

Gene Expression of Malignant Lymphomas Developed in Mice Continuously Exposed to Low-Dose-Rate Gamma-Rays

Katsuyoshi FUJIKAWA, Satoshi TANAKA, Ignacia BRAGA-TANAKA III, Kazuaki ICHINOHE, Kimio TANAKA, Yoichi OGHISO
Department of Radiobiology

Abstract

We previously found that the life-shortening in B6C3F1 mice continuously irradiated at a low-dose-rate (LDR) (20 mGy/22h/day) for about 400 days with an accumulated dose of 8000 mGy was caused by early death from a variety of neoplasms including malignant lymphomas (MLs). In this study, we investigated changes in gene expressions of 20 MLs each from irradiated mice and non-irradiated control mice by using a microarray to characterize the gene expression profile of MLs induced by LDR irradiation. Hierarchical clustering analysis on genes related to cell growth, cell death and immune response identified 11 MLs which had a gene expression profile characterized by up-regulation of *Alk* and *Cd30* genes and down-regulation of *Bax* gene. Such *Alk*-positive MLs were found in 9 cases (45%) in the irradiated group, but only 2 cases (10%) in the non-irradiated control group. These results suggest a possibility that development of *Alk*-positive MLs might contribute to life-shortening of mice continuously irradiated with LDR gamma-rays.

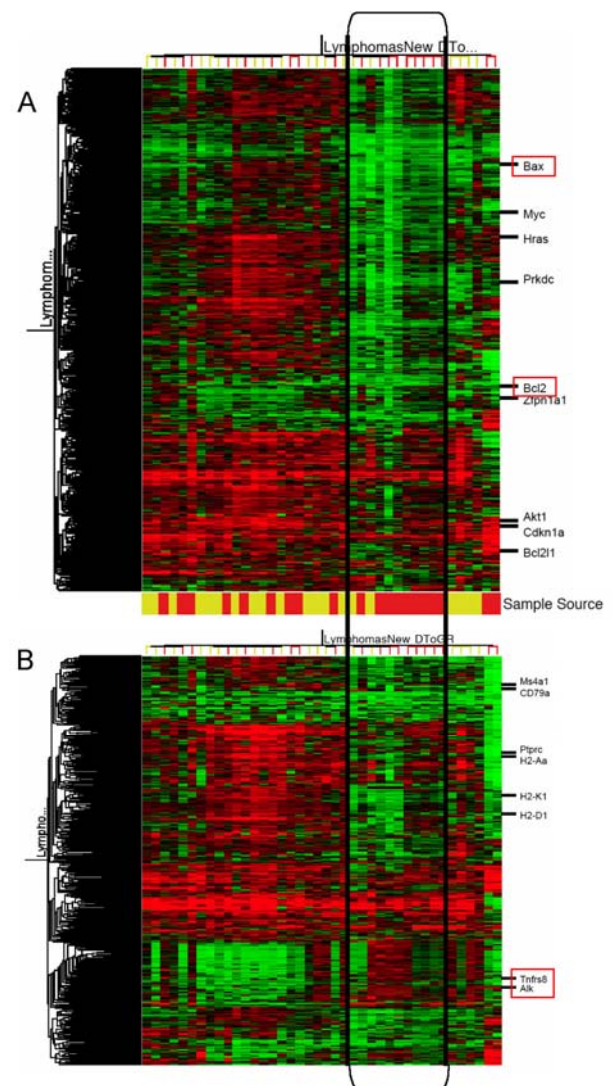


Fig. 1 Hierarchical clustering of genes relating to (A) cell growth and cell death (1694 genes), and (B) immune response (457 genes). Color bars on the bottom of panel A indicate sample sources: yellow shows MLs from non-irradiated mice; red shows MLs from mice long-term irradiated by gamma-rays at a LDR (20 mGy/22h/day) for 8000 mGy.