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Report:

The analysis is not finished. We include here a preliminary abstract submitted to the IUCr XVII @ Seattle

We are studying the structures of some orbiviruses. These are animal viruses, which belong to the same family as the better known rotaviruses and reoviruses, which cause significant human disease ¹. Bluetongue virus is the classic orbivirus; it has a proteinaceous capsid from which an outer layer can be stripped away to reveal a 700 Å core particle². The core is robust and penetrates the host cell intact, it contains a small number of proteins with enzymatic activity and much larger numbers of VP3 and VP7. VP7 forms the outer surface of the core and is present at the level of 780 copies per core, arranged on a T= 13 lattice².

We have determined, by X-ray crystallography, a number of structures of this molecule³ (Grimes *et* al., unpublished). We have combined the information from the X-ray structures of VP7 with that from electron cryomicroscopy (Prasad, unpublished) and used simple fitting procedures to place the X-ray structure in the EM map.

We have separately crystallized the whole core of 2 serotypes: BTV-1 and BTV- 10. BTV-1 crystallized in space group P2₁2₁2, a=798Å, b=825Å, c=756Å, BTV- 10 crystallized in space group P4₁2₁2, a=b=1120Å, c=1592Å. Data have been collected at the SRS (UK) & ESRF (Fr) for BTV-1 and at the ESRF for BTV- 10. Both structures have been solved at low resolution using the cry-em phasing model.. The resolution is being extended for both structures and the unusual architecture will be discussed.

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- [3] Grimes, J., Basak, A., Roy, P. and Stuart, D. Nature, 373, 167-170 (1995)
- [5] Burroughs, N., Grimes, J., Mertens, P. and Stuart, D. *Virology*, *210*, 217-220, 1995