We have developed a data collection system which can fit for both time resolved Laue and LOT, and name it as time-resolved camera system. Typical nature of this camera for time-resolved Laue is that imaging plate cassette with 800x800mm detector area can be moved quickly while rotating fast shutter is chopping the X-ray to get m-sec order of time resolution spots whose images are aligned along horizontal direction. Chopping is better than the streaks as following reasons; 1. Easy to get accurate integration intensity data. 2. Back ground can be reduced extensively. 3. To reduce the dose of X-ray to the crystal and to reduce the crystal damage. The evaluation of this system has been done by crystal of w-amino acid aminotransferase whose space group 122 (a=137.9, b=124.7, and c=61.5Å) and cell dimensions are a=137.9, b=124.7, and c=61.5Å. The normal Laue data collected from 42 frames with 400x800mm. The recovery is 62% within 2Å resolution. The R (I) is 8.4%. Time resolved Laue data was collected from three shots at 2mm interval. The R factor(I) between three spots is 0.07 for 3580 reflection in a frame which corresponds to 75% of single spots exposure in the same condition. Time-resolved experiment using LOT has been done by this system switching to as the Weissenberg camera. In the case of tetragonal lysozyme using flow cell, independent data up to 1.8Å has been collected within 15 min with two frames. Rmerge(I) is 0.045.

The data used in this study was a 2.6Å set of 0.25° oscillation data collected at room temperature using a Mar Research 30 cm image plate scanner on crystals of the Neurophysin-hyclrin I complex (space group P41_2_1_2, a=b=68.7Å and c=113.6Å). The 0.25° images were combined to form the 0.5°, 0.75°, 1.00°, 1.25° and 1.5° used in the analysis. Each data set was then processed using X-GEN, XDS, MOSFILM and DENZO. The results of our analysis will be presented. Work supported by NIH grant GM-41936.

PS01.04.12 AN ANALYSIS OF DATA COLLECTION STRATEGIES AND DATA REDUCTION SOFTWARE FOR IMAGE PLATE DATA. Bing Hui1, John Rose2 and Bi-Cheng Wang2, 1Dept. of Crystallography, University of Pittsburgh, Pittsburgh, PA 15260, U.S.A., 2Dept. of Biochemistry & Molecular Biology, University Georgia, Athens, GA 30602, U.S.A.

In designing a strategy for macromolecular data collection, one of the most often asked questions is “What scan range should I use?” The answer may vary depending on the facilities used for data collection and the programs used for data processing. Intuitively, narrow oscillation data slices (0.1-0.25°) should give a better signal-to-noise ratio than large oscillation data slices (say, 0.5-2.0°). However most image plate data is collected using a large oscillation data slice due in part to the slow readout time of the commercial detectors, the decay of diffraction quality with time and the initial lack of data reduction software for narrow oscillation data slices. In addition, there appears to be no reported systematic study on the relation of scan range to data quality for image plate data which prompted us to do a systematic study on this subject.

The data used in this study was a 2.6Å set of 0.25° oscillation data collected at room temperature using a Mar Research 30 cm image plate scanner on crystals of the Neurophysin-hyclrin I complex (space group P41_2_1_2, a=b=68.7Å and c=113.6Å). The 0.25° images were combined to form the 0.5°, 0.75°, 1.00°, 1.25° and 1.5° used in the analysis. Each data set was then processed using X-GEN, XDS, MOSFILM and DENZO. The results of our analysis will be presented. Work supported by NIH grant GM-41936.

PS01.04.10 TIME-RESOLVED PROTEIN DATA COLLECTION SYSTEM WITH LARGE IMAGING PLATE. K.Sakabe, N.Kamiyai, N. Watanabe2, S. Adachi1, K. Sasaki3, S.Ikemizu1, T.Higashit, & N. Sakabe3, Dept. of Chem. Nagoya Univ., Chiusa, Nagoya, 464 Japan, 1IRIKEN, Hiroswa 2-1, Wako, Saitama, 351 01 Japan, 2PP, KEX, Tsukuba 305 Japan, 3College of Medical Technology, Nagoya Univ. Higashi, Nagoya, 461. 4Institute of Applied Biochem., Univ. of Tsukuba, Tsukuba Ibaraki 305 Japan, 5Rigaku Corporation Matsubara, Akishima, Tokyo 196 Japan

Crystallographers are investigating ever larger unit cells. HI-STAR with high resolution mode and Dual HI-STAR for large unit cells. However, the new calibration method, using amorphous Iron foil placed at the crystal position and generating the commerical detector area as following reasons; 1. Easy to get accurate integration intensity data. 2. Back ground can be reduced extensively. 3. To reduce the dose of X-ray to the crystal and to reduce the crystal damage. The evaluation of this system has been done by crystal of w-amino acid aminotransferase whose space group 122 (a=137.9, b=124.7, and c=61.5Å) and cell dimensions are a=137.9, b=124.7, and c=61.5Å. The normal Laue data collected from 42 frames with 400x800mm. The recovery is 62% within 2Å resolution. The R (I) is 8.4%. Time resolved Laue data was collected from three shots at 2mm interval. The R factor(I) between three spots is 0.07 for 3580 reflection in a frame which corresponds to 75% of single spots exposure in the same condition. Time-resolved experiment using LOT has been done by this system switching to as the Weissenberg camera. In the case of tetragonal lysozyme using flow cell, independent data up to 1.8Å has been collected within 15 min with two frames. Rmerge(I) is 0.045.