assayed for surface marker and p53 genotype. In a significant fraction of the mice 7 wks after 6 Gy-irradiation, we observed an abnormal increase of relative cell number of $CD4^+CD8^+$ thymocytes remaining in the thymus of highly irradiated mice and such abnormal thymocytes could be detected even 5 weeks after the irradiation. The abnormal $CD4^+CD8^+$ thymocytes were shown by PCR analysis of sorted cells to contain cells with p53–/– genotype. The data suggest that p53–/– thymocytes may appear as prelymphoma cells within several weeks post irradiation in $CD4^+CD8^+$ thymocyte subpopulation of irradiated p53 heterozygous mice.

34 Dose-response Relationship of Thymic Lymphoma Induction by Gamma Radiation and Induction of Non-thymic Lymphomas at Very Low Doses in SCID Mice

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SCID mice which have the defect of DNA-dependent protein kinase catalytic subunit, exhibit the limited activities of repair from DNA double strand breaks and are sensitive to ionizing radiation. In order to study the relationship between repair capacity for DNA double strand breaks and carcinogenesis, and the responsibitily at the low dose of gamma rays, the effects of ionizing radiation on tumor induction were studied using scid homozygote (scid/scid), and C.B-17(+/+)mice. Carcinogenesis experiments showed the significant increase of the incidence of thymic lymphomas at 25 cGy to sublethal dose. At very low dose(5 and 10 cGy), non-thymic B or T cell lymphomas were incuced in SCID mice, whereas there was no induction of these lymphomas in wild-type mice. No tumors other than lymphomas were observed, because of the life shortning effect by the induction of thymic lymphomas. Thus SCID mice is highly sensitive to the induction of non-thymic lymphomas at very low doses.

35 Arg/Pro TP53 codon 72 polymorphism in radiation-associated human thyroid tumors

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Common polymorphism in the TP53 gene (encoding Arg72Pro in p53) was analyzed in radiation-associated post-Chernobyl and spontaneous series of adolescent and adult papillary thyroid cancer (PTC) in patients of Russia by real-time PCR allelic discrimination assay and direct sequencing. Reference data for sporadic PTC were available for German caucasians. The distributions of sequencing variants in both radiation-associated series, but not in spontaneous one differed significantly from the reference group. Radiation-associated groups harbored at least heterozygous 72Pro significantly more often, and homozygous 72Arg less often than the reference group. The radiation-associated and spontaneous adult groups statistically differed from each other for these indexes. Data imply the different distribution of allelic forms of the TP53 in PTCs of diverse ethiopathogenic groups.

36 Detection of Illegitimate Sites by Intracisternal A-particle-mediated Retrotransposition in Radiation-induced Tumors.

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Genomic DNA of acute myeloid leukemia (AML) cells induced by x-ray in C3H/He mice is frequently accompanied with illegitimate insertion of the cDNA of the intracisternal A-particle (IAP) DNA element that is present in normal murine genome in two thousand copies per haploid and is closely related with provirus form of retrovirus in the structure. We established the PCR-based method to detect the characteristic integration site of IAP cDNA in tumors. From genomic DNAs of 11 lines of radiation-induced AML cells from C3H/He mice, 21 sites of the unique integration sites of IAP cDNA were amplified by this method. In contrast, occurrence of only 4 insertion of IAP cDNA were newly observed among 40 lines of thymic lymphoma cells from C3H/He mice. Since insertion of IAP element with H-type LTR was observed in all the characteristic site, suggesting that activation of the H-type LTR of IAP is common feature in hematopoietic tumors in C3H/He mice.

37 Transcriptional Regulation of Long-terminal Repeat of Intracisternal A-particle that Contributes Gene Rearrangement in Radiation-induced Myeloid Leukemia in C3H Mice.

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Mouse genome possesses 2000 copies of the retrotransposon, intracisternal A-particle (IAP) DNA element, that closely resembles to provirus of retrovirus. We have previously classified long-terminal repeat (LTR) of IAP elements in genome by its nucleotide sequence variation to type-A to H. The integration of IAP cDNA with H-type LTR into genomic DNA to generate