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Identification a dynamic atlas of the RNA editome in developmental skeletal muscle in pigs

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A-to-I RNA editing meditated by ADAR enzymes is a widespread post-transcriptional event in mammals. However, A-to-I editing in skeletal muscle remains poorly understood. By integrating strand-specific RNA-seq, whole genome bisulfite sequencing and genome sequencing data, we comprehensively profiled the A-to-I editome in developing skeletal muscles across 27 prenatal and postnatal stages in pig, an important farm animal and biomedical model. We detected 198,892 A-to-I editing sites and found that they occurred more frequently at prenatal stages and showed low conservation among pig, human and mouse. Both the editing level and frequency decreased during development and were positively correlated with ADAR enzyme expression. The hyper-edited genes were functionally related to the cell cycle and cell division. A co-editing module associated with myogenesis was identified. The developmentally differential editing sites were functionally enriched in genes associated with muscle development, their editing levels were highly correlated with expression of their host mRNAs and they potentially influenced the gain/loss of miRNA binding sites. Finally, we developed a database to visualize the Sus scrofa RNA editome. Our study presents the first profile of the dynamic A-to-I editome in developing animal skeletal muscle and provides evidence that RNA editing is a vital regulator of myogenesis.

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