Plant virus structures. A touch of local colour

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The first high resolution structures of crystalline RNA viruses appeared almost fifteen years ago The characterization of tomato bushy stunt virus[1] and the 17-fold double disc of tobacco mosaic virus coat protein[2] at near-atomic resolution (2.9 Å) is a landmark in virology and structural biology. Since then, major advances in X-ray crystallographic techniques, particularly the availability of synchrotron sources, coupled with the explosive growth of computing power, needed to process and analyse vast amounts of diffraction data, have permitted the structure determination of over a dozen other RNA viruses[3,4]. The spherical, RNA plant viruses appear to be constructed using very similar design principles, with the virions having icosahedral symmetry, containing sixty identical asymmetric units. Most often, the asymmetric units contain three copies of a single protein, each residing in a slightly different environment. All the six RNA plant viruses characterized so far have been isolated in the temperate zones of the world (northern Europe and north America). Subramanya *et al.*[5] now report the first structure of a RNA plant virus isolated from the tropics.

Sesbania grandiflora, a plant occurring in fields around the temple town of Tirupati in Andhra Pradesh, is often afflicted by a mosaic disease (Figure 1), caused by a virus first isolated by Sreenivasulu and Nayudu[6], working at the Botany Department of S. V. University, Tirupati. A partial sequence determination of the 31 kDa coat protein from sesbania mosaic virus (SMV) has revealed an amino acid identity of 69% (109 out of the 159 residue determined so far) with the protein of the cowpea strain of southern bean mosaic virus (SBMV)[5]. The structure of the sesbania virus, SMV, at 4.7 Å is now revealed by the crystallographic work of Subramanya and Murthy[5], at the Indian Institute of Science, Bangalore. Working with crystals in the rhombohedral space group R3, using three-dimensional X-ray diffraction data collected using an area detector and employing molecular replacement procedures involving the known SBMV structure[7], these authors have obtained an electron density map, which permits clear tracing of the three independent polypeptide chains of the coat protein (Figure 2). The polypeptide fold is very similar to that of the previously determined SBMV protein[7]. Even at the moderate level of resolution of the SMV structure, most aromatic side-chains can be clearly identified. The most striking finding is the identification of four icosahedrally independent sites, which may correspond to cation binding positions. Three of the sites are in locations similar to that observed in the structures of related viruses, SBMV and tomato bushy stunt virus (TBSV). The remaining site is, however, at a location in which the closest residue in SBMV is isoleucine, whose hydrocarbon side-chain is incapable of cation coordination. Interestingly, this residue has been mutated to aspartic acid in SMV. The cation at this site bridges three nearly parallel helices from the three subunits, leading the authors to speculate that helical dipoles might contribute to stabilization of the bound cation. Many spherical plant viruses swell on treatment with EDTA, presumably due to a leaching out of the bound cation resulting in altered subunit interactions. Future structural work might address the precise nature of the swelling process, which may be of importance in the life cycle of the virus. The clarification of the issue of whether the SMV and SBMV structures differ in other significant ways must await extension of the SMV structure to higher resolution.

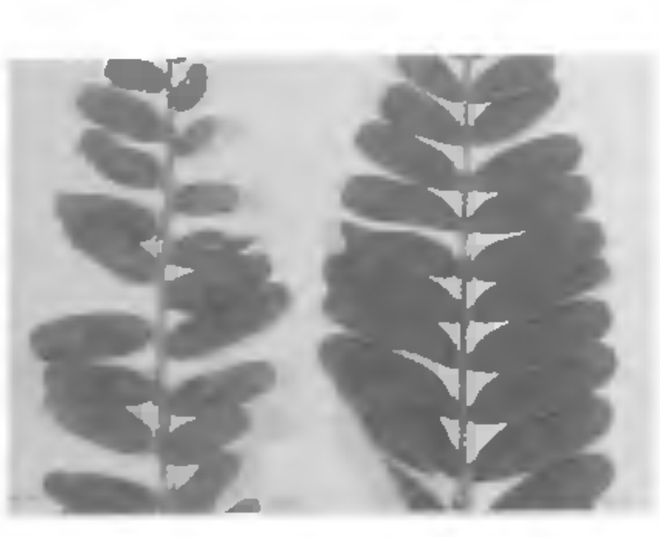

Figure 1. Typical symptoms elicited on *Sesbania grandiflora* plants by sesbania mosaic virus infection, (left) infected plant, (right) normal plant

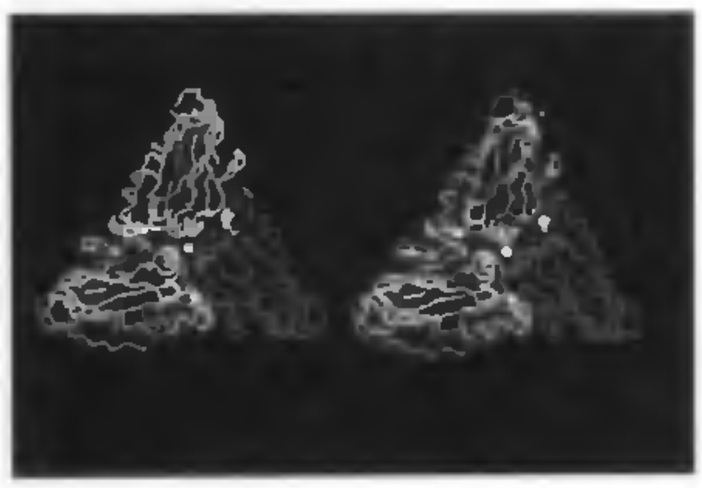

Figure 2. Stereodiagrams of the polypeptide fold of the protein subunits in one icosahedral asymmetric unit of sesbania mosaic virus particle The spheres corresponds to the positions of divalent cations Structure determination of the demetallized virus particle shows that only one of the three cations (cation between blue-red subunit interface) related by quasi three-fold axis is effectively removed by EDTA treatment Figure provided by H S Subramanya and M R N Murthy

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