DATE: Day 8 Month 5 Year 2019

SUMMARY of
2018 RESEARCH RESULTS REPORT
For International Collaborative Research with IPR, Osaka University

Research Title		Crystal structure of galactosidase from *Arabidopsis*
Applicant	**Name**	Chun-Jung Chen
	Affiliation	National Synchrotron Radiation Research Center
	Present Title	Scientist/Professor (Deputy Director)
Research Collaborator (Host PI)		Prof. Atsushi Nakagawa

Summary

Galactosidases are the initial enzyme in the metabolic pathway of the raffinose and sachyose catabolism, which catalyze the hydrolysis of the terminal linked α-1,6-galactosyl residue from galacto-oligosacharides. We have solved the structure of the enzyme at resolution 2.8 Å, which contained two molecules in one asymmetry unit. The crystal structure of the enzyme fold into three domains — the N-terminal domain, the catalytic domain and the C-terminal domain. The structures of mutant complexes with varied substrates were also determined at high resolution with the solved wild-type *apo*-structure as the search model using SPring-8 BL44XU beamline. These structural studies provide a better understanding of the key residues involved in the active site and the catalytic mechanism as well as domain functions of this enzyme.

Besides the work of galctosidases, we also published a few papers in the last project year related to previous collaborative projects based on the continuous collaboration and the provided BL44XU beamtime. The crystal structure of quinol:fumarate reductase from *Desulfovibrio gigas* provides structural insights into the electron/proton transfer pathways in bacteria (*Sci. Rep.* 8(1):14935). The various crystal structures of shrimp nodaviruses, including *Penaeus vannamei* (PvNV) and *Macrobrachium rosenbergii* nodaviruses (MrNV), reveal the mechanisms of capsid assembly, viral infection and particle polymorphism. The shrimp nodaviruses cause white-tail disease in shrimps, with high mortality. The structural insights of the shrimp nodaviruses derived from our study provide opportunities for the rational design of antivirals, such as a recombinant MrNV-LP into *M. rosenbergii* as a potential vaccine against white-tail disease (*Commun. Biol.* 2:72). On the basis of this study of nodaviruses, we recently develop a novel phasing method to obtain a non-crystallographic symmetry constraint map, which is efficient, and equivalent to a conventional non-crystallographic symmetry averaging map. Using the non-crystallographic symmetry constraint map, the structure of *T*=1 PvNV surface-domain sub-viral particle including twining data was newly determined.

***Deadline: May 17, 2019**
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