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| 14. ABSTRACT |
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RPPR Final Report
as of 31-Oct-2018

Agency Code:

Proposal Number: 62436MS

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INVESTIGATOR(S):

Name: Ph.D Bogdan Dragnea

Email: dragnea@indiana.edu

Phone Number: 8128560087

Principal: Y

Organization: **Indiana University at Bloomington**

Address: 509 East 3rd ST, Bloomington, IN 474013654

Country: USA

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Report Date: 30-Jun-2017

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Final Report for Period Beginning 01-Oct-2013 and Ending 30-Mar-2017

Title: Materials design. Optical interactions in virus-based materials

Begin Performance Period: 01-Oct-2013

End Performance Period: 30-Mar-2017

Report Term: 0-Other

Submitted By: Ph.D Bogdan Dragnea

Email: dragnea@indiana.edu

Phone: (812) 856-0087

Distribution Statement: 1-Approved for public release; distribution is unlimited.

STEM Degrees:

STEM Participants:

Major Goals: The major goals of the project were to:

- 1) Construct a photothermal microscope for manipulating nanoparticles through optical forces and measure their optical scattering and absorption spectra as they organize under optical radiation forces.
- 2) Engineer a coherent array of hundreds of light emitting molecules supported by a symmetric biomolecular template formed of a virus capsid.
- 3) Determine conditions required for collective relaxation and the nature of light emitted (coherence, dynamics), i.e. conditions in which the fluorophores act as an optical antenna array. Identify photonic and molecular structure characteristics, specifically the role of symmetry leading to super-radiance.
- 4) Assemble the super-radiant virus-like particle around a plasmonic nanoparticle and determine how the chromophore array couple to radiation and localized plasmon modes.
- 5) Measure collective absorption cross-section using the instrument developed in aim (1), and the samples of aim (2) and (4). Develop collective coupling model based on findings.

Accomplishments: We have published 6 papers related to different aspects of the 4 broader goals. We have a patent related to an application that is emerging from goals 3-4. Highlights from unpublished work are:

- discovery of collective relaxation at room temperature from a virus-supported fluorophore array. Radiation appears to be temporally coherent. A manuscript is under consideration at Nature.
- proof-of-principle for detection of nanoparticle-induced phase transformation in molecular materials using photothermal. The new approach should be of interest for technologies related to nanoparticle-sensitized bolometers. Manuscript in final form.

RPPR Final Report as of 31-Oct-2018

Training Opportunities: Trainees:

- Joseph Holmes, Ph. D. candidate, 3rd year, Physics, IU. Has been enrolled in the APS Bridge program for underrepresented groups.
- Maryam Zahedian, Ph. D. candidate, 5th year, Chemical Physics, IU.
- Sajnee Desai, undergraduate, pursuing double major Chemistry and Physics, Honors.
- Sidra Ahmad, undergraduate, pursuing double major Chemistry and Physics, Honors. Nominated for the Goldwater scholarship.
- Amberly Xie, freshman, IU STARS program.

We have created two demos which have been used at the Wonderlab Science museum and at the Bloomington Science Fest, October 2018.

Results Dissemination: Invited talks (2015-2018):

- SPIE San Diego, August 2018
- International Center for Theoretical Physics (ICTP) Trieste, June 2017.
- Lehigh University, Chemistry Department invited talk, October 2018.
- Ohio University, Athens, Chemistry Department invited talk, May 2018.
- International Center for Theoretical Physics, Trieste, 2017
- Eindhoven Technical University, Netherlands, 2017
- University of North Carolina, Charlotte, 2016
- Harvard University, SEAS, 2015
- DOE Contractor meeting, Boston, 2015
- Aspen Center for Physics, 2015
- Berea College, 2015

Honors and Awards: IU Trustees Teaching Award

Protocol Activity Status:

Technology Transfer: Patent application, August 2018

title: Virus-enabled targeted vector for imaging, August 2018

PARTICIPANTS:

Participant Type: Postdoctoral (scholar, fellow or other postdoctoral position)

Participant: Irina Tsvetkova

Person Months Worked: 1.00

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Title: "STRUCTURE AND MECHANOCHEMISTRY OF" "ICOSAHEDRAL VIRUSES AND VIRUS SHELLS STUDIED" "BY ATOMIC FORCE MICROSCOPY"

Authors: Cheng Zeng

Acknowledged Federal Support: Y

1 Collective emission from arrays of virus-supported chromophores

2 Irina B. Tsvetkova^a, Arathi Anil Sushma^a, Joseph C.-Y. Wang^b, William L. Schaich^c, and Bogdan G.
3 Dragnea^{a*}

4 ^aChemistry Department, Indiana University Bloomington, IN, 47405, USA

5 ^bDepartment of Molecular and Cellular Biochemistry, Indiana University Bloomington, IN, 47405, USA

6 ^cPhysics Department, Indiana University Bloomington, IN, 47405, USA

7 *Correspondence and requests for materials should be addressed to B.D. (email: dragnea@indiana.edu)

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11 Over the years, spectacular improvements in chromophore photostability, wavelength
12 range, biological integration, detectors and detection techniques, have pushed the limits of
13 fluorescence imaging to realms never thought possible before¹⁻³. Despite these improvements,
14 most fluorescence imaging techniques continue to rely on the incoherent spontaneous
15 emission from many independent chromophores. However, a system's collective behavior can
16 be much more than the sum of its parts⁴. For instance, the indistinguishability of microscopic
17 quantum constituents can lead to coherent behavior via quantum, symmetry-enforced
18 selection rules⁵. Such collective relaxation processes can be much faster and more efficient
19 than those encountered near the thermodynamic limit. Indeed, certain molecular phenomena
20 that are central to life on earth appear to rely on quantum coherence⁶. Thus, light-harvesting
21 complexes - macromolecular assemblies in photosynthetic organisms, exploit the tight spatial
22 organization of proteinaceous multi-chromophore assemblies to enable coherent exciton
23 transport in short times and over distances many times larger than the size of molecular
24 constituents^{7,8}. In a similar yet distinct vein, here we show that harnessing of organizational

25 principles present in viruses leads to collective behavior, in the form of coherent optical
26 emission from hundreds of chromophores bound to a nanoscopic molecular framework. Thus,
27 while at first fluorescence quenching ensues as the number of chromophores chemically-
28 conjugated to the surface of a virus particle increases, when the number of chromophores per
29 particle is nearing the maximum number of surface sites allowable, a sudden brightening of the
30 emitted light and a shortening of the excited state lifetime are observed. This radiation
31 brightening is observed under short pulse excitation only; steady-state excitation is
32 characterized by conventional concentration quenching for any number of chromophores per
33 particle. The results are consistent with efficient, collective relaxation at room temperature
34 when the emitters are placed on a symmetric template, suggesting a way towards novel, virus-
35 enabled imaging vectors with qualitatively different optical properties than state-of-the-art
36 agents. Such biophotonic particles could be of interest for laser-guided surgery^{9,10}, optogenetic
37 manipulation¹¹, and other applications that would benefit from bright, deep-subwavelength
38 light sources¹².

39
40 Control of the probability of spontaneous emission through cooperation among emitters
41 has a venerable history, and includes phenomena such as stimulated emission and lasing,
42 super-radiance, amplified spontaneous emission, photon echo, and magnetic resonance decay.
43 Most of these phenomena have been already worked into powerful spectroscopy tools^{13,14}.

44 In super-radiance (SR)¹⁵⁻¹⁷, a sub-wavelength ensemble of indistinguishable, excited
45 two-level quantum emitters is prepared in, or spontaneously attains, a correlated state which
46 couples into a common electromagnetic field as a single, massive radiating dipole¹⁸. Because of

47 its substantially-accelerated radiative decay as the number of cooperating chromophores
48 increases, in the years before the invention of the laser, SR was suggested as a way towards
49 generating short coherent pulses of light, without a cavity. However, this promise has proven
50 difficult to fulfill. The reason is that the coherent behavior emerges only when the quantum
51 emitters are indistinguishable and the cooperative radiative decay of the system is faster than
52 any other phase breaking (decoherence) process. Thus, SR could be observed at low
53 temperature only for non-interacting (non-aggregated) emitters such as atomic gases¹⁶,
54 molecular centers in crystals¹⁹, and quantum dots²⁰. On the other hand, tightly bound
55 molecular crystals and arrays²¹ and in the light-harvesting complexes of certain photosynthetic
56 microorganisms⁸ exhibit accelerated radiative decays from excitonic states at close to room
57 temperature. Only recently, coherent relaxation at room temperature was observed in
58 ensembles of non-interacting (sparse) diamond N-vacancies²².

59 Here we present experiments suggesting that coherent relaxation of non-interacting
60 emitters at room temperature can even occur in soft matter, namely in arrays of molecular
61 dyes, provided two conditions are present: 1) Excitation is done by high-intensity pulsed
62 irradiation, and 2) the dyes are located on, and interacting strongly with a three dimensional,
63 symmetric molecular scaffold of a size much smaller than the wavelength of light. Condition (2)
64 presumably ensures the equivalence of local environments and thus optical indistinguishability
65 of individual chromophores, while condition (1) ensures that initially nearly all chromophores
66 are in the excited state. We note that these experimental design features represent a molecular
67 assembly embodiment of the so-called “Dicke optical bomb”⁴.

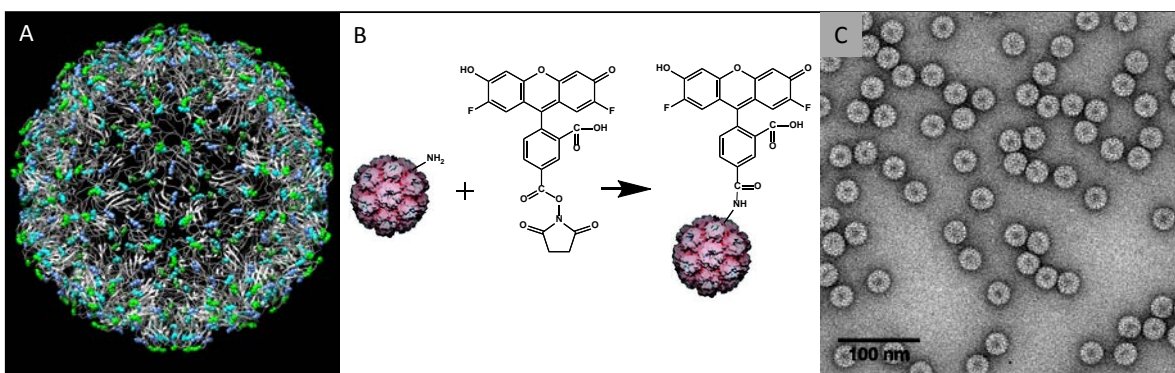


Figure 1. A) Molecular model of BMV with structure surface exposed lysines. B) Lysine bioconjugation reaction scheme. C) TEM image of near-saturation labeled BMV.

68 The symmetric molecular scaffold or template in this work is a Brome mosaic virus
 69 (BMV) particle, which has an icosahedral capsid formed of 180 identical self-assembled
 70 proteins²³. A common bioconjugation reaction of surface-exposed lysines was used to
 71 covalently attach the fluorescein derivative dye, Oregon Green™ 488 carboxylic acid
 72 succinimidyl ester (OG), at specific locations on the virus (Fig. 1A, B, SI)²⁴. The average number
 73 of chromophores was controlled by varying the molar ratio between capsid and dye in the
 74 reaction media, and by adjustment of buffer conditions (SI).

75 The degree of labeling was estimated from UV/Visible absorption spectra of purified
 76 BMV-chromophore conjugates (Fig. 2A) and confirmed by matrix assisted laser
 77 desorption/ionization-time of flight spectrometry (MALDI-TOF) (SI). From the molecular
 78 structure of the virus particle (Fig. 1A), based on steric constraints, we expect a maximum of
 79 $N_{max}=300$ chromophores per particle. The smallest distance between two nearest-neighbors at
 80 this labeling density is ~ 19 Å (see table in Fig. SI-1). Therefore, unlike the case of J and H
 81 molecular aggregates²⁵, negligible nearest neighbor electronic coupling is expected here.
 82 Indeed, no changes in the form of spectral shifts or broadening/narrowing of the bands could

83 be observed in the absorption and emission spectra as a function of N , at low excitation
 84 intensity (Fig. 2). Concentration quenching was, however, noticeable (see Fig. 2B, inset). This is
 85 consistent with previous works²³, although, as reported for other dye-labeled virus-like
 86 particles²⁶, the quenching rate was below that typically observed in free-dye solutions.

87 Absorbance spectra showed a bathochromic shift for the main absorbance peak of dye-
 88 conjugated BMV samples, independent of N , from 491 nm for the free dye to 496 nm,
 89 indicating that the dye is coupled to the protein (Fig. 2A). To obtain further information on the
 90 dye-surface geometry we attempted single particle reconstruction of cryo-electron microscopy
 91 images. The structures of BMV and dye-saturated BMV are indistinguishable at the 7 Å
 92 resolution of our experiment (Fig 1C, SI). Interestingly, although no extra density could be
 93 attributed to the presence of OG molecules, the OG-conjugated BMV particles (BMV-OG) are
 94 more stable to physical and chemical manipulations than wtBMV. Specifically, when dialyzed in
 95 disassembly buffer conditions for 24 hours, wtBMV is completely disassembled, while dye-
 96 saturated BMV remains intact, with no noticeable morphological changes (SI). The added

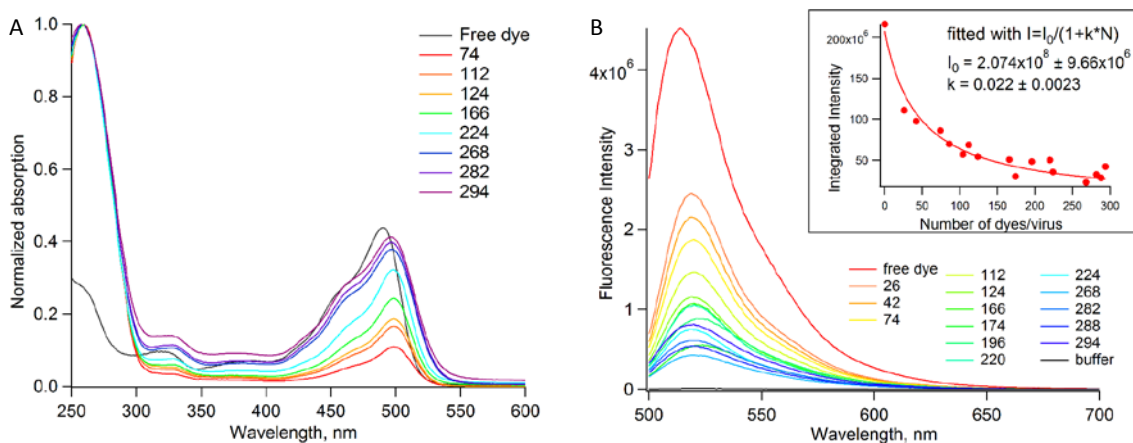


Figure 2. A) Uv-vis absorption and B) fluorescence emission spectra of free dye and BMV-OG. Inset in B) shows fit corresponding to the Stern-Volmer equation describing concentration quenching for spectrally-integrated, steady-state fluorescence intensity vs N .

97 resilience of the BMV-OG particles to environmental challenges suggests that the
98 chromophores interact strongly with the capsid, in a way that stabilizes it.

99 Since the emission rate of an ensemble of coherent radiators is a nonlinear function of
100 the number of excited chromophores and because the dephasing rate scales as N , coherent
101 behavior will be favored under strong population inversion and/or reduction of dephasing
102 rates. To obtain a strong population inversion, we have used pulsed excitation from a
103 supercontinuum laser (120 ps pulse duration, maximum 500 μW average power at the sample).
104 To investigate the possible onset of accelerated emission, we measured an effective
105 fluorescence lifetime as estimated from the mean photon arrival times, and the time-integrated
106 photon counts from single BMV-OG particles as a function of the average N , by fluorescence
107 lifetime microscopy (FLIM) with time-correlated single photon counting (TCSPC) (see Supporting
108 Information).

109 Fig. 3 shows the distributions of the fluorescence lifetime and time-integrated photon
110 counts from single particles for two situations: In Fig. 3A the sample was irradiated with 90% of
111 the maximum laser power (450 μW at the sample), while in Fig. 3B. only 15% of the maximum
112 laser power (75 μW at the sample) was used. In both, Fig. 3A and 3B, as N increases to ~ 200 ,
113 both photon counts and lifetime decrease. This is consistent with a nonradiative relaxation rate
114 increase due to the concentration quenching effect observed in steady-state spectroscopy (Fig
115 2B inset and SI). However, as N increases above ~ 200 , bright particles with short lifetimes
116 appear in Fig. 3A but not in Fig. 3B. This is consistent with a significant avoidance of
117 concentration quenching.

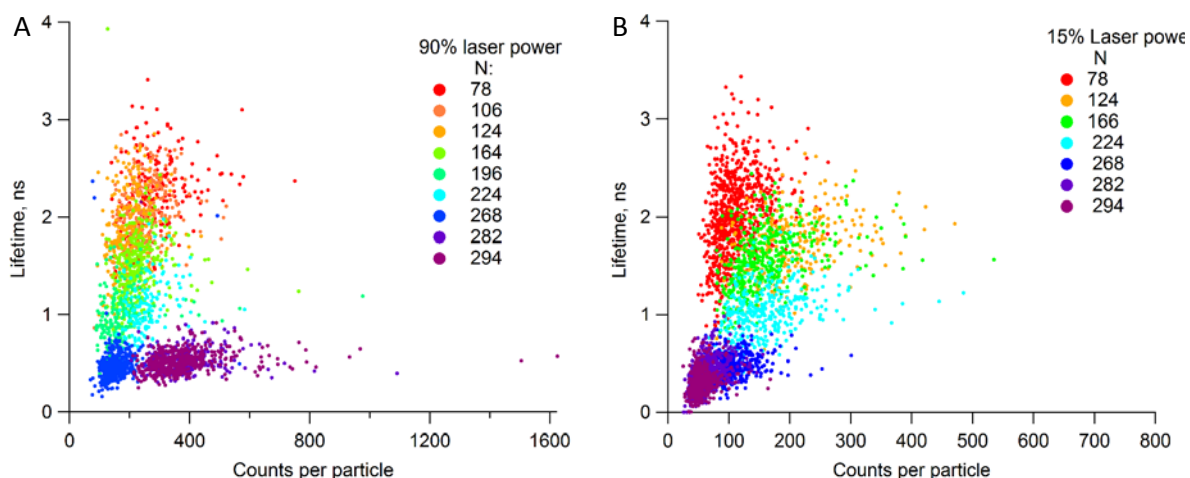


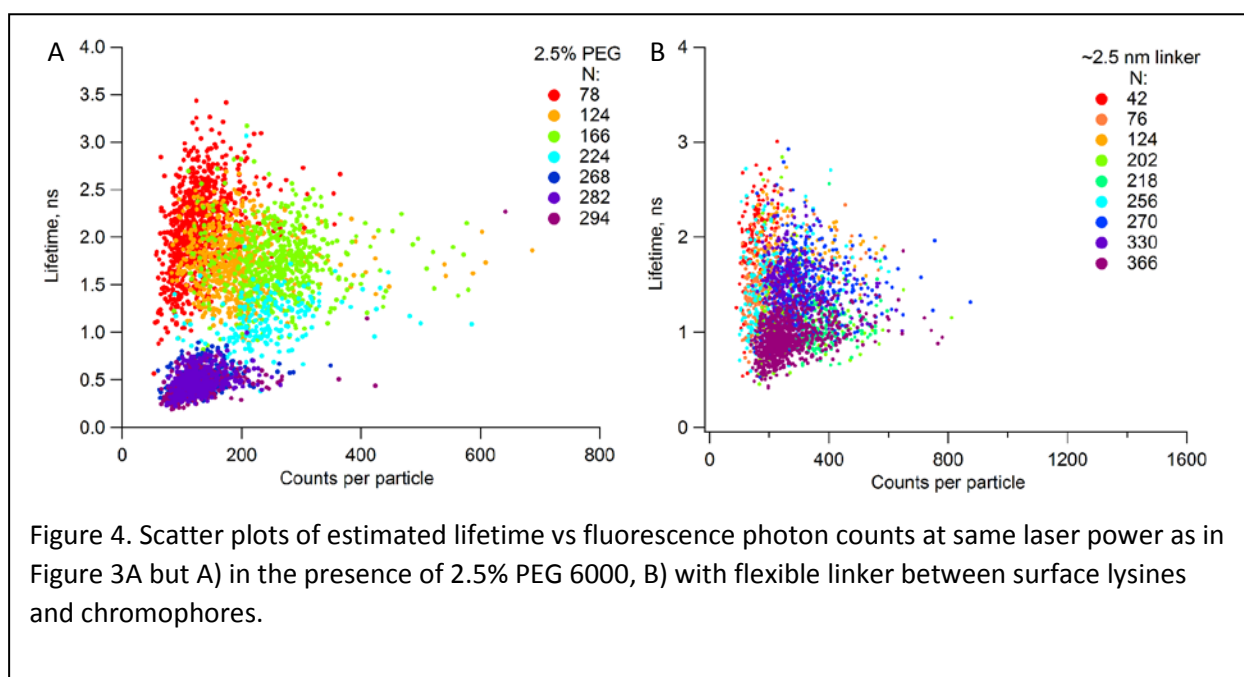
Figure 3. A) Scatter plots of estimated lifetime vs fluorescence photon counts collected from hundreds of labeled BMV particles by single-particle FLIM (each dot represent single virus particle). The different colors represent samples with different average number of chromophores per particle (N). Symbols show the maximum probability point for each distribution. B) Same as (A), except for the excitation power, which is 6x less than in (A).

118 We consider several possible explanations for the strongly nonlinear behavior in Fig 3A.
 119 At the first sight, a possible mechanism could be amplified spontaneous emission (ASE)²⁷. In
 120 ASE, chromophores absorb light, and start decaying by spontaneous emission. If the emitted
 121 light passes through a region containing inverted molecules, it may de-excite these, being
 122 amplified in the process. The decay accelerates, shortening the emitted pulse duration.
 123 Unlike coherent phenomena, ASE is much less sensitive to phase breaking processes, and
 124 therefore we would expect it to occur even in the presence of static and dynamic fluctuations
 125 (disorder). To test this idea, we added polyethylene glycol (PEG, MW 6000) to the dye-BMV
 126 solution (Fig. 4A). PEG exerts depletion forces on the viral coat protein, and can increase the
 127 osmotic pressure on the virus shell²⁸. As a result, PEG is known to induce a measurable (~ 10 Å)
 128 average radius compression at concentrations above 2.5%²⁹. Furthermore, adsorption of PEG is

129 likely to disrupt the protein/dye interaction and/or change the local environment of the dye³⁰.
130 Upon 2.5% PEG addition, the brightening effect observed in Fig. 3A is completely suppressed.

131 In an additional experiment investigating the role of dye-virus template interaction, we
132 have added a 25 Å linker between the chromophore and the coat protein (see reaction scheme
133 in SI), thus reducing the possibility of chromophore interacting with the virus shell, pushing the
134 chromophore into solution, and making the chromophore more prone to positional
135 fluctuations. Similar to the PEG experiment, this treatment also significantly disrupted the trend
136 in Fig. 3A. Note that, under this approach, some of the dye molecules were still conjugated
137 directly to the surface-exposed lysines, which further added to the heterogeneity of the dye
138 environment (see SI, MALDI data). We conclude that ASE is an unlikely explanation for the
139 observed accelerated decay and the brightening of emission.

140 Since the density of chromophores in our case is well below that calculated for attaining
141 the stimulated emission threshold in nanolasers³¹, the remaining working hypothesis is that the



142 observed accelerated emission is due to superradiance. Four factors favor this hypothesis: i)
143 immobilization of emitters on a rigid molecular scaffold at identical local environments is
144 expected to lead to a reduction of inhomogeneous broadening by suppressing dynamics along
145 some of the molecular degrees of freedom, ii) the strong dye - virus template interaction may
146 decrease the effectiveness of phase breaking processes, iii) the role played by symmetry
147 suggesting involvement of quantum selection rules, iv) the population inversion requirement.

148 We note that avoidance of fluorescence quenching is known to occur in photosynthetic
149 organelles, even at low excitation intensity. Thus, while emission from a 0.1 M chlorophyll
150 solution is completely quenched, chlorophylls bound in light harvesting complexes of certain
151 photosynthetic bacteria are strongly fluorescent at room temperature even as the
152 concentration reaches 0.25 - 0.5 M, *i.e.* concentration quenching is effectively suppressed. The
153 reason for this difference is believed to be the result of the spatial organization of chlorophyll
154 molecules in photosynthetic LHCs not being random³². The same complexes are believed to
155 exhibit super-radiant behavior at room temperature, in solution, although, it is important to
156 note that in the LHC case, SR is likely of the type observed in molecular aggregates, in stark
157 contrast from the type of molecular organization we are dealing with here.

158 In conclusion, collective relaxation akin to SR has been achieved in solution, and at room
159 temperature using a biological, virus template approach. A volume much smaller than the
160 wavelength of light, high chromophore densities, and a near perfectly symmetric molecular
161 arrangement, create a set of circumstances in which the photophysical properties of
162 multichromophore particles are significantly different from those of individual chromophores.
163 This discovery may lead to new virus-enabled vectors with qualitatively enhanced optical

164 emission properties, complemented by possibilities of further chemical or genetic manipulation
165 for targeting in biomedical applications, and potentially other uses that could benefit from
166 bright, deep-subwavelength light sources.

167

168 **Methods**

169 **BMV purification**

170 wtBMV was expressed in *Nicotiana benthamiana* via *Agrobacterium*-mediated gene delivery
171 according to previously described protocol³³. Seven days after infection, *N. benthamiana* leaves
172 were homogenized in virus buffer [250 mM NaOAc, 10 mM MgCl₂ (pH 4.5)] and then
173 centrifuged at 6000 rpm for 25 minutes using an Eppendorf F-35-6-30 rotor. The supernatant
174 was layered on a 10% sucrose cushion in virus buffer and centrifuged at 26,000 rpm for 3 hours
175 using a Beckman SW 32Ti rotor. The pellets were resuspended in 38.5% CsCl (w/v, virus buffer)
176 and were kept overnight in the cold room. Next day, solution was centrifuged at 10,000 rpm for
177 10 minutes in the BIO-Rad to remove the undissolved pellets. After that, supernatant was
178 centrifuged at 45,000 rpm at 4 °C in a 100 Ti rotor. The resulting virus band was collected and
179 dialyzed against SAMA [50 mM NaOAc, 8 mM Mg(OAc)₂ (pH 4.6)] buffer for 24 hours, with
180 three changes. Virus concentration was measured by Nanodrop.

181 **Fluorescent modification of wtBMV**

182 Surface exposed lysines of wtBMV were labelled by bioconjugation with Oregon Green 488
183 carboxylic acid, succinimidyl ester. Concentrated stock of wt-BMV was diluted in phosphate
184 buffer (100 mM, pH 8.5) or sodium bicarbonate buffer (100 mM, pH 7.5) to concentration of
185 10¹³ particles/ml. Dye was freshly prepared in DMSO and mixed with BMV solution at different
186 ratios ranging from 1000 to 20000 dyes/capsid. The reaction was left for 2-3 hours at room
187 temperature, then free dye was removed via dialysis or filter wash with virus storage buffer at

188 pH 4.5. The wash step was done until there was no presence of free dye in supernatant by UV-
189 Vis.

190 **Bioconjugation of Oregon Green dye through a linker**

191 The concentrated stock of wt-BMV was diluted in phosphate buffer (100 mM, pH 7) to a
192 concentration of 10^{13} particles/ml, followed by reacting with 100x excess of Sulfo-SMCC
193 (sulfosuccinimidyl 4-(N-maleimidomethyl) cyclohexane-1-carboxylate) for 1 hour at room
194 temperature. Excess SMCC was removed from the mixture by passing it through a Sephadex
195 column (PD-10) with multiple washes using SAMA buffer with pH 6. The concentration of the
196 virus in the BMV-SMCC mixture was recorded with Nanodrop, and then a bi-functionalized
197 polyethylene glycol with thiol and amine end was mixed in to react for another hour at room
198 temperature. The concentration of BMV-SMCC linker was determined, and it was subjected to
199 mass spectrometry to analyze the masses. Further, OG488 was added in the same proportions
200 as for BOG samples, followed by removal of excess dye using dialysis.

201 **Transmission Electron Microscopy**

202 Electron-transparent samples were prepared by placing 10 μ L of dilute sample onto a carbon-
203 coated copper grid. After 10 min, the excess solution on the grid was removed with filter paper.
204 It was stained with 10 μ L of 2% uranyl acetate for 10 minutes and the excess solution was
205 removed by blotting with filter paper. The sample was then left to dry for several minutes.
206 Images were acquired at an accelerating voltage of 80 kV on a JEOL JEM1010 transmission
207 electron microscope and analyzed with the ImageJ Processing Toolkit to estimate the diameters
208 of the particles.

209 **Steady State Absorption and Emission Spectroscopy**

210 Absorbance spectra were recorded with a Varian Cary 100 Bio instrument. The concentration of
211 wtBMV and the labeling efficiency of dyes were obtained from the UV-Visible absorbance
212 spectra. Fluorescence measurements were done on a QuantaMaster™ fluorescence
213 spectrometer (Horiba) with the following parameters: excitation wavelength: 488 nm; emission
214 wavelength: 515 nm. The excitation and steady state emission spectra of 100 nM solutions
215 were an average from at least three independent measurements. wt-BMV and OG488 were
216 used as reference standards whose optical characteristics were compared against labeled-BMV.

217 **Fluorescence Lifetime Imaging Microscopy (FLIM)**

218 The lifetime measurements were carried out with a Leica TCS SP8 SMD in FLIM configuration.
219 The sample was excited at a wavelength of 488 nm from a supercontinuum laser emitting
220 pulses of 120 ps at 40 MHz. The time-average maximum power was 500 μ W at the sample. The
221 collection spectral window was 500 nm to 550 nm. Data analysis was done with SymPhoTime
222 64 (PicoQuant) software, ImageJ Processing Toolkit, and IgorPro.

223 **Matrix Assisted Laser Desorption/Ionization-Time of Flight Spectrometry**

224 Fluorescent dye labeled BMV samples were buffer-exchanged to water. The diluted samples
225 were mixed with α -cyano-4-hydroxycinnamic acid (CCA) matrix in 1:5 ratio (varies depending
226 upon the concentration of the sample. Myoglobin and CytochromeC protein mixture was used
227 as the calibrant, which was introduced in 1:1:5 ratio with respect to the CCA matrix. Matrix
228 Assisted Laser Desorption/Ionization- Time of Flight (MALDI-TOF) Mass Spectrometry was done

229 on Bruker Autoflex III in the linear mode. A 355 nm frequency tripled beam Nd-YAG laser was
230 incident on the 384-well steel plate of 1 μ L spot size.

231 **Cryo-electron microscopy**

232 Cryo-EM frozen hydrated specimen was prepared as follows: 4 μ L sample of Oregon Green
233 labelled BMV capsid was loaded onto a glow-discharged Quantifoil R2/2 300 meshed copper
234 grid that has an addition ultrathin layer of carbon film. The grid was quickly frozen by using a
235 FEI VitrobotTM Mark III. The humidity in the chamber was set to 100% and the blotting time is 4
236 sec. The frozen hydrated specimen was then transferred to a Gatan 626 cryo-holder and kept
237 under liquid nitrogen temperature (approximately -172°C) for the subsequently data collection.
238 The grid was imaged using a 300-kV JEOL JEM-3200FS equipped with in-column energy filter
239 and a DE-64 direct electron detection camera. The energy slit width was set to 20 eV and a
240 nominal magnification of x60000 (equivalent to 0.854 Å per pixel) was used to collect the 141
241 25-frame movie stacks. The movie stacks were aligned, dose-weighted, and summed using
242 MotionCor2³⁴. The first 2 and the last 10 frames were discarded, leaving the total dose to be
243 less than 30 e⁻/Å². The defocus value for each micrograph was estimated using CTFIND4³⁵. A
244 total of 31378 particles were semi-manually picked using e2boxer.py³⁶. Reference-free 2D
245 classification was performed on the whole particle set using Relion 2.1³⁷ and the particles
246 within class averages that are shown to be either clear noise or significant overlap were
247 discarded at this point. The class averages that show clear capsomer density were then used to
248 build the initial low-resolution model using e2initialmodel.py. This initial model was further
249 refined using Relion 3D auto-refine with a total of 12522 particles and a post-processing
250 procedure to a final resolution of 7 Å. The 3D model of Oregon Green labeled BMV was

251 visualized and analyzed using UCSF Chimera ³⁸. The atomic coordinates of native BMV (PDB
252 code 1SJ9) solved by X-ray crystallography was fitted into the cryo-EM density to analyze the
253 potential binding positions for Oregon Green.

254

255 **References**

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335
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341 processed the data and wrote a first draft of the manuscript, J.C.-Y.W. performed the cryo-em

342 experiments and structural analysis, WLS contributed to the drafting and critical revision of the
343 manuscript, B.D. conceived and designed the research, and contributed to data analysis and manuscript
344 preparation.

345 **Supplementary information** is available for this paper

Supporting information for

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Collective emission from arrays of virus-supported chromophores

Irina B. Tsvetkova^a, Arathi Anil Sushma^a, Joseph C.-Y. Wang^b, William L. Schaich^c, and Bogdan G. Dragnea^{a*}

^aChemistry Department, Indiana University Bloomington, IN, 47405, USA

^bDepartment of Molecular and Cellular Biochemistry, Indiana University Bloomington, IN, 47405, USA

^cPhysics Department, Indiana University Bloomington, IN, 47405, USA

*Correspondence and requests for materials should be addressed to B.D. (email: dragnea@indiana.edu)

18 **Virus modification and characterization**

19 Virions of the Brome mosaic virus (BMV), with T = 3 icosahedral symmetry provided the
20 symmetric template for bio-conjugation⁷. The 28 nm-diameter BMV capsid is composed of 180
21 identical copies of a single coat protein. BMV can be disassembled into protein dimers and RNA
22 genome and reassembled⁸. Conditions for obtaining empty virus-like particles⁹ or hybrid
23 nanoparticles containing synthetic cores¹⁰⁻¹² have been extensively studied.

24 The chemical surface modification of BMV capsid has been studied¹³. wtBMV has 12
25 lysines per coat protein among which residues K64, K83, K105, K111, and K165 (Fig. 1A, S1) are
26 surface-exposed and have been shown to efficiently undergo chemical modification by
27 thioimide reagents¹⁴. These reactive lysines provide, in principle, for 900 possible labeling
28 sites on the virus surface, for further modification. We analyzed the likelihood of dye locations
29 and nearest-neighbor distances on the surface of BMV by measuring distances between lysines
30 residues in the full virus molecular model using the Chimera software. The average nearest
31 distance between reactive surface exposed lysines is about 2 nm (Fig. S11).

32 Lysines are commonly addressed through reaction with active esters (e.g, succinimidyl,
33 sulfosuccinimidyl, or tetrafluorophenyl esters)¹⁵ (Fig. 1B). Changing the molar ratio of
34 chromophores to the virus in the reaction media varied the average number of chromophores.
35 The labeling reaction was done in two buffer conditions to obtain better control over N. Fig. S12
36 shows the dependence of <N> on the dye input concentration at the reaction onset.

37 The efficiency of labeling in BMV-chromophore conjugates was determined by UV-
38 Visible absorption spectroscopy and supported by Matrix Assisted Laser Desorption/Ionization-

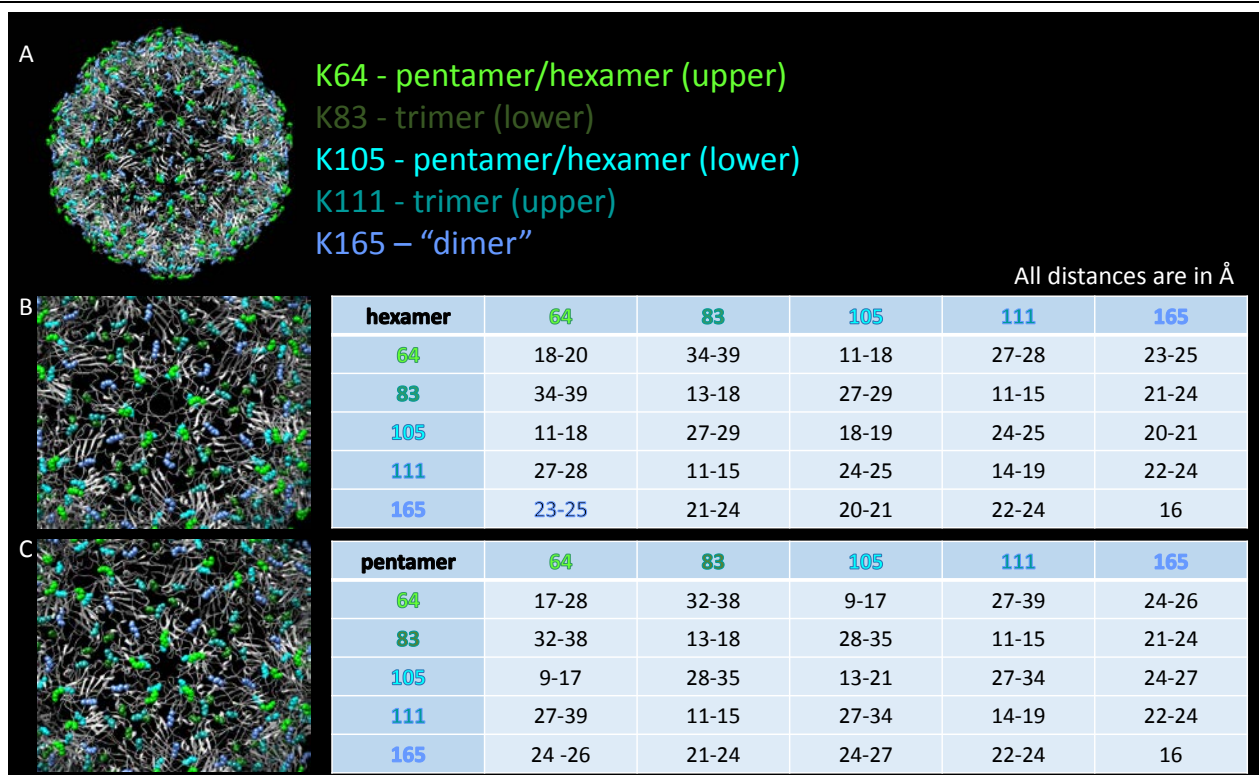


Figure SI1. Analysis of distances between possible labelling sites. A) Full virus model and color description, B) hexamer view and table with distances for hexameric subunit, C) same as B but for pentameric subunit. Note: From structure analysis K165, K64, K111 are likely to be labelled and K83 and K105 are less likely.

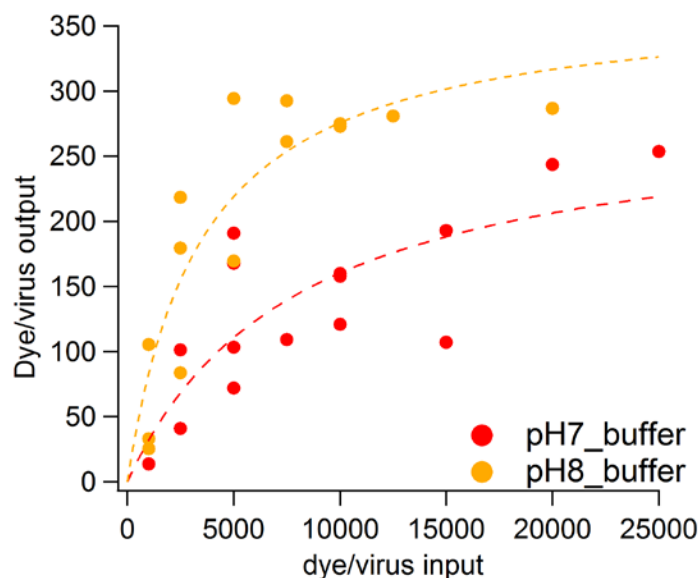


Figure SI2. Bioconjugation reaction output vs dye input in reaction mixture for two buffer conditions (dashed lines are binding isotherm fitting).

40 Time of Flight Spectrometry (MALDI-TOF). The average number of chromophores per particle
41 was calculated from extinction data using the Beer-Lambert law and the molar extinction
42 coefficient ($\epsilon = 70,000\text{cm}^{-1}\text{M}^{-1}$) for Oregon green at 496 nm in buffer at pH 8. BMV is most
43 stable in buffers with pH 4-5. Therefore concentration measurements were done in these
44 conditions. As a consequence of the pH change, the extinction coefficient had to be adjusted. In
45 order to do account for the change in the extinction coefficient, the free dye absorbance
46 spectrum was measured for a pH range from 4 to 8 at varied concentrations from 0.05 μM to
47 0.5 μM . Thus we obtained an ϵ at pH 4.6 of $33641\text{cm}^{-1}\text{M}^{-1}$.

48 MALDI-TOF (Fig. S13) was used to provide molecular weight information of labeled
49 proteins. For BMV labeled through lysine modification, there are two peaks present below 200
50 dyes/virus, which correspond to unlabeled protein and proteins with one dye. For samples with
51 a dye/virus ratio of above 200, a third peak appeared which corresponds to two dyes per coat
52 protein. Also, the height of unlabeled protein peak decreased significantly. By fitting the peaks
53 we can estimate the degree of labeling from MALDI experiments. The table in Figure S13
54 provides the comparison between the labeling load calculated from UV-Vis spectra and from
55 MALDI-TOF spectra. Although there is a difference in absolute numbers between two methods,
56 the trend is the same. It is likely that MALDI-TOF underestimates the degree of labeling due to
57 the particle stability against laser-induced fragmentation being dependent on labeling.

58 Particle morphology was imaged by negative stained TEM and Cryo-EM images and dye-
59 conjugated BMV is indistinguishable from wtBMV (Fig. S14). The inset in Fig S14A shows the
60 rotationally averaged particle image with two structural layers: the outer capsid layer and the
61 inner RNA layer. No observable disruption on the labeled capsid surface can be detected

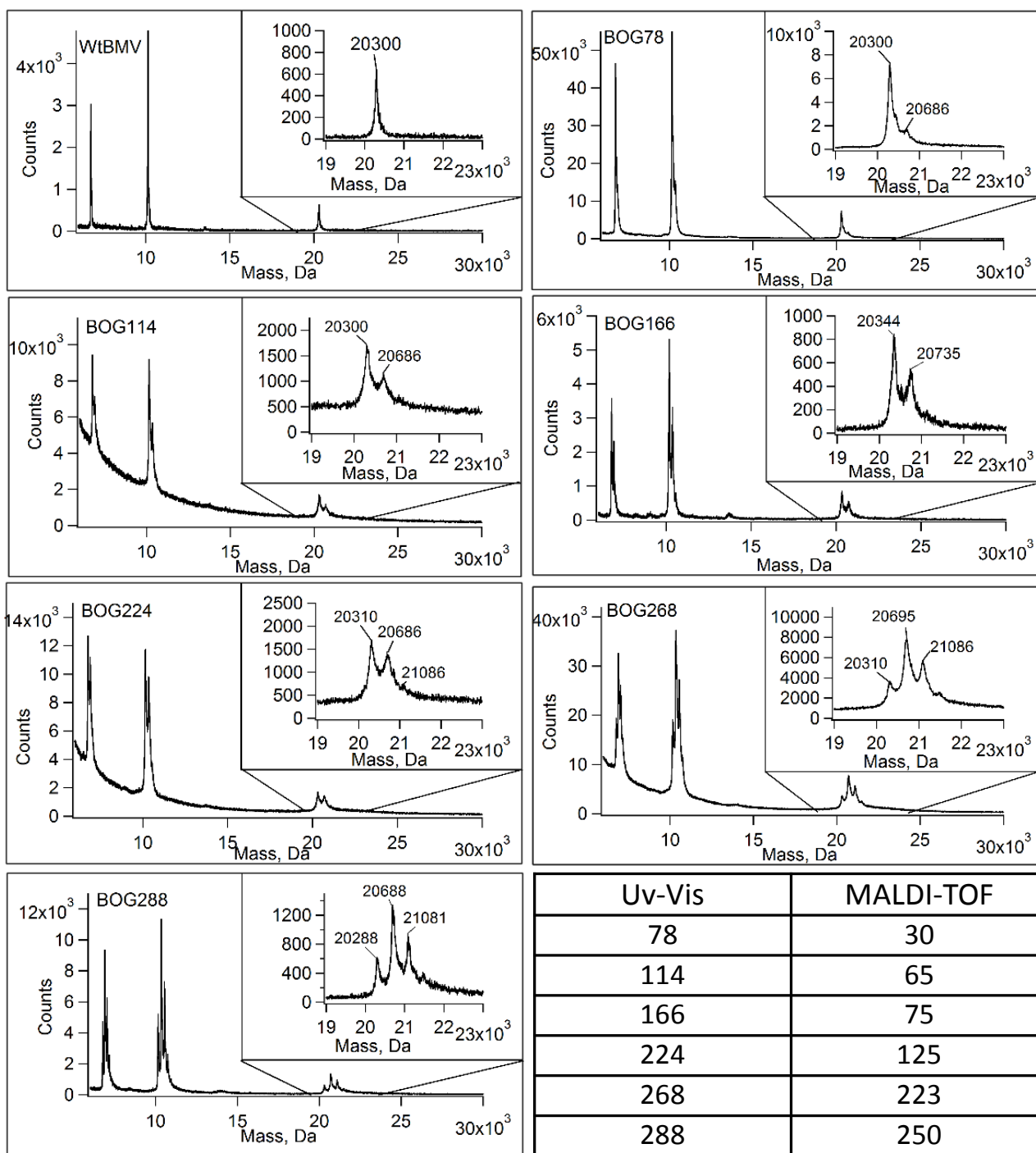


Figure S13. MALDI-TOF spectra for wtBMV and bioconjugated samples with different N and table with comparison of dye loading calculated from UV-Vis and MALDI spectra.

63 (Fig SI4B). A total of 12522 particles from 141 micrographs were used to compute the final 3D
 64 reconstruction to 7Å resolution (estimated by Fourier shell correlation at 0.143). At the 3D
 65 level, the labeled BMV capsid also exhibits an overall architecture of T=3 surface lattice that is
 66 comparable to the native virus (Fig SI4C). There are 12 pentameric capsomer protrusions
 67 located at the fivefold axes and 20 hexameric capsomer protrusions located at threefold axes.
 68 Docking of the X-ray crystallographic structure (PDB code 1JS9) into the cryo-EM density map

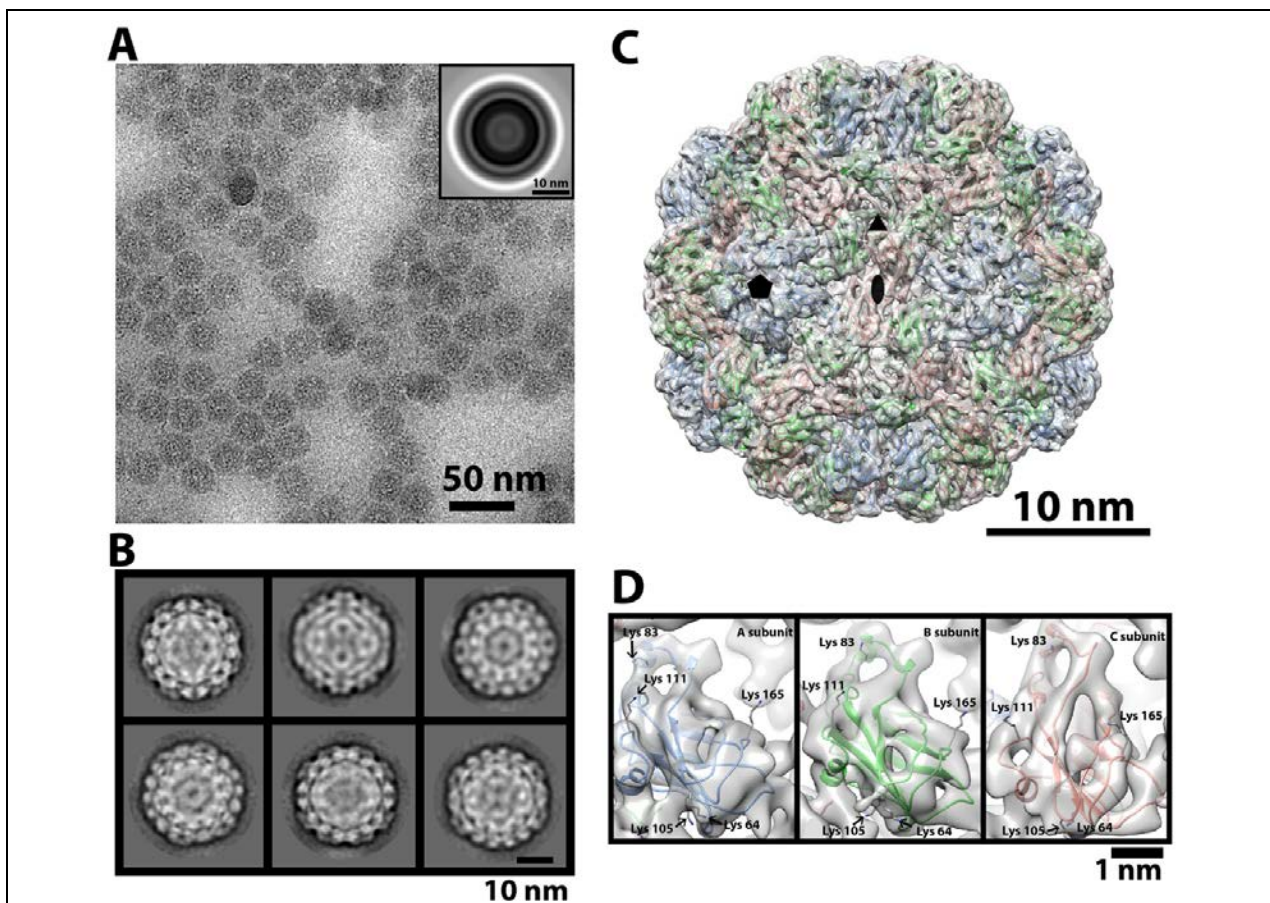


Figure SI4. Cryo-EM analysis of Oregon Green labeled BMV. (A) A representative cryo-EM micrograph of BMV particles vitrified in a thin layer of ice. Inset shows the rotationally aligned averaged image. (B) Selected typical class averages calculated from reference-free 2D classification. (C) The cryo-EM structure of Oregon Green labeled BMV (transparent grey) fitted with the atomic structure of BMV (PDB code 1JS8). (D) Close-up views of each subunits show Lys 64 has become buried within the electron density map.

69 reveals excellent agreement (Fig SI4C). Out of five possible locations on the BMV capsid protein
70 that may interact with Oregon Green: Lys 64, Lys 83, Lys 105, Lys 111, and Lys 165. Lys 64 was
71 found to be mostly buried inside the cryo-EM density (FigSI4D). Other Lys positions are either
72 partially exposed or fully exposed.

73 Since at the current resolution in the cryo-EM reconstruction no extra density could be
74 attributed to Oregon Green molecule, we surmise the dye must be very close to the BMV
75 surface. This is supported by the dye-conjugated BMV particles being more stable to physical
76 and chemical manipulations with respect to wtBMV, which suggests that the chromophore
77 interacts strongly with the capsid, stabilizing it. Specifically, when dialyzed in disassembly buffer

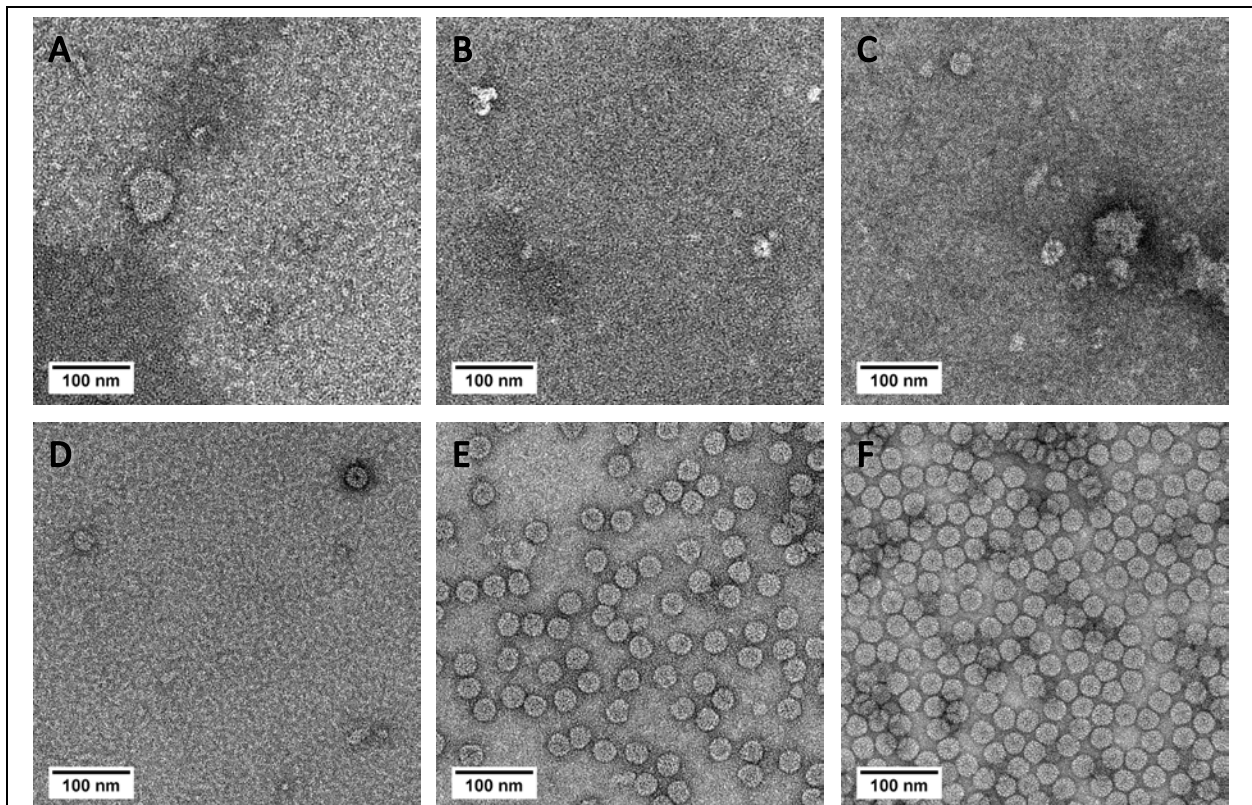
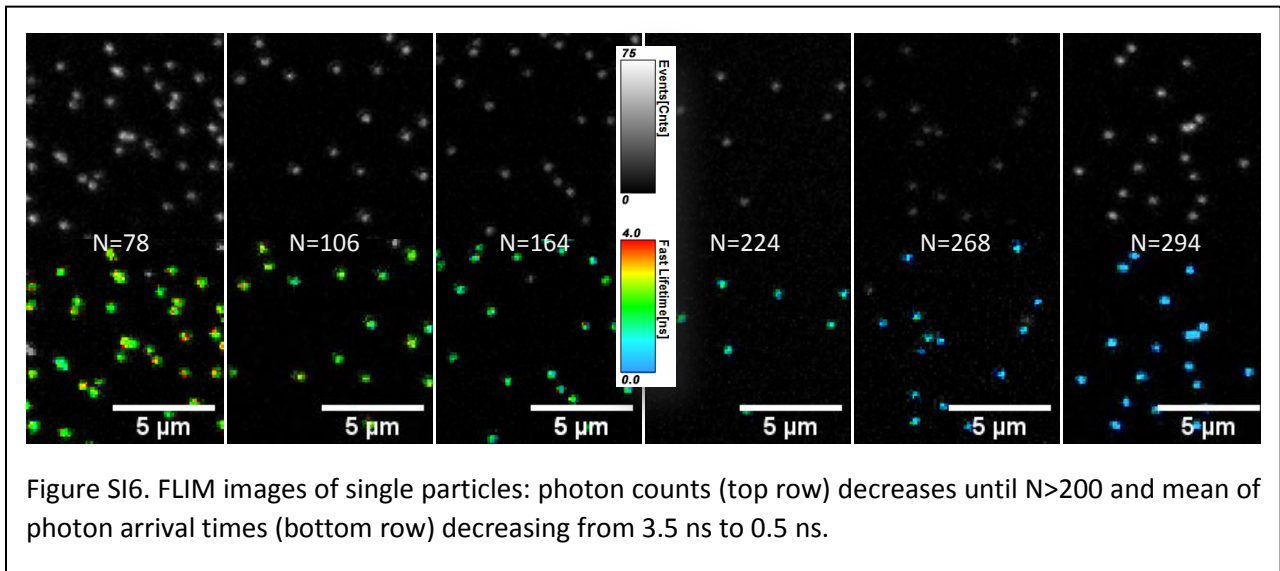


Figure SI5. Stability test. TEM images of samples after overnight dialysis in disassembly buffer: A) wtBMV, B) BOG74 , C) BOG 196, D) BOG 224, E) BOG 268 and F) BOG 288 after drying-reconstitution cycle.

78 conditions for 24 hours, wtBMV is completely disassembled (Fig. SI5A) but dye-conjugated BMV
79 with dye ratio above 200 has the same morphology as in virus-storage buffer (Fig. SI5D-E).
80 Additionally, the $\langle N \rangle = 288$ sample was completely dried under vacuum overnight and
81 reconstituted with SAMA buffer. Again, the $\langle N \rangle = 288$ virus particles retained their native
82 morphology and optical properties (by FLIM).



83

84

85 **Fluorescence life-time imaging considerations**

86 FLIM images are presented in Figure SI6. Non-monotonic changes of photon counts
87 (grey scale) and lifetime (color scale) as function of the average number of dyes per virus
88 particle are visible. The scatter plots presented in the main text were obtained by integrating
89 the photon counts from single virus areas and measuring the mean of photon arrival times for
90 at least 200 single virus particles, and from at least 5 images obtained from different regions in
91 the sample.

92 We used the mean photon arrival time per pixel as a measure of the single particle
93 lifetime instead of a histogram fit due to the noise in the individual histograms of arrival times
94 at low counts per pixel. In support for this approach giving a fair representation of the lifetime,
95 we integrated the arrival times over all pixels associated with virus particles and used the
96 ensemble histogram for exponential fitting to find the overall sample lifetime. The value thus
97 obtained matched well the averaged mean photon arrival time per pixel.

98 It is important to note here that the fluorescence life-time microscopy setup is based on
99 the time correlated single photon counting (TCSPC) scheme. While this scheme clearly indicates
100 that the emitted number of photons depends non-linearly on $\langle N \rangle$, for quantitative studies
101 TCSPC has the drawback that it relies on the assumption of uncorrelated photon emission
102 statistics, more specifically, on the assumption of one or less photons per pulse. Thus, after the
103 excitation pulse, detection of arrival of the first emitted photon triggers the readout and one
104 event is recorded in the histogram at the arrival time. The TCSPC card is not able to count for a
105 period known as “dead-time” after this event, which in our case is 90 ns. For correlated
106 photons, counts and lifetimes may appear skewed when the TCSPC scheme is used. Work is
107 underway to implement a second-order photon correlation setup, which will be able to provide
108 the true photon correlation statistics.

109 It is worth noting that at the maximum laser power employed in our setup, we expect
110 photon emission at each pulse. With this assumption and taking into account losses in FLIM set-
111 up (reflections, detector quantum yield, and electronics dead time) we calculated the maximum
112 measurement limit to be 60 photon counts/pixel. By integration over 9 pixels/particle, to
113 include all photons from a single virus, the maximum counts for particle emitted at every pulse,

114 is in the range of 300-350 counts/particle (because of bell-shaped point-spread function). This is
115 also the maximum we have obtained for samples with $N > 200$. Therefore, the maximum counts
116 obtained for samples with $N > 200$, supports efficient excitation and subsequent emission at
117 every pulse. This is only possible if we assume collective relaxation is more effective than non-
118 radiative quenching.

119

120 **Additional supporting images for control sample characterization:**

121 The flexible linker was added between chromophore and virus surface by first reacting
122 the lysines with hetero-bifunctional SMCC (succinimidyl 4-(N-maleimidomethyl)cyclohexane-1-
123 carboxylate, ~ 8 Å long) and then, adding thiol-TEG-NH₂ (~ 17 Å long), followed by conjugation of
124 OG-488 dye (Fig. SI8A). In this case, it should be noted that some of the dyes were attached to
125 the surface exposed lysines, adding to the heterogeneity of the system and further disrupting
126 symmetry (Fig. SI8B).

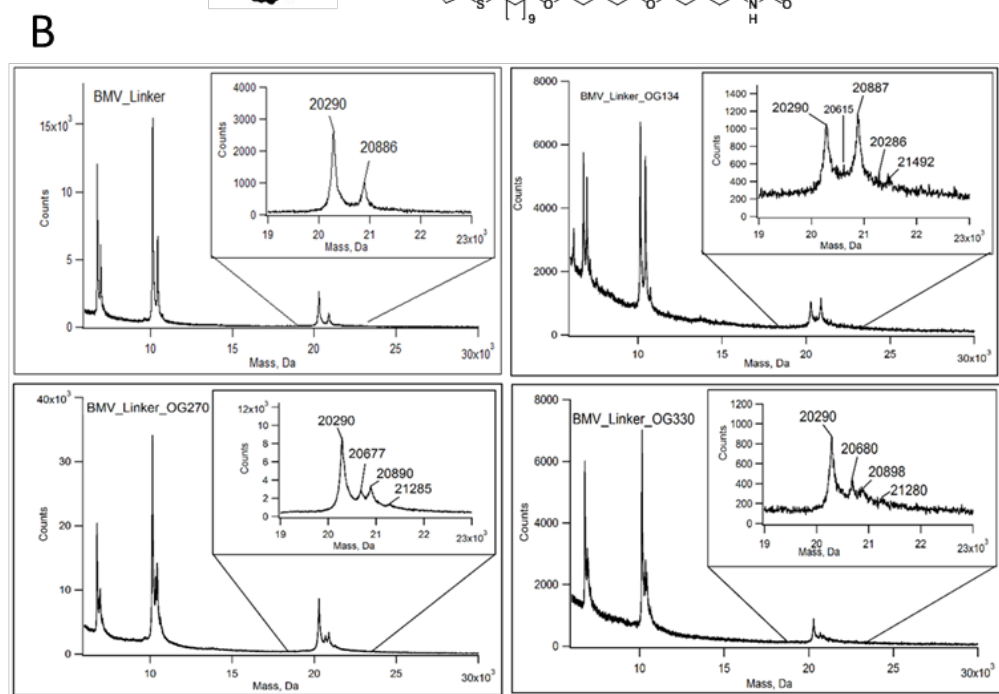
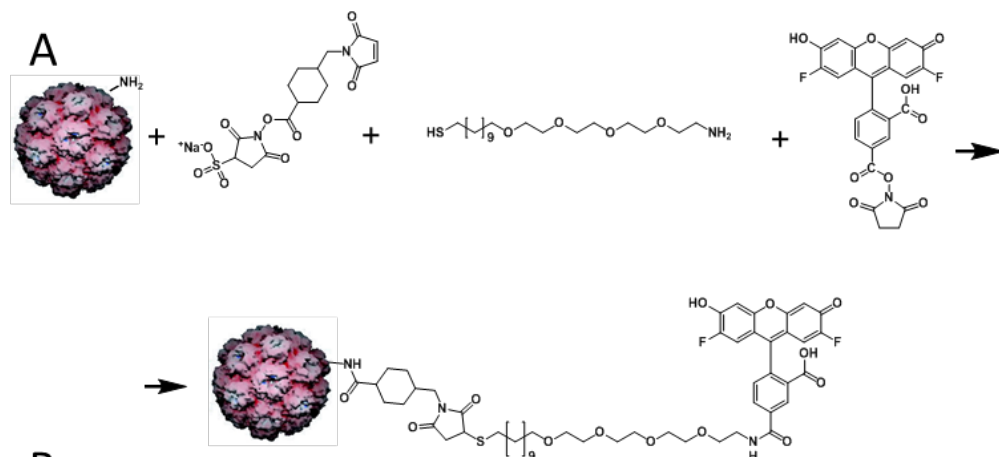


Figure S18. A) Scheme of bioconjugation through a linker, MALDI-TOF spectra for BMV with flexible linker and samples with dye attached through linker for different N.

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