STATICS AND KINEMATICS OF SYMMETRIC SWELLING VIRUSES

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<u>Summary</u> Some viruses in biology vary their diameter in response to pH change, and retain icosahedral symmetry during its swelling motion. In this research, a mechanical ball-jointed model of the virus was set up, then mobility and self-stresses were analysed with symmetry-adapted techniques. Also investigated was the uniqueness of fully symmetric kinematic paths of swelling, through analytical relationships between geometrical variables of the model.

MODELLING THE COWPEA CHLOROTIC MOTTLE VIRUS

The CCMV (Cowpea Chlorotic Mottle Virus) has recently received much attention, partly because of its icosahedral symmetry, rarely observed in biological systems, but more interestingly because, if there is a change in pH, the virus starts to behave as a mechanism, leading to a symmetric enlargement of the original object [1]. Expansion is produced by screw-like motion of each polygonal morphological unit (capsomere) of the virus coating: pentagonal and hexagonal elements (called pentamers and hexamers) undergo a radial translation and rotation in a way that original symmetry of the structure is preserved. Fig. 1 shows computer-aided image reconstruction of native (a) and swollen (b) form of a CCMV [2].

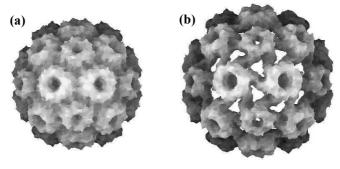


Fig. 1: native and swollen form of a CCMV capsid

Numerical data obtained by cryo-electron microscopy reveals two important factors: (i) there is a double protein chain between adjacent capsomeres; (ii) internal deformations of capsomeres are relatively small compared to the dimension of swelling. It looks therefore plausible to reproduce and analyse the swelling motion by a ball-jointed mechanical model composed of rigid elements.

Mechanical model

In the mechanical model of a CCMV (referred to as 'double-link expandohedron' [3] henceforth), capsomeres are represented by regular pentagons and hexagons forming a truncated icosahedron in the closed configuration. Pairs of rigid bars that substitute protein links are arranged such that two endpoints of each bar lie somewhere in the planes of connected polygons respectively. An additional requirement is that double link connections between hexagons must obey C_2 symmetry, in order to respect overall symmetry conditions. We assume that contact points give a pattern of C_5 and C_6 symmetry on pentagons and hexagons. For example, Fig. 2a represents the closed configuration of a model where connection points are located along the edges of somewhat smaller polygons (for clarity, only these shrunk polygons are displayed instead of original ones).

For the numerical analysis of the model, polygons are represented by position coordinates of their mid-points and another triplet of numbers that characterises the rotation of the polygon. The set of 32 polygons (12 pentagons and 20 hexagons) is constrained by $12\times5 + 20\times6 = 180$ rigid bars. A compatibility matrix is set up which relates the change of length of each bar to the geometric variables describing the position of the polygons. In this way, $6\times(12+20) = 192$ kinematic variables and 180 constraints define a 180-by-192 matrix to be analysed.

Symmetry-adapted analysis

Singular value decomposition (SVD) of a compatibility matrix gives directly all independent states of self-stress and mechanisms, but in a general Cartesian coordinate system; much more progress can be made if they are put into a

symmetry-adapted form. With the help of the Great Orthogonality Theorem of Group Representation Theory, it is possible to generate matrices that transform both states of self-stress (constraints) and mechanisms (variables) into a symmetry-adapted basis where matrices take a block-diagonal form [4].

For the symmetry-adapted compatibility matrix of the CCMV model, performing SVD on each block separately shows that there is a fully symmetric mechanism, but no fully symmetric state of self-stress; a direct proof for the finiteness of that fully symmetric (swelling) mechanism [4]. Therefore the expandohedron described above seems to be an appropriate model for the expanding virus, and a general configuration of the expandohedron is shown in Fig. 2b. We note, however, that in addition there were three states of self-stress and other eight mechanisms of different symmetry properties that implies the existence of other possible inextensional mechanisms that are not investigated here.

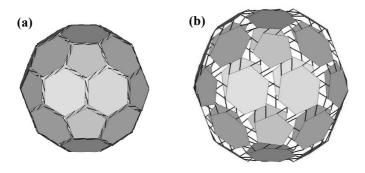


Fig. 2: Closed and general configuration of the expandohedron

POSSIBLE PATHWAYS OF SWELLING

If once the rotation (α) of a hexagon is given for any configuration, the corresponding radius of inscribed sphere (R_6) can be computed from a quadratic polynomial. Therefore there are generally two possible radii for a given angle, and the $R_6 - \alpha$ relationship gives an irregular egg-like diagram. The limit points mark the minimum and maximum rotation allowed, but in fact only a part of the upper curve is physically admissible because of self-intersections (the lower part corresponds to shrinkage rather than expansion).

Once all of the connection points on the polygons and link lengths are defined, the pentagons must fit in a compatible way to their surrounding hexagons – measurements on the CCMV indicate that the radius characterising the translation of the pentagons (R_5) is greater than R_6 . Analysis of the expandohedron shows that the explicit formula for R_5 leads to a fourth-order polynomial in α . Numerical experiments revealed that there are possible initial geometrical data that allow for four real roots of this polynomial, even within the physically admissible domain of expansion, while other geometries (and other α) produces two or zero real roots. Detailed analysis showed that changes in number of real roots in several cases occur at the same configurations where there are kinematic bifurcations. Thus even in the fully symmetric mode the expansion is not uniquely determined by the generic model. Instead it will be necessary to refine the initial geometry with parameters (link lengths, node coordinates within polygons) taken from experimental data obtained from electron microscopy. Then it will be possible to have a better insight into the problem: which of the different kinematic pathways is really physically admissible?

CONCLUSIONS

A rigid, ball-jointed mechanical model of a CCMV was found to be appropriate to reproduce some aspects of experimentally observed swelling: double-link expandohedra certainly have a finite symmetric expansion mode. Analytical rotation-translation relationships were determined for hexagons and pentagons that showed limit points and possible bifurcations within the physically admissible kinematic pathway, showing that symmetric expansion can be performed in different ways for a given geometry. Measurements on the exact virus geometry, however, will help to find the correct kinematic path.

References

- [1] Speir J. A., Munshi S., Wang G., Baker T. S., Johnson J. E.: Structures of the native and swollen forms of cowpea chlorotic mottle virus determined by X-ray crystallography and cryo-electron microscopy. *Structure* **3**:63-78, 1995.
- [2] Reddy V., Natarajan P., Okerberg B., Li K., Damodaran K., Morton R., Brooks III C., Johnson J.: VIrus Particle ExploreR (VIPER), a Website for Virus Capsid Structures and Their Computational Analyses. *J. of Virology* **75**:11943-11947, 2001.
- [3] Kovács F., Tarnai T., Guest S. D., Fowler P. W.: Double-link expandohedra: a mechanical model for expansion of a virus, *Proc. R. Soc. Lond. A* (submitted), 2003.
- [4] Kangwai R. D., Guest S. D.: Detection of finite mechanisms in symmetric structures. *International Journal of Solids and Structures* **36**:5507–5527, 1999.