

The cryo-EM structure of the Broad Bean Stain Virus reveals a common capsid assembly mechanisms among comoviruses

LAI KEE HIM, J.¹, LECORRE, F.¹, ZEDDAM, J.², BLANC, S.², TRAPANI, S.¹ and BRON, P.¹

¹ Centre de Biochimie Structurale - CNRS 5048 - INSERM U1054 - Montpellier, France, ² Biologie et Génétique des Interactions Plante-Parasite - INRA - Montpellier, France

The *Broad bean stain virus* (BBSV) is a seed-borne virus that infects *Fabaceae*, causing severe and widespread disease in Europe, North Africa, Asia, Middle East and Australia. The symptoms range from mild to severe and occasionally inducing plant death. BBSV is part of the *Comoviridae* subfamily. It has a bipartite, positive-sense and single-stranded RNA genome. The two segments, RNA-1 and RNA-2, are separately encapsidated in icosahedral particles that have a maximum diameter of about 30 nm and comprising of 60 copies of large and small coat proteins. The RNA-2 codes for the two capsid proteins, which are processed by the action of the RNA-1-encoded proteinase. In this context, we have investigated the structural organization of the coat protein of BBSV by cryo-electron microscopy and single particle analysis. We present here the cryo-electron microscopy density map of the BBSV at 3.8 Å resolution, allowing us to compute the atomic model of the capsid protein giving access notably to residues involved in RNA/capsid interactions. The structural analysis of the C-terminal domain of the small coat protein reveal a maturation cleavage between Leu567 and Leu568 and interactions with different parts of neighbouring small coat protein at the level of the pentameric turret. This specific interaction pattern previously identified as key in the assembly of the *Cowpea mosaic virus* is then present in other comoviruses suggesting a common capsid assembly mechanism throughout all comovirus species.