Basic Characterization of a Multiple CCD X-ray Detector and its First On-Beamline Test

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1. Introduction

This is a status report for the current year on the Multiple Charge-Coupled-Device X-ray Detector Project that the SR Structural Biology Research Group of RIKEN and the Station Equipment Group of JASRI have been conducting in collaboration with EEV in the UK.

A 4×4 array CCD X-ray detector system was successfully constructed and examined with a conventional X-ray generator system last year [1, 2]. Then the groups proceeded on to a systematic analysis of the acquired X-ray image data, and performed the first test at the RIKEN Beamline I in order to evaluate the imaging capability.

2. Basic Characterization

Among the detector parameters examined were the (1) image distortion, (2) spatial resolution, (3) non-uniformity, and (4) dynamic range.

Image distortion is usually attributed to the optical deformations occurring in the fibre-optics-tapers used in a CCD X-ray detector. In the present work, it was evaluated by the use of lattice images produced with the X-ray generator system [1]. In reference to the precisely located lattice points, it was found that the image distortion was on the order of 0.1 mm and 2 mm at the centers and at the edges of the CCD X-ray detector modules, respectively.

By fitting a Gaussian distribution function to the lattice points observed, their horizontal and vertical spreads were estimated to be 164 ±13 μm (FWHM) and 188 ± 25 μm (FWHM), respectively. Since these values are very close to the extension of the incident X-ray beam, it is highly conceivable that the spatial resolution of the MCCDX is much better than these values.

In order to investigate the non-uniformity quasi-flat field of an X-ray beam are the two most conceivable sources of this significant fluctuation observed in the noise image.

While evaluating the MCCDX system with the conventional X-ray generator system, X-of the X-ray sensitivity that the MCCDX system inherently possesses, the system was irradiated with a quasi-flat field of an X-ray beam achieved with the X-ray generator system by the elimination of all associated optical components. Since the global structure observed in the flat-filed images should have corresponded to the non-uniformity, the low-frequency spatial components were extracted from the images and fitted to a 2D Gaussian distribution function. It was found in all of the CCD X-ray detector modules that the sensitivity decreased down to 80% at the edges with respect to the value at the center.

The high-frequency components contained in the flat-field images, on the other hand, represented the noise levels associated with the X-ray intensity measurements. It was found that the standard deviation of the noise amplitude distribution of the image was as high as 2% of the maximum intensities that the MCCDX could measure, while that of a dark image is better than 0.02% in the MCCDX system. Spatial and temporal variations of the

Fig. 1 X-ray transmission image with the fine structure of veins clearly resolved.

ray transmission images of a twig with leaves were taken to demonstrate the overall imaging capability of the system. Figure 1 displays one of the X-ray transmission images with the fine structure of veins clearly resolved.

3. The First On-Beamline Test

Having confirmed that the MCCDX can attain the designed functional specification, it was subjected to its first on-beamline test, on December 4, 1997 at RIKEN beamline I, and acquired X-ray diffraction images of well-known protein samples. Figure 2 displays a typical X-ray diffraction pattern of Lysozyme observed during the first test.

In reference to the results reported in the present work, one can expect the MCCDX to function as a significant part of RIKEN Beamline I where research on advanced protein crystallography is being performed based upon the trichromatic concept [3]. Various tests, however, are waiting to be done for the MCCDX the following year, to confirm whether it has been successfully installed not only in terms of hardware, but also in terms of software. To that end, the MCCDX will be acquiring a vast amount of X-ray diffraction images of protein samples during the period of commissioning.

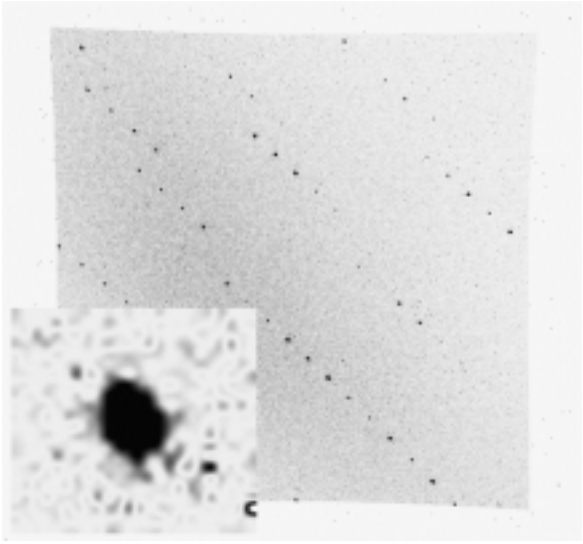

Fig. 2 Typical X-ray diffraction pattern of Lysozyme observed during the first on-beamline test. A diffraction spot magnified is shown at the left-bottom corner.

References

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