

Identification of the common radiation-sensitive and glucose metabolism-related expressed genes in the thymus of ICR and AKR/J mice

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서론

Our goal was to identify the common radiation-sensitive expressed genes in the thymus of ICR and AKR/J mice on 100 days after irradiation. Thus, we performed microarray analysis for thymus of ICR and AKR/J mice, respectively. We categorized differential expressed genes by the analysis of DAVID Bioinformatics Resources v6.7 and GeneSpring GX 11.5.1 and validated gene expression patterns by QPCR analysis.

재료 및 방법

Animals

Seven-week-old female ICR mice (23.9 ± 1.17 g) and female AKR/J mice (24 ± 1.37 g) were purchased from Shizuoka Laboratory Center (Japan) and maintained under specific-pathogen-free conditions.

High- and low-dose-rate irradiation

A γ -ray generator (IBL 147 C; CIS Bio-International, France) was used for generating high-dose-rate irradiation (^{137}Cs , 0.8Gy/min). we reared mice in a long-term low-dose-rate irradiation facility equipped with a ^{137}Cs source and exposed the mice at 0.7 mGy/h until the cumulative dose reached 1.7Gy.

Whole genome microarray

Thymus from 100-day-old mice after high- and low-dose-rate irradiation were collected and analyzed by whole genomic microarray using an Agilent oligo microarray (44K, 60-mer oligonucleotide).

Quantitative reverse transcription PCR

PCR was performed in duplicate using SYBR green (Qiagen, Hilden, Germany) and a 7500 real-time PCR machine (Applied Biosystems, Foster city, USA). The relative abundance of specific mRNA levels was calculated by normalizing to β -2-microtubulin and 18srRNA expression by the $2^{-\Delta\Delta\text{ct}}$ method.

Statistical analyses

All data are presented as mean ± SD and ANOVA test was analyzed by SAS system release 8.02.

결과 및 고찰

Comparison of body weight, organs weight between ICR and AKR/J mice

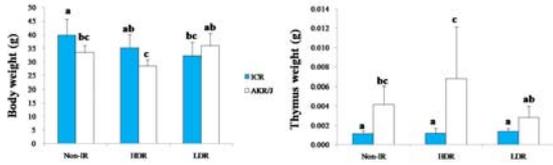


Fig.1. Comparison of body weight and thymus weight between irradiated ICR and AKR/J mice

Comparison of the pathways in the thymus of ICR and AKR/J mice

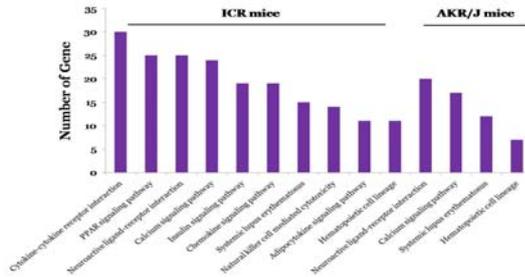


Fig. 2. Comparison of the pathways in the thymus of non-irradiated mice

Comparison of the pathways in the thymus of low-dose-rate irradiated ICR and AKR/J mice

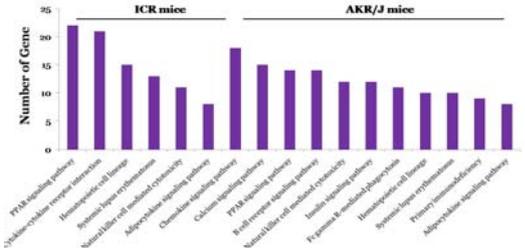


Fig. 3. Comparison of the pathways in the thymus of low-dose-rate irradiated mice.

Comparison of the pathways in the thymus of high-dose-rate irradiated ICR and AKR/J mice

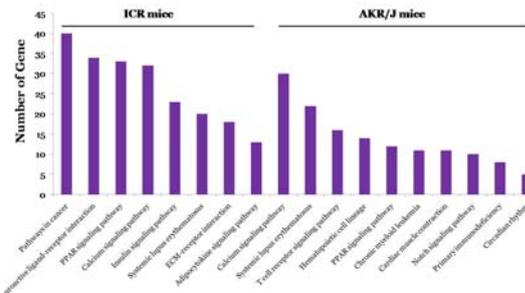


Fig. 4. Comparison of the pathways in the thymus of high-dose-rate irradiated mice.

The validation and pathway of the common radiation-sensitive genes in the ICR and AKR/J mice

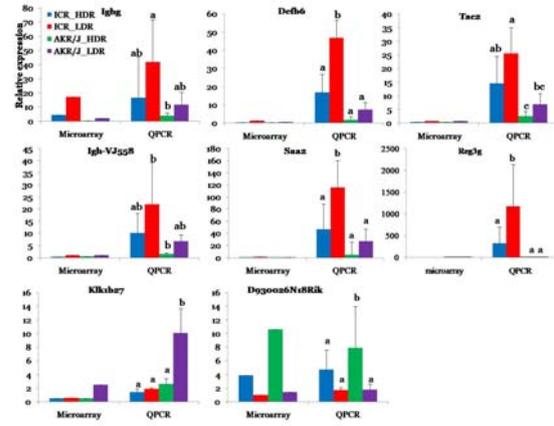


Fig. 5. The QPCR analysis and pathway analysis for validating microarray.

결론

Our result demonstrated that radiation-sensitive expressed genes and signaling pathways in the thymus of irradiated ICR and AKR/J mice.

참고 문헌

1. Huang DW, Sherman BT, Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID Bioinformatics Resources. Nature Protoc. 2009;4(1):44-57.
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