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Identification of Genes Expressed in Preovulatory Follicles during Ovulation in Rodent Ovary

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The LH surge triggers ovulation by activating cascade of genes. We investigated ovulation-associated genes using differentially expressed gene (DEG) kit and DNA microarray analysis. *In vitro* kinase assay revealed the activation of PKC zeta within 20 minutes after LH treatment in preovulatory follicles. Genes regulated by PKC zeta pathway were then identified using DEG kit. Thirteen genes including testin were stimulated by PKC zeta activation. MTT assay showed that treatment of preovulatory granulosa cells with mirystoylated-PKC zeta reduced viable cells, indicating a role of PKC zeta pathway in apoptosis. Northern analysis revealed that gonadotropin treatment increased testin expression within 3 hr in preovulatory granulosa cells both *in vivo* and *in vitro*. *In situ* hybridization analysis demonstrated that testin was also expressed in atretic follicles as well as in preovulatory granulosa cells. In addition, we identified LH-regulated genes in cultured mouse preovulatory follicles using DNA microarray analysis. Interestingly, factors important for the transition from proliferation to differentiation were stimulated by LH. Those factors include interferon alpha, runx1, B-cell translocation gene and cyclin G. Cyclin G expression was increased within 1 hr after LH treatment in granulosa cells of preovulatory follicles. FACS analysis demonstrated an increase in Go/G1 phase 6~8 hr after LH treatment, suggesting that those differentiation related factors may play an important role in ovulation. Our findings demonstrate several important genes for ovulation.