



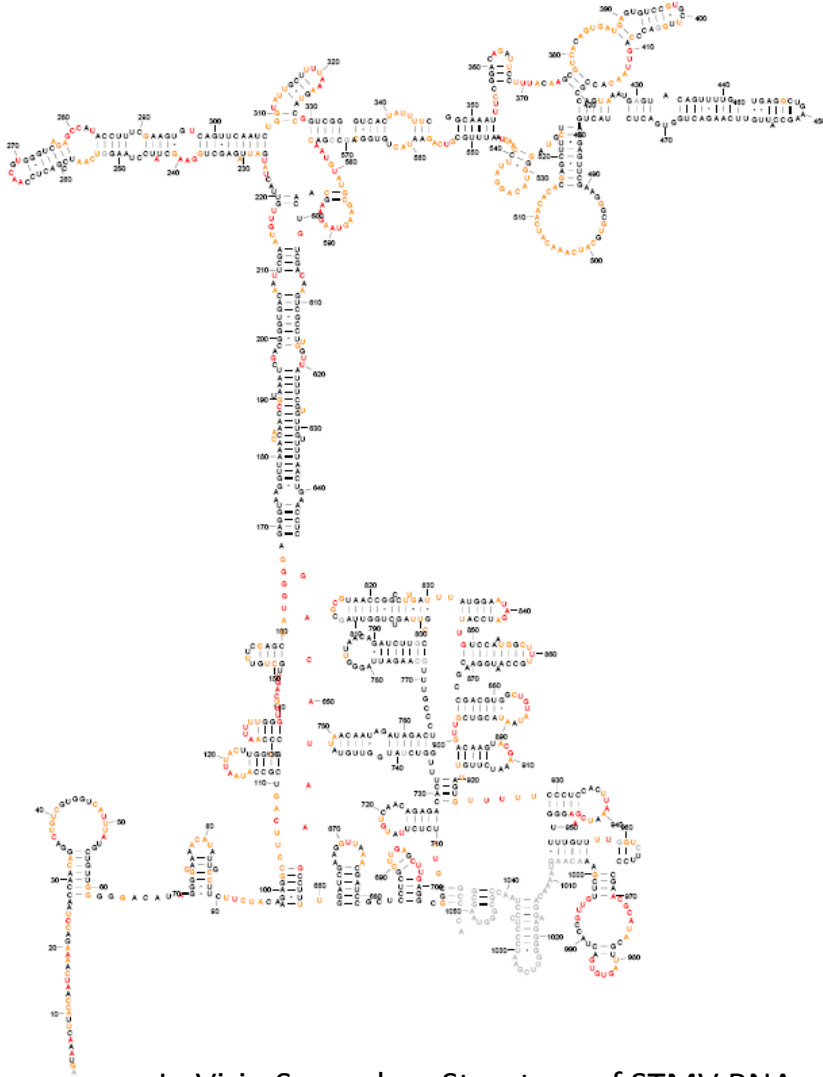
## Background

- RNA forms complex secondary structures including various functional domains
- SHAPE chemistry gives reactivity data that is used with folding programs to create structures for biological RNAs
- There are hypothesized structural changes of the RNA genome structure inside versus outside the viral capsid
- Existing model potentially identify 30 helices of 9 base pairs each that interact with the sides of the icosahedral protein coat.

## Goals

- Determine the secondary structure of the very 3' end of the RNA using Locked Nucleic Acids in a specially designed primer
- Modify existing protocol and carry out SHAPE experiments to obtain nucleotide reactivity inside the viral capsid
- Compare in virio and ex virio structures to existing models

# Results



In Virio Secondary Structure of STMV RNA

- In Virio structure is consistent with three pseudoknots in the 3' region
- Major Y-structure is conserved from ex virio to in virio
- 19 out of 30 capsid-binding helices identified
- Less local base pairing than in prior models