*, *MDH2* and *ME1* have the remarked significant positive correlation with adipocyte volume across the six adipose tissue types. We conclude that there are breed-, gender- and tissue-specific expression patterns of *ME1*, *MDH1* and *MDH2*, which highlight their potential as candidate genes for selecting for fat volume in pigs.

Key words: Pig; *MDH1*; *MDH2*; *ME1*; mRNA; Adipose; qRT-PCR