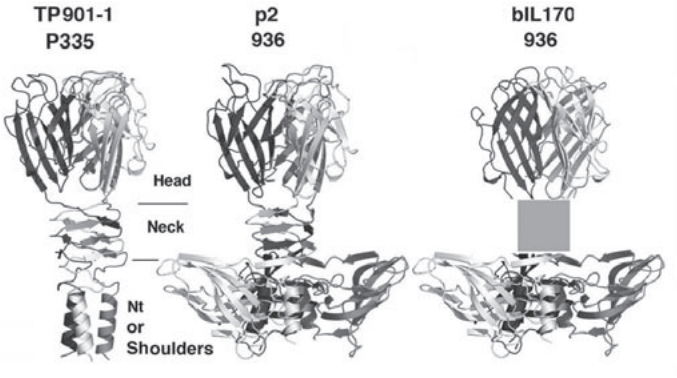
and those of adenoviruses or reoviruses, which invade mammalian cells, suggests that these viruses, despite evolutionary distant targets and the different chemical nature of their genomes (DNA vs RNA), might have a common ancestral gene. Results on RBPs of other lactococcal phages (bIL170 and TP901-1) 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*

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

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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), had 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

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

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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

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

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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 trimer, 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