

Molecular study of the radiolysis of concentrated proteins by accelerated ions

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In order to better describe the biological effects of ionizing radiation, understanding the mechanisms of radiolysis at the molecular scale is a key step. Proteins are by far the most abundant biomolecules in the cell, yet very few studies describe their radiolysis by accelerated ions. The aim of our team is therefore to develop a systematic study of these effects on protein biomolecules, from amino acids to whole proteins, and with various ions, energies and dose-rates.

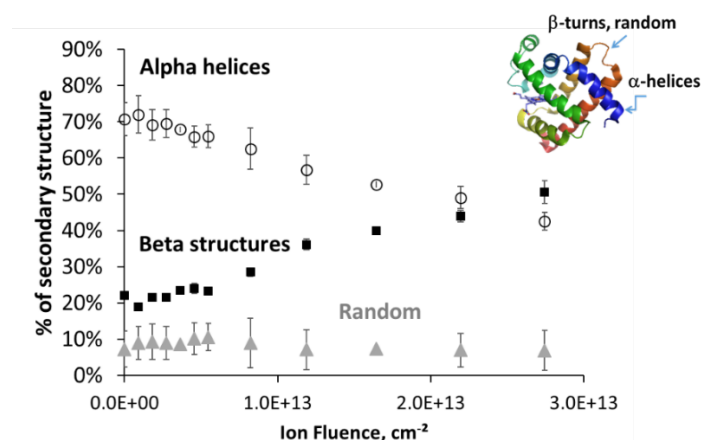


Figure 1 Evolution of the secondary structure of myoglobin under irradiation by 2 MeV protons, as a function of cumulative ion fluence. Error bars were determined with a duplicate of irradiation

In this work, myoglobin, a small heme-protein, was irradiated by accelerated ions of a few MeV energies, in highly concentrated native gels, 20 % w/w, similar to protein content in the cell. The impact of ions on its secondary structure was followed by mean of infrared spectroscopy, showing reproducible and organized change in its conformation, from alpha helices to mostly beta-structures (Figure 1). UV-Visible spectra were also recorded under irradiation, and the combination of the data allowed identifying the formation of a significant quantity of carbon monoxide under irradiation.

The results obtained with low-energy protons will be presented and compared to helium and carbon ions, and the possible source for carbon monoxide will be discussed. Results obtained with other proteins (HSA, beta lactoglobulin) will be compared.