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Analysis of the spatiotemporal expression of major genes in the TGF-β/*Smad* signaling pathway and correlation analysis using Hu sheep muscle tissue

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ABSTRACT. The mRNA expression levels of key genes (*Smads*, *MSTN*, and *MyoG*) in the TGF-β/*Smad* signaling pathway in Hu sheep at different growth stages (2 days, 2 months, and 6 months of age) and in different skeletal muscles (longissimus dorsi muscle and soleus muscle) and different genders were detected; and correlation of the *Smad* family (*Smad*2, *Smad*3, *Smad*4, and *Smad*7), *MSTN*, *MyoG* expressions was analyzed in Hu sheep. The results showed that the expression of *Smads* was higher in the soleus muscle than in the longissimus dorsi muscle; the expressions of *Smad*2, *Smad*3, and *Smad*4 were significantly higher in 2-day-old sheep than in sheep belonging to the other age groups ($P < 0.05$); the expressions of *Smad*2, *Smad*4, and *Smad*7 were higher in rams than in 2-day-old ewes, but lower in rams than in 2-month-old and 6-month-old ewes; and the expression of *Smad*3 was higher in rams than

in 2-day-old and 2-month-old ewes, but lower in rams than in 6-month-old ewes. In the 2 different muscle tissues, expression of *Smad*2 was significantly positively correlated ($P < 0.01$) with that of *Smad*3. The expression of *Smad*3 was significantly positively correlated ($P < 0.01$) with that of *Smad*4, which showed that the *Smad* family genes could have an inhibitory effect on the TGF-β/*Smad* signaling pathway.

Key words: Hu sheep; *Smads*; *MSTN*; *MyoG*; Gene expression

