Contribution ID: **116** Type: **Posters**

A new scavenger that reduces radiation damage in solution and crystalline protein samples

Tuesday, 16 June 2015 17:40 (1h 50m)

Radiation damage is a serious problem in synchrotron light sources, limiting the quality of the collected data. This issue is critical for structural biology techniques, like Biological Small Angle X-ray Scattering (BioSAXS), and Macromolecular Crystallography (MX). Common strategies to reduce radiation damage in SAXS are flowing the sample through the beam, or adding small molecules such as dithiothreitol (DTT) or polyols such as glycerol to the sample. However, DTT is not advisable in proteins with disulphide bonds, and glycerol may reduce signal-to-noise ratio at high concentrations. In MX, the primary strategy is cooling the samples to cryogenic temperatures. However, radiation damage is a complex phenomenon not completely understood, and still a milestone for structural biology studies at current synchrotron radiation facilities.
The scavenging properties of several small molecules that have not been investigated as scavengers for SAXS and MX were analysed. Lysozyme was used in both experiments, as this is a model protein for SAXS and MX. All the assays were performed at near room temperature. The results show that the so-called SMX1 compound has similar efficacy as DTT or glycerol in decreasing radiation damage in solution scattering experiments. SMX1 also shows scavenging properties in MX experiments on lysozyme crystals at room temperature. Protective effects of SMX1 on enzyme function of lysozyme irradiated in solution were also studied. Altogether, the results show that SMX1 can be considered a new alternative scavenger for structural biology techniques. This study is part of an ALBA Synchrotron Light Source project in radiation damage on biological macromolecules, in collaboration with the Spanish Nuclear Safety Council (CSN). This project is being carried out as collaboration between NCD-BL11 and XALOC-BL13, which are the ALBA beamlines dedicated to SAXS and MX, respectively.

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Session Classification: Special Session - Coffee and poster discussion: ALBA users and AUSE members

Track Classification: VII AUSE Congress