

Gene expression analysis by micorarray in neonatal uterus exposed to diethylstilbestrol

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Introduction: Neonatal period is important period for normal uterine development and differentiation in mice. Neonatal diethylstilbestrol (DES) exposure induces disorganized uterine myometrial layers, less uterine glands and uterine adenocarcinoma. However, molecular mechanism of these uterine abnormalities is unknown. Thus, we compared global gene expressions between neonatal and adult uterus, and also examined specific gene expressions in neonatal mouse uterus exposed to DES.

Methods: Adult female mice were injected with oil vehicle alone one week after ovariectomy. Neonatal mice (0-day-old) were injected with 3 µg DES per pups or oil vesicle alone. Uterui were dissected 6 hours after the injection. cRNA preparation was used to inoculate Murine U74A version 2 GeneChip Expression Arrays (Affymetrix, Inc.).

Result: The mRNA of nearly 10,000 genes from neonatal and mature uterus was analyzed by microarray analysis. Neonatal control mouse uterus showed 264 upregulated genes and 266 downregulated genes as compared to mature ovariectomized control mouse uterus. Upregulated genes in neonatal control mouse uterus were related to cell cycle, transcription and muscle development. While, downregulated genes in neonatal control uterus were related to transcription, defense response, enzymes. Neonatal mouse uterus exposed to DES revealed upregulation of 35 genes and downregulation of 29 genes. The upregulated genes by DES in neonatal uterus have no classified tends. However, half of the downregulated genes by DES in neonatal uterus were related to cytoskeleton and muscle development. In conclusion, genes related to uterine muscle development and differentiation were expressed in neonatal mouse uterus, and DES repressed these genes 6 hours after the injection, which may result in disorganization of uterine myomefrium and other uterine abnormalities.