The organization of the protein on the surface of the virus creates 22Å-long, 70Å-wide protrusions on the icosahedral threefold axes, and 15Å depressions on the twofold axes. Cylindrical structures around icosahedral 5-folds are surrounded by 15Å-deep 'canyons'. In analogy 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 responsible 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.

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.


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