

Z3 14 **DNA microarray analysis of gene expression regulated by estrogen in the rat uterus**

Han Seung Kang*, Jeong Min Yu, Dae Yong Shim, Seong Jin Yoo, and Sung Goo Kang

Department of Biology, College of Natural Science, University of Inje

The uterus during estrus cycle synthesizes a complex of signaling molecules with specific spatial and temporal modes of expression and which are critical for cell proliferation and differentiation. The mechanisms underlying the differential pattern of synthesis of these associated proteins is not understood very well. Previous studies have shown that the ovarian hormones modulate these cellular events through the gene expressions. In the present study, we used for a functional genomics approach applying cDNA expression array technology to identify novel candidate genes involved in the regulation of uterine cell proliferation and differentiation during estrus cycle. Animals were sacrificed on pro-estrus, ovariectomized(OVX)+estradiol(E) treated and OVX rats. Total RNA was isolated from the uterus. ³²P-labelled cDNA was generated from 20 ug total RNA and hybridized with the Atlas Rat 1.2 Array II cDNA expression array(Clontech). Using this approach, we found several genes whose expression in rat uterus was altered with estrus cycle. For example, the expression of 7 genes including secreted protein acidic & rich in cysteine (SPARC), clathrin heavy chain, were more strongly expressed at pro-estrus, OVX+E than OVX. Our long term goal is to determine the role of these differentially expressed genes during estrus cycle.