



Development-related expression patterns of protein-coding and miRNA genes involved in porcine muscle growth

F.J. Wang, L. Jin, Y.Q. Guo, R. Liu, M.N. He, M.Z. Li and X.W. Li

Institute of Animal Genetics and Breeding,
College of Animal Science and Technology, Sichuan Agricultural University,
Ya'an, Sichuan, China

Corresponding author: X.W. Li
E-mail: xuewei.li@sicau.edu.cn

Genet. Mol. Res. 13 (4): 9921-9930 (2014)
Received January 9, 2014
Accepted August 19, 2014
Published November 27, 2014
DOI <http://dx.doi.org/10.4238/2014.November.27.21>

ABSTRACT. Muscle growth and development is associated with remarkable changes in protein-coding and microRNA (miRNA) gene expression. To determine the expression patterns of genes and miRNAs related to muscle growth and development, we measured the expression levels of 25 protein-coding and 16 miRNA genes in skeletal and cardiac muscles throughout 5 developmental stages by quantitative reverse transcription-polymerase chain reaction. The Short Time-Series Expression Miner (STEM) software clustering results showed that growth-related genes were downregulated at all developmental stages in both the psoas major and longissimus dorsi muscles, indicating their involvement in early developmental stages. Furthermore, genes related to muscle atrophy, such as *forkhead box 1* and *muscle ring finger*, showed unregulated expression with increasing age, suggesting a decrease in protein synthesis during the later stages of skeletal muscle development. We found that development of the cardiac muscle was a complex process in which growth-related genes were highly expressed

during embryonic development, but they did not show uniform postnatal expression patterns. Moreover, the expression level of miR-499, which enhances the expression of the *β -myosin heavy chain*, was significantly different in the psoas major and longissimus dorsi muscles, suggesting the involvement of miR-499 in the determination of skeletal muscle fiber types. We also performed correlation analyses of messenger RNA and miRNA expression. We found negative relationships between miR-486 and *forkhead box 1*, and miR-133a and *serum response factor* at all developmental stages, suggesting that *forkhead box 1* and *serum response factor* are potential targets of miR-486 and miR-133a, respectively.

Key words: Muscle growth; Porcine; Expression pattern; qRT-PCR