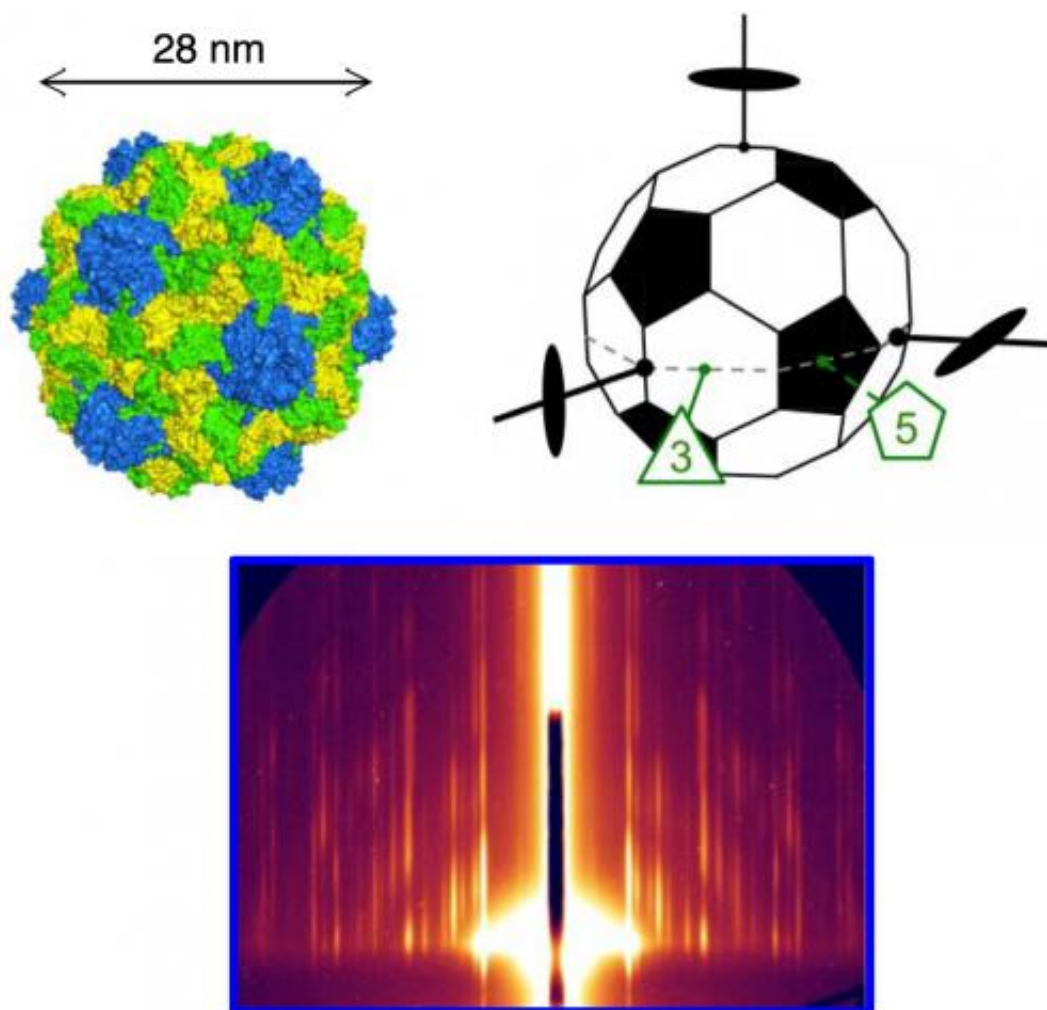


Two-dimensional crystalline structure assembled from outer shells of a virus

February 21 2014, by Mona S. Rowe



Above: At left, the protein shell of TYMV consists of 180 copies of a protein subunit, with 60 subunits forming 12 pentamers (blue) and 120 subunits forming 20 hexamers (yellow and green). At right, the truncated icosahedron, which resembles a soccer ball, illustrates the virus orientation. **Below:** Grazing-incidence small-angle x-ray scattering (GISAXS) pattern from 2D crystals of

TYMV bound to a cationic lipid monolayer at the air-water interface.

(Phys.org) —From steel beams to plastic Lego bricks, building blocks come in many materials and all sizes. Today, science has opened the way to manufacturing at the nanoscale with biological materials. Potential applications range from medicine to optoelectronic devices.

In a paper published in *Soft Matter*, September 2013, scientists announced their discovery of a two-dimensional crystalline structure assembled from the outer shells of a virus. A virus consists of a protein shell protecting an interior consisting of either DNA or RNA.

"We are excited about the potential of virus-like particles as building blocks for creating new nanostructures," said the paper's lead author, Masafumi Fukuto, a physicist in the Condensed Matter Physics and Materials Science Department at Brookhaven National Laboratory. "For the particular virus that we studied, we discovered two new forms of 2D crystals that are distinct from previously observed hexagonal and square crystals."

The team used as their model system the turnip yellow mosaic virus (TYMV), which infects cruciferous vegetables like cabbages, cauliflower and broccoli. TYMV's protein shell resembles a soccer ball, which is characterized by a set of many axes with rotational symmetry, including two-fold axes between a pair of hexagons, three-fold axes through the center of hexagons, and five-fold axes through pentagons. This is known as icosahedral symmetry: all 20 hexagons are identical and all 12 pentagons are identical.

Fukuto described their work as new because it focuses on the structural diversity in the 2D arrays that arise from the constituent particle's high

symmetry and regular shape. "Viruses have been used in previous studies of self-assembly, but in nearly all of those studies, the virus particles were treated as spheres and the ordered 2D arrays observed were hexagonal lattices," he said. "Second, this work is unique for demonstrating a rational approach to 2D crystallization that is based on controlling the interactions of [virus particles](#), which occur at the surface of an aqueous solution where the 2D arrays are formed."

Critical work was done at Brookhaven Lab's National Synchrotron Light Source (NSLS). Explained Lin Yang, one of the paper's coauthors, "We used beamline X22B to identify the right conditions to generate the TMV crystals. Then we measured them at X9 to reveal the 2D structure." Yang is an NSLS beamline scientist in Brookhaven's Photon Sciences Directorate.

Another attractive feature of these viral protein shells as building blocks is that their exterior and interior surfaces can be modified by genetic and chemical methods. According to Fukuto, this capability has already been exploited by others to generate nanoscale reaction vessels and containers to deliver imaging and therapeutic agents.

Thinking further down the road, Fukuto said that the next challenge will be to take advantage of the modification capabilities to control anisotropic interparticle interactions and assemble virus-like particles into more complex architectures. One way to think about anisotropy is to imagine Lego pieces with black and white patches like soccer balls. Depending on the types of the patches facing each other, two pieces may or may not fit together. How these patches interact with each other would therefore determine what could be built out of the pieces.

To date, the team has studied only protein shells of native plant viruses. In the future, they will study virus-like particles whose protein shells have been artificially modified to enhance or suppress the formation of a

particular crystal structure. The control over interparticle interactions will also be essential for generating ordered structures out of a mixture of different virus-like particles.

"We also would like to extend our studies to 3D assembly," said Fukuto. "New beamlines at NSLS-II will offer advantages through improvements in both resolution and sample throughput. The 3D assembly is expected to involve a greater degree of structural diversity and larger sample parameter space than for the simple 2D case that we have analyzed. Both the improved resolution and sample throughput will be helpful in addressing these issues."

Fukuto named the SMI and LIX beamlines at NSLS-II as offering better resolution for biological samples. SMI is an acronym for Soft Matter Interfaces and LIX stands for High-brightness X-ray Scattering for Life Sciences. CMS, the Complex Materials Scattering beamline, will allow faster sample throughput.

More information: Science Paper: Crystallization, structural diversity and anisotropy effects in 2D arrays of icosahedral viruses:
pubs.rsc.org/en/content/article...g/2013/sm/c3sm51853a

Provided by Brookhaven National Laboratory

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