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**Proteomic determination of the biological sequelae of electron irradiation.**

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Radiobiological-based treatment planning, where radiation dose is varied according to the regional biological variations in tumor tissue e.g. hypoxia, is becoming increasingly available and represents a radically different approach to improving the radiocurability of tumors. However, many of the current algorithms are based upon radiobiological phenomenon that have been studied for decades, e.g., the oxygen effect, and few utilize recent information on biological parameters that influence radiation response, e.g. EGFR status. With regard to electron treatment planning, there is a paucity of studies that have looked at the biological consequence of exposure to electrons of differing energies. The assumption is that there is a uniform cell killing per unit dose within the treatment volume. We have recently applied proteomic analysis to determine the impact that exposure to low and high-energy electrons have on the proteome of tumor cells; preliminary data suggests that a completely different spectrum of proteins are expressed 24 hours after exposure to 50 cGy of high versus low LET electrons. Changes in the cellular proteome provide an indication of the different cellular responses elicited in response to damage induced by high and low energy electrons. Should these protein changes reflect a different high versus low energy electron mediated cell inactivation, then algorithms may have to be developed that take into account the energy distribution within the dose field. A new technique called MALDI-imaging is capable of resolving proteomic differences at various sites in a tissue slice, thus allowing for a spatial determination of proteins within an irradiated tumor volume. In the future it may thus be feasible to determine the exact dose distribution with an irradiated field and determine the efficacy with which radiation kills tumor or normal cells.