

Structural analysis of bacterial transporter protein

Taiji NAKAE*¹, Hiroyuki AKAMA¹, Hiroaki SAKAI²

¹Tokai Univ., Bouseidai, Isehara, Kanagawa 259-1193, Japan

²Osaka Univ., 3-2, Yakadaoka, Suita, Osaka 565-0871, Japan

Introduction

The MexAB-OprM efflux pump of *Pseudomonas aeruginosa* exports xenobiotic including antibiotics out of cells contributing to multiantibiotic of this hospital pathogen. The pump assembly consists of the proton conducting transporter MexB, the membrane fusion protein MexA, and the outer membrane protein OprM. [1, 2, 3]

The aim of this study is to obtain atomic level three dimensional structure of these medically important and scientifically interesting transporter proteins and contribute to understanding of multidrug resistance.

Experiments and Results

We collected the data of native crystals using an ADSC detector and synchrotron radiation with 1 Å wavelength at 100 K.

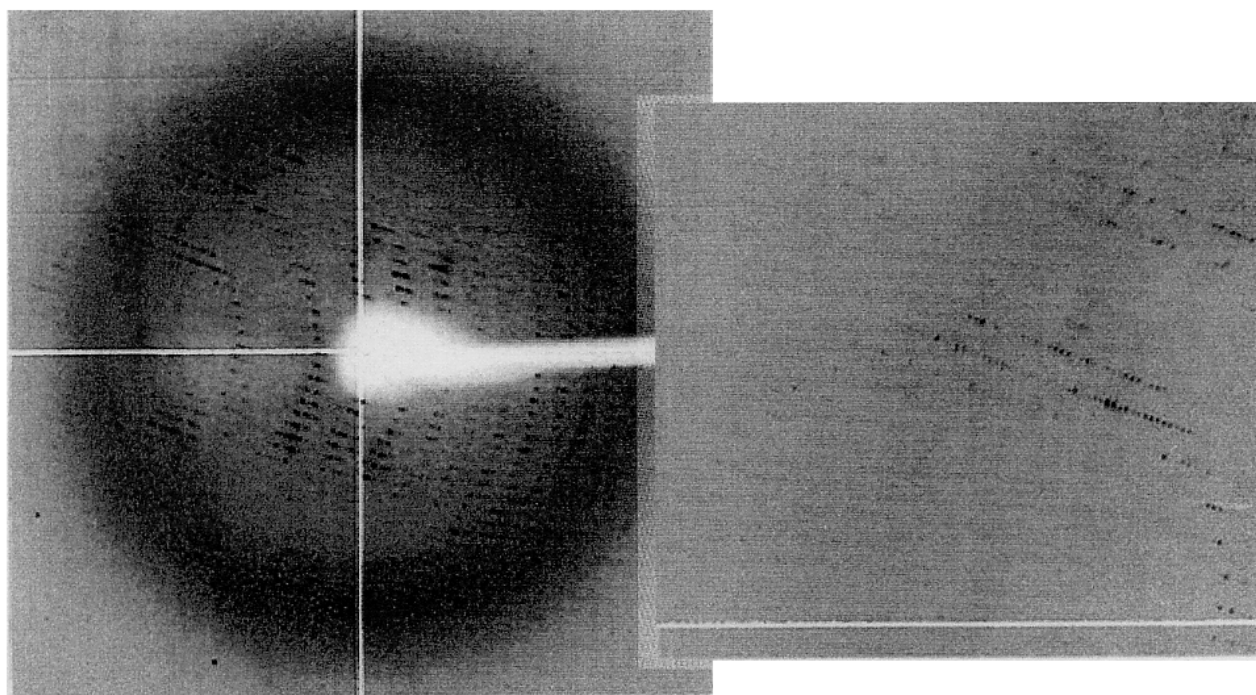
The data were processed using MOSFLM program package. OprM was belonging to monoclinic space group C2 with unit cell parameters of $a = 145 \text{ Å}$, $b = 85 \text{ Å}$, $c = 352 \text{ Å}$ and $\beta = 97 \text{ deg}$. The crystals diffracted beyond 3.5 Å, but we have been perplexed with anisotropic diffractive pattern. (figure)

The data collections and the analysis of derivative crystals is now in progress.

References

- [1] H. Yoneyama et al., J. Biol. Chem. Vol.275, No.7, pp. 4624-4638 (2000).
- [2] A. Nakajima et al., J. Biol. Chem. Vol.275, No.39, pp. 30064-30068 (2000).
- [3] L. Guan et al., J. Biol. Chem. Vol.274, No.15, pp. 10517-10522 (1999).

Figure Diffractions of OprM and this zoom-up (right).
Camera length was 350 mm.



* nakae@is.icc.u-tokai.ac.jp