RADIONUCLIDE ANTIBODY-CONJUGATES: DEVELOPMENTS AND APPLICATIONS TO OBTAIN A TARGETED CANCER THERAPY

Gjorgieva Ackova Darinka[1], Smilkov Katarina[1], Petre Makreski[2], Trajče Stafilov[2], Duatti Adriano[3], Janevik-Ivanovska Emilija[1]

[1]Department of Pharmacy, Faculty of Medical Sciences, University Goce Delčev – Štip, R. Macedonia

[2]Department of Chemistry, Faculty of Natural Sciences and Mathematics, University "Ss. Cyril and Methodius" – Skopje, R. Macedonia

[3]Department of Chemical and Pharmaceutical Sciences, University of Ferrara, Ferrara, Italy

Understanding the behaviour and function of biomolecules at the molecular level is key to the discovery and development of new drugs, as well as diagnostic techniques. The characterization of therapeutic monoclonal antibodies (mAbs) poses many challenges compared to those of low-molecular mass drugs because of their inherent complexity due to their protein nature. Achievements in this field of science have changed the way that drugs are being designed and developed nowadays. Vibrational spectroscopy techniques, like Fourier Transform Infrared (FTIR) spectroscopy and Raman spectroscopy (RS) have helped to determine the secondary structure of complex protein molecules, as well as protein-ligand complexes. Other advantages of these techniques include the need of very low sample concentration and the ease of sample preparation. Therefore, they are gaining growing importance in the field of medicine and pharmacology.

Our group has demonstrated the use of these tools to understand protein-ligand interactions in therapeutically important mAb, rituximab, conjugated with three different bifunctional chelating agents (*p*-SCN-Bn-DOTA, *p*-SCN-Bn-DTPA and 1B4M-DTPA) with no available structural information of obtained complexes. A special interest was directed to the secondary structure of the antibody. In spite of the fact that Raman spectra show characteristic fingerprints which can be used for molecular identification, we detected the most important protein groups, and noted the a-helix and the b-sheet structures in the molecule.

The high-throughput approach presented here has significant potential for analyzing the stability of biotherapeutics as well as any other biological molecules which are used as anti-cancer therapeutic drugs.