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RFID Tag System for Sample Tracking at Structural Biology Beamlines

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Abstract. We have developed and operated a sample exchange system on the macromolecular crystallography beamlines at the Photon Factory for high-throughput experiments, remote operations, and automated experiments. Automated data collection experiments are carried out according to the sample data description files. To prevent human error when preparing the samples and the files, each cassette and cryo-pin is assigned an ID. We implemented a barcode reader on the sample exchanger to identify a commercially available pin with a 2-D barcode. The barcode can be read after the robot picks up the pin from a liquid nitrogen dewar. However, several pins could not be identified due to frost growth on the barcode. To achieve 100% identification, herein we report the development of a sample tracking system with an RFID tag. The small RFID tag is fixed on the base of the cryo-pin and a reader is fixed on the tip of sample rotation axis. Preliminary tests reveal a 100% success rate when the tag-reader distance is less than 0.6 mm.

INTRODUCTION

For high-throughput protein crystallography, various sample exchange robots have been developed at structural biology beamlines [1-7]. Users insert their samples into cassettes and bring them to the beamlines. To identify the cassettes, a one-dimensional barcode is labeled on the SPACE cassette [2] and the ALS puck [3]. The SPINE sample holder and puck [4-6] have two-dimensional barcodes used for identification.

We have developed and implemented sample exchange robots at the macromolecular crystallography beamlines of the Photon Factory for high-throughput experiments, remote operations, and automated experiments [7]. In our experimental system, automated data collection experiments are carried out according to predetermined experimental conditions, which are described in the sample data files. We began offering beam time for fully-automated experiments to users at PF-AR-NE3A. Because cassettes from several users are placed in the same liquid nitrogen dewar, the position of each cassette is important. However, because the cassettes used by our robot, SSRL cassettes or Universal VI-pucks, lack barcodes, the barcode of the pin at the predetermined position is used to identify the cassettes.

We previously implemented a two-dimensional barcode reader on the sample exchange system. Typically, most barcodes can be read after the robot picks up the pin from the cassette, but some cannot be read due to frost growth on the barcode. Additionally, heavy use of the barcoded pins makes it difficult to read over time as the barcodes become blurred. If a barcode cannot be read, the operator is required to relate manually the lost barcoded cassette in

the dewar. However, if multiple barcodes are not recognized, the operator must enter the experimental hutch to check the cassettes visually.

Usage of Radio Frequency ID (RFID) tags have been proposed to manage numerous biomedical samples [8-10]. In the field of protein crystallography, RFID tags have been proposed to identify cryo-pins [11-13] and cassettes [12-13]. We have originally developed an RFID tagged cryo-pin and a reader with a magnet, which can read easily the tag on the rotation axis of a goniometer.

RFID TAG AND READER

Figure 1 (a) shows an RFID tag used in our identification system. The dimensions of the RFID tag are 3.6 mm (w) x 2.5 mm (d) x 0.9 mm (h), and the reading frequency is 13.56 MHz. The RFID tag is affixed to the hole at the center of the bottom of the cryo-pin using a glue designed for very low temperatures (Fig.1 (b)). Since the depth of the hole is a little larger than the height of the tag, the tip of the goniometer's rotation axis definitely touches the base.

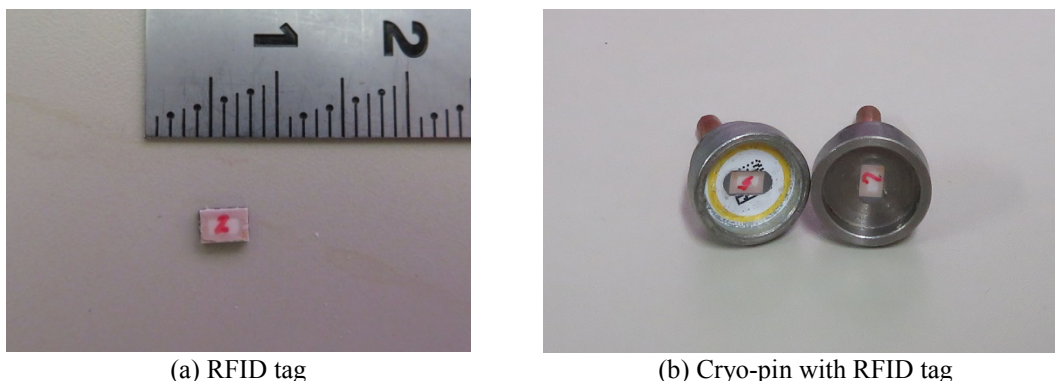


FIGURE 1. RFID tag and cryo-pin.

We manufactured an RFID reader which can be placed on the rotation axis with a built-in static magnet. Figure 2 shows the setup of our reader on the goniometer of AR-NW12A beamline in KEK. The reader is screwed to the rotation axis tightly. For the preliminary experiments at the beamline, the cable is taken from the side of the reader and connected to a PC via a USB. In future, we pass the coaxial cable through inside the rotation shaft and connect it to the PC using slip rings.

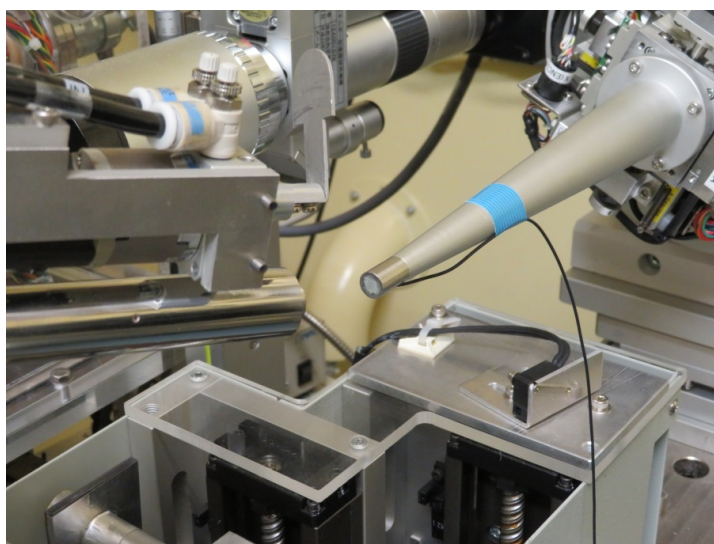


FIGURE 2. RFID reader on the sample rotation axis.

TEST EXPERIMENTS

Cryo-pins with RFID tags were put into a liquid nitrogen dewar, and reading tests were conducted after mounting the pin on the goniometer. Errors were not revealed in the preliminary tests. To check the stability of the RFID system, we investigated the relationship between the tag-reader distance and the success rate. Figure 3 shows our equipment used to investigate the success rate. The stage upon which the reader is affixed can be moved by a micrometer head. The cryo-pin is held by a 3D-printed acrylic part.

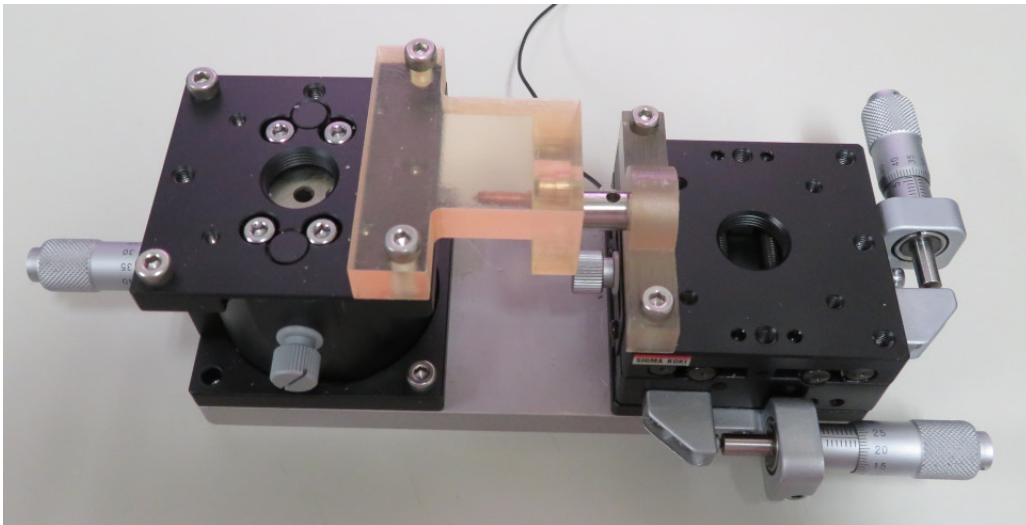


FIGURE 3. Equipment employed to investigate success rate

We measured the success rate while changing the distance between the reader and the tag on the cryo-pin. For comparison, we also prepared five RFID tagged cryo-pins and an RFID tag. Figure 4 plots the success rate as a function of distance. Because the distance between the tag and the reader is not zero when the pin is on the reader, Fig. 4 shows the corrected distance. When the tag-reader distance was less than 0.6 mm, the success rate was 100%. To ensure compatibility with the beamlines and the 2D barcode reader, the RFID has a thin barcode sticker.

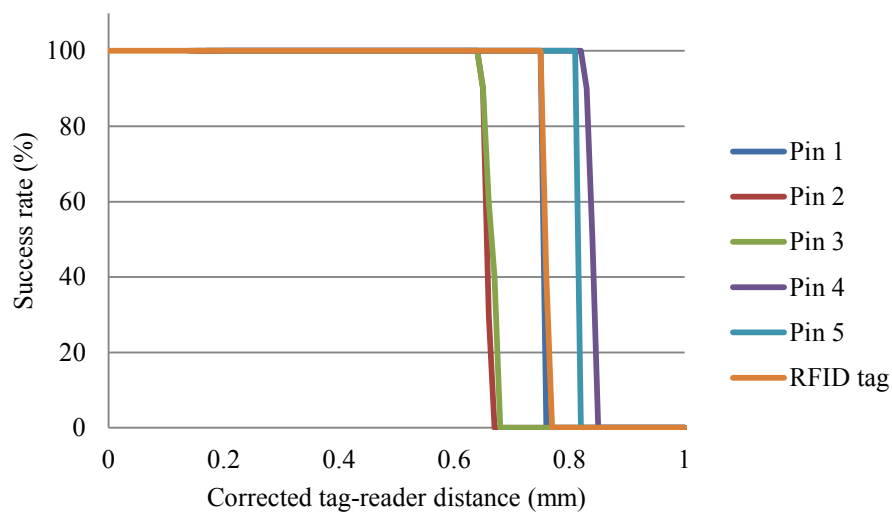


FIGURE 4. Relationship between the success rate and the tag-reader distance

CONCLUSIONS

To prevent misreading a two-dimensional barcode on the cryo-pin, we developed a new identification system using RFID tags. We manufactured a cryo-pin with a tag. The reader can be fixed on the rotation axis of the goniometer. The preliminary tests revealed a 100% success rate when the tag-reader distance was less than 0.6 mm. We are going to implement the reader on the sample rotation axis using a slip ring for long term experiments.

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REFERENCES

1. A. E. Cohen, P. J. Ellis, M. D. Miller, A. M. Deacon and R. P. Phizackerley, *J. of Applied Crystallography* 35, 720-726 (2002).
2. G. Ueno, R. Hirose, K. Ida, T. Kumasaka and M. Yamamoto, *J. of Applied Crystallography* 37, 867-873 (2004).
3. G. Snell, C. Cork, R. Nordmeyer, E. Cornell, G. Meigs, D. Yegian, J. Jaklevic, J. Jin, R. C. Stevens and T. Earnest, *Structure* 12, 537-545 (2004).
4. A. Beteva, F. Cipriani, S. Cusack, S. Delageniere, J. Gabadinho, E. J. Gordon, M. Guijarro, D. R. Hall, S. Larsen, L. Launer, C. B. Lavault, G. A. Leonard, T. Maris, A. McCarthy, J. McCarthy, J. Meyer, E. Mitchell, S. Monaco, D. Nurizzo, P. Pernot, R. Pieritz, R. G. B. Ravelli, V. Rey, W. Shepard, D. Spruce, D. I. Stuart, O. Svensson, P. Theveneau, X. Thibault, J. Turkenburg, M. Walsh and S. M. McSweeney, *Acta Cryst. D62*, 1162-1169 (2006).
5. F. Cipriani, F. Felisaz, L. Launer, J. -S. Aksoy, H. Caserotto, S. Cusack, M. Dallery, F. di-Chiaro, M. Guijarro, J. Huet, S. Larsen, M. Lentini, J. McCarthy, S. McSweeney, R. Ravelli, M. Renier, C. Taffut, A. Thompson, G. A. Leonard and M. A. Walsh, *Acta Cryst. D62*, 1251-1259 (2006).
6. L. Jacquamet, J. Joly, A. Bertoni, P. Charrault, M. Pirocchi, X. Vernede, F. Bouis, F. Borel, J. -P. Périn, T. Denis, J. -L. Rechatin and J. -L. Ferrer, *J. of Synchrotron Radiation* 16, 14-21 (2009).
7. M. Hiraki, S. Watanabe, L. M. G. Chavas, Y. Yamada, N. Matsugaki, N. Igarashi, S. Wakatsuki, M. Fujihashi, K. Miki, S. Baba, G. Ueno, M. Yamamoto, M. Suzuki, A. Nakagawa, N. Watanabe and I. Tanaka, *AIP Conf. Proc.* 1234, 673-676 (2010).
8. C. H. P. Durst, F. R. Ihmig, C. C. Fuchs, M. Biel, M. Daffertshofer and H. Zimmermann, *Proc. of I-KNOW* (2006).
9. S. Housseman, N. Absi, D. Feillet and S. Dauzère-Pérès, *Proc. of 2009 Winter Simulation Conference*, 2065-2077 (2009).
10. R. van der Togt, P. J. M. Bakker and M. W. M. Jaspers, *J. of Biomedical Informatics* 44, 372-383 (2011).
11. J. M. Ziegler and B. Simpson, *US 2007/0205899 A1* (2007).
12. G. Papp, C. Rossi, R. Janocha, C. Sorez, M. Lopez-Marrero, A. Astruc, A. McCarthy, H. Belrhali, M. W. Bowler and F. Cipriani, *Acta Cryst. D73*, 829-840 (2017).
13. G. Papp, F. Felisaz, C. Sorez, M. Lopez-Marrero, R. Janocha, B. Manjasetty, A. Gobbo, H. Belrhali, M. W. Bowler and F. Cipriani, *Acta Cryst. D73*, 841-851 (2017).