Long-term alteration of gene expression without morphological change in testis after neonatal exposure to genistein in mice: toxicogenomic analysis using cDNA microarray.

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In this study, we carried out toxicogenomic analysis using in-house cDNA microarray to ascertain the long-term effects of neonatal exposure to genistein, also known as phytoestrogen, on testicular gene expression in mice. Male ICR mice, 1 day after birth, were exposed for 5 days to genistein (1000 µg/mouse/day) or diethylstilbestrol (DES) (50 µg/mouse/day), used as an example of a potent estrogen, and their testes were used when they were 12 weeks old. Since exposure to DES was been reported to induce morphological changes and alteration of gene expression in reproductive organs, DES was used as a positive control. Genistein-treated mice did not show any histological abnormalities or increased apoptotic cells in testes, but these abnormalities and increases were found in DES-treated mice. On the other hand, mRNA expression analysis using in-house cDNA microarray revealed that 2 down-regulated genes (GeneBank accession No. W49392 and AI430907) were detected in genistein-treated mouse testes. Moreover, real-time PCR analysis revealed that mRNAs of the W49392 gene, estrogen receptor α (ERα) and androgen receptor (AR), were down-regulated in the testes of both genistein-treated and DES-treated mice. In our present study using toxicogenomic analysis, long-term alteration in testicular mRNA expression, without morphological change in testes, was detected after neonatal treatment with genistein, indicating that the W49392 gene, in addition to ERα and AR, might be useful as a biological marker for predicting the effects of neonatal exposure to DES and genistein.