X-ray microscopy & cell structure

Gerd Schneider

BESSY m.b.H., Albert-Einstein-Str. 15, 12489 Berlin, Germany, e-mail: **Schneider@bessy.de**

The x-ray microscope installed at the 3rd generation storage ring BESSY II is dedicated for applications in life, environmental and materials sciences. It covers the photon energy range between 250 - 600 eV. Currently, the spatial resolution is about 25 nm. To protect biological cells from radiation damage caused by X-rays, imaging of the samples has to be performed at cryogenic temperatures, which makes it possible to take multiple images of a single cell as required for tomography [1]. Due to the small numerical aperture of zone plates, X-ray objectives have a depth of focus on the order of several microns. By treating the X-ray microscopic images as projections of the sample absorption, computed tomography can be performed [2,4]. Since cryogenic biological samples are resistant to radiation damage, it is possible to reconstruct frozen-hydrated cells imaged with a full-field X-ray microscope. This approach is used to obtain 3-D information about the location of specific proteins in cells. To localize proteins in cells, immunolabelling with strongly X-ray absorbing nanoparticles was performed [3]. To detect protein distributions inside of cells, X-ray microscopy tomography of immunolabelled frozen-hydrated cells was performed. As a first example, the distribution of the nuclear protein, male specific lethal 1 (MSL-1) in the *Drosophila melanogaster* cell was studied [4]. In the talk, the current status and future aspects of biological x-ray microscopy will be discussed.

References

[1] G. Schneider, "Cryo X-ray microscopy with high spatial resolution in amplitude and phase contrast", *Ultramicroscopy* **75**, Nov. 1998, 85 - 104

[2] D. Weiß, G. Schneider, B. Niemann, P. Guttmann, D. Rudolph, and G. Schmahl, "Computed tomography of cryogenic biological specimens based on X-ray microscopic images", *Ultramicroscopy* **84**, 2000, 185 - 197

[3] S. Vogt, G. Schneider, A. Steuernagel, J. Lucchesi, E. Schulze, D. Rudolph, and G. Schmahl: "X-ray microscopic studies of the Drosophila dosage compensation complex", *Journal of Structural Biology* **132**, 2000, 123 - 132

[4] G. Schneider, E. Anderson, S. Vogt, C. Knöchel, D. Weiss, M. LeGros, C. Larabell: "Computed tomography of cryogenic cells," *Surf. Rev. Lett*., Vol. 9, No. 1 (2002) 177- 183