



Non-Ionizing Radiation & Children's Health

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PLATFORM PRESENTATION ☒

Other Childhood Cancers - Current Molecular Approaches To Address Environmental Risk Factors

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Cancer is caused by changes in the genome and/or epigenome of somatic cells, removing the cell from the tight control on cell division and apoptosis regulating the behaviour of normal cells. There is clear evidence, that environmental factors can affect the frequency of specific cancers in specific populations, which, in turn, could help to reduce the frequency of these cancers. Analysis of the genome and transcriptome of the cancer, and the genome of the patient provides new possibilities to identify the mechanisms behind these environmental effects offers a number of new possibilities to identify these environmental effects, and the mechanisms, through which they increase cancer frequency. Specific environmental factors can for example leave a 'footprint' in the genome of the tumor cell, sometimes allowing the identification of the mechanisms responsible. Analysis of the genome of lung cancer has for example identified the characteristic mutation footprint of tobacco smoke (Pleasant et al., *Nature*, 2010, 463(7278), 184-190). Similarly, viral agents will be identified by deep sequencing of DNA or RNA from the tumor sample. Alternatively, we can expect, that specific environmental effects will specifically increase the frequency of specific cancer subtypes. Deep sequencing and modelling provides a highly effective way to identify such subtypes, increasing the power of the statistical analysis. We are using a combination of high throughput sequencing of genome and transcriptome of both tumor and patient to establish predictive models (virtual patients), which ultimately will reflect the response of real patients to specific therapies in oncology and other areas of medicine. This type of analysis will however also provide the basis for a much more stringent analysis of potential environmental effects of cancer formation than feasible up to now..