diffraction data. The data collection was performed at Station X7 using X-rays of 1.08 Å wavelength. The diffraction patterns were recorded on the newly installed image plate system made by Mar research. A total of abot 50 useful images were processed and the space group of the crystals was determined as C2, a=575.4Å, b=323.7Å, c=558.4Å, β=108.5°. There is a whole virus particle in the asymmetric unit, which results in a 60 fold nonocrysatllographic averaging in phase determination by the molecular replacement method. About 50% unique data were collected to 3.5Å resolution and the Rmerge was 11.5% for data with $I/\sigma>2.0$. A locked rotation function was calculated using data to 4.0 Å resolution and the virus orientation was clearly identified in the unit cell. Work is now continued on the translation of the virus particles in the unit cell. Once the position of the virus particles is known, phases could be first derived from the BeAn coordinates and improved by electorn density averaging over the 60 fold noncrysatllographic symmetry. The final structure of GDVII will reveal the differences between the highly-viruslent group and the persistent group on the capsid. We shall learn more about the relationship bewteen virus infection and demyelination and persistence infection.

MS-03.02.03 STRUCTURE OF THE VIRION AND EMPTY CAPSIDS OF A22 IRAQ 24/67 FOOT-AND-MOUTH DISEASE VIRUS. By S. Curry*, R. Abu-Ghazaleh, W. Blakemore, E. Fry†, T. Jackson, A. King, S.Lea†, J.Newman, D. Stuart†. AFRC Institute for Animal Health, Pirbright Laboratory, Pirbright, Woking, U.K. †Laboratory of Molecular Biophysics, Oxford University, U.K.

We have crystallized and determined the three-dimensional structure of A22 Iraq 24/64 foot-and-mouth disease virus (FMDV). We now have representative structures of at least one subtype from three of the seven serotypes defined for FMDV. The results of the structural analysis of A22 Iraq confirm and extend the findings from the comparison of O and C type viruses.

A22 Iraq crystallized in space group I222; a data set 70% complete to 3Å was collected. Structure factors were phased using a partially refined model of $A10_{61}$ (Fry, E. *et al.* unpublished) FMDV and a $2|F_O| - |F_C|$ electron density map was calculated at 3Å resolution. This map, averaged over the fifteen protomers in the asymmetric unit, was of high quality and enabled an initial model to be built. Refinement is in progress.

Preliminary analysis of the structure reveals that structural differences between A22 Iraq and other serotypes are confined to external loops. As observed for O1BFS (Acharya, R. *et al.* (1989), *Nature (London)*, **337**, 709-716.) and CS8-c1 (Lea, S. *et al.* manuscript in preparation) FMDV, the longest surface loop which connects strands G and H of the beta-barrel core of VP1 is largely disordered. This GH loop is an important antigenic feature and also implicated in binding to the cellular receptor. The mobility of this feature appears to be strongly conserved in FMDV. The implications of this finding will be discussed. Elsewhere on the surface of the virion there are shifts of several Ångströms in the positions of surface oriented loops. Moreover, there is evidence that structural alterations in one loop due to sequence variation can affect the conformation of adjacent loops. This structural information is being used to interpret the large amount of serological data available for serotype A FMDV.

Empty capsids of FMDV lack the genomic RNA and are reported also to lack the cleavage of the precursor VP0 into VP2 and VP4 which is simultaneous with encapsidation and contributes to the stability of the virion. In order to probe both the mechanism of VP0 cleavage and the RNA-protein interactions on the interior of the capsid, we have determined the structure of empty capsids of A22 Iraq. Curiously, in these capsids VP0 has largely been cleaved into VP2 and VP4. Our investigation into the reasons for this finding will be presented.

Empty capsids crystallized isomorphously with the virus. A difference map revealed that the external surface structures of the virus and empty capsid are identical. However, on the interior surface the n-termini of VP1 and VP2 and the c-terminus of VP4 appear to be disordered in the empty capsid relative to the virus. These termini are all close to the interface between pentameric subunits which are assembly intermediates in FMDV. The presence of RNA in the virus appears to be necessary to stabilize these portions of the capsid polypeptides.

MS-03.02.04 THE STRUCTURE OF CANINE PARVOVIRUS. By Hao Wu*, Jun Tsao, Michael Chapman, Walter Keller, Mavis Agbandje, and Michael Rossmann, Dept. of Biol. Sci., Purdue University, West Lafayette, IN, 47907. *Current address: Dept. of Biochem. and Mol. Biophys., Columbia University, New York, NY 10032.

The structures of canine parvovirus (CPV) full and empty particles have been determined to atomic resolution. The structure of CPV empty capsid has also been refined recently.

Each subunit of the virus possesses an anti-parallel β barrel motif that has been found in most viruses whose structures are known. On the viral surface, there are canyons around the fivefold axes and prominent spikes at the three-fold axes. With analogy to Rhinovirus14, the canyons might be the receptor binding sites. Residues related to the antigenic properties as well as the host range determinants of the virus are found on the threefold spikes. Extensive interactions are observed among the threefold related subunits. Five β hair-pins at each fivefold axis make up a β cylindrical structure. A substantial volume of electron density is shown to be DNA, corresponding to about 13% of the virus genome. Different protein conformations are observed at the region where DNA binds.

MS-03.02.05 STRUCTURAL STUDIES OF TYPE B NEURAMINIDASE. By Clinton L. White*, Musiri N. Janakiraman, W. Graeme Laver, Gillian M. Air and Ming Luo; Center for Macromolecular Crystallography, University of Alabama at Birmingham, Birmingham, Alabama, USA.

