Gene expression in swine granulosa cells and ovarian tissue during the estrous cycle

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ABSTRACT. The components of the insulin-like growth factor (IGF) system appear to be involved in regulation of ovarian follicular growth and atresia in the pig. We investigated the expression pattern of mRNAs for IGF1 (*IGF1*), its binding proteins (*IGFBP1*, *IGFBP2*, *IGFBP3*, and *IGFBP5*), and epidermal growth factor in swine follicle cells and ovarian tissue throughout the estrous cycle using the real-time quantitative PCR technique. The results of gene expression were analyzed using linear regression with gene expression as a dependent variable and days of estrous cycle as an independent variable. Additionally, an analysis was made of the correlation of expression levels with plasma concentration of follicle-stimulating hormone, luteinizing hormone, estradiol-17β, progesterone, and prolactin. Expression of mRNA of all of these genes was detected in granulosa cells and ovarian tissue. *IGFBP3* mRNA showed a quadratic expression pattern ($P \leq 0.001$) and was significantly and positively correlated with progesterone ($r = 0.81$; $P \leq 0.01$) but negatively correlated with prolactin ($r = -0.596$; $P \leq 0.05$). Expression

of the other genes was unaffected by the stage of the estrous cycle. Real-time quantitative PCR effectively detected all transcripts, including the very low levels of *IGFBP1* transcripts, and could be used for studies of follicle dynamics.

Key words: Follicular development; Growth factors; RT-PCR