Life Science:

X-ray imaging is a relatively new application of synchrotron radiation. It is still not widely recognized as a major tool in biology. However, since the emergence of third-generation synchrotron radiation facilities, imaging techniques have been developed extensively. Even though there are other competitive methods for structural studies, high resolution synchrotron imaging is now established as a useful tool in biology, as well as in many other fields of sciences. In particular, microtomography, which enables one to investigate the three-dimensional structure of an object at high resolution, is a unique method. As a result of intensive development, several variations of the imaging techniques are now available.

Professor Takahashi used high resolution tomography to investigate a fossil flower. The study revealed the structure of a flower smaller than 3 mm in size, and from its details, it is now established as a new fossil species. Dr. Mizutani also used microtomography to visualize neurons in the brain. The samples were stained with high-Z elements to enhance contrast. A neuronal network was beautifully visualized at sub-micron resolution.

Professor Takeda' s group used phase-contrast tomography to investigate the microstructures of glomeruli and tubular structures of the kidney. This technique makes use of a Bonse-Hart type interferometer. Its advantage over conventional absorption-based tomography is its much higher density resolution. Thus, biological samples with only small density variations can be visualized. The kidney of a human disease model hamster was studied, and the details of the lesions were detected.

Medical Biology

Dr. Maeshima and Dr. Nishino used X-ray coherent diffraction. This technique is different from other imaging techniques in that it does not record an image but reconstructs it from the X-rays scattered by an object. This reconstruction is performed entirely by a computer and facilitated by oversampling the scattering intensity distribution. Just as with the other imaging techniques, a 3D structure can be obtained by rotating the sample and recording many scattering data. They used this technique to visualize a human chromosome. The 2D resolution was 38 nm and the 3D resolution was 120 nm. This technique is just an early stage of application because it is expected to become a more powerful tool when combined with XFEL, which will be available in a few years.

There are two other reports using diffraction. Dr. Inui used small-angle scattering to investigate the function of PGDS, a protein that may be useful as a drug delivery vehicle. It is interesting to note that small-angle scattering is based on the same principle as the diffraction imaging used by Maeshima and Nishino. The difference is that within the X-ray beam, there is only one object with a fixed orientation in the case of diffraction imaging, whereas there are nusmerous identical objects with random orientations in small-angle scattering. Dr. Oda used a fiber diffraction technique to study the structure of an actin filament, which is a ubiquitous component of cell motility. Information obtained by electron microscopy was combined with the fiber diffraction data to reveal the structural change in actin monomers when they assemble into a filament.

These articles make a good showcase of a variety of techniques for studying non-crystalline biological samples using synchrotron radiation. They help us to recognize how these structure-oriented X-ray techniques, from projection imaging (radiograph) to fiber diffraction and eventually to crystalline diffraction, are related to each other.

Naoto Yagi

"Lupinasu" - *Lupin*