to diagnostically radiation damage in the presence of thermal burns. The results show: 1) The fMPCEs induced by single burns (¢ó¡ãburn 10% and 20% individually) were varied in control range at 24 h and became lower than control when the sampling time was prolonged to 48 h and 72 h. 2) There were good dose and time response of the fMPCEs induced by single radiation injuries (1, 3, 5 Gy individually) at 24 h, 48 h and 72 h. 3) The fMPCEs induced by combined radiation-burn injury (10%¢ó¡ãburn + 1, 3, 5 Gy individually; 20% ¢ó¡ãburn + 1, 3, 5 Gy individually) showed the fMPCEs increased following radiation dose increased at 24 h, but under the same radiational exposure, the fMPCEs of combined injury groups was significantly lower than single radiation groups, and the fMPCEs of 20% combined injury groups was lower than 10% combined injury groups. At the mean time, the percentages of PCE (PCE%) were found to proportionally increase after combined radiation-burn injuries. The reason of the fMPCEs decreased may be due to burns damage can stimulate some new erythercytes to produce and dilute the MPCE, It was possible to canculate radiation dose lower when the fMPCE was used as biologcal indicator of radiation injury under combined radiation-burn exposure.

Keyword(s): micronuclei; combined radiation-burn injury; mouse

P IX.14 Preliminary study of detection of excision-repairable DNA lesions with cytosion arabinoside-cytokinesis-block micronucleus test (ARA-CBMNT)

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It was already found that cytosine arabinoside (ARA) can inhibite the activities of DNA polymerisate enzyme, thereby, the DNA Lesions in Go phase can be fixed and expressed as micronuclei (MN) in M phase. The micro-quantity whole blood culture method was used in this study. The productions of MN in the cultured human lymphocytes with and without ARA were compared. We observed the baseline (no mutagen) of MN frequencies (¡ë) in +ARA group is increased 6.4-fold of that in - ARA group, 3.3-fold increased for 1 Gy x-rays, 3.5-fold increased for 1 Gy œÃ-rays, and 6.3-fold increased for Ultraviotet Light. These observations suggested that combined ARA-CBMNT method may enhance the sensitivities of exposure to mutagens that predominantly induce DNA excision repairable lesions, and the micro-quantity whole culture method is also suitable for ARA-CBMNT.

Keyword(s): micronuclei; human lymphocytes; cytosine arabinoside (ARA)

P IX.15 Chlamydomonas reinhardtii as a model system for DNA repair study

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The DNA repair machinery appears to have the capability of finding and dealing differentially with many types of damages to the DNA in the restoration of its normal function. It means there exist several repair systems which organisms developed for maintaining the integrity of the genome in connection with its vulnerability to physical and chemical damage and the chances for error inherent in the replication process. Progress in understanding of DNA repair starts with the isolation of repair-deficient mutants, following by the genetic and molecular analysis and the study of mutant phenotypes. We have isolated and described a number of mutants with sensitivity to DNA damaging agents in *C reinhardtii* which constitutes the very convenient model system for dissection of DNA repair. This research was focused on establishing the non-excision repair pathways. The different repair pathways were assessed on the basis of single and double repair-deficient mutants responses to UV-light, X-irradiation and alkylating agents treatments. Molecular analysis of pyrimidine dimer excision from the DNA of repair-deficient strains proved their repair genes involvement in non-excision repair. Genetic analysis revealed that these repair pathways are determined by several genes, three of which have been located into the first linkage group and they form a cluster of repair genes determining DNA repair based on other mechanisms than excision of damages from DNA in Chlamydomonas *reinhardtii*.

Keyword(s): Repair pathways; Genetic analysis; *Chlamydomonas reinhardtii*

P IX.16 Characterization of an Arabidopsis thaliana homologue of the human ATM gene

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A partial cDNA fragment from Arabidopsis with homology to ATM was identified. The homology spans the putative Pi3 kinase domain and extends into the upstream region. BLAST searches indicate that the Arabidopsis cDNA is most closely related to ATM, then the human ATR gene and the yeast TEL1 gene. A corresponding genomic clone was isolated and its physical map position was determined. It lies on the lower arm of chromosome 3, next (less than 100 kb away) to an I/Spm element. This tranposable element is being used for a localized saturated mutagenesis in order to tag the ATM homologue. Progress in the sequencing and tagging of the gene will be described.

Keyword(s): Arabidopsis; ATM homologue

P IX.17 Homologous recombination in CHO cell lines defective in DNA damage processing

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DNA homologous recombination was studied using a DNA construct bearing tandem copies of LacZ marker gene containing a non-overlapping deletion. Four cell lines were used in this study: xrs6 cell line - Ku86 deficient, defective in dsb repair; Pa13 and Pb4 cell lines sensitive to DNA crosslinking agents, probably defective in DNA crosslink repair; parental CHO-K1 cell line. After electroporation, stable transfectants containing a single copy of plasmid intergrated into the genome were isolated and the rate of spontaneous and induced homologous recombination between the two copies of LacZ gene was estimated. The rate of spontaneous recombination in CHO-K1 cells was 1.9 event/locus/cell generation/105. The rate of spontaneous recombination in Pb4 cells was similar to the wt cells, on average 3.0 events/locus/cell generation/105; in Pa13 was about 10-fold higher than in wt cells, on average 23.0 events/locus/cell generation/105. In xrs6 cells we found a very high rate of spontaneous recombination, on average 600.0 events/locus/cell generation/105, i.e. 300 times higher than in wt cells. No induction of spontaneous recombination was found after 2 Gy gamma-irradiation, or treatment with diepoxybutane. Our results confirmed the role of dsb in initiation of homologous recombination. It seems also that homologous recombination does not play any role in processing of DNA crosslinks.

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