and those of adenoviruses or reoviruses, which invade mammalian cells, suggests that these viruses, despite evolutionary distant targets and the different chemical nature of their genomes (DNA vs RNA), might have a common ancestral gene. Results on RBPs of other lactococcal phages (bIL170 and TP901-1) will also be presented, which further illustrate the modular nature of these proteins in the viral world, and their insertion in the viral baseplate.

Keywords: receptor binding protein, bacteriophage, Lactococcus lactis

P04.13.309

Crystallization and structure determination of recombinant hepatitis E-virus-like particle

Naoyuki Miyazaki1,2,3, Che-Yen Wang2,3, Akifumi Higashiura1, Atsushi Nakagawa1, Tian-Cheng Li4, Naokazu Takeda1, Li Xing1,3, Tsukihara Tomitake1, Tatsuo Miyamura1, R. Holland Cheng2,3

1Institute for Protein Research, Laboratory of Protein Synthesis and Expression, 3-2 Yamadaoka, Suita, Osaka, 565-0871, Japan, 2Molecular and Cellular Biology, University of California, Davis, CA 95616, USA, 3Department of Biosciences at Novum, Karolinska Institute, Halsovagen 7, 14157 Huddinge, Sweden, 4Department of Virology II, National Institute of Infectious Diseases, Tokyo, Japan, E-mail: naoyukimiyazaki@protein.osaka-u.ac.jp

Hepatitis E virus (HEV) causes water-borne epidemics with a substantial mortality rate in pregnant women. It accounts for the major part of enterically transmitted hepatitis infection worldwide. The major structural protein is derived from open reading frame 2 of the viral genome, which forms the virus-like particles (VLPs) as expressed in insect cells. Single crystals of HEV-VLPs obtained by the hanging-drop vapor-diffusion methods at 293 K diffracted X-rays to 3.8 Å resolution, and the atomic structure of the HEV-VLP has been determined by phase extension from a low-resolution electron microscopy structure. The structure of the capsid protein of HEV has three domains, which exhibit similarities to the caliciviruses, agents of acute nonbacterial gastroenteritis.

Keywords: virus structure, virus coat proteins, viral structure and function

P04.13.308

Structure of the SARS coronavirus nucleocapsid protein RNA-binding dimerization domain

Chwan-Deng Hsiao, Chun-Yuan Chen, Chung-ke Chang, Tai-huang Huang

Academia Sinica, Institute of Molecular Biology, No. 128, Academia Rd. sec. 2, Nankang, Taipei, N/A, 115, Taiwan, E-mail: hsiao@gate.sinica.edu.tw

Coronavirus nucleocapsid proteins are basic proteins that encapsulate viral genomic RNA to form part of the virus structure. The nucleocapsid protein of SARS-CoV is highly antigenic and associated with several host-cell interactions. Our previous studies using nuclear magnetic resonance revealed the domain organization of the SARS-CoV nucleocapsid protein. RNA has been shown to bind to the N-terminal domain (NTD), although recently the C-terminal half of the protein has also been implicated in RNA binding. Here, we report that the C-terminal domain (CTD), spanning residues 248-365 (NP248-365), has stronger nucleic-acid-binding activity than the NTD. To determine the molecular basis of this activity, we have also solved the crystal structure of the NP248-365 region. Residues 248-280 form a positively charged groove similar to that found in the infectious bronchitis virus (IBV) nucleocapsid protein. Furthermore, the positively charged surface area is larger in the SARS-CoV construct than in the IBV. Interactions between residues 248-280 and the rest of the molecule also stabilize the formation of an octamer in the asymmetric unit. Packing of the octamers in the crystal forms two parallel, basic helical grooves, which may be oligonucleotide attachment sites, and suggests a mechanism for helical RNA packaging in the virus.

Keywords: severe acute respiratory syndrome coronavirus, nucleocapsid, viral packaging

P04.13.310

The N-terminal induced-fit loops of capsid protein of Rice dwarf virus stabilize capsid of the virus

Hisashi Naitow1, Naoyuki Miyazaki2, Tomitake Tsukihara2, Atsushi Nakagawa2, Toshihiro Omura3, Nobuo Kamiya4

1RIKEN Harima Institute / RIKEN SPring-8 Center, 1-1-1 Kouto, Sayo-cho, Sayo-gun, Hyogo, 679-5148, Japan, 2Institute for Protein Research, Osaka University, 3National Agricultural Research Center, 4Material Science & Chemistry, Graduate School of Science, Osaka City University, E-mail: naitow@spring8.or.jp

Induced-fit loops were observed in the N-terminal region of the P8 outer-capsid protein of Rice dwarf virus. In thirteen independent P8 molecules, each of the loops had a different conformation. These induced-fit loops appeared to stabilize and strengthen the binding between the respective P8 outer-capsid proteins and the P3 core-capsid protein, with the heterologous bindings, in the double-layered capsid, having disparate symmetry. Among five kinds of P8 trimmer, all the P8 proteins in the P-trimers that were located at the five-fold axes exhibited some disorder in the N-terminal region. This observation, together with the total binding energy between the P-trimer and vertical P3 and horizontal P8 was lowest among the trimers, suggests that it would be this trimer that would be released when one of the outer-capsid trimers is shed from the core particle to mediate the biological activity of the virus. In figure, the thirteen
independent P8 molecules are superimposed on one of the P3 core-capsid protein. Caα trace of the P8 molecule is shown in a stick model. Start and end of the two induced-fit loops, shown in gray stick, are indicated in terms of residue number.

Keywords: virus coat proteins, virus assembly, viral structure and function

P04.13.311

*Acta Cryst.* (2008). A64, C328

**The structure of baculovirus intracellular polyhedrin crystals reveals homoplasmy of viral polyhedra**

Fasseli Coulibaly1, Elaine Chiu1, Keiko Ikeda2, Sascha Gutmann1, Peter W Haebe1, Clemens Schulze-Briese1, Hajime Mori3, Peter Metcalf1

1University of Auckland, School of Biological Sciences, Thomas Building, 2A Symonds Street, Auckland, Auckland, 1001, New Zealand, 2Swiss Light Source at Paul Scherrer Institute, Villigen, Switzerland, 3Altana Pharma AG, Konstanz, Germany, 4Kyoto Institute of Technology, Kyoto, Japan, E-mail: f.coulibaly@ auckland.ac.nz

Because insect viruses often remain in soil or leaves for prolonged periods before finding suitable hosts, they have evolved different strategies to preserve their infectivity in such conditions. The most striking of these survival strategies are polyhedra, crystals of the viral polyhedrin protein which form a tough matrix protecting virus particles. Virus particles embedded in polyhedra can remain infectious for decades in the soil but, once ingested by new larvae, polyhedra readily dissolve in the alkaline environment of mid-guts initiating a new infectious cycle. Recently, the first atomic structure of polyhedra revealed the architecture of such infectious crystals produced by the silkworm cyivirus, a RNA virus belonging to the Reoviridae family. To understand how this strategy evolved in the viral world, we have engaged in the structural analysis of polyhedra produced by baculoviruses, DNA viruses completely unrelated to cyivirus. I will present the 2.3Å structure of baculovirus polyhedra determined by X-ray crystallography from crystals 5-10 micrometers in diameter purified from infected cells. These crystals belong to the P23 space group with cell edge parameters of 103Å, just like cyivirus polyhedra. They are also made of polyhedrin trimers and extremely dense and robust except in alkaline conditions. Despite these functional and structural similarities, baculovirus and cyivirus polyhedrin proteins are unrelated and the way they pack in polyhedra is strikingly different. This evolutionary convergence to very similar crystalline architectures from different building blocks is reminiscent of the wide use of the icosahedral symmetry in virus particles.

Keywords: apoptosis, protein homology, viral protein

P04.13.313


**Structure of influenza H5N1 nucleoprotein and its interaction with RNA**

Pang-Chai Shaw1, Andy Ka-Leung Ng1, Hongmin Zhang2, Jiahui Wang2, Kemin Tan3, Shannon Wing-Ngor Au1

1Chinese University of Hong Kong, Department of Biochemistry, The Chinese University of Hong Kong, Shatin, Hong Kong, NT, China, 2Department of Medical Oncology, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, USA, 3Midwest Center for Structural Genomics and Structural Biology Center, Argonne National Laboratory, Argonne, IL, USA, 4Department of Microbiology, The Chinese University of Hong Kong, Shatin, Hong Kong, NT, China, E-mail : pshaw@cuhk.edu.hk

Influenza is a contagious respiratory illness causing annual epidemics. The threat of a pandemic outbreak of influenza virus H5N1 has become a major concern worldwide. The nucleoprotein (NP) plays both structural and functional roles in influenza viruses and represents an attractive drug target. Here we report the 0.33nm crystal structure of H5N1 NP, which is composed of a head domain, a body domain and a tail loop. Our structure resolves the important linker residues (residues 397-401, 429-437) that connect the tail loop with the remainder of the molecule and a flexible, basic loop (residues 73-91) located in an arginine-rich groove surrounding Arg150. Using surface plasmon resonance, this basic loop and arginine-rich groove, but mostly a protruding element containing Arg174 and Arg175, were found to be important in RNA binding. A possible mechanism by which NP associates with RNA is as follow. First, the flexibility of the basic loop (residues 73-91) may allow it to sample the environment and capture RNA. The captured RNA could

C328