

## Poster Presentation

MS037.P11

### *Structure assembly mechanism of rice dwarf virus*

Akifumi Higashiura<sup>1</sup>, Yusuke Nakamichi<sup>1</sup>, Naoyuki Miyazaki<sup>1</sup>, Kenta Tsutsumi<sup>1</sup>, Kazuyoshi Murata<sup>2</sup>, Toshihiro Omura<sup>3</sup>, Atsushi Nakagawa<sup>4</sup>

<sup>1</sup>Institute For Protein Research, Suita, Japan, <sup>2</sup>Supportive Center for Brain Research, National Institute for Physiological Sciences, Okazaki, Japan, <sup>3</sup>National Agricultural Research Center, Tsukuba, Japan, <sup>4</sup>Institute For Protein Research, Osaka University, Suita, Japan

E-mail: atsushi@protein.osaka-u.ac.jp

Rice Dwarf Virus (RDV), the causal agent of rice dwarf disease, infects rice plants and negatively affects rice production in East Asia. RDV is transmitted to rice plants by vector insects, leafhoppers. RDV is a member of the genus Phytoreovirus of the family Reoviridae. The Reoviridae has a wide host range, including human, animals and plants. RDV has an icosahedral double-layered shell with the diameter of approximately 70 nm and contains 12-segmented double stranded RNAs (S1 to S12) as the genome. The genome encodes 7 structural (P1, P3, P5, P7, P8, P9) and 5 nonstructural (Pns4, Pns6, Pns10, Pns11, Pns12) proteins. The inner shell formed by P3 proteins contains the genome and transcription complexes (TC). The TC is composed of an RNA polymerase (P1), a capping enzyme (P5) and nucleic acid binding proteins (P7). The outer shell mainly composed of P8 proteins, and a small number of P2 and P9 proteins. P2 protein is essential for the infection of insect cells. The double shell structure, including inner capsid (P3), outer capsid (P8) and fragments of RNA binding (P7) proteins, of RDV was determined at 3.5Å resolution by X-ray crystallography[1]. This structure suggested the self-assembly mechanism of capsid proteins via both homologous and heterologous interactions. The nonstructural proteins Pns6, Pns11 and Pns12 of RDV were reported as major constituents of a viral factory, called viroplasm. The viroplasm assembles in the cytoplasm of infected cells. The replication and assembly of RDV are thought to take place inside viroplasm.

We are studying molecular mechanism of assembly of virus particle based on the atomic structures. Structures of capsid proteins (P3 and P8), the capping enzyme (P5), P2 and viroplasm major component protein (Pns12) were determined by the combination of X-ray crystallography and EM analysis. These structures, together with the intermediate state structure of virus assembly determined by cryo-EM single particle analysis, suggested the structure assembly mechanism of RDV.

[1] Nakagawa, A. et al. (2003). *Structure*, 11, 1227-1238.

**Keywords:** [X-ray crystallography](#), [Electron microscopy](#), [virus structure](#)