Structural Aspects of Recognition
and Assembly in Biological Macromolecules
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RECOGNITION AND SPECIFICITY IN ASSEMBLY OF ICOSAHEDRAL VIRUSES: TBSV AND TCV

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SUMMARY

There are at least three essential problems of recognition in assembly of simple, RNA-containing icosahedral viruses: (1) correct inter-subunit non-covalent bonding; (2) correct variation of this bonding according to position in the structure in order to satisfy quasi-equivalence; (3) recognition of viral RNA. The structures of tomato bushy stunt and turnip crinkle viruses (TBSV and TCV, respectively) show how the design of a protein subunit can meet these structural requirements. The fundamental motif is one of flexibly connected, specifically folded domains. Each of the two principal domains (denoted "P" and "S") that form the tightly bonded viral shell folds around a "classical" hydrophobic core and presents both polar and non-polar residues for contact with neighboring subunits. Striking features of contacts that have more than one state (i.e. where homologous surfaces approach each other differently in quasi-equivalent positions) are extensive patches of H-bonds and salt bridges, demarcated by strips of non-polar residues. One important S-domain contact appears to contain two neighboring sites for divalent cations, with ligands from both apposed subunits. These sites are probably the locus of divalent-cation controlled alkaline expansion of TBSV and TCV particles, which occurs at pH 7 when such cations are absent. The N-terminal portion of the molecule is particularly remarkable. The proximal 35 residues, spatially disordered on 120 of the 180 subunits, form an extended structure on the remaining 60. The interdigitation in sets of three of these extended arms determines the size and curvature (triangulation number) of the shell. There is evidence that the distal 70 residues (the extreme N-termunus) fold into a relatively compact domain with a role in RNA binding. This part of the subunit is always spatially disordered and cannot be seen in a high resolution electron-density map.