

Satellite Tobacco Mosaic Virus: An All-Atom Three-Dimensional Model.

... then a surprise ...

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The X-ray crystal structure of STMV revealed a structure containing 30 double-helical RNA segments, with each helix having nine base pairs and an unpaired nucleotide at the 3' end of each strand. Based on this structure, Larson and McPherson proposed a model of 30 hairpin-loop elements occupying the edges of the icosahedron and connected by single-stranded regions (*Curr Opin Struct Biol* 11:59-65 (2001)). More recently, Schroeder *et al.* (*Biophys J* 101:167-175 (2011)) have combined the results of chemical probing with a novel helix searching algorithm to propose a specific secondary structure for the STMV genome, compatible with the Larson-McPherson model. I will discuss our all-atom model of STMV, which includes the complete protein and RNA sequences and the Schroeder RNA secondary structure (Zeng *et al.*, *J Struct Biol*, in press (Oct 2012)). As far as we know, this is the first all-atom model for the complete structure of any virus.

We have recently determined the secondary structure of the STMV RNA genome, transcribed *in vitro*, using SHAPE probing. I will present this structure, compare it with the secondary structure model of Schroeder *et al.* (which was based on chemical probing in partially disrupted viruses), and discuss the implications for the assembly of STMV.