



ANALYSIS OF L,D-TRANSPEPTIDASE INVOLVED IN LYSOZYME SENSITIVITY IN Corynebacterium glutamicum

<u>Akira Kumagai</u>, Masaaki Wachi; Department of Bioengineering, Tokyo Institute of Technology, Yokohama 226-8501, Japan; kumagai.a.ab@m.titech.ac.jp

Key words: Corynebacterium glutamicum, MtrAB two-component system, L,D-transpeptidase

Introduction. Corynebacterium glutamicum is a Gram-positive bacterium that belongs to the mycolic acid containing actinomycetes. C. glutamicum is widely used for industrial production of L-glutamic acid. Glutamic acid production by C. glutamicum is induced by biotin limitation, penicillin treatment or fatty acid ester treatment. All these treatments affect cell surface structures of C. glutamicum. However, the reason why these treatments induce L-glutamate production is still unclear. In this study, to clarify the relationship between the cell surface structure and the Lglutamate production of C. glutamicum, we analyzed lysozyme sensitive mutants of C. glutamicum and identified a new gene responsible for lysozyme sensitivity.

Methods. *C. glutamicum* wild-type strain KY9611 and a lysozyme sensitive mutant strain KY9708 were used in this study. Cells were grown in L medium at 30° C. Growth was monitored by measuring OD₆₆₀.

Results. C. glutamicum KY9708 was isolated as a lysozyme sensitive mutant. We found that KY9708 carries a missense mutation in the mtrB gene encoding the sensor kinase of the two component system MtrAB. The mtrB mutation in KY9708, named mtrB9708, was transferred into a wild-type strain by sacB gene mediated successive homologous recombination. The constructed defined mtrB9708 mutant strain also showed lysozyme sensitivity (Fig. 1A). MtrAB twocomponent system is known to regulate genes involved in formation of cell surface structures (1). To identify a gene(s) responsible for lysozyme sensitivity under control of MtrAB, microarray analysis was carried out. 16 genes were found, expression of which were decreased in the mutant strain compared to the wild type. We then constructed expression plasmids of these genes. As a result, it was found that plasmid expressing NCal2388 suppressed lysozyme sensitivity of the *mtrB* mutant strain (Fig. 1B). NCgl2288 gene encodes a homolog of L,Dtranspeptidase. which is involved in modification of peptidoglycan.

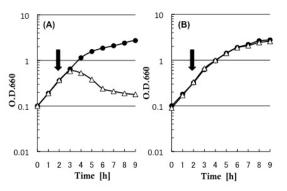


Fig.1 Suppression of lysozyme sensitivity of the *mtrB* mutant by NCgl2388. (A) mtrB9708/pECt (empty vector), (B) mtrB9708/pNCgl2388. Lysozyme (25 μg/mL) was added at 2 h. ●: control, Δ: + lysozyme.

We then constructed a NCgl2388 deletion mutant strain. As expected, the Δ NCgl2388 mutant strain also showed lysozyme sensitivity (Fig. 2).

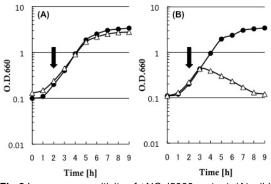


Fig.2 Lysozyme sensitivity of ΔNCgl2388 mutant. (A) wild type, (B) ΔNCgl2388. Lysozyme (25 μg/mL) was added at 2 h. •: control, Δ: + lysozyme.

Conclusions. These results indicate that NCgl2388 under control of the MtrAB twocomponent system is responsible for lysozyme sensitivity. Decreased expression of NCgl2388 may cause a defect in peptidoglycan layer, which renders cells lysozyme sensitive.

Acknowledgements. This work was supported in part by a grant-in-aid for Scientific Research (B) to M.W. from the Japan Society for Promotion of Science.

References.

1. Möker N., Brocker M., Schaffer S., Krämer R., Morbach S., Bott M. (2004) *Mol. Microbiol.*, **54**, 420-438.