

Electrostatic theory of viral self-assembly

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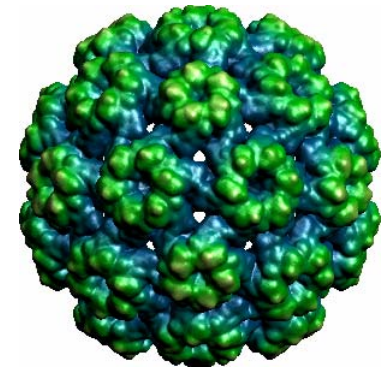
Outline

- Optimization of viral structure stability
- Kinetics of viral self-assembly

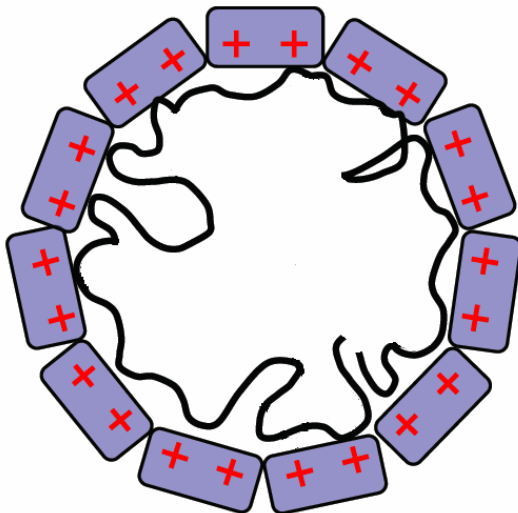
Icosahedral viruses

- Self-assembly from a solution of capsid proteins and ss RNA.
- The number of capsid proteins is $60T$, $T=1, 3, 4, 7, \dots$
- The absolute value of ss RNA charges is approximately twice larger than the total capsid charge.

CCMV (T=3)

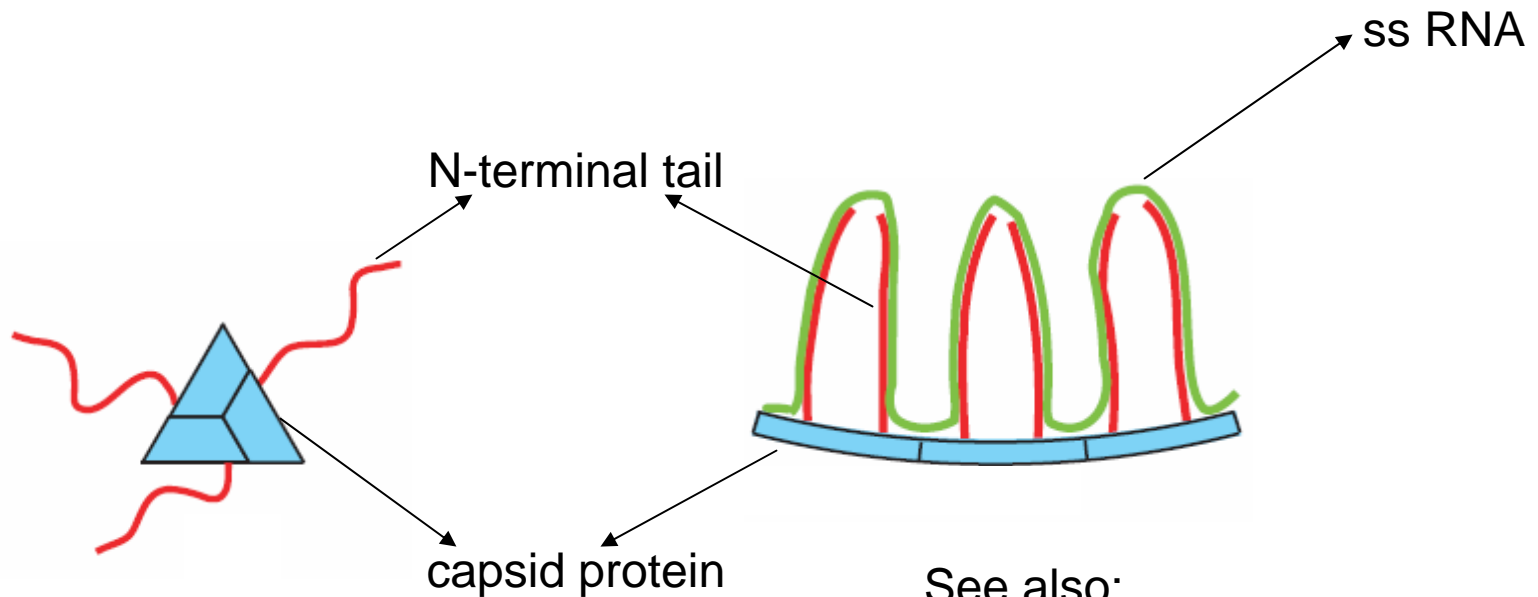


<http://viperdb.scripps.edu/>



P. van der Schoot and R. Bruinsma,
Phys. Rev. E 71, 061928 (2005).

For many viruses the capsid protein has long N-terminal tail, which carries all positive charge.

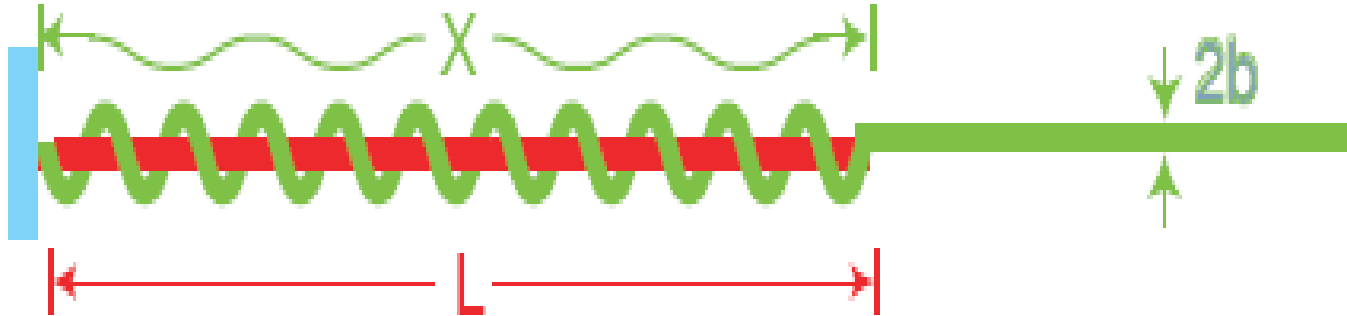


See also:

V. A. Belyi and M. Muthukumar,
PNAS 103, 17174 (2006)

Virus	Q_r	q_p	q_t	N_t	η_r / η_t	N_d / N_t	R	R
							(exp)	(theor)
Brome Mosaic	3030	10	9	48	2.8	0.44	1.7	2.8
Cowpea Chlorotic Mottle	2980	7	9	49	2.8	0.63	2.4	2.8
Nodamura	4540	13	18	52	1.5	0.79	1.9	1.8
Pariacoto	4322	13	14	47	1.8	0.61	1.8	1.9
Sesbania Mosaic	4149	6	6	57	5.0	0.89	3.8	5.0
Rice Yellow Mottle	4450	17	12	52	2.3	0.79	1.5	2.3
Southern Bean Mosaic	4136	16	14	58	2.2	0.89	1.4	2.2
Cocksfoot Mottle	4082	15	13	54	2.2	0.88	1.5	2.2
Average	3944	12	12	52	2.6	0.74	2.0	2.6
Cucumber Mosaic	3214	15	12	66	2.9	0.59	1.2	2.9
Tomato Aspermy	3391	14	12	67	2.9	0.55	1.3	2.9
Carnation Mottle	4003	10	11	81	3.9	1.00	2.2	3.9
Tobacco Necrosis	3700	9	10	79	4.1	0.90	2.3	4.1
Tomato Bushy Stunt	4776	12	13	92	3.7	0.91	2.2	3.7
Average	3817	12	12	77	3.5	0.79	1.8	3.5

N-terminal tail overcharged by ss RNA (with total length S)



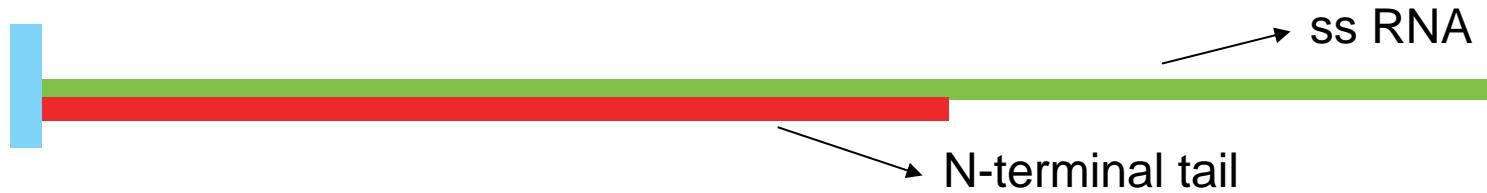
$$\text{Free energy: } F(X) = L \left(\frac{-X\eta_r + L\eta_t}{L} \right)^2 \ln \left(\frac{r_s}{b} \right) + (S - X)\eta_r^2 \ln \left(\frac{r_s}{b} \right)$$

Optimize $F(X)$ with respect to X

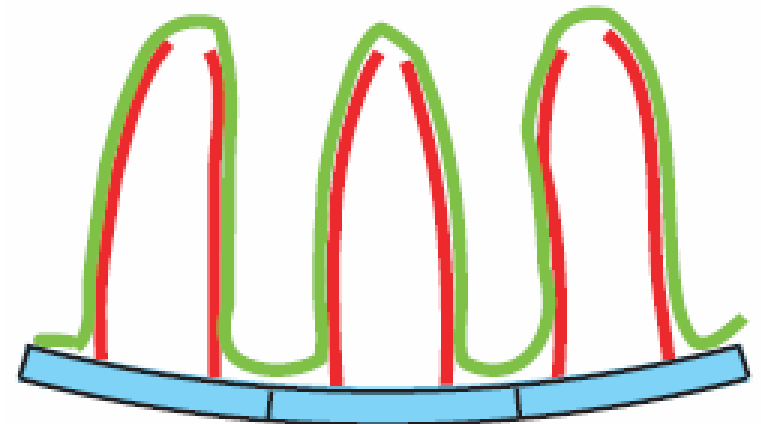
At $\eta_r / \eta_t < 2$ ss RNA wraps around the N-terminal tail

$$X = (\eta_t / \eta_r + 1/2)L$$

At $\eta_r / \eta_t > 2$ both polymers are stretched



Viruses are most stable when the total contour length of ss RNA is close to the total length of the tails.



Virus	Q_r	q_p	q_t	N_t	η_r / η_t	N_d / N_t	R	R
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Very long tails



$$\eta_t^* \sim 2\eta_t,$$

$$R_{\text{theor}}^* \sim R_{\text{theor}} / 2$$

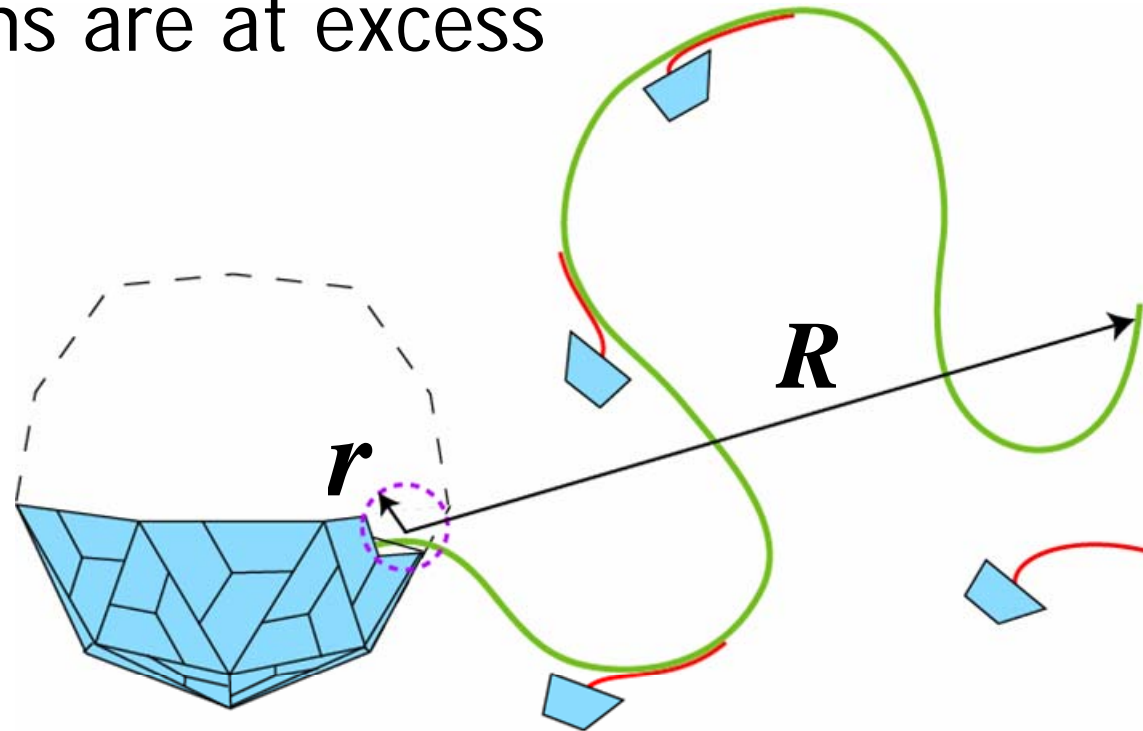
The ss RNA speeds up the self-assembly when the capsid proteins are at excess

Without antenna:

$$J_3 = 4\pi Dcr$$

With antenna:

$$J = 4\pi DcR$$



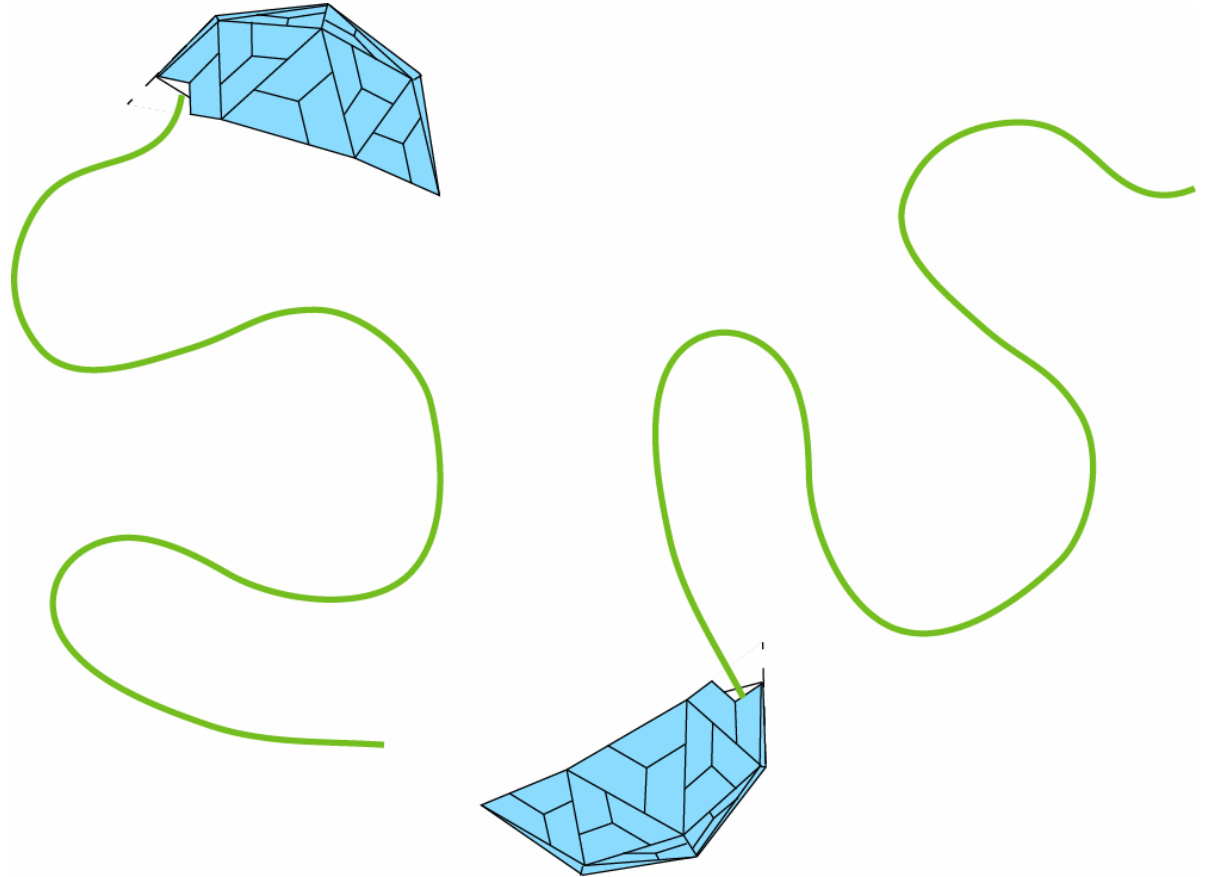
For a typical T=3 virus
 ss RNA ~ 3000 bases ~ 2100 nm
 radius of antenna R ~ 60 nm
 size of capsid protein r ~ 4 nm
 number of proteins M = 60T = 180

$$\tau_a = \tau_0 (r / R) = \tau_0 / 15$$

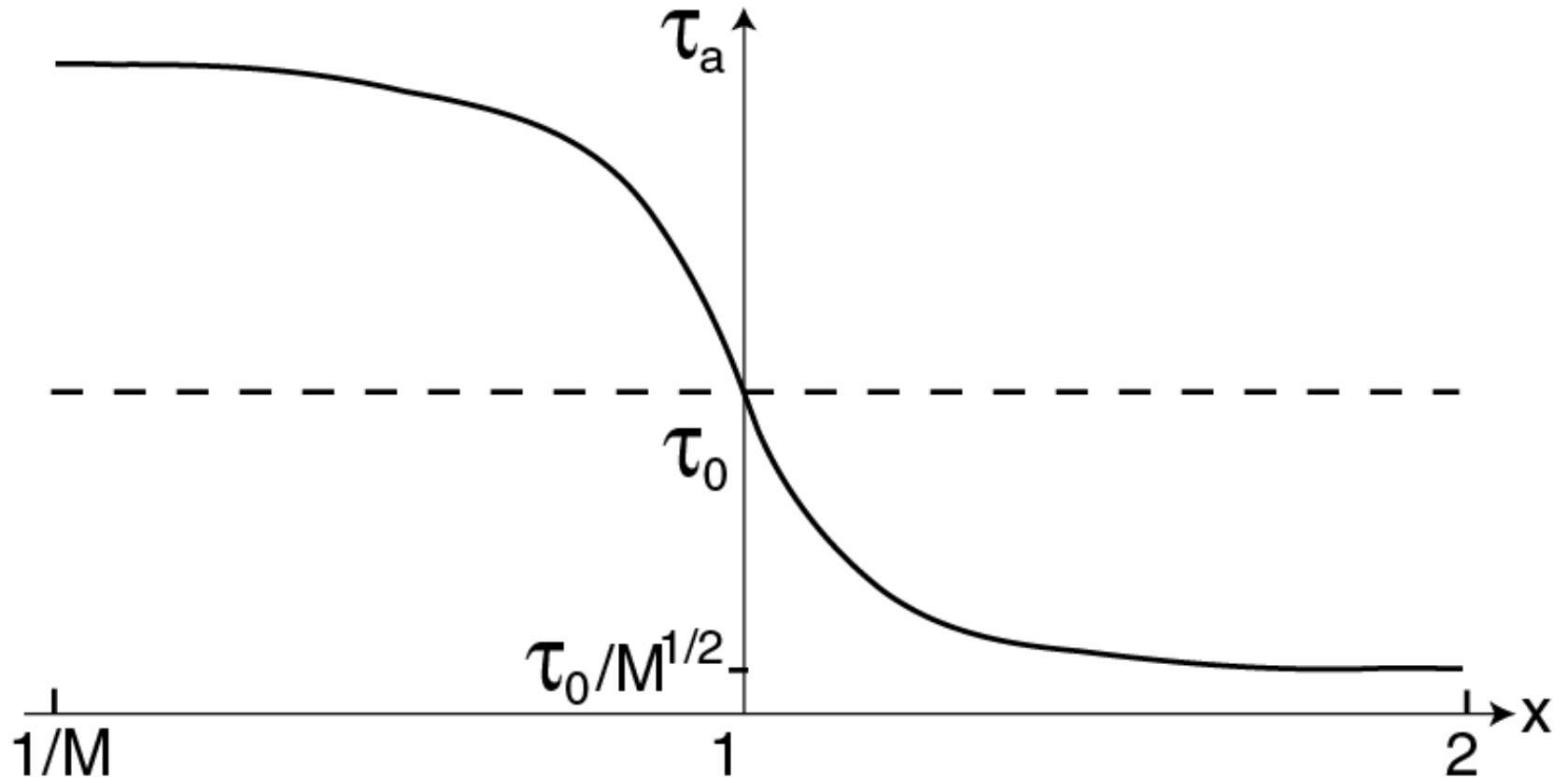
$$\tau_0 = M / 4\pi cDr$$

The ss RNA tail slows down the self-assembly when the ss RNA molecules are at excess

Kinetic trap



Assembly time τ_a as a function of ratio $X = c / Mc_R$,
 $\tau_0 = M / 4\pi cDr$ is the assembly time without the
 antenna effect.



excess of RNA ← stoichiometry → excess of protein

Assembly from short RNA

CF can grow only via CF-CF collisions and merging.
Typical size of fragment grows with time:

$$n = n(t), \quad c(n) = c / n,$$

$$\tau(n) = 1 / 4\pi D(n)r(n)c(n) = n / 4\pi Drc,$$

$$\tau_a = M\tau(n) / n = M / 4\pi Drc = \tau_0.$$

Excess of capsid proteins or of ss RNA plays NO role!

Summary

- Viruses are most stable when the total contour length of ss RNA is close to the total length of the tails.
- When capsid proteins are at excess, the ss RNA antenna speeds up self-assembly.
- When ss RNA molecules are at excess, the ss RNA tail slows down self-assembly.