Biological Science

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Structural analysis of bacterial transporter protein

Taiji NAKAE*[1], Hiroyuki AKAMA[1], Tomitake TSUKIHARA[2], Atsushi NAKAGAWA[2]
[1]Tokai Univ., 143, Shimokasuya, Isehara, Kanagawa 259-1193, Japan
[2]Osaka Univ., 3-2, Yamadaoka, Suita, Osaka 565-0871, Japan

Introduction

The MexAB-OprM xenobiotic-antibiotic exporter of *Pseudomonas aeruginosa* transports structurally and functionally diverse antibiotics and renders the cells multiantibiotic resistance. This is a large problem in hospitals. The pump consists of inner membrane spanning transporter MexB [1], periplasmic clamp protein MexA [2, 4], and the outer membrane duct protein OprM [3, 5].

An aim of this study is to reveal atomic level three-dimensional structure of these medically important and scientifically interesting transporter proteins and contribute to better understanding of the mechanism of multi-drug transport. We believed that determination of the crystal structure of MexB is medically relevant because *P. aeruginosa* often infects immunocompromised patients and shows multidrug resistance. Such study also provide impact in advancement of science because mechanism of multicomponent drug efflux system is not well understood yet.

Experiments and Results

We collected the data of MexB crystals using an ADSC Q315 detector and synchrotron radiation source with 450mm distance at 100 Kelvin. These wavelengths are 0.90000 to 1.01324Å

The data were processed using HKL2000 program package. MexB belongs to primitive hexagonal space group $P6_3$ with unit cell parameters of $a = b$ =116.8Å, c = 231.7Å, $\alpha = \beta = 90.0°$, $\gamma = 120.0°$. Detailed analysis of MexB is in progress.

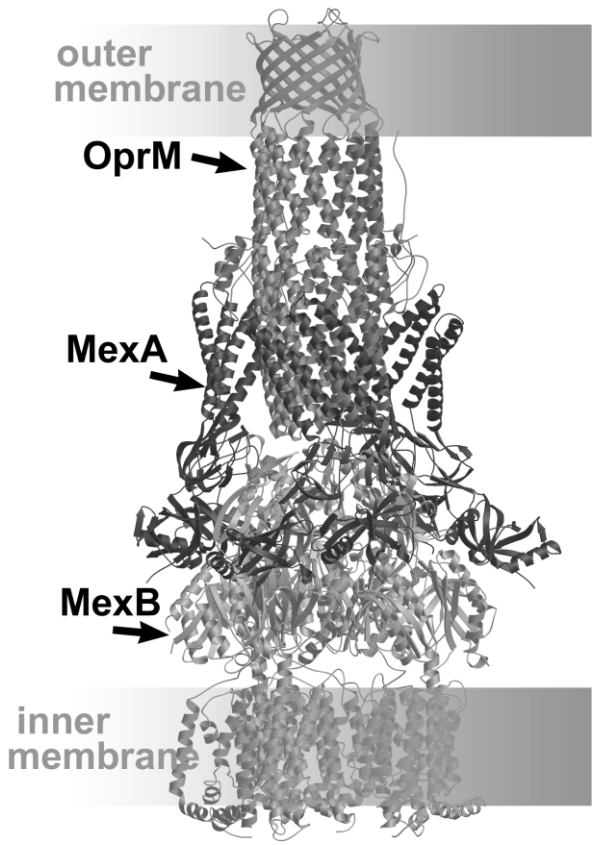

Fig.1. Fitting model of the MexA subunit with the MexB and OprM subunits. Figure shows a side-view. Structure of the OprM and MexA subunits has been solved already [4, 5]. The MexB model was simulated based on the AcrB structure of *E. coli*. Stoichiometric number of MexA, MexB and OprM is based on biochemical quantification of these subunits [6]. The α-helical hairpin domain of the MexA dimer is likely to interact with α-helix bundle of OprM, and the disordered domain of MexA, which is the most distant from the α-helical hairpin, is likely to interact with the MexB subunit by hydrophobic interaction.

References

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