Synchrotron radiation and protein crystallography in Japan

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N. Sakabe has been developing IP diffractometers at the Photon Factory since the early 1980s. Before SPring-8 began operations, all of protein crystallographers were dependent on him for the collection of intensity data. Many Japanese and foreign crystallographers determined a number of novel crystal structures using his detectors at the Photon Factory. S. Wakatsuki has built a new undulator beamline equipped with a CCD detector, which is user friendly and high-quality beamline. The Photon Factory has one undulator and three bending magnet beamlines and SPring-8 has four undulator and six bending magnet beamlines for protein crystallography.

In the 1980s less than ten groups were working on protein crystallography in Japan. Many new research groups studying protein crystallography were organized by scientists both inside and outside of universities from 1990. The number of protein structures determined at high resolution has gradually increased. Nine membrane protein structures have been determined at high resolution using X-ray methods. In 1995 T. Tsukihara's group at Osaka University and S. Yoshikawa's group at Himeji Institute of Technology succeeded in structural determination of a bovine respiratory membrane protein complex, cytochrome c oxidase. This structure, the first membrane protein structure determined from mammalian cells, was a marked breakthrough not only in crystallographic studies of membrane proteins, but also in the field of bioenergetics. C. Toyoshima of the University of Tokyo determined the structure of the sarcoplasmic reticulum calcium pump in 2000. He successfully demonstrated the mechanism of calcium pumping by serial structural analyses of reaction intermediates. T. Okada's endeavor to crystallize a G protein-coupled receptor resulted in successful structure determination by a collaboration of SPring-8 group lead by Dr. M. Miyano and Prof. R. E. Stenkamp's group of University of Washington in 2000. Collaborating with A. Yamaguchi of Osaka University, three young crystallographers, M. Murakami, S. Nakashima and E. Yamashita, determined the structure of the bacterial multidrug efflux transporter AcrB in 2002 and elucidated a transportation mechanism.

K. Namba of Osaka University elucidated the mechanism of bacterial flagellar assembly and function by combining cryo-electron microscopic structures and X-ray structures. A. Nakagawa elucidated structure organization of a double-shelled RNA virus based on the structure of Rice Dwarf Virus at 3.5 Å resolution. Many other physiologically important protein structures have been determined since the mid 1990s in Japan. Outstanding structural studies on recombination, replication, transcription, and translation have been performed by K. Morikawa of BERI, T. Hakoshima of Nara IST, S. Yokoyama of RIKEN and the University of Tokyo, I. Tanaka of Hokkaido University and O. Nureki of Tokyo Institute of Technology. After setting up a Structural Biology Center in the Photon Factory, S. Wakatsuki has made significant progress in understanding the structural biology of lysosomal protein transport.

In 2002, the Japanese government started a large structural genomics program, "Protein 3000." In addition to the high-throughput structural genomics approach led by S. Yokoyama at RIKEN, eight target oriented structural genomics projects led by I. Tanaka of Hokkaido University, S. Wakatsuki of the Photon Factory, M. Tanokura of the University of Tokyo, K. Miki of Kyoto University, A. Nakagawa of Osaka University, and others are included in Protein 3000. Most of the Japanese protein crystallographers and many biochemists have joined this program. Consequently, crystallography has become a more familiar method for biochemists.