Although the viruses are quite different in many of their properties, the polypeptide topologies of their surface domains are quite similar. The major technological advances which have made it possible to determine structures with molecular weights in the range of 2 to 10 \(^{10}\) have been:

1. commercially available and reliable rotating anode generators, now being augmented by synchrotron sources, to generate high intensity X-rays,
2. fine-focusing X-ray sources and focusing mirrors to obtain the necessary resolution of Bragg maxima for very large unit cells,
3. the development of oscillation photography in conjunction with fast film scanners to measure hundreds of thousands of reflections while the crystal is rapidly decaying due to radiation damage; and
4. the molecular replacement method which utilizes the non-crystallographic symmetry of viruses to help in the determination of heavy atom positions and to greatly improve the accuracy of phase determination.

Both TBSV and SBM\(\text{V}\) have an external diameter of around 300 \(\text{\AA}\) and a protein coat of 30 \(\text{\AA}\) or more thickness. Their interior is filled with RNA. The 180 protein subunits per virus have icosahedral symmetry. Although the viruses are quite different in many of their properties, the polypeptide topologies of their surface domains are remarkably similar. TBSV possesses an additional protruding domain. Investigation of other viruses such as satellite tobacco necrosis virus (Lunge et al., Nature, 285, 373-377, 1980) will help to show whether this remarkable similarity is the result of divergence from a primordial plant virus or of constraints required for self-assembly into an icosahedral particle.

The basic amino terminal arm of SBM\(\text{V}\), TBSV and many other spherical and bacilllius-shaped plant viruses is intimately involved in RNA interaction and the assembly of the protein subunits into a coat of appropriate diameter. The surface domain of SBM\(\text{V}\) is an eight-stranded anti-parallel 8-barrel. Protein-protein interactions are mediated by the binding of cations and hydrophobic interactions. Removal of calcium causes the virus to swell and then disassemble. Protein-nucleic acid interactions are also enhanced by a basic surface on the interior of the surface domain.

Anomalously scattering effects are also a promising tool in membrane structure research, as is apparent from investigations going on at SSRL (Stanford, USA) and EMBL (Heidelberg, Germany). It also may have an impact on fibre diffraction.