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DNA Array Analysis of Changes in Gene Expression Profile in DHEA-induced PCO

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Under normal conditions, women produce a single dominant follicle that participates in a single ovuation each menstrual cycle. But Polycystic ovary syndrome(PCOS) conditions, folliculogenesis does not proceed normally. This condition leads to the accumlation of large numbers of small graffian follicles in which the theca interstitial cells (TIC) produce abnormally large amounts of androgen.

PCOS is probably the most common endocrine disorder, affecting women of reprodutive age with 5-10% prevalence estimate. Chronic anovulation, hyperandrogenism, hirsutism, obesity, infertility and polycystic ovaries are clinical hallmarks of women with PCOS. Its etiology remains unknown.

To investigate the gene expression pattern of ovary in PCO-induced rat, we used cDNA expression analysis. Total RNA was extracted from the ovary of pco-induced rat and reverse-transcribed in the presence of [α^{32}P]-dATP. Which were hybridized to Atlas™ Rat Toxicology 1.2 array (Clontech) representing approximately 1176 rat genes. We compared gene expression between ovary of pco-induced immature female rats and control. Differential gene expression profiles were revealed (LIFR-alpha, ADRA1A, Heat shock 90-kDa protein A, PDGFRA). Reverse transcription-polymerase chain reaction(RT-PCR) was used to validate the relative expression pattern obtained by the cDNA array.

The precise relationship between the altered expression of genes and PCO is a matter of further investigation. This study was supported by Korea Science and Engineering Foundation(KOSEF)

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