



Expression profiles of differentially expressed genes affecting fecundity in goat ovarian tissues

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ABSTRACT. Although RNA-Seq is an effective method for identifying and exploring novel functional genes in mammals, it has rarely been applied to study fertility-related genes in the goat. In this study, RNA-Seq was used to screen the estrus ovaries of uniparous and multiparous Anhui white goats (AWGs). In total, 15,890 genes were identified and 2201 of these were found to be differentially expressed between the genetic libraries from uniparous and multiparous goats. Compared to the uniparous library, 1583 genes were up-regulated and 618 genes were down-regulated in the multiparous library. The *FER1L4* gene showed the level of highest up-regulation in the multiparous library, while *SRD5A2* expression showed the greatest down-regulation.

In order to determine the functions of *FER1L4* and *SRD5A2* in goats, the expression profiles of the two genes in different tissues from AWGs and Boer goats at diestrus were analyzed by quantitative PCR. *FER1L4* and *SRD5A2* showed tissue specific expression patterns and were highly expressed in ovaries from both AWGs and Boer goats. *FER1L4* was more highly expressed in ovaries from multiparous than uniparous AWGs. In contrast, *SRD5A2* was expressed at a lower level in multiparous AWGs. These results indicated that *FER1L4* and *SRD5A2* may be associated with the high fecundity of AWGs.

Key words: Goat; Ovary; Fecundity; Differentially expressed genes; Tissue expression profile