



**Photoresponsive endosomal escape enhances gene delivery
using liposome-polycation-DNA (LPD) nanovector**

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1 Photoresponsive endosomal escape enhances gene
2 delivery using liposome-polycation-DNA (LPD)
3 nanovector

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14 **KEYWORDS:** light responsiveness, gene delivery, endolysosomal escape, imaging analysis

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19 **ABSTRACT**

20 Lipid-based nanocarriers with stimuli responsiveness have been utilized as controlled release
21 systems for gene/drug delivery applications. In our work, by taking advantage of high
22 complexation capability of polycations and the light triggered property, we designed a novel
23 photoresponsive liposome-polycation-DNA (LPD) platform. This LPD carrier incorporates
24 verteporfin (VP) in lipid bilayers and the complex of polyethylenimine (PEI)/plasmid DNA
25 (pDNA) encoding EGFP (polyplex) in the central cavities of liposomes. The liposomes were
26 formulated with cationic lipids, PEGylated neutral lipids and cholesterol molecules, which
27 improve their stability and cellular uptake in the serum-containing media. We evaluated the
28 nanocomplex stability by monitoring size changes over six days, and the cellular uptake of
29 nanocomplex by imaging the intracellular route. We also demonstrated light triggered the
30 cytoplasmic release of pDNA upon irradiation with a 690 nm LED light source. Furthermore this
31 light triggered mechanism has been studied at subcellular level. The activated release is driven by
32 the generation of reactive oxygen species (ROS) from VP after light illumination. These ROS
33 oxidize and destabilize the liposomal and endolysosomal membranes, leading to the release of
34 pDNA into the cytosol and subsequent gene transfer activities. Light-triggered endolysosomal
35 escape of pDNA at different time points was confirmed by quantitative analysis of colocalization
36 between pDNA and endolysosomes. The increased expression of the reporter EGFP in human
37 colorectal cancer cells was also quantified after light illumination at various time points. The
38 efficiency of this photo-induced gene transfection was demonstrated to be more than double
39 compared to non-irradiated controls. Additionally, we observed reduced cytotoxicity of the LPDs
40 compared with the polyplexes alone. This study have thus shown that light-triggered and

41 biocompatible LPDs enable improved control of efficient gene delivery which will be beneficial
42 for future gene therapies.

43 **1. INTRODUCTION:**

44 Gene therapies currently under development against cancer, genetic disorders, and other
45 diseases utilize diverse genetic materials including antisense oligodeoxynucleotides
46 (asODN), small interfering RNA (siRNA), plasmids and other forms of nucleic acids^{1, 2}.
47 While viral transfection remains the established method of their delivery, recently, various
48 nanoscale nonviral vectors have been identified to deliver these genetic materials into cells
49 with several advantages³⁻⁵. Many of these are comparatively easy to prepare, and they have
50 attractive properties such as minimal immunogenicity and excellent biocompatibility⁶, as
51 well as the ability of loading long DNA fragments.⁷⁻⁹ Besides, the enhanced permeability
52 and retention (EPR) effect enables these nanoscale carriers to preferentially accumulate in
53 tumour tissue¹⁰, and they can also be molecularly targeted^{11, 12}. This EPR effect can
54 markedly reduce side-effects towards non-cancer tissue during therapy. All these
55 advantages point to the possibility of nonviral carriers to play a vital role in the future
56 clinical gene/drug delivery systems⁸.

57 Among nanoscale nonviral gene vectors, cationic phospholipids (lipoplexes), polymers
58 (polyplexes) and lipid-polymer hybrids (lipopolyplexes) have been widely developed for
59 various delivery strategies¹³. Lipoplexes are constructed from phospholipid molecules
60 which generally consist of hydrophobic tails and hydrophilic heads. These molecules
61 reassemble to form liposomal or micellar structures able to encapsulate nucleic acids and
62 prevent them from degradation¹⁴. In cationic liposomal gene carriers, two main forces
63 contribute to the lipoplex formation. One is the elasticity forces driven by the lipid

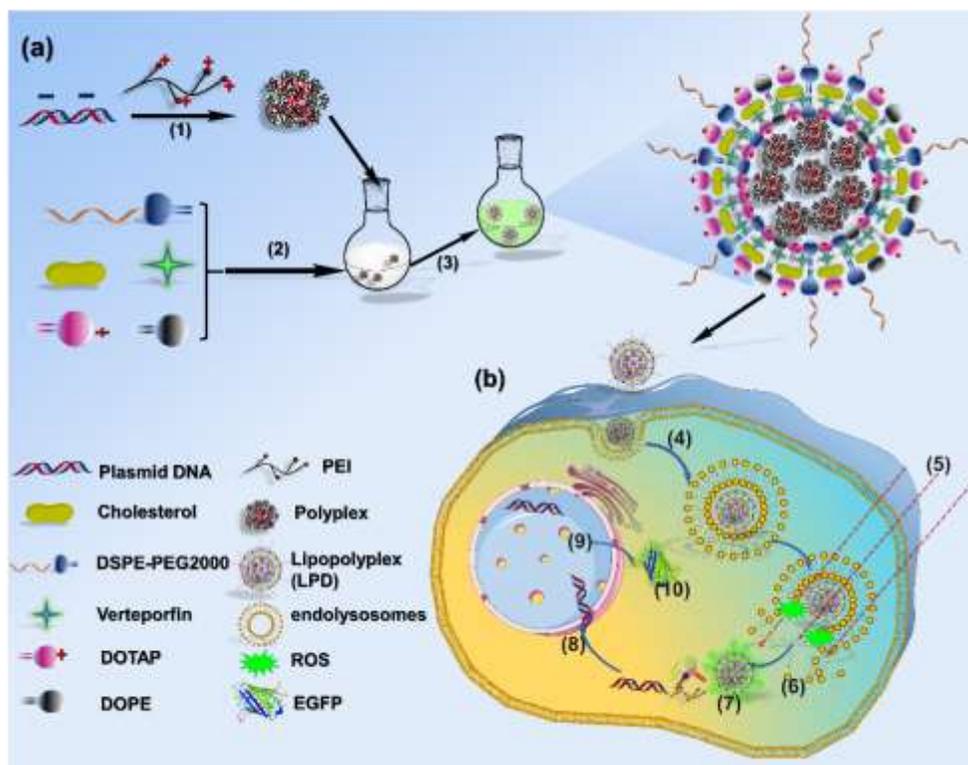
64 hydrophobic moiety, the other is the electrostatic force between the negatively charged
65 nucleic acid cargos and the positively charged groups in lipid molecules¹⁵. Their relative
66 balance may be correlated with lipoplex morphologies and the effectiveness of
67 transfection¹⁶. Moreover, the fusogenic mechanism induced by the liposomal structure
68 affects cellular internalization of liposomes within the endocytosis pathway, and may
69 promote endosomal escape via membrane destabilization, resulting in content release from
70 liposomes into the cytoplasm^{17, 18}. To achieve the on-demand content release, several types
71 of stimulus-responsive liposomes have been designed whose bilayer would be destabilized
72 by physiological and external stimuli¹⁹⁻²³. These triggering approaches include changes in
73 pH²⁰, temperature²¹, ROS²², magnetic fields²⁴, ultrasound²⁵ or light²³. Among these, the
74 light-triggering modality has attracted intense interest, due to precise control of different
75 parameters of light, the feasibility of spatiotemporal manipulation (including optical fibre
76 delivery directly into the body) and non-invasiveness of light irradiation. In addition to the
77 controllability of lipid-like delivery systems, their stability in the physiological
78 environment is also crucial for *in vivo* applications. This can be achieved by either
79 adjustment of lipid components or the modification of liposome surface. For instance,
80 incorporating cholesterol (Chol) in liposomal formulations can improve resistance to
81 liposome aggregation in a physiological environment, protect them from protein binding
82 and mechanical breakage²⁶ and prolong their half-lives. Additionally further surface
83 modification with polyethylene glycol (PEG) the uptake by the mononuclear phagocyte
84 system and extends their blood-circulation time by forming the “stealth liposomes”²⁷.
85 Importantly, PEG groups may facilitate conjugation with different targeting ligands

86 including folic acid, antibodies, and cell penetration peptides (CCP)²⁸. All of these are
87 important in *in vivo* applications²⁹.

88 Polycation vectors such as PEI³⁰ and poly-L-lysine (PLL)³¹ have been widely used for the
89 formulation of DNA-polymer complexes (polyplexes) for improved DNA delivery into
90 cells. The delivery of polyplexes into cells is facilitated by their high cationic charge density
91 at physiological pH³². Although PEI has good physical stability, is easy to manipulate and
92 is moderately resistant to enzymatic degradation³³, its drawbacks such as high cytotoxicity
93 and limited transfection activity have hindered its applications *in vivo*^{8, 34, 35}. They are
94 determined by the physicochemical properties of PEI structures and molecular weight. For
95 example, branched PEI with a high molecular weight (for example, 25 kD) shows
96 substantial transfection activity but suffers from the greater cytotoxicity (80%, at 60 $\mu\text{g}/\text{mL}$
97 in Lovo cells)³⁶, compared with PEI of lower molecular weight³⁷⁻³⁹. To achieve the optimal
98 balance between cytotoxicity and transfection efficiency, different strategies for PEI
99 modification have been explored, including combining the PEI/DNA complex with various
100 phospholipids to form the LPD complexes (named lipopolyplexes)⁴⁰.

101 The purpose of our work is to further enhance the transfection efficiency of such LPD by
102 using external stimuli, for example, light. To the best of our knowledge, few work on photo-
103 responsive LPD as a gene vector has been studied. To this end, we herein developed
104 PEGylated and light-triggered liposomes incorporating large PEI (branched, 25 kD)/pDNA
105 (4.7 kbp) complexes based on our previous work⁴¹. This photoresponsive LPD successfully
106 delivered gene and achieved gene expression in HCT116 cell line, which is considered as
107 an typical *in vitro* model to study gene therapy of colorectal cancer⁴². The pDNA loading
108 capability of LPD was assessed by gel electrophoresis under different N/P molar ratios (N

109 indicates PEI nitrogen and P represents phosphate of pDNA). To enhance the stability of
110 LPDs, in addition to PEGylation, Chol was also added to the liposome formulations. The
111 liposome stability with different Chol contents was measured by dynamic light scattering
112 (DLS) and differential scanning calorimetry (DSC). In order to enable light triggering, we
113 used verteporfin (VP). VP is one of the photosensitizer drugs clinically used for
114 photodynamic therapy. VP can rapidly and effectively generate reactive oxygen species
115 (ROS) under 690 nm photoirradiation⁴³. When VP is incorporated in the liposome, the ROS
116 production upon irradiation can destabilise the liposomal membranes⁴¹. We hypothesize
117 here that, after the liposomes have been endocytosed by cells where they eventually localize
118 in the endosomes or lysosomes, the ROS can further destabilize the endolysosomal
119 membranes, resulting in the escape of entrapped pDNA out of the endolysosomal
120 compartments into the cytoplasm, in which the released pDNA can play the role of gene
121 expression. To demonstrate this process of light activated release of pDNA from the
122 endolysosomes, subcellular tracking of endolysosomal escape of pDNA was carried out by
123 confocal microscopy imaging and quantitative analysis of colocalization. Finally, light-
124 enhanced transfection efficiency was examined using flow cytometry to determine the
125 fraction of transfected, EGFP-expressing cells for different light illumination periods. The
126 details of this approach are shown in Scheme 1.



127

128 **Scheme 1** (a) Schematic illustration of preparation of LPD and (b) intracellular events in the course
 129 of light-triggered gene transfer, (1) Polyplex complexation (2) Dried in vacuum (3) Hydration (4)
 130 Cellular uptake (5) 690 nm photoirradiation (6) Endolysosomal escape (7) Vector dissociation (8)
 131 Nuclear translocation (9) Gene transcription (10) EGFP expression.

132 2. Experimental

133 2.1 Materials

134 Lipids (DOTAP: Catalog No. 890890 and DOPE: Catalog No. 850375, DSPE-PEG (2000)
 135 Amine: Catalog No. 880128) were purchased from Avanti Polar Lipids (Alabaster, AL,
 136 USA). Dulbecco's modified Eagle's medium (DMEM: Catalog No. 11965-092), fetal
 137 bovine serum (FBS: Catalog No. 10437-028), trypsin (Catalog No. 15400054),
 138 LysoTracker (Catalog No. L7528), Hoechst 33342 (Catalog No. H3570), Phosphate-

139 buffered saline (PBS: Catalog No. 10010023) and Dulbecco's Phosphate-buffered saline
140 (DPBS: Catalog No. 14190250) solution, Hank's Balanced Salt Solution (HBSS: Catalog
141 No. 14175145) solution, 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES:
142 Catalog No. 14185052) buffer, TAE Buffer (Tris-acetate-EDTA, 50×, Catalog No. B49)
143 optiMEM (Catalog No. 31985070) solution were purchased from ThermoFisher (Scoresby,
144 Vic, Australia). McCoy's 5A medium (product no: ATCC® 30-2007™), were purchased
145 from the ATCC. Uranyl acetate (Catalog No. 73943), paraformaldehyde (Catalog No.
146 P6148), chloroform (Catalog No. 372978), cholesterol (Catalog No. C8667),
147 Fluoromount™ aqueous mounting medium (Catalog No. F4680), DNase I
148 (Deoxyribonuclease I, Catalog No. D5025), phosphotungstic acid (PTA, Catalog No.
149 P4006) and 2', 7'-Dichlorofluorescein diacetate (DCF-DA) (Catalog No. D6883) were
150 purchased from Sigma-Aldrich (Castle Hill, NSW, Australia).

151

152 **2.2 Plasmid DNA and cell lines**

153 The plasmid pEGFP-N1 (GenBank: U 55762.1) encoding the enhanced green fluorescence
154 protein, EGFP (4.7 kbp), was obtained from the Chinese People's Liberation Army Military
155 Academy of Medical Sciences (Beijing, China). It was amplified in the *E. coli* DH5α strain,
156 extracted and purified using the Qiagen Plasmid Midi Kit. The concentration of the pEGFP-
157 N1 solution was determined with NanoDrop 2000 (ThermoFisher, Vic, Australia). The
158 fluorescein labelled pDNA was prepared using the Label IT® Nucleic Acid Labelling
159 Reagents (Mirus Bio LLC., WI USA) as per the manufacturer's instructions.

160 A human colorectal cancer cell line, HCT116 (product no: ATCC® CCL-247™) were
161 purchased from ATCC (Manassas, VA USA). McCoy's 5A medium supplemented with

162 10% FBS and 1% Antibiotic-Antimycotic was used to culture the HCT 116 cells. DMEM
163 supplemented with 10% FBS and 1% Antibiotic-Antimycotic was used as the culture
164 medium of the HCT 116 cells. The cells were grown at 37 °C with 5% CO₂ in the cell
165 incubator. When cells reached about 90% confluence, they were detached with trypsin and
166 transferred into petri dishes or well plates for different experimental purposes.

167

168 **2.3 Preparation of liposomes and LPDs**

169 Liposomes with different formulations were prepared via a thin-film method⁴⁴ with some
170 modifications. Briefly, lipid components at different mole ratios were mixed with VP at the
171 fixed amount in 5 mL chloroform in a round flask (Scheme 1). The mixture solvent was
172 then evaporated under argon gas stream with a rotary evaporator (Buchi R-300, Flawil
173 Switzerland) for 15 min at 50 °C. The thin lipid film was formed at the bottom of the flask
174 and subsequently hydrated with HEPES buffer (40 mM, pH 7.4) by vigorous stirring for 30
175 min until the suspension was homogenized. The hydrated liposome suspension was
176 extruded 11 times through a 200 nm polycarbonate membrane in a mini-extruder (Avanti
177 Polar Lipids). The final liposome suspension was purified by using 3000 MW dialysis tubes
178 for 24h at 37 °C in 500 µL DI water prior to further use. To determine the encapsulation
179 amount of VP loaded inside of liposomes, we added Triton X-100 (0.1%) to as-prepared
180 liposome solution, resulting in VP release. The VP fluorescence (excitation/emission:
181 425/690 nm) was recorded on a Fluorolog-Tau-3 system and compared with the
182 corresponding VP calibration standard curve. To determine the encapsulation efficiency of
183 VP loaded inside liposomes at different time points (6 h, 12h, 24h, 36h, 48h), dialysis was

184 conducted. The leaked VP was calculated compared with the corresponding VP standard
185 curve via the fluorophotometer measurement.

186 The HN buffer (150 nM NaCl and 10 mM HEPES, pH 7.4) is the complexation buffer used
187 for LPD formation. Polyplexes (PEI/pDNA complexes) with different N/P ratios⁴⁵ were
188 prepared by incubation of pDNA with different amounts of PEI solution at 37 °C in the HN
189 buffer for 30 min. For the preparation of the LPD, the as-prepared lipid film was hydrated
190 with the solution of preformed polyplexes for 30 min at room temperature. The hydrated
191 lipopolyplex solution was freshly prepared prior to cell experiments and measurements.

192 **2.4 Characterization**

193 The zeta potential and size distribution of liposome samples with and without PEGylation
194 were determined by DLS using a Zetasizer 3000HSA (MALVERN Instruments,
195 Worcestershire, UK). After 2 min balance at 25°C, each sample was measured in triplicate
196 and data were collected as the mean \pm standard deviation (SD). The size of liposome
197 suspended in different solutions including HEPES buffer, optiMEM medium and 10% FBS
198 solution were also measured at different time points.

199 Prior to transmission electron microscopy (TEM) imaging of liposome samples, the TEM
200 grid specimens were prepared using the negative staining method. Briefly, a copper grid
201 was placed onto a drop of 10 μ L liposome, LPD or polyplex suspension, allowing the grid
202 to absorb samples for 3 min, followed by staining with 2% (w/v) phosphotungstic acid for
203 another 3 min. After air-dry of samples overnight, the grid specimens were then observed
204 under a TEM (Philips CM 10) with an acceleration voltage of 100 KV. Images were
205 captured with the Olympus Megaview G10 camera and processed with iTEM software.

206 The absorption and fluorescence spectra of liposomes and pure VP were measured with a
207 UV-VIS spectrometer (Cary 5000, Varian Inc.) and a Fluorolog-Tau3 System (HORIBA
208 Scientific) with 425 nm Xe lamp excitation, respectively. To determine the encapsulation
209 efficiency of VP loaded inside liposomes, Triton X-100 (0.1 %) was added to as-prepared
210 liposome solution, resulting in destabilization of liposomal structure and VP release. The
211 VP fluorescence (Ex/Em: 425 nm/690 nm) was recorded on a Fluorolog-Tau-3 system and
212 its concentration was calculated from the standard curve of free VP solution.

213 For thermal stability measurement, differential scanning calorimetry (DSC2010, TA
214 Instruments, Delaware, US) was used to characterize the temperature of liposome phase
215 transitions (T_m). Briefly, about 10 μL of each sample was placed on an aluminium pan
216 which was covered with an aluminium lid. The pans were heated in a linear gradient (1
217 $^{\circ}\text{C}/\text{min}$, rising from 25 to 100 $^{\circ}\text{C}$) in a nitrogen environment, alongside with a reference
218 pan containing 10 μL of HEPES buffer. The peak on each enthalpy graph was indicated
219 with T_m of each sample (data was acquired and exported from the Universal Analysis
220 software).

221 **2.5 Gel electrophoresis**

222 To evaluate the pDNA loading ability of liposomes and determine the best N/P ratio, the
223 electrophoresis using 1% agarose gel (w/v) in TAE (1 \times) buffer was conducted. The
224 complex solution with various N/P ratios was loaded into the agarose gel. The gel was pre-
225 stained with SYBR Safe DNA stain before running electrophoresis, which was carried for
226 40 min at a constant voltage of 90 V. Electrophoresis images were then visualized using
227 Gel Imaging U: Genius3 (Syngene, UK). The image acquisition was done using the
228 software GeneSys.

229 **2.6 Enzymatic degradation assay**

230 To assess the capability of LPD for protection of pDNA from DNase I, enzymatic digestion
231 assay was conducted. The LPDs with different N/P ratios were suspended in 1× DNase I
232 Reaction Buffer (10 mM Tris-HCl, 2.5 mM MgCl₂, 0.5mM CaCl₂, pH 7.6) to a final volume
233 of 50 μl. Two units of DNase I were then added and mixed thoroughly. The mixture solution
234 was incubated at 37°C for 10 minutes, followed by gel electrophoresis analysis described
235 above.

236 **2.7 Cellular uptake of liposomes and endolysosomal escape with light triggering**

237 HCT 116 cells (5×10^4 /well) were plated on the coverslips in a 24-well plate and incubated
238 overnight at 37 °C in a humidified 5% CO₂ atmosphere. The cells were then incubated with
239 500 μL of optiMEM solution containing LPD LPDs (10 μg/mL) for different periods. After
240 incubation, the old media were removed and the cells were washed three times with PBS
241 solution (1 ×, pH 7.4). For the assessment of light-triggered endolysosomal escape of
242 fluorescein labelled pDNA molecules, light irradiation (690 nm, 15 mW/cm²) using a red
243 LED light source (Fedy, Shenzhen, China,) were carried out for 4 min after 2 hr of
244 incubation of cells with the LPD . For endolysosome staining, LysoTracker (50 nM in
245 optiMEM) was added into the cell culture medium in each well and incubated for one hour
246 before the cells were collected to be fixed. The cells were fixed with 2% paraformaldehyde
247 (10 min, 37°C) and stained with Hoechst 33342 (5 μg/mL) (10 min, 37 °C). After staining,
248 each coverslip was washed by the PBS solution three times and then mounted onto a glass
249 slide. The glass slide was imaged using a Leica SP2 confocal laser scanning microscopy
250 (CLSM) system. The excitation wavelengths of 405 nm, 488 nm, and 543 nm were used
251 for the confocal imaging of VP, fluorescein labelled pDNA and LysoTracker, respectively.

252 Their fluorescence emission was imaged at for 460 ± 10 nm Hoechst 33342, 525 ± 25 nm
253 for fluorescein, 590 ± 10 nm for LysoTracker and 700 ± 25 nm for VP.

254 **2.8 Assessment of gene transfection after light illumination**

255 HCT 116 cells were seeded on a 24-well plate at the density of 1×10^5 cells/well, followed
256 by overnight incubation. 500 μ L of optiMEM solution containing LPDs (N/P = 25) was
257 added to each well. After 2 h incubation, the cells were exposed to the 690 nm LED light
258 (0.15 mW/cm^2) for 2 min, 4 min, 6 min respectively, followed by additional one hour
259 incubation. The old medium was replaced by the fresh one and the cells were incubated for
260 another 22 h. The EGFP expression in the cells was imaged using a CLSM system. The
261 transfection efficiency of different samples was measured using flow cytometry
262 (CytoFLEX S, Beckman Coulter, Australia). The cells were washed twice and harvested in
263 the DPBS buffer at the concentration of 10^6 cells mL^{-1} , followed by flow cytometry
264 measurements of the percentage of cells expressing EGFP.

265 **2.9 Detection of cellular ROS generation after light illumination**

266 DCF-DA is a non-fluorescent molecule, which can be rapidly oxidized by cellular ROS to
267 the fluorescent DCF. This allows it to be the indicator of a broad range of ROS⁴⁶. In order
268 to quantify ROS generation upon light irradiation, the HCT116 cells (5×10^4 /well) were
269 cultured in the petri dishes overnight. After removing the culture medium, the cells were
270 incubated with 500 μ L of the optiMEM solution containing LPDs (10 $\mu\text{g/mL}$). After 2 h
271 incubation at 37 $^\circ\text{C}$, the medium was removed and the cells were washed with 500 μ L of
272 $1 \times$ HBSS solution five times. 200 μ L of $1 \times$ HBSS containing DCF-DA (25 μM) was
273 subsequently added to the cells, followed by incubation for 30 min at 37 $^\circ\text{C}$, while protected
274 from light. After incubation, the cells were illuminated by 690 nm LED light for different

275 time periods (2 min, 4 min and 6 min). After light irradiation, the DCF-DA solution was
276 removed and cells were washed with PBS three times, followed by imaging under a Leica
277 SP2 CLSM system. For comparison, the control cells were incubated with 100 μ L of the
278 optiMEM solution containing H₂O₂ at different concentrations (1 μ M, 10 μ M and 100 μ M)
279 for 2 hours followed by addition of DCF-DA and CLSM imaging. For the determination of
280 ROS, cells were cultivated in 96-well plates, instead of petri dishes, and followed by the
281 same procedure as described above. After treatment, the mean DCF fluorescence intensity
282 in each group was determined by flow cytometry.

283 **2.10 Cell viability assays**

284 The HCT 116 cells were seeded into 96-well plates (1×10^4 per well) and cultured for 24 h
285 at 37°C. The old medium was then removed and the optiMEM solution containing
286 liposomes (10 μ g/well, encapsulating VP), lipopolyplex (10 μ g/well) and pure PEI (10
287 μ g/well) were added to each well. After 2 hours of incubation, the cells were washed with
288 PBS three times to remove unbound samples. The fresh medium was then added to the cells,
289 followed by another 24 hr incubation. For the light irradiation alone, the cells were exposed
290 to 690 nm light source (15 mW/cm²) for 1 min, 2 min, 4 min and 6 min, respectively. After
291 light treatment, the fresh medium was added to the cells for another 24 hr incubation. The
292 toxicity of the liposomes, LPDs, pure PEI solution and 690 nm light in cells was assessed
293 using the MTS kit (Promega, WI, USA) as per manufacturer's instructions. Cell viability
294 was calculated as a percentage of the absorbance in treated cells compared with the
295 untreated control cells.

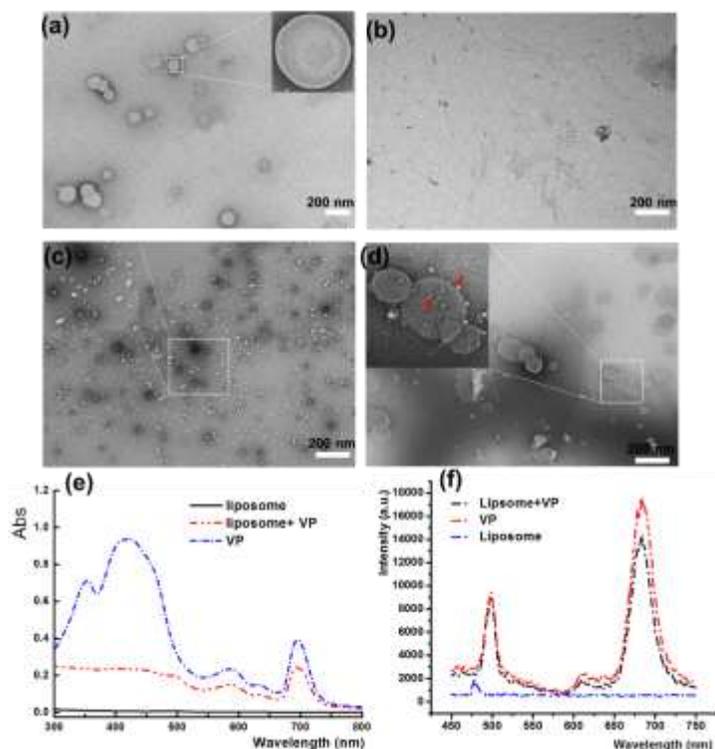
296 **2.11 Statistical analysis**

297 All quantitative data were shown as mean \pm SD from at least three parallel groups. *P* values
298 were determined by Student's t-tests or two-way ANOVA (analysis of variance) using
299 Prism 5 (GraphPad). **p* <0.05, ***p* <0.01, ****p* <0.001 and *****p* <0.0001 were thought
300 to be statistically significant.

301 3. RESULTS AND DISCUSSION

302 3.1 Characterization of pDNA and liposome samples

303 The morphology and optical properties of pure pDNA molecules, polyplexes and LPD
304 samples were determined by using spectrophotometry and TEM. The plasmid map was
305 plotted using Vector NT and its absorption spectrum is shown (Figure S1a). The absorbance
306 ratios between 260 nm and 280 nm Abs₂₆₀/Abs₂₈₀) and between 260 nm and 230 nm
307 (Abs₂₆₀/Abs₂₃₀) were calculated to be about 1.8 and 2.0, suggesting high purity of DNA
308 molecules⁴⁷. The TEM images in Fig. 1 show the structure of liposomes loaded with VP
309 (Fig. 1a), pDNA (Fig. 1b), polyplexes (Fig. 1c) and LPDs (Fig. 1d). The PEI/pDNA
310 polyplexes (indicated by red arrows) were observed inside the liposomes as well as on the
311 surface of the liposomes (Fig. 1d). In addition, the VP absorption peak at 690 nm was
312 slightly blue-shifted to a shorter wavelength at 685 nm when loaded inside liposomes
313 compared to VP alone (Fig. 1e), which was consistent with the reported study that
314 liposome's encapsulation causes a blue shift of the loading cargoes⁴⁸. However, the
315 fluorescence spectrum of liposome-formulated VP was not obviously changed compared
316 to pure VP solution (Fig. 1f). These results indicated that VP was encapsulated in the
317 liposomes. The amount of VP loaded inside liposomes was calculated to be approximately
318 112 μ g/mL.



319
320 **Figure 1** Characterization of different liposome samples. Representative TEM images of (a)
321 liposome loaded with VP, (b) pure pDNA, (c) polyplexes and (d) LPDs. The red arrows indicate
322 the polyplexes. (e) The absorbance and (f) fluorescence spectra of pure liposomes, liposomes
323 loaded with VP and pure VP.

324

325 3.2 Stability studies of liposome formulations

326 Size distribution and zeta potential of liposome formulations with varying Chol content was
327 determined by the DLS method, as shown in Table S1 and Fig S1b. The mean size of
328 liposomes increased with increasing Chol content, up to 150 nm for Chol levels exceeding
329 50%. These results are consistent with the literature⁴⁹. All the PDI values of nanoparticle
330 suspension are around 0.40, varying slightly between groups with different Chol content.
331 These values indicate a relatively narrow size distribution of the as-prepared LPD⁵⁰. The

332 zeta potential reduced gradually with the increasing Chol%, because of an increase in the
333 negatively charged hydroxyl group (-OH) on cholesterol.

334 Chol is a very important component in the liposomal structure which helps to control the
335 rigidity of the lipid bilayer⁵¹. In order to determine the optimized Chol% for the stabilized
336 liposomes, DLS measurements within six days and DSC assay have been conducted. As
337 shown in Figure S2a and b in the supporting data, the size and corresponding PDI of
338 liposomes with 33% Chol was largely unchanged during 6-day incubation time, compared
339 with other Chol contents; similar results were reported earlier⁵². However, because
340 cholesterol has a very small hydrophilic head and is, therefore, less efficient in shielding
341 the hydrophobic interaction, the excess addition amount of Chol would lead to undesired
342 destabilization of lipid bilayers⁵³. Hence, 33% Chol was chosen to formulate liposomes for
343 following experiments.

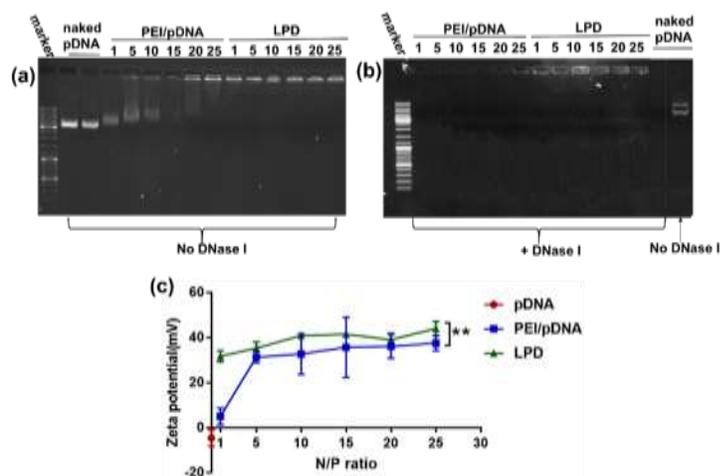
344 In addition, the DSC heatflow diagram (Figure. S2c) exhibits the phase transition
345 temperature (T_m) of each liposome with various Chol%. In the absence of Chol, liposomes
346 didn't show any phase change peaks. However, when the Chol fraction reached 50%, the
347 phase transition could be observed. This is because the higher content of cholesterol allows
348 the formation of the anhydrous cholesterol domain in bilayer structure²⁶, which facilitates
349 the phase transition from solid-gel to a liquid crystal phase. Compared to the liposomes
350 having 50% Chol where the T_m was 55 °C, the liposomes with a higher proportion of
351 cholesterol (66.7%) exhibited a higher T_m of 72 °C. The increase in T_m confirms that the
352 addition of cholesterol to the liposome formulation contributes to enhanced stabilization of
353 as-prepared liposomes.

354 To further demonstrate the stability of PEGylated liposomes in the physiological
355 environment, DLS measurements were conducted to monitor the size changes of PEGylated
356 and non-PEGylated liposomes in the serum-reduced medium (optiMEM) and serum-
357 containing solution (10% FBS cell culture medium). As shown in Figure. S3, the size of
358 conventional liposomes was increased by a factor of two after 6 hr incubation in both the
359 optiMEM medium and normal cell culture medium. However, the PEGylated liposomes
360 liposomes demonstrated a smaller size change did not change so largely compared to non-
361 PEGylated groups ones at the same experimental conditions. In addition, the change of
362 encapsulation efficiency (Figure S3c) of VP with different dialysis time also demonstrated
363 that PEGylated liposomes can lead less leakages of the loaded VP molecules compared to
364 the non-PEGylated groups. These findings indicate that the PEGylation enhances the
365 stability of liposomes during 6 hr incubation compared to the liposomes without
366 PEGylation. The optimal formulation of liposomes with the higher stability is the molar
367 ration of 1:1:1:1 for DOTAP, DSPE-PEG, DOPE and Chol. In addition, VP release profile
368 from liposomes with and without PEGylation also indicated that PEGylated liposomes have
369 higher stability compared to the non-PEGylated ones (Figure 3c).

370 **3.3 The DNA loading capability of LPDs measured by gel electrophoresis**

371 In the presence of polycations or cationic liposomes, the DNA molecules can self-assemble
372 into polyplexes and/or lipoplexes due to electrostatic attraction. An ideal polycation-based
373 gene carrier should have the capability to load a high amount of negatively charged DNA
374 and facilitate cellular uptake. To determine the DNA loading capability of LPD with
375 different N/P ratios used in this study, the agarose gel retardation assays were conducted.
376 The naked DNA molecules without any loading vehicles were clearly observed from the

377 gel, however, less DNA was detected with an increased N/P ratio (Fig. 2a). When the value
 378 of N/P ratio reached 25:1, free DNA could not be detected in the agarose gel lanes,
 379 indicating that the maximal amount of DNA molecules can be loaded into the PEI/pDNA
 380 polyplexes when N/P ratio reached 25:1.



381
 382 **Figure 2** Gel retardation assays of polyplexes and LPDs with different N/P ratios (a) without and
 383 (b) with DNase I digestion. (c) Zeta potentials of pDNA, PEI/pDNA, LPD with various N/P ratios.
 384 ** $p < 0.01$.

385
 386 It's worth mentioning that LPDs have the higher capacity of condensing negatively charged
 387 DNA, compared with the PEI/pDNA polyplex, which was confirmed by the fact that less
 388 DNA migrated from the gel wells than the polyplex at same N/P ratio (Fig. 2a.). The
 389 condensation of DNA molecules also contributes to the prevention of enzymatic
 390 degradation. To demonstrate the reduced enzymatic degradation of DNA in polyplexes and
 391 LPDs, the DNase I, a strong endonuclease that non-specifically cleaves DNA, was
 392 respectively added into pDNA, polyplex and LPDs for the enzymolysis assay. As shown in
 393 Fig. 2b, DNA loaded inside the LPDs at all N/P ratios were clearly visualised in the gel

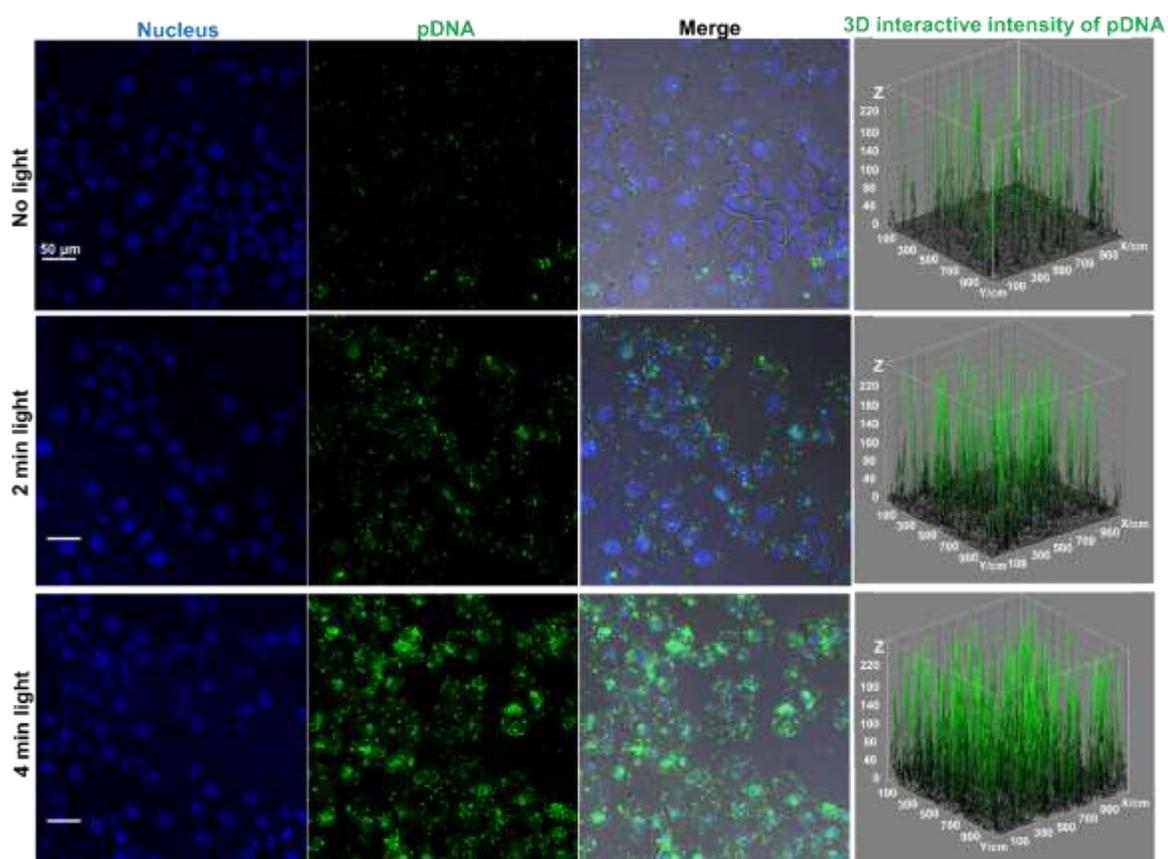
394 wells even after the DNase I reaction, while DNA in the polyplex at high N/P ratio only
395 can be observed. For the polyplex at low N/P ratio less than 20 and pure pDNA, there was
396 no clear indication of DNA after enzymatic degradation. These results indicated that the
397 encapsulation of polyplexes into the liposomal cavity can significantly reduce the
398 enzymolysis effect on cleaving DNA molecules. Therefore, by using this LPD structure,
399 exogenous genetic materials can be protected against undesired enzymatic degradation and
400 delivered to the cells of interest. Additionally, the zeta potential of polyplexes and LPDs
401 with varying N/P ratios was also measured. As shown in Fig. 2c, the zeta potential of
402 different complexes increases with increasing N/P ratio, with higher positive values for
403 LPDs than the polyplex group. This increased positive charge of LPDs would facilitate
404 their cellular uptake through endocytosis pathway due to the preferential interaction
405 between the positively charged delivery platform and negatively charged cell membranes.

406 **3.4 Cellular uptake of LPDs, light-triggered ROS generation, and pDNA release**

407 Fig. S4 in shows representative CLSM images of the internalized LPDs in HCT 116 cells
408 after different periods of incubation (1, 2 and 3 hr). After 3 hr incubation, the perinuclear
409 rings with red fluorescence signal from VP were clearly observed, compared with the cells
410 during 1 hr and 2 hr incubation. Therefore, we chose 3 hr incubation time in this study.

411 Light-induced cellular ROS generation from LPDs was evaluated by using the DCF-DA
412 assay. In principle, the cell-penetrable nonfluorescent DCF-DA molecules can be oxidized
413 by ROS molecules, resulting in the production of fluorescent DCF. The fluorescence
414 intensity of DCF was increased with light illumination, indicating that a higher amount of
415 ROS was generated from VP loaded inside LPDs than that in non-irradiated cells (Figure.
416 S5). By comparing with the H₂O₂-treated groups which were considered as positive

417 controls⁵⁴, the DCF intensity in the cells treated by LPDs and 6 min illumination was almost
418 equivalent to that produced by 100 μM H_2O_2 .
419 Additionally, cellular pDNA release from LPDs was assessed by irradiating cells with LED
420 light (690 nm, 15 mW/cm^2) for 2 and 4 mins, respectively. As shown in Fig. 3, the increased
421 green signal from the released pDNA (labelled with fluorescein) was clearly observed with
422 light illumination, with the maximum intensity being achieved at 4-min illumination,
423 compared with the absence of illumination. These data indicate that the release of pDNA
424 molecules from the endolysosomal compartments can be enhanced by light irradiation. The
425 reason could be attributed to photochemical damage of endolysosomal membranes caused
426 by increased ROS production due to light exposure.

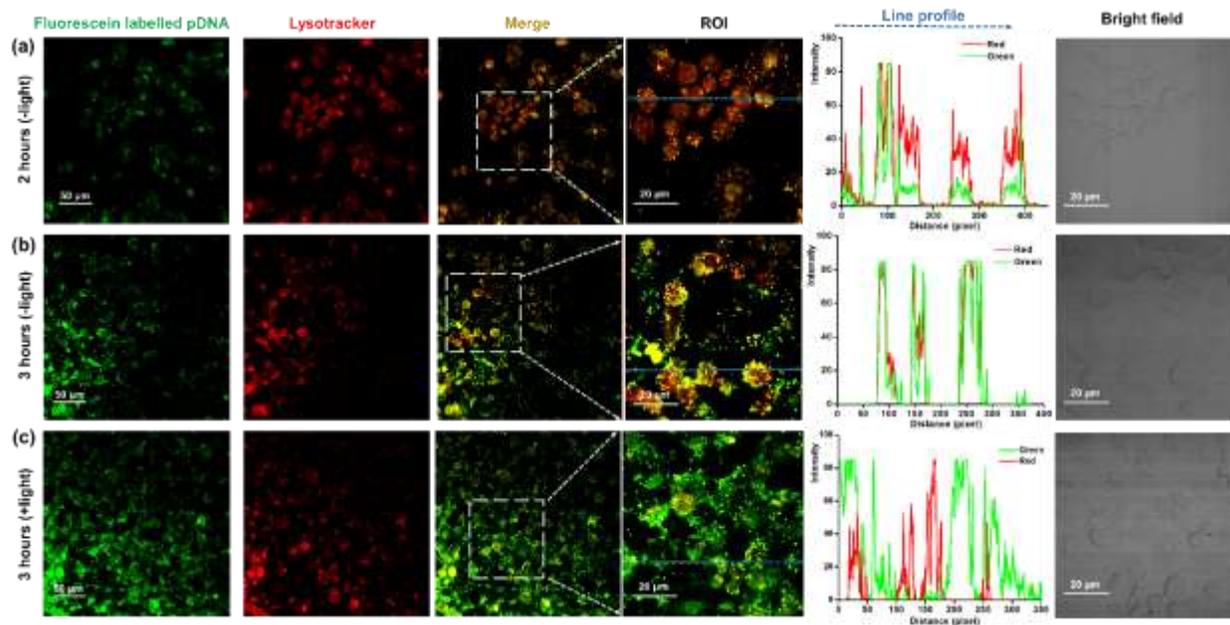


427

428 **Figure 3** CLSM images and 3D interactive intensity plot of fluorescein-labelled pDNA
429 release after photoirradiation for different periods: 0, 2, and 4 min. The merge panel
430 represent the images merged by the blue, green and bright field channels. Scale bars = 50
431 μm .

432 **3.5 Quantitative analysis of endolysosomal escape of pDNA after light illumination**

433 To further characterise the enhanced cellular release of pDNA from light-triggered LPDs,
434 intracellular trafficking, and endolysosomal escape were recorded by using CLSM and
435 analysed by the object-based colocalization of fluorescence intensity (Fig. 4), which was
436 done by using the line profile in ImageJ software. After 2 hr incubation, most fluorescein
437 labelled pDNA was observed to be internalized in cells, which was confirmed by the pixel
438 intensity profile (the line profile panel in Fig. 4). These data also show that most of the
439 green signal from fluorescein (pDNA) overlap with the red signal from LysoTracker
440 (endolysosomes) although its intensity is lower than the LysoTracker signal (Fig. 4a). After
441 3 hr incubation, a stronger overlap between the green and red signal was observed,
442 indicating that the entrapment of LPDs inside the endolysosomes was enhanced after 3 hr
443 incubation, compared to 2 hr (Fig. 4b). However, after a subsequent 4-min light irradiation
444 and another 1 hr incubation, most pDNA molecules escaped outside the endolysosomal
445 compartments. This was confirmed by the reduced overlap between the green and red
446 channels, as shown in Fig. 4c.



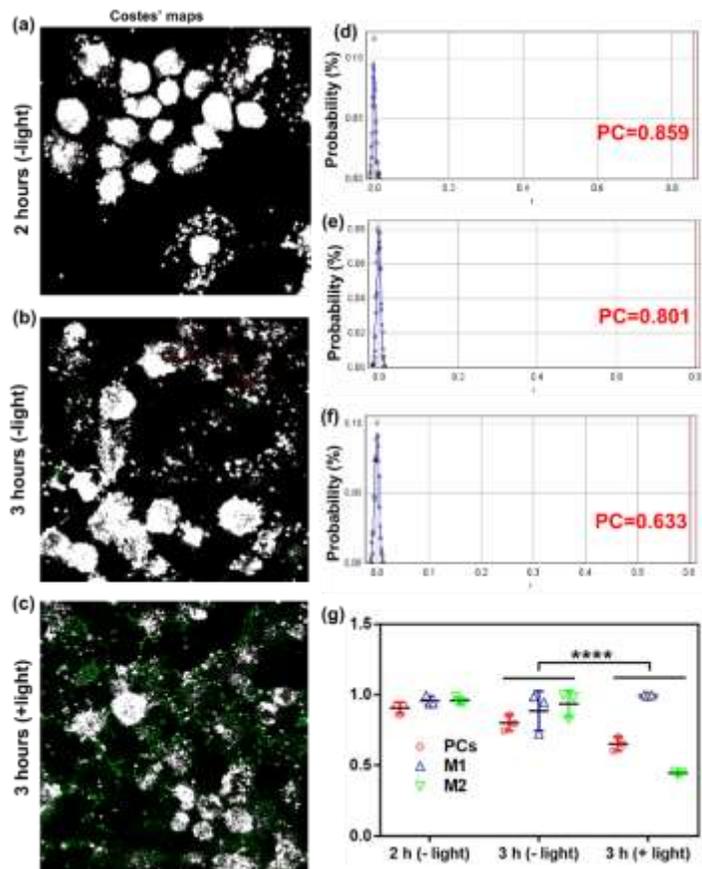
447
 448 **Figure 4** CLSM images of colocalization between the endolysosomes (LysoTracker, red channel)
 449 and fluorescein-labelled pDNA (green channel) (a) after 2 hr incubation, (b) after 3 hr incubation
 450 and (c) after 3 hr incubation and 4-min light illumination. The line profile plots indicate the
 451 intensity distribution of green and red channels through the blue lines in the magnified view of
 452 ROI in the merged panel. The right panel presents the bright field pictures of ROI.

453
 454 To confirm the light-induced escape of pDNA, the colocalization of regions of interest
 455 (ROI) shown in Fig. 4 was further quantified using the Costes' approach, Mander's
 456 coefficient and the Pearson's coefficient (PC) analysed by using ImageJ. Fig. 5a, b and c
 457 show the Costes' maps of the ROIs in Fig 4a, b and c, respectively. Based on the Costes'
 458 approach, the colocalization between pDNA and endolysosomes was represented by a
 459 white overlay of red signal from LysoTracker and the green signal from fluorescein. A large
 460 white area was respectively observed after 2-hr and 3-hr incubation suggesting that most
 461 LPD nanoparticles were internalized into the endolysosomes (Fig. 5a and b). However, in

462 the presence of light illumination, green areas appeared and white areas were significantly
463 reduced, indicating that most LPD nanoparticles were released from endolysosomal
464 compartments into the cytoplasm (Fig. 5c).

465 Based on the Costes' colocalization analysis, the PC value was also evaluated. The PC
466 ranges from -1 to 1, with -1 indicating a negative correlation, 1 indicating a positive
467 correlation and 0 standing for no correlation. The PC value was 0.859 and 0.801 after 2 h
468 and 3 h incubation without light illumination, respectively, which indicated that most
469 pDNA molecules were colocalized with endolysosomes (Fig. 5d and e). However, the value
470 of PC decreased to 0.633 after light illumination (Fig. 5f), consistent with the pDNA release
471 from the endolysosome compartments.

472 Furthermore, the Mander's coefficient, varying from 0 to 1, was calculated to determine
473 the overlap fraction of two channels. Here, M1 is defined as the proportion of the green
474 signal coincident with the red signal over its total intensity and M2 is the fraction of green
475 signal coincident with the red one⁵⁵. As shown in Fig. 5g, M2 (indicated by green triangles)
476 was only 44.5% after light illumination, compared with control cells without light
477 illumination (M2 = 99.6%), suggesting that more DNA molecules escaped from
478 endolysosomes after light treatment.



479

480 **Figure 5** (a), (b) and (c) are the Coste's maps of Fig. 4 (a), (b) and (c), respectively, showing
 481 colocalization between pDNA and endolysosomes. (d), (e) and (f) are plots of the distributions of
 482 the Pearson's coefficients (PCs) of (a), (b) and (c) respectively. (g) Manders' coefficient analysis
 483 and PCs. **** $p < 0.0001$.

484

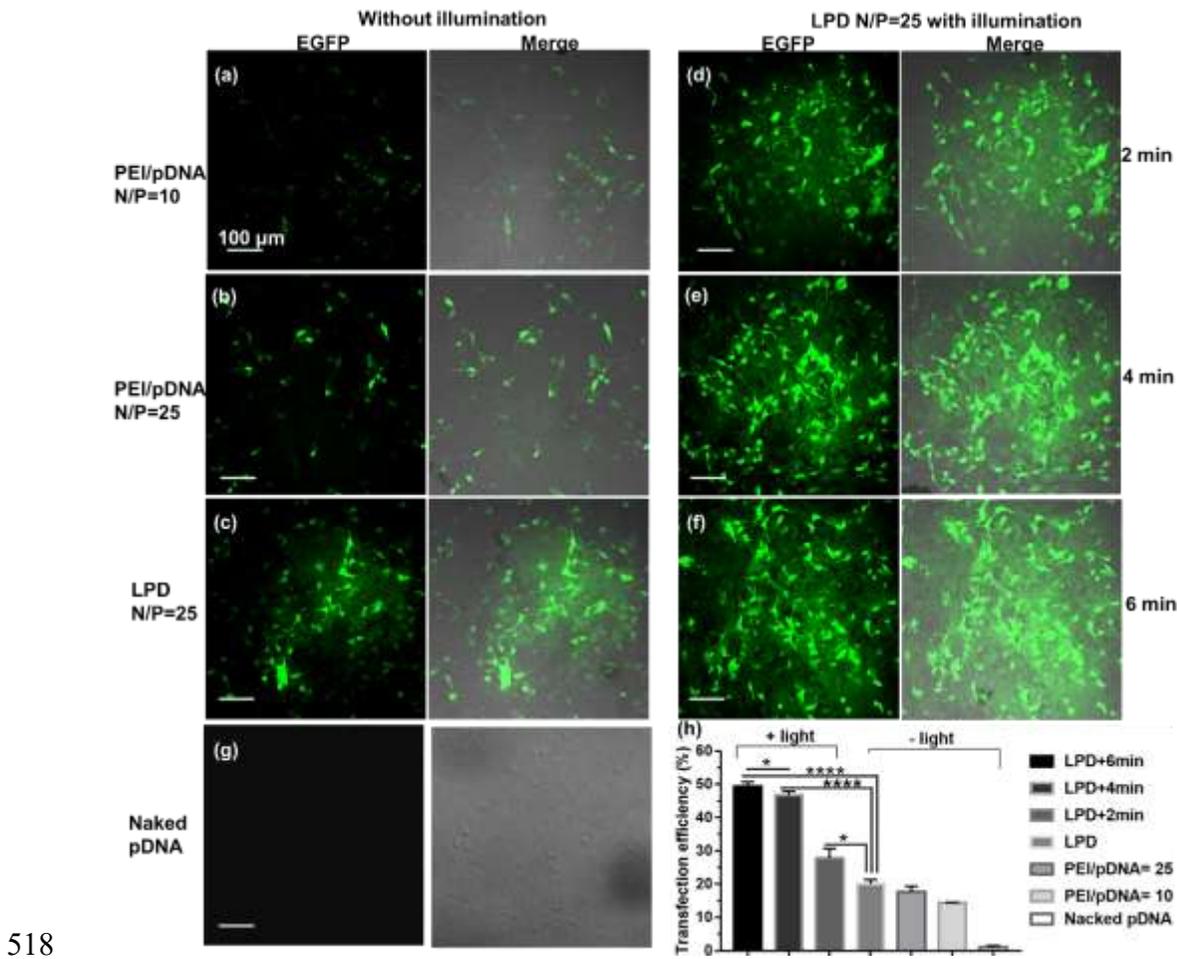
485 3.6 Gene transfection under light irradiation

486 The CLSM images and quantitative analysis of EGFP expression in HCT 116 cells after
 487 light-triggered pDNA release are shown in Fig.6. When cells were treated with LPD
 488 (N/P=25) alone, a slightly higher EGFP fluorescence intensity was observed, compared
 489 with PEI/DNA (N/P=25) treated cell group (Fig. 6b, c, and h). However, with light
 490 illumination, LPD produced enhanced transfection efficiency. The maximum EGFP

491 expression level was achieved after 4 min illumination ($49.3 \pm 1.4 \%$), to a value of over
492 twice that in the LPD transfected cells without light irradiation ($20.1 \pm 1.3 \%$, Fig. 6h). It
493 should be mentioned that, compared with 2 min illumination, the EGFP fluorescence after
494 4 min illumination shows slightly increasing signal in CLSM images (Fig. 6e and f), but its
495 intensity is changed in a statistically significant fashion (Fig. 6h, $*p < 0.5$). These results
496 are consistent with the pDNA release profile under light irradiation shown in Fig. 3. For
497 comparison purposes, the cells were also transfected with PEI/pDNA polyplexes (N/P=10
498 and pure pDNA but without light illumination). A lower EGFP fluorescence intensity was
499 observed in these groups, compared with cells transfected by LPDs (Fig. 6a, c, and g),
500 indicating the limited transfection efficiency of PEI/DNA complexes (N/P=10) and pure
501 DNA molecules. Additionally, we evaluated EGFP fluorescence intensity in HCT 116 cells
502 transfected with pure DNA, PEI/DNA complexes and LPDs with and without light
503 illumination by flow cytometry. The representative intensity histograms are shown in
504 Figure S6. The fluorescence intensity of the LPD-transfected groups was increased with
505 prolonged photoirradiation, which confirmed the enhanced transgene efficiency of LPD by
506 photoirradiation.

507 The maximum transfection efficiency achieved in this study is comparable with previously
508 published work where the combination of branched PEI (BPEI)/pDNA with reduced
509 graphene oxide (rGO) was used to release pDNA under light illumination⁵⁶. In this earlier
510 work, the transfection efficiency of the PEG–BPEI–rGO/pDNA (N/P=20) nanocomplexes
511 in PC-3 and NIH/3T3 cells (with 20-min irradiation at a wavelength of 808 nm, at a light
512 irradiance of 6 W/cm^2) was 2-3 times compared with nanocomplexes alone. However, the
513 involvement of graphene-based materials in this earlier study requires a detailed evaluation

514 of the toxicity of these materials prior to clinical translation. By contrast, the liposome
 515 delivery system used in our work has a high potential for clinical translation due to the long
 516 and successful history of using liposomes for encapsulating agents such as Doxorubicin for
 517 clinical use.

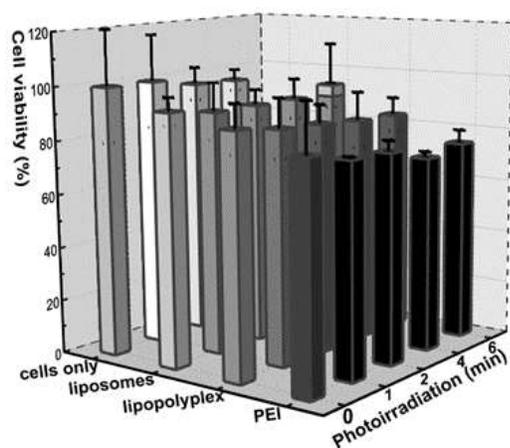


518
 519 **Figure 6** CLSM images (a-f) of EGFP expression in HCT 116 cells after 48 hr of transfection with
 520 and without light illumination. Scale bars = 100 μ m. (h) transfection efficiencies of different
 521 groups. * $p < 0.05$ and **** $p < 0.0001$, compared to the LPD group without light.

522

523 3.7 Cellular cytotoxicity assays of different nanocomplexes and light illumination

524 A series of cell viability tests after the nanocomplex and light treatments were performed
525 to estimate the potential toxicity effect on cells. As shown in Fig. 7, for the light treatment
526 alone, the cell viability was not changed significantly compared to the controls. Among the
527 delivery systems considered in this work, with same concentration at 10 $\mu\text{g}/\text{well}$, PEI has
528 higher toxicity to cells, about 32% cells being affected when treated with PEI and
529 illuminated for 4 min. By contrast, the liposomes and LPDs did not affect cell viability,
530 even under photoirradiation for different time periods. For example, about 17% cells were
531 killed by LPDs after 6-min illumination. This could be a result of the light-triggered ROS
532 generation from VP. However, more than 80% cells were still alive in liposome and LPD
533 groups, indicating that these delivery platforms are relatively biocompatible.
534 In this study, PEI polyplexes still exhibited their intrinsic cytotoxicity (around 70% cell viability
535 in our experimental conditions). However, the cytotoxicity was significantly reduced by
536 incorporating PEI/pDNA complexes into liposomes. The results on cell viability after treatment
537 with our lipopolyplex and light illumination was even comparable with other liposome-PEI hybrid
538 vectors alone (more than 80% cell viability)⁵⁷.



539

540 **Figure 7** Cytotoxicity of liposomes (10 $\mu\text{g}/\text{well}$), lipopolyplex (10 $\mu\text{g}/\text{well}$) and PEI (10 $\mu\text{g}/\text{well}$)
541 on HCT 116 cells in combination with photoirradiation.

542 4. CONCLUSION

543 In summary, a photoresponsive LPD system was developed for pDNA delivery and release
544 *in vitro*. The complexation of DNA and PEI and formation of the LPD nanoconstruct
545 enhanced the loading capacity of pDNA into the liposomal vehicles. Subsequent
546 encapsulation of polyplexes inside liposomes overcame the disadvantages in high
547 cytotoxicity of PEI and photosensitizer molecules. The addition of cholesterol and
548 PEGylated lipids in liposome formulation improved the stability and biocompatibility of
549 nanocomplexes in the physiological environment, which is very important for the use of
550 light-triggered liposomes in *in vivo* applications, in particular, on-demand gene release. The
551 VP molecules introduced into the liposome cavity generated ROS after light illumination,
552 enabling endolysosomal escape of pDNA via a photochemical internalization mechanism.
553 This dynamic process has been demonstrated by quantitatively analysing image-based
554 colocalization between nanocomplexes and endolysosomes. After light triggering, pDNA
555 was released and modified the expression of encoded EGFP in HCT116 cells. The
556 enhancement of EGFP fluorescence intensity by a factor of two was achieved with light-
557 triggered LPD delivery system, compared with the control group without light illumination.
558 In this project, 690 nm LED (15 mW/cm^2) was used as a light source, whose maximum dosage (6
559 min irradiation) was calculated to be 5.4 J/cm^2 . This is much lower than clinic and *in vivo* dose
560 (25-500 J/cm^2) of the light source used for activating VP in photodynamic therapy^{58, 59}. In addition,
561 the wavelength of 690 nm located within “therapeutic window” can penetrate tissues deeper (5-10
562 mm) with less photodamage to biological tissues compared with visible light⁶⁰. Given these

563 excellent properties of this light source, we believe this system can be feasible for *in vivo* work. In
564 addition to pDNA used in this study, our light responsive LPD system can efficiently
565 deliver other nucleic acids including siRNA, microRNA and larger plasmids with specific
566 functions. These genetic materials can be delivered in a temporally controllable way by
567 combining such delivery vehicle with light, thus providing a potential for enhanced
568 transfection efficiency and therapeutic effect in gene therapy *in vivo*. Further clinical
569 translation is also achievable with our liposomal nanocarrier since the key agents including
570 lipids and VP are widely used in clinical practice.

571

572 **Conflicts of interest**

573 There are no conflicts to declare.

574 **Supporting Information.**

575 Electronic supplementary information (ESI) available. See DOI: XXXXX

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583

584 **ABBREVIATIONS**

585 asODN: Antisense oligodeoxynucleotides; BPD-MA: Benzoporphyrin derivative monoacid; BPEI:
586 Branched polyethylenimine; CLSM, Confocal laser scanning microscopy; DDS, Drug/gene
587 delivery systems; DOPE, 1,2-Dioleoyl-sn-glycero-3-phosphoethanolamine; DOTAP, N-[1-(2,3-
588 Dioleoyloxy)propyl]-N,N,N-trimethylammonium methyl-sulfate; EGFP, Enhanced green
589 fluorescent protein; FDA, Food and drug administration; LED, Light-emitting diode; LPEI, Linear
590 polyethylenimine; NIR, Near-infrared; PCI, Photochemical internalization; pDNA, Plasmid DNA;
591 PDT, Photodynamic therapy; PEG, Poly-(ethylene glycol); PEI, Polyethylenimine; PLGA,
592 Poly(D,L-lactide-co-glycolide); PLL, Poly-L-lysine; ROS, Reactive oxygen species; siRNA,
593 Small interference RNA; TEM, Transmission electronic microscopy; VP, Verteporfin; DLS,
594 Dynamic light scattering; DCF, 2', 7'-dichlorofluorescin; DCF-DA, 2', 7'-Dichlorofluorescin
595 diacetate; PBS, Phosphate-buffered saline; HEPES, 4-(2-hydroxyethyl)-1-
596 piperazineethanesulfonic acid; TAE, Tris-acetate-EDTA; HBSS, Hank's balanced salt solution;
597 DMEM, Dulbecco's modified Eagle's medium; FBS, Fetal bovine serum; DPBS, Dulbecco's
598 Phosphate-buffered saline; DSC, Differential scanning calorimetry; EPR, Enhanced permeability
599 and retention; DMSO, Dimethyl sulfoxide; PTA, Phosphotungstic acid

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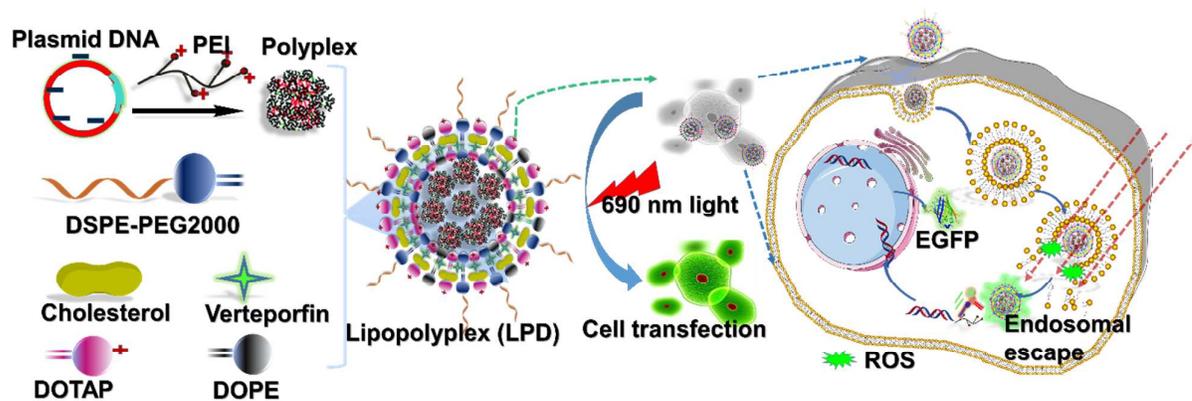
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Graphical Table of Contents

Light-triggered endolysosomal escape enhances gene delivery by photoresponsive LPD nanoparticles.

Highlights:

1. Photo responsive lipid-based hybrid nanoparticles were successfully applied for light enhanced the cytoplasmic release of pDNA followed by gene expression
2. Light-triggered endolysosomal escape of pDNA at different time points has been studied at subcellular level, confirming by quantitative analysis of colocalization between pDNA and endolysosomes