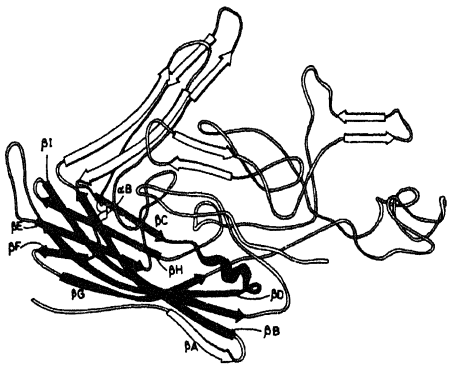

Figure 1. Ribbon drawing of the three-dimensional fold of canine parvovirus VP2. The secondary-structure elements have been identified by correspondence to those of the plant virus, southern bean mosaic virus. The shaded region corresponds to the eight-stranded β-barrel motif found in the coat protein structures of most of the plant and animal icosahedral viruses. [Redrawn from the original with permission from Prof. M. G. Rossmann, © American Association for the Advancement of Science.]

of other spherical viruses. However, this motif is only a third of the VP2 protein and the remaining part of the polypeptide folds into a mostly irregular structure. Similar large-scale unordered structures are not usually observed in the folded structure of globular proteins. Surprisingly, this structure appears as an insertion between the β-strands β-G and β-H and consists of 219 residues. This region also corresponds to the 'FMDV loop' of animal picornaviruses. These similarities in the polypeptide folds of different viruses are meaningful in terms of plant and animal virus evolution.

The organization of the protein on the surface of the virus creates 22-Å-long, 70-Å-wide protrusions on the icosahedral threefold axes, and 15 Å depressions on the twofold axes. Cylindrical structures around icosahedral 5-folds are surrounded by 15-Å-deep 'canyons'. In anology with rhinoviruses, the structure of which was also determined by the Rossmann group a few years ago, the authors suggest that the canyon near the icosahedral 5-folds might be the site of receptor attachment. Rhinoviruses are resposible for common cold in humans. According to the 'canyon hypothesis' (Figure 2) proposed by the Rossmann group, the receptor-recognition site, where residues must be conserved to allow virus particles to continue to bind cell-surface receptors of susceptible cells, is deeply buried inside the canyon or pit and is inaccessible to antibody molecules. The residues accessible to antibody molecules are on the surface of the virus and do not participate in recognition. Random mutations at these sites can lead to the evolution of new serotypes. These findings on receptor recognition and our understanding of mechanisms of immune surveillance hold promise for design of rational drugs targeted against residues lining the canyon floor. Another interesting feature of this work is the observation of partially ordered nucleic-acid structure. Approximately 13% of the ss-DNA genome is icosahedrally ordered and is visible in the electron-density map. Each protein subunit appears to be in an invariant contact with 11 nucleotides. This is the second clear example of ordered nucleic acid in icosahedral virus particles. However, the functional implications of ordered nucleic-acid structure is not yet clearly understood.

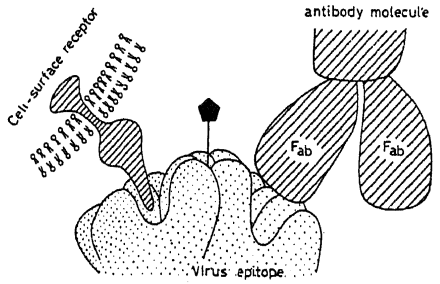

Figure 2. The 'canyon hypothesis' provides a mechanism by which picornaviruses are believed to evade the host immune system. The receptor-binding site is deeply buried on the surface of the virus and hence binding of the large antibody molecules to the site is sterically hindered. New serotypes evolve by mutation of residues outside the canyon. [Reproduced with permission from Prof. M. G. Rossmann, © American Association for the Advancement of Science.]

The three-dimensional structure of canine parvovirus will provide a firm foundation for designing future experiments to elucidate the receptor-recognition and antigenic sites of parvoviruses.

1. Tsao, J. *et al.*, *Science*, 1991, **251**, 1456.

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