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Identification of Differential Gene Expression during Primordial to Primary Follicle Transition in Mouse Ovaries by ACP technology

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Transition of the resting primordial follicle to the growing primary follicle is a critical process for female reproduction, but its mechanism is poorly understood. The present study was conducted to investigate gene expression profile at the primordial-primary follicle transition process.

We isolated total RNA of female mouse ovary at day1 (contains only primordial follicles) and day5 (contains primordial and primary follicles) and synthesized cDNA using annealing control primers (ACP; Seegene, Inc., Seoul, Korea). ACP provides annealing specificity and sensitivity to the template and allows to identify only authentic differentially expressed genes (DEGs). We used total 80 ACPs for PCR, observed PCR products on 2% agarose gel, cloned 42 DEGs using TOPO TA cloning vector, sequenced, and analyzed by BLAST search. Sequences of 34 clones significantly matched database entries while 4 clones were novel and 4 clones were EST. Two of 34 genes were specifically expressed only in day 5 ovaries (Sui1-rs1, Apg3p/Aut1p-like), and rest of 32 genes were expressed in both stages but were differential in amount. Differential expression was confirmed using semiquantitative RT-PCR, and there was no false positive. Anx11 and Pepp2-pending were highly expressed genes in day1-, while BPOZ, Ches1, Kcmf1, NHE3, Nid2, Ninj1, SENP3 and Survivin were highly expressed genes in day5-ovary. List of genes would provide insight for further study of mechanism regulating primordial-primary follicle transition.

Key words) *mouse, folliculogenesis, differential gene expression, ACP*