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of Cu(II) and Cr(III) ions were masked. The method was applied to the analysis of Cr(VI) in industrial water with recoveries of 95.2 - 104.3 % and a mean RSD (n=6) of 5.6%.

Keywords: chromium(VI), catalytic method, sulphanilic acid, p-aminobenzoic acid, industrial water

ORAL PRESENTATION 4

ALTERED DRUG RESISTANCE AND NEUROLOGIC DISORDERS IN DROSOPHILA MELANOGASTER WITH A DEFICIENT HISTAMINE-GATED CHLORIDE CHANNEL

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The recent identification and characterization of two genes, encoding histamine-gated chloride channel subunits from Drosophila melanogaster, has confirmed that histamine is a major neurotransmitter in the visual system of the fruitfly. One of the cloned genes, hclA, corresponds to ort (ora transientless), mutations in which affect histaminergic synaptic transmission in the Drosophila visual system. We identified a mutational change (a null mutation) in the genomic and RNA copies of hclA derived from flies with the ort[1] allele. This correlates with new phenotypes observed in the mutant strain. We found hypersensitivity to neurotoxins of the avermectin group in both the ort[1] adult flies and third instar larvae compared to Oregon R wild-type animals. In contrast, the mutation makes male and female adults more resistant to treatment with diethyl ether, and the animals show substantially prolonged recovery from paralysis after diethylether anaesthesia, as well as an impaired recovery from paralysis after mechanical shock, as revealed by the bang sensitivity test. The examination of several other alleles ort (with identified mutations in hclAs) in the same tests revealed the allele-specific responses. Altogether, our data give direct evidence that in vivo a HCLA subunit-containing receptor has a distinct role in the response to general anaesthesia and the neurotoxins, as well as indicate that its function is not limited by the frames of the visual system.

TOPICS: 1) Ion channels and membrane trafficing; 2) Metabolic disorders; 3) Molecular structure and function

OCTOBER 15, 2003 – WEDNESDAY

HALL B

LECTURE 1

INACTIVATION OF MELANOMA CELLS IRRADIATED WITH GAMMA RAYS AND LOW ENERGY PROTONS

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Radiotherapy and particularly proton therapy is very efficient in eliminating malignant growths, but it is also very delicate, since healthy tissue surrounding ill tissue should not be affected at all or very little by the irradiation. The main characteristics of protons, such as their well defined range, relatively small lateral scattering, and high energy deposition density, just before the end of the range, make them particularly suitable when malignant growths are deeply embedded or are close to critical organs, where there is a high demand to minimize the destruction of the neighbouring and overlaying tissue.

In order to obtain better results in eliminating malignant cells, the aim of this in vitro study was to investigate the difference in response of HTB63 human melanoma cells to irradiation with either gamma rays or protons considering dynamics of cell growth. Single irradiation with gamma rays using doses from 2 to 20 Gy exhibited weak inactivation of human melanoma cells in vitro. The best effect, 26% of growth inhibition was obtained after single irradiation with gamma ray using dose of 16 Gy. Using the same doses of proton irradiation, with energy at the target of 22.6 MeV, significant melanoma cell growth inhibition was induced. Doses of 12 and 16 Gy provoked growth inhibition of 48.9 and 51.2% respectively. Estimated RBEs for inactivation of HTB63 cells ranged from 1.02 to 2.22. The electrophoretical analyses of DNA samples and flow cytometric evaluation have shown a small percentage of apoptotic cells after both types of irradiation.

The inhibitory effect of protons on melanoma growth, in contrast to gamma rays, can be explained considering specific physical properties of protons, especially taking in account good dose distribution.

LECTURE 2

LARGE SCALE MACROMOLECULAR SIMULATIONS BY SYMPLECTIC INTEGRATION METHODS

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Among the main theoretical methods of investigation of the dynamic properties of biological macromolecules, such as proteins, are molecular dynamics (MD) simulation and harmonic analysis. MD simulation is a technique in which the classical equation of motion for all atoms of a molecule is integrated over a finite period of time. The resulting trajectory is used to compute time-dependent properties of the system. Harmonic analysis is a direct way of analyzing vibrational motions. Harmonicity of the potential function is a basic assumption in the normal mode approximation used in harmonic analysis. This is known to be inadequate in the case of proteins because anharmonic effects, which