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Isolation and characterisation of exosomes for siRNA delivery to cancer cells

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Dr. Wing-Fu Lai
Corresponding Guest Editor
Methods and Techniques for the Development of Drug Delivery Systems
Journal of Visualised Experiments (JoVE)

16th July 2018

Dear Dr. Lai,

We would very much appreciate it if you could consider the following manuscript for the Methods and Techniques for the Development of Drug Delivery Systems Collection in *Journal of Visualised Experiments (JoVE)*.

Isolation and characterisation of exosomes for siRNA delivery to cancer cells

Farid N. Faruqu, Lizhou Xu, Khuloud T. Al-Jamal

There is an increasing interest in developing exosomes as drug delivery vectors, particularly for the delivery of siRNA in RNAi-based gene silencing applications. This is mainly due to their intrinsic capability of intercellular delivery of RNA. The protocol described in this manuscript is proposed for the production of exosomes from immortalised cell lines with high yield and purity for *in vitro* siRNA delivery to cancer cells.

Culture of the cells of which the exosomes were derived from were done in bioreactor flasks to increase the exosome yield. The exosomes were then isolated by ultracentrifugation onto a single sucrose cushion to achieve high purity of the exosomes. Fluorescently-tagged non-specific siRNA was loaded into the exosomes *via* electroporation, and were then delivered to PANC-1 (human, pancreatic adenocarcinoma) cells *in vitro*. Efficiency of siRNA uptake by the PANC-1 cells were analysed by flow cytometry.

Bioreactor flask culture coupled with isolation using a sucrose cushion yielded exosomes of high yield and minimal non-exosomal vesicle and protein contamination, assessed by the particle:protein (P:P) ratio. Although the encapsulation efficiency of the siRNA into exosomes were quite low (10-20%), ~40% PANC-1 cells treated with the siRNA-encapsulated exosomes were positive for the siRNA in just 4 h post-treatment. It is hoped that the proposed protocol would be applied in obtaining high quality exosomes as carriers for various siRNA against different oncogenic targets for *in vitro* and *in vivo* delivery and therapy studies.

Thank you for your consideration of our work and please do not hesitate to contact me for any further query.

I look forward to hearing your response.

Sincerely yours,

A handwritten signature in black ink, appearing to be 'K. Al-Jamal'.

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TITLE:

Preparation of Exosomes for siRNA Delivery to Cancer Cells

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KEYWORDS:

Exosome, Isolation, Characterization, siRNA Delivery, Cellular Uptake, Nanocarrier

SUMMARY:

An exosome is a new generation of drug delivery carriers. We established an exosome isolation protocol with high yield and purity for siRNA delivery. We also encapsulated fluorescently labelled non-specific siRNA into exosomes and investigated the cellular uptake of siRNA-loaded exosomes in cancer cells.

ABSTRACT:

Extracellular vesicles, in particular exosomes, have recently gained interest as novel drug delivery vectors due to their biological origin, abundance, and intrinsic capability in intercellular delivery of various biomolecules. This work establishes an isolation protocol to achieve high yield and high purity of exosomes for siRNA delivery. Human Embryonic Kidney cells (HEK-293 cells) are cultured in bioreactor flasks and the culture supernatant (hereon referred to as conditioned medium) is harvested on a weekly basis to allow for enrichment of HEK-293 exosomes. The conditioned medium (CM) is pre-cleared of dead cells and cellular debris by differential centrifugation and is subjected to ultracentrifugation onto a sucrose cushion followed by a washing step, to collect the exosomes. Isolated HEK-293 exosomes are characterized for yield, morphology and exosomal marker expression by nanoparticle tracking analysis, protein quantification, electron microscopy and flow cytometry, respectively. Small interfering RNA (siRNA), fluorescently labeled with Atto655, is loaded into exosomes by electroporation and excess siRNA is removed by gel filtration. Cell uptake in PANC-1 cancer cells, after 24 h incubation at 37 °C, is confirmed by flow cytometry. HEK-293 exosomes are 107.0 ± 8.2 nm in diameter. The exosome yield and particle-to-protein ratio (P:P) ratio are $6.99 \pm 0.22 \times 10^{12}$ particle/mL and $8.3 \pm 1.7 \times 10^{10}$ particle/ μ g, respectively. The encapsulation efficiency of siRNA in exosomes is ~ 10 -20%. Forty percent of the cells show positive signals for Atto655 at 24 h post-incubation. In conclusion, exosome isolation by ultracentrifugation onto sucrose cushion offers a combination of good yield and purity. siRNA

could be successfully loaded into exosomes by electroporation and subsequently delivered into cancer cells *in vitro*. This protocol offers a standard procedure for developing siRNA-loaded exosomes for efficient delivery to cancer cells.

INTRODUCTION:

Exosomes are a subtype of extracellular vesicles (EV) ranging from 50-200 nm in diameter, secreted by various cell types such as immune cells¹⁻², cancer cells³⁻⁶ and stem cells⁷. Exosomes have also been shown to be present in various physiological fluids⁸⁻¹¹. The combination of the inherent ability of exosomes to carry various biomolecules (*e.g.*, RNA and proteins)¹²⁻¹⁴ and the effective delivery of these biomolecules into recipient cells¹⁵⁻¹⁷ attracted interest for their potential as nano-scale drug delivery vectors. Various small molecules that serve as anti-cancer and anti-inflammatory drugs have been demonstrated to be successfully loaded into exosomes and delivered to target cells¹⁸⁻²⁷. Interestingly, nucleic acids such as siRNA²⁸⁻²⁹ and microRNA³⁰ have also been successfully loaded into exosomes *via* electroporation and delivered to target cells.

Recently, RNA interference (RNAi) *via* small interfering RNA (siRNA) has gained more interest as the preferred mechanism in gene silencing due to its high specificity, potent effect, minimal side effects and ease of siRNA synthesis²⁸⁻²⁹. siRNAs are double-stranded RNA molecules ranging from 19 to 25 nucleotides in length that triggers sequence-specific catalytic mRNA knockdown. Due to its large molecular weight and polyanionic nature, passive uptake of naked siRNA into cells is hindered²⁸⁻²⁹. It is also not possible for naked siRNA to be injected into the systemic circulation due to rapid degradation by plasma nucleases³¹. Thus, encapsulation of siRNA in a nanocarrier would aid the effective delivery and uptake of siRNA into the target cells.

An exosome is an ideal system for siRNA encapsulation as its structure is comprised of a hollow, aqueous core enveloped by a phospholipid bilayer. Exosomes not only have good stability in the blood but also have natural targeting properties to deliver functional RNA into cells³². The study conducted by Alvarez-Erviti *et al.* successfully demonstrated effective delivery of siRNA to the brains of mice using engineered exosomes with virtually no complications³¹. It is hypothesized that exosome-based therapy is relatively safer than other therapies as exosomes do not replicate endogenously as cells would and therefore do not exhibit metastatic properties¹⁵.

Various methods have been reported to successfully isolate exosomes from either cell culture or physiological fluids. The most popular method uses ultracentrifugation to pellet exosomes from the starting material³¹⁻³³. This method can be quite harsh on exosomes and usually co-precipitates proteins from the sample. Combining ultracentrifugation with a density-based separation such as sucrose gradients is becoming more common, to reduce protein and non-exosomal contamination in the isolated exosomes^{19,34}. Size-exclusion chromatography (S) allows separation of exosomes from other types of extracellular vesicles (EV) by size and can also result in minimal protein contamination but is limited by small amount of starting material it can process³⁵⁻³⁶. Immunoaffinity capture uses beads coated with antibodies that bind to exosomal surface proteins such as tetraspanins or other cell-specific marker that allows specific capture of exosomes rather than EVs or other proteins, as well as isolating sub-population of exosomes from

whole samples, but again is limited by the amount of starting material and is costly³⁶⁻³⁷. Polymer-based precipitation of exosomes used to be popular too, but since it is a rather crude precipitation, it leads to a higher non-exosomal vesicle and protein contamination³⁸⁻³⁹.

Electroporation has been reported for its inefficiency as a method to load exosomes with siRNA due to protein aggregation^{15,28,31}. Transfection-based approaches were demonstrated to have better loading efficiency and protein stability, but is undesirable due to its toxicity and side effects of transfection agents in altering cellular gene expression²⁸. Thus, electroporation has been more widely used in siRNA loading into exosomes as it is a safer method. However, an optimized encapsulation method needs to be established in order to deliver adequate amounts of siRNA to the target site for a potent gene knockdown.

Here, we propose an exosome isolation protocol using density-based ultracentrifugation onto just a single 25% (w/w) sucrose cushion prepared in deuterium oxide, rather than a sucrose density gradient. This is a cost-effective method that circumvents the laborious density gradient preparation and allows processing of large volumes of starting material, yet results in intact exosomes of high yield and purity suitable for subsequent loading with siRNA. Fluorescent Atto655-conjugated non-specific siRNA was loaded into Human Embryonic Kidney cells (HEK-293 cells) derived exosomes *via* electroporation and delivered to human pancreatic adenocarcinoma (PANC-1) cancer cells *in vitro*.

PROTOCOL:

1. Cell Culture in a Bioreactor Flask

[Place **Figure 1** here]

1.1 Culture HEK-293 cells in **normal medium** (see **Table of Materials**; 5% CO₂, 37 °C) and expand them into 4 x T75 flasks (until 90% confluent).

1.2 Wet the membrane of the bioreactor flask by adding 50-100 mL of normal medium in the medium reservoir of the bioreactor flask.

1.3 Collect all HEK-293 cells from the 4 x T75 and resuspend them in 15 mL of **exosome-depleted medium** (see **Table of Materials**).

1.4 Add the HEK-293 cell suspension to the cell compartment of the bioreactor flask using a 20 mL syringe connected to a blunt fill needle (see **Table of Materials**), with care to remove any bubble that might have formed.

1.5 Fill the medium reservoir of the bioreactor flask with **normal medium** up to 500 mL and keep the flask in the incubator (5% CO₂, 37 °C) for a week.

2. Conditioned Medium (CM) Harvesting from the Bioreactor Flask

133
134 2.1 After 1 week, discard all the medium in the medium reservoir of the bioreactor flask.

135
136 2.2 Remove all the medium in the cell compartment (*i.e.*, the **CM**) using a 20 mL syringe
137 connected to a blunt fill needle.

138
139 2.3 Add 50-100 mL of **normal medium** to the medium reservoir.

140
141 2.4 Add 15 mL of **exosome-depleted medium** to the cell compartment by removing the old
142 medium and adding fresh **exosome-depleted medium** using a 20 mL syringe connected to a blunt
143 fill needle.

144
145 2.5 Fill the medium reservoir of the bioreactor flask with **normal medium** up to 500 mL and keep
146 the flask in the incubator (5% CO₂, 37 °C) for another week.

147
148 NOTE: The culture can be continued for more than a year. For step 2.2, the CM from the first
149 harvest will not be used for exosome isolation and is discarded. For the 2nd and subsequent
150 harvest, the CM is kept for exosome isolation.

151 152 3. Exosome Isolation onto a Sucrose Cushion

153
154 [Place **Figure 2** here]

155
156 3.1 Pre-clear the CM (from step 2.2) by differential centrifugation and filtration as follows.

157
158 3.1.1 Centrifuge at 500 x g for 5 min at 4 °C. Transfer the supernatant into a new tube and discard
159 the pellet. Repeat this centrifugation step once more, recovering the supernatant and discarding
160 the pellet.

161
162 3.1.2 Centrifuge the supernatant from step 3.1.1 at 2000 x g for 15 min and 4 °C and then discard
163 pellet. Filter the recovered supernatant once through 0.22 µm filters.

164
165 3.2 During pre-clearing, prepare 25% (w/w) sucrose solution in deuterium oxide by accurately
166 weighing out 1.9 g (± 0.001 g) of sucrose in a universal tube, and then topping up with deuterium
167 oxide until the weight reaches 7.6 g (± 0.001 g).

168
169 3.3 Fill up an ultracentrifuge tube (see **Table of Materials**) with 22.5 mL of pre-cleared CM. Make
170 up the CM to 22.5 mL with 0.22 µm-filtered PBS if the current volume is less than that.

171
172 3.4 Place a glass pipette (see **Table of Materials**) in the tube and, through it, add 3 mL of sucrose
173 solution so that the solution forms a separate layer beneath the CM.

174
175 3.5 Carefully place the tube containing layered CM/sucrose solution into the bucket of a swing-
176 out rotor (see **Table of Materials**), and secure the bucket into the rotor.

3.6 Place the rotor into the ultracentrifuge (see **Table of Materials**) and spin at 100,000 x g for 1.5 h at 4 °C.

3.7 Collect 2 mL of the sucrose layer and add this to an ultracentrifuge bottle (see **Table of Materials**) containing 20 mL of filtered PBS for a washing step.

3.8 Place the tubes into a fixed-angle rotor (see **Table of Materials**) and spin at 100,000 x g for 1.5 h at 4°C.

3.9 Carefully remove the supernatant with a 10 mL serological pipette and resuspend the pellet with 400 µL filtered PBS. Keep this exosome stock at 4 °C or -80 °C for short-term and long-term storage respectively.

4. Characterization of Exosome Size and Yield by Nanoparticle Tracking Analysis (NTA)

4.1 Make 1:1,000-1:50,000 dilutions of the exosome stock in 1 mL (minimum 750 µL) volume so as to obtain 20-80 particles in the viewing frame of the NTA instrument (see **Table of Materials**) display.

4.2 Inject the diluted exosome stock into the NTA instrument sample chamber using a 1 mL syringe, and insert the temperature probe of a thermometer into the temperature probe inlet.

4.3 Set the NTA software (see **Table of Materials**) for recording as follows: 3 standard measurements, 30 s each, manual temperature option unchecked; and enter the dilution factor under the **Advanced** tab.

4.4 Set the camera level to 13 and run the capture script on the NTA software, injecting a fresh batch of sample and entering the temperature of the sample chamber when prompted after each reading.

4.5 Set the threshold to 4 for the subsequent analysis part, and note the average modal size and particle concentration of the exosome stock from the measurements.

5. Characterization of Exosome Purity by Particle:Protein Ratio Determination

5.1 Measure the protein content of the exosome stock by a bicinchoninic acid (BCA) protein assay kit (see **Table of Materials**) as follows.

5.1.1 Prepare the **defined standards**.

5.1.1.1 Prepare the standard of the highest concentration (500 µg/mL) by adding 45 µL of BSA stock solution (2 mg/mL – provided in the assay kit) to a microcentrifuge tube, and make it up to 180 µL with PBS.

221
222 5.1.1.2 Fill 8 microcentrifuge tubes with 90 µL of PBS.

223
224 5.1.1.3 Make serial dilutions (factor: 0.5) by taking 90 µL from the highest BSA standard and
225 adding this into the 1st microcentrifuge tube with PBS (mix well), then taking 90 µL from this tube
226 and adding it into the 2nd microcentrifuge tube.

227
228 5.1.1.4 Repeat this until the 7th microcentrifuge tube. The 8th tube will be just PBS (*i.e.*, the blank:
229 0 µg/mL).

230
231 5.1.2 Prepare the **exosome samples** by making 1:2 dilution of samples with PBS in a total volume
232 of 90 µL (45 µL of sample, 45 µL of PBS).

233
234 5.1.3 Prepare the BCA working reagent mix.

235
236 5.1.3.1 Calculate the total volume of BCA working reagent mix needed (50 µL per well, in
237 duplicates, including standards).

238
239 5.1.3.2 Mix the individual BCA reagents according to the following ratio: 25 parts reagent A: 24
240 parts reagent B: 1 part reagent C.

241
242 5.1.4 Perform the assay and analysis.

243
244 5.1.4.1 Add 40 µL of each standard and exosome sample prepared above into a well of a 96-well
245 plate (duplicates for each standard and sample).

246
247 NOTE: Since this is a colorimetric assay, proper pipetting technique is crucial to achieve accurate
248 results. Change pipettes after adding each standard/sample replicate into each of the wells

249
250 5.1.4.2 Add 50 µL of the protein assay working reagent mix into each well, and incubate the plate
251 at 37 °C for 30 min.

252
253 NOTE: To minimize deviations between replicates, add the protein assay working reagent into
254 the 1st replicate of a standard/sample, followed by the 2nd replicate of the same sample/standard,
255 before adding it to the 1st replicate of another sample/standard.

256
257 5.1.4.3 Measure the absorbance at 562 nm on the plate reader (see **Table of Materials**).

258
259 5.1.4.4 Plot a standard curve from the absorbance values of the standards, and work out the
260 protein concentration in each sample using the equation of the curve.

261
262 5.2 Calculate the particle:protein ratio by dividing the exosome yield obtained earlier with the
263 protein concentration of the exosome stock measured above.

264

6. Characterization of Exosomal Marker Expression by Flow Cytometry

6.1 Incubate 40 μL of exosomes ($\geq 1 \times 10^{11}$ particles/mL) with 10 μL of aldehyde/sulphate latex beads (undiluted from stock) for 15 min at room temperature (RT).

6.2 Add 5 μL of 100 μM BSA solution (see **Table of Materials**) to the exosome-bead mixture to achieve a 10 μM final concentration and incubate for 15 min at RT.

6.3 Add 1 mL of PBS and incubate for 75 min at RT in a microcentrifuge tube with mild agitation on a rocking shaker (~ 150 rpm).

6.4 Centrifuge the suspension at 580 x g for 5 min at RT and discard the supernatant.

6.5 Resuspend the pellet with 1 mL of 100 mM glycine solution (see **Table of Materials**) and incubate for 30 min at RT.

6.6 Centrifuge the suspension for 5 min at 580 x g. Discard the supernatant and resuspend the pellet with 1 mL of 3% FBS/PBS (see **Table of Materials**).

6.7 Repeat this washing step and resuspend the pellet in 350 μL of 3% FBS/PBS.

6.8 Divide the suspension into 7 tubes, each containing 50 μL of suspension and incubate them with fluorophore-conjugated anti-CD81, anti-CD9 and anti-CD63 antibodies and their corresponding isotype controls (1:10 dilution), respectively, for 45 min at 4 $^{\circ}\text{C}$. Keep 1 of the tubes as an unstained control but undergoing the same processing.

6.9 Add 1 mL of 3% FBS/PBS to each tube, centrifuge for 5 min at 580 x g and discard the supernatant.

6.10 Resuspend the pellet with 200-400 μL of 3% FBS/PBS and analyze the sample on the flow cytometer (see **Table of Materials**) under the appropriate channels.

7. Characterization of Exosome Morphology by Transmission Electron Microscopy (TEM)

7.1 Fix exosome aqueous dispersions at proper concentrations such as 10^{10} p/mL in fixing solution (see **Table of Materials**) for 15 min.

7.2 Place the samples on 300 mesh carbon coated copper grids and leave to air dry.

7.3 Negatively stain the samples with 0.22 μm -filtered aqueous uranyl acetate (see **Table of Materials**) for 4 min followed by two 50% methanol/ H_2O wash (see **Table of Materials**).

7.4 Air dry the sample.

7.5 Observe the samples under TEM (see **Table of Materials**). Set the accelerating voltage at 80 kV and the spot size at 2. Use objective aperture with all samples.

NOTE: Freshly isolated exosome particles should be used for microscopy observation to obtain optimal images.

8. siRNA Encapsulation into Exosomes by Electroporation

8.1 Pre-chill the electroporation cuvette (see **Table of Materials**) on ice for 30 min before electroporation.

8.2 Mix 7.0 µg of exosomes (32 µL from 7×10^{12} p/mL stock in PBS) with 0.33 µg of siRNA (12 µL from 2 µM stock in RNase-free water) in the microcentrifuge tube. Make up the volume to 150 µL with citric acid buffer (see **Table of Materials**). The exosome to siRNA molar ratio is 1:60 in this case.

8.3 Transfer the mixture to electroporation cuvette. Cap the cuvette and place it in the cuvette holder of the electroporator (see **Table of Materials**). Rotate the turning wheel 180° clockwise.

NOTE: The wheel must be turned completely to the locked position, in order for the cuvette to contact the electrodes.

8.4 Select desired electroporation program (*e.g.*, X-01, X-05, A-20, T-20, T-30, *etc.*) and start electroporation by pressing the **Start** button.

NOTE: A successful pulse is indicated by showing “OK” on the display.

8.5 Once electroporated, remove the cuvette after turning back the wheel 180° counter-clockwise. Withdraw the sample from the cuvette with the plastic pipette for further processing.

9. Removal of Free siRNA Using Size Exclusion Chromatography (SEC)

9.1 Equilibrate the SEC column (2.9 cm [H] x 1.3 cm [W]; see **Table of Materials**) by passing 3.5 mL of filtered PBS twice.

9.2 Dissolve 150 µL of electroporated sample in 350 µL of filtered PBS and transfer this to the SEC column to perform the free siRNA removal.

9.3 Collect the first 500 µL fraction that eluted from the column (F0).

9.4 Add 500 µL of filtered PBS to the column and collect the next 500 µL fraction (F1).

9.5 Repeat the above step until a total of 10 x 500 µL fractions (up to F9) is collected. F1 and F2 should contain the siRNA-encapsulated exosomes.

9.6 Wash the column with filtered PBS (twice, at least) to remove any sample residues.

10. *In Vitro* Uptake of siRNA-Loaded Exosomes into PANC-1 Cells

10.1 Seed PANC-1 cells in 24-well flat-bottom plates (see **Table of Materials**) at a density of 50,000 cells per well 24 h prior to the uptake study and incubate the cells in the incubator (5% CO₂, 37 °C).

10.2 Electroporate HEK-293 exosomes (7.0 µg) with Atto655-siRNA (0.33 µg) as per **Step 8**.

10.3 Purify electroporated exosome as per **Step 9** and resuspend in 100 µL of PBS.

10.4 Add 50 µL of the electroporated exosomes to PANC-1 cell and incubate at 37 °C and 5% CO₂ for 4 h.

10.5 Collect cells after incubation.

10.6 Wash the cells with 1 mL of sterile PBS and resuspend in 200 µL of PBS in polystyrene round-bottom tube (see **Table of Materials**).

10.7 Analyze cells by flow cytometer (see **Table of Materials**) with 10,000 events acquired per sample.

NOTE: Un-electroporated exosome-siRNA mixture samples and untreated cells with filtered PBS were used as controls.

REPRESENTATIVE RESULTS:

The physicochemical characterization of exosomes isolated from HEK-293 cells (HEK-293 Exo) are summarized in **Table 1**. The size measured using nanoparticle tracking analysis (NTA) instrument was 107.0 ± 8.2 nm. Exosome yield from the HEK-293 cells, also analyzed using the NTA instrument, was $6.99 \pm 0.22 \times 10^{12}$ p/mL from ~24 mL of CM (obtained from 2 rounds of harvest). Purity of the HEK-293 Exo assessed by calculating the particle-to-protein ratio (P:P) was $8.3 \pm 1.7 \times 10^{10}$ p/µg.

The size distribution of isolated HEK-293 Exo is shown in **Figure 3A**. Morphological analysis using transmission electron microscopy (TEM) showed the HEK-293 Exo were spherical structures slightly above 100 nm in size (**Figure 3B**). This result agrees with that from NTA measurement (**Figure 3A**). The isolated HEK-293 Exo were positive for CD81, CD9 and CD63, which are canonical markers used to identify vesicles as exosomes (**Figure 3C**).

For purification of exosomes using size exclusion chromatography (**Figure 4**), the percentage recovery of exosomes was calculated by dividing the total exosome particle number recovered in the 10 fractions collected (F0-F9) with the initial exosome particle number used, while the

percentage recovery of siRNA was calculated by dividing the total fluorescence intensity obtained from F3, F4 and F5 with the total fluorescence intensity obtained from all 10 fractions collected. The recovery of exosome and siRNA post-purification was calculated as 75.0% and 80.4%, respectively. The encapsulation efficiency of siRNA in exosomes was ~10-20%, calculated using the siRNA standard curve established (**Figure 4C**).

Qualitative analysis of *in vitro* uptake of exosomes loaded with the fluorescent Atto655-siRNA by flow cytometry showed that PANC-1 cells treated with siRNA-encapsulated exosomes recorded the largest shift in fluorescence signal (**Figure 5A**). PANC-1 cells treated with siRNA-encapsulated exosomes recorded a higher percentage of population positive for the Atto655 signal (39.4%) compared to that treated with unloaded exosomes and siRNA mixture (0.56%), which corroborated the observation above (**Figure 5B**). The degree of cellular uptake of siRNA (expressed as the fold difference in mean fluorescence intensity (MFI) values from that of untreated cells) was also observed to be significantly higher in PANC-1 cells treated with siRNA-encapsulated exosomes (MFI fold difference = 5.1) compared to that treated with the exosome-siRNA mixture (MFI fold difference = 1.1) (**Figure 5C**). These observations demonstrated that the siRNA-encapsulated exosomes were internalized by the PANC-1 cells and that they effectively delivered the siRNA intracellularly.

Figure Legends:

Figure 1: Culture of cells in bioreactor flask for exosome production. (A) Simplified anatomy of the bioreactor flask. (B) Starting culture in the bioreactor flask. See **Table of Materials** for the composition of normal and exosome-depleted medium (C) Harvesting conditioned medium (CM) and maintenance of culture in the bioreactor flask.

Figure 2: Isolation and characterization of exosomes. (A) Pre-clearing harvested conditioned medium (CM) from dead cells and cell debris. (B) Isolating exosomes from CM onto sucrose cushion. (C) Washing step to remove sucrose and contaminating proteins. (D) Isolated exosomes were then subjected to physicochemical, biochemical and morphological characterization.

Figure 3: Biochemical and morphology analysis of HEK-293 exosomes. (A) Size distribution of HEK-293 exosomes using Nanoparticle Tracking Analysis (NTA). The curve shows a superimposed histogram from 3 different captures at 30 s interval with red areas denoting standard deviation between measurements (n = 3). (B) Transmission Electron Microscopy (TEM) images of the naïve HEK-293 exosomes. Scale bar: 100 nm. (C) Detection of exosomal markers CD81, CD9 and CD63 using flow cytometry on HEK-293 exosomes. Exosomes were coupled to aldehyde/sulphate latex beads prior to detection. Exosome-beads complex were subsequently stained with fluorophore-conjugated anti-CD81, anti-CD9 and anti-CD63 antibodies. Degree of expression of the markers are expressed as the fold difference in median fluorescence intensity (MFI) values from that of the control (exosome-beads complex stained with the corresponding isotype). Values are expressed as mean \pm SD, where n = 3.

Figure 4: Exosome purification post-electroporation. (A) Elution profiles (F0-F9) of Atto655-siRNA and electroporated exosomes using size exclusion chromatography. (B) NTA analysis of both Atto655-siRNA and exosome from F0 to F9 using size exclusion chromatography. (C) The calibration curve of Atto655 labelled siRNA. Fluorescence intensities were obtained by - plate reader at Ex/Em: 640-10/680 nm; Gain 2800. Values are expressed as mean \pm SD (n = 3).

Figure 5: Cellular uptake of siRNA-encapsulated exosomes into PANC-1 cells at 4 h. (A) Histograms comparing cellular uptake of unloaded exosomes + siRNA mixture and siRNA-encapsulated exosomes. (B) Comparison of the uptake of unloaded exosomes + siRNA mixture at 4h by pseudocolor plot. (C) The fold difference in mean fluorescence intensity (MFI) values of the samples tested compared to that of untreated cells. Values are expressed as mean \pm SD, where n = 3. *** P < 0.001. NS: not significant. One-way ANOVA was used for statistical analysis.

Table 1: Physicochemical characterization of exosomes.

DISCUSSION:

Obtaining a decent exosome yield from cultured cells, which are enough for several rounds of *in vitro* or *in vivo* studies, is still a challenge. According to the manufacturer, the bioreactor flasks were intended for production of antibodies and proteins with high yield from culture of various immortalized cell lines. This allows the cells to continuously enrich the culture medium with the desired product, resulting in a concentrated conditioned medium (CM) in the cell-compartment. Theoretically, the same concept would be beneficial in exosome production from various cell lines, and indeed culturing these cells in the bioreactor flasks was demonstrated to significantly increase the exosome yield⁴⁰. The large medium reservoir continuously supplies nutrients to and removes wastes from the cell compartment through a 10 kDa semi-permeable membrane, allowing prolonged culture without requiring a large volume of medium to be in contact with the cells, or regular flasks changing, which can ultimately save the overall cost and labor of high-scale exosome production⁴⁰. It was also demonstrated that the morphology, phenotype as well as the immunomodulatory functions of exosomes isolated cells long-term bioreactor flasks cultures are similar to that sourced from cells cultured in regular 75 cm² flasks⁴⁰. Culture of other immortalized cell lines as exosome sources in the bioreactor flask would therefore help increase their exosome yield while maintaining their integrity and function. This form of culture is however not applicable to primary cells with limited division cycles, and those that cannot be cultured in high density.

Since harvest of the CM is done weekly, and the cells in culture were never passaged, it can be assumed that the cells in the bioreactor flask are not growing in a monolayer like the regular cell culture. They are most likely to form clusters with necrotic centers, or simply detach from the surface and die when the cells are too confluent for a monolayer. Visual inspection of the cell compartment of the bioreactor flask is not possible to confirm this assumption, but is reflected by the large number of dead cells obtained during the CM harvesting. Regular removal of poorly adherent and non-viable cells from the bioreactor flask can prevent the build-up of materials on the semi-permeable membrane that can adversely affect the exchange of gas, nutrients and waste between the cell compartment and the medium reservoir, thus allowing prolonged culture

in the bioreactor flasks for >6 months⁴⁰. In this context, this non-regularity of cell growth in the bioreactor flasks is ideal as we speculate that it mimics the actual condition of tumor growth *in vivo* more closely than the conventional monolayer cell culture, and it is hoped that the exosomes produced by the cancer cells in the bioreactor flask would be more similar to that secreted by tumors *in vivo*. This would be particularly beneficial in studies looking into the role of tumor-derived exosomes in the progression of the tumor pathology. Tumor-derived exosomes have been reported to intrinsically and preferentially home to their tissue of origin³², therefore having exosomes produced in a system mimicking their *in vivo* production would also be desirable in studies looking at exploring the passive targeting ability of exosomes as drug nanocarriers.

The P:P ratio was reported as a parameter to assess the purity of isolated exosomes from contaminating proteins from the culture medium of physiological fluids from which exosomes were sourced from⁴¹. The P:P ratio of $8.3 \pm 1.7 \times 10^{10}$ p/μg obtained in this study falls within the high purity range proposed in the study. This ratio highlights the danger of using protein concentration to express the yield or dose of exosomes isolated or used in downstream studies respectively, as this does not reflect the true amount of exosomes available in the sample given the problem of protein contamination during isolation. NTA *via* instruments such as NanoSight, which measures the concentration of exosomes in terms of particle number, is a more sensible and accurate way of quantifying exosomes.

Highly accurate weighing during the preparation of the 25% sucrose solution in deuterium oxide is crucial as this method is a density-based isolation. Exosomes have a rather narrow range of flotation density in sucrose solution so accurate preparation of the sucrose cushion will reduce contamination of non-exosomal vesicles such as apoptotic bodies or Golgi-derived vesicles during isolation⁴². It is advised not to keep leftover sucrose solution and using it even after one day so as to avoid risk of factors that can alter its density such as loss or addition of water in the solution by either evaporation or condensation of air in the tube. Use of a swing-out rotor is also essential during centrifugation onto the sucrose cushion to allow even migration of exosomes from the CM to the sucrose solution.

Withdrawing the sucrose solution post-centrifugation is also a delicate step, and it involves finding a compromise between maximizing the amount of exosomes recovered, and not too much that protein from culture medium is introduced to the exosome sample withdrawn. The interface between the sucrose solution and the condition medium is where proteins from the culture medium would collect post-centrifugation, and can usually be seen as a dark brown ring that sits on the interface. In our hands, withdrawing 2 mL of the sucrose cushion from the initial 3 mL added is the optimum volume that agrees with the compromise mentioned above. The volumes described in this protocol are for the specific rotors used; therefore, it is advised to optimize the volume of sucrose to be withdrawn when scaling up or down the volumes for the types of rotors available in different facilities. It is also important to avoid the area right at the center of the bottom of the tube when withdrawing the sucrose, as this is where particles of higher density than sucrose will sediment and can usually be seen as an off-white pellet.

The washing step with a relatively large amount of PBS helps to further reduce the degree of protein contamination during exosome isolation⁴¹. This step is also essential in removing excess sucrose from the exosomes so as to avoid osmotic damage to the exosomes themselves or the biomolecules within the exosomal lumen, as well as reducing the risk of bacterial and/or fungal growth in the exosome stock. Preparing the sucrose solution in deuterium oxide rather than water helps to reduce the amount of sucrose needed to achieve the exosome flotation density for isolation, hence reducing the risk of both osmotic damage and microbial contamination. After the first centrifugation onto the sucrose cushion, the exosome-containing sucrose layer withdrawn and added to the PBS can be stored at 4 °C and processed the following day if faced with time constraints.

To the best of our knowledge, the exosome/siRNA molar ratio is an important factor in determining the efficiency of electroporation. In this protocol, we used 1:60 as the exosome to siRNA molar ratio. As the encapsulation ability of different types of exosomes are different, we strongly suggest this to be optimized on a case-by-case basis. However, the encapsulation efficiency proposed herein can always be a parameter for selecting the optimal electroporation conditions.

In addition, aggregation of siRNA is believed to be one of the most common problem in electroporation. It is proven that electroporation can induce strong aggregation of siRNA, making it even harder to enter exosomes. siRNA aggregations are often mistakenly interpreted as encapsulation of siRNA into exosome therefore proper controls were used in this study as the formation of siRNA aggregates is unavoidable during electroporation²⁸. The percentage encapsulation efficiency of our purification method was calculated by using normalized values to minimize the influence from other sources such as background noise, exosome and siRNA aggregations that would affect the data reliability. Based on our findings, there was negligible siRNA aggregations observed in the control sample *i.e.*, using electroporated and un-electroporated siRNA.

This protocol has successfully demonstrated the encapsulation of siRNA into exosomes and their subsequent intracellular delivery of the siRNA to cancer cells *in vitro*. Therefore, various types of exosomes from different cell lines can be isolated and characterized using the proposed protocol, and subsequently loaded with various therapeutic siRNA for different types of oncogenic targets over-expressed in different cancers. An interesting application would be to explore the siRNA delivery and uptake efficiency using various permutations of exosome source-target cell pair *in vitro*. This can then be translated to animal models to assess the efficiency of both the delivery and therapeutic efficiency of siRNA-encapsulated exosomes *in vivo*.

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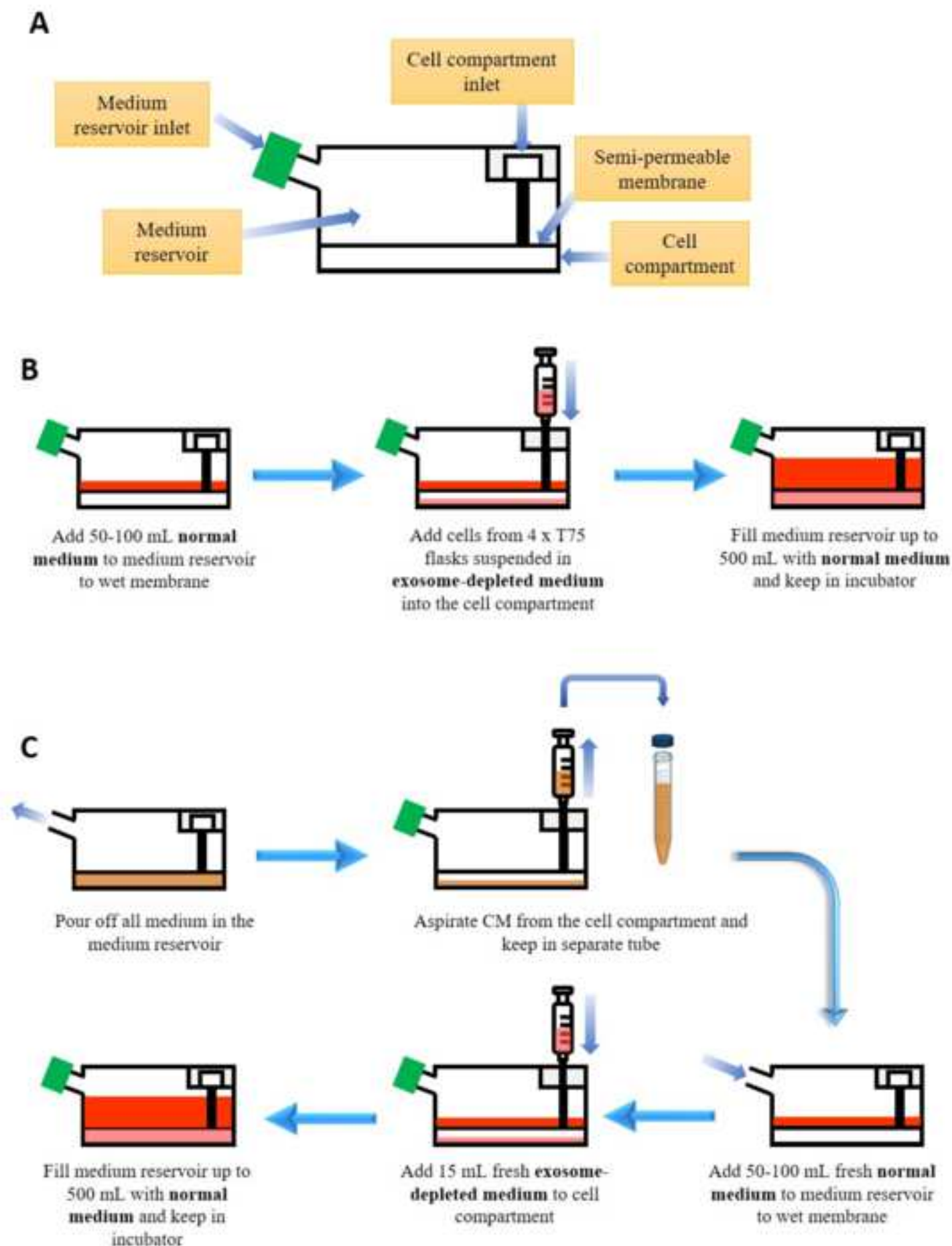
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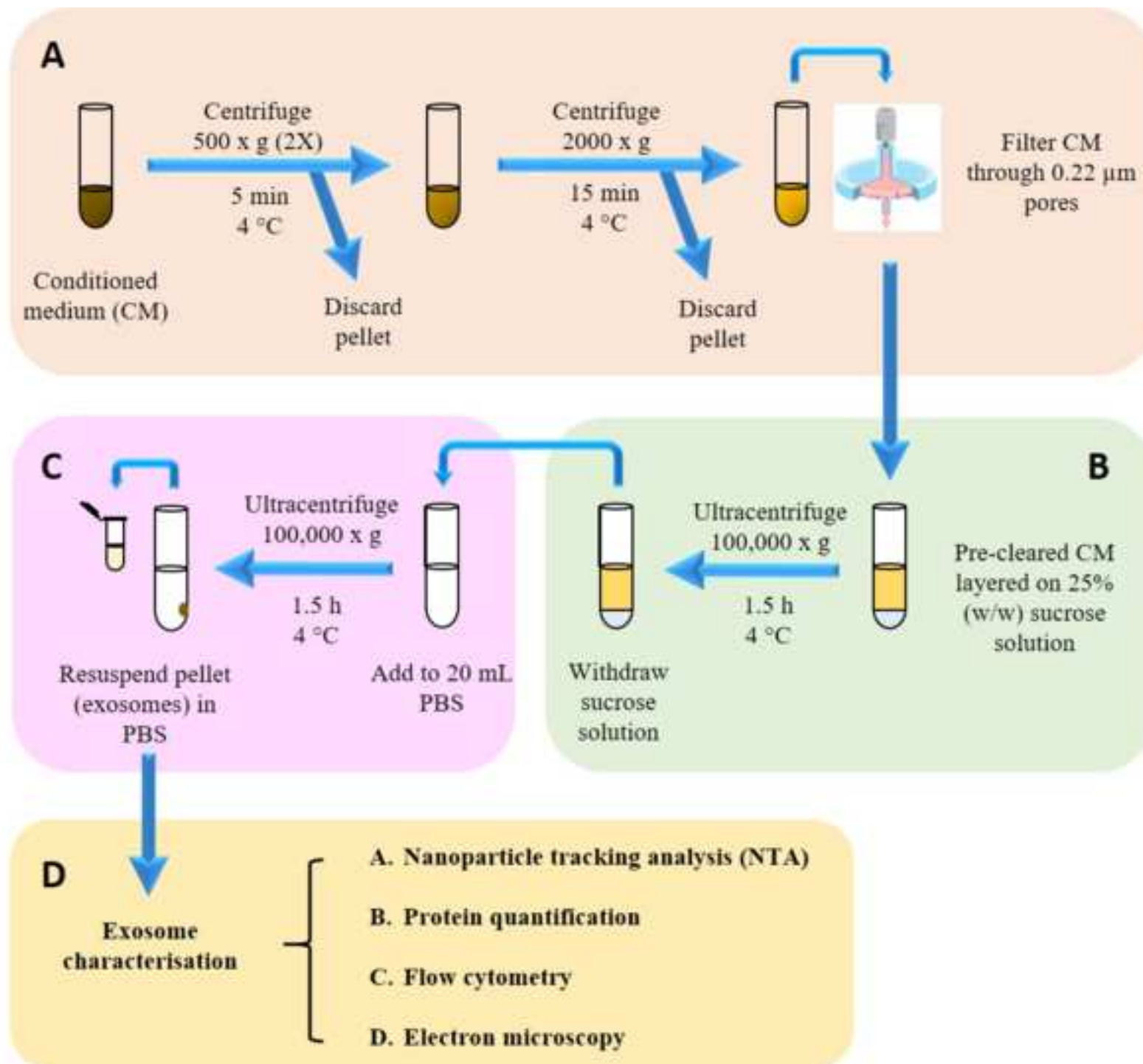
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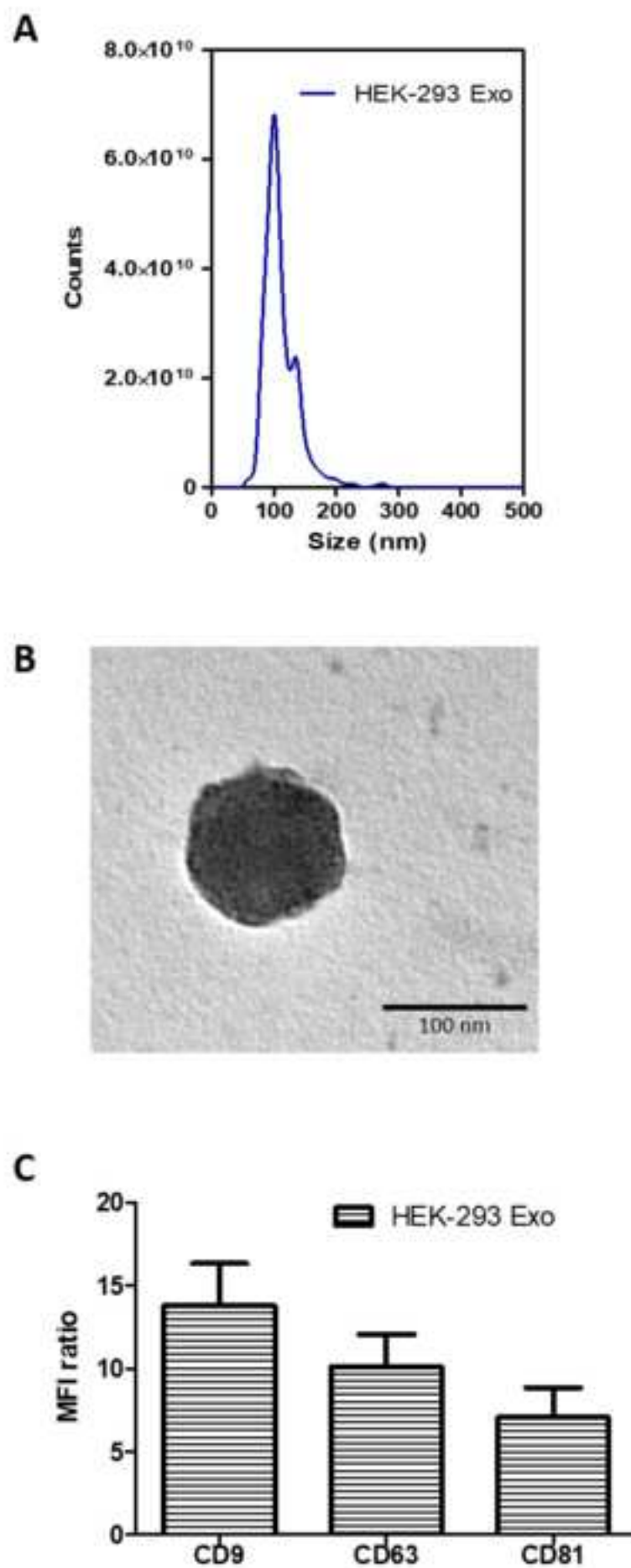
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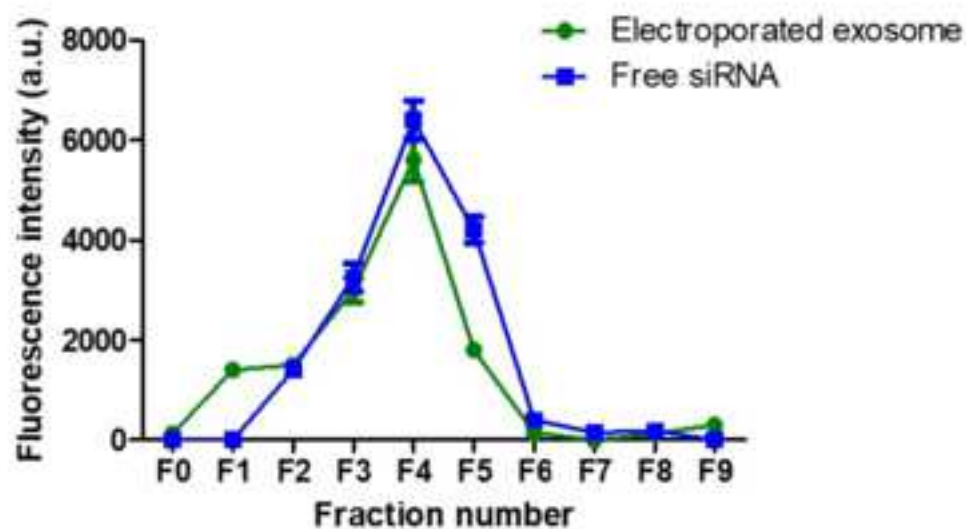
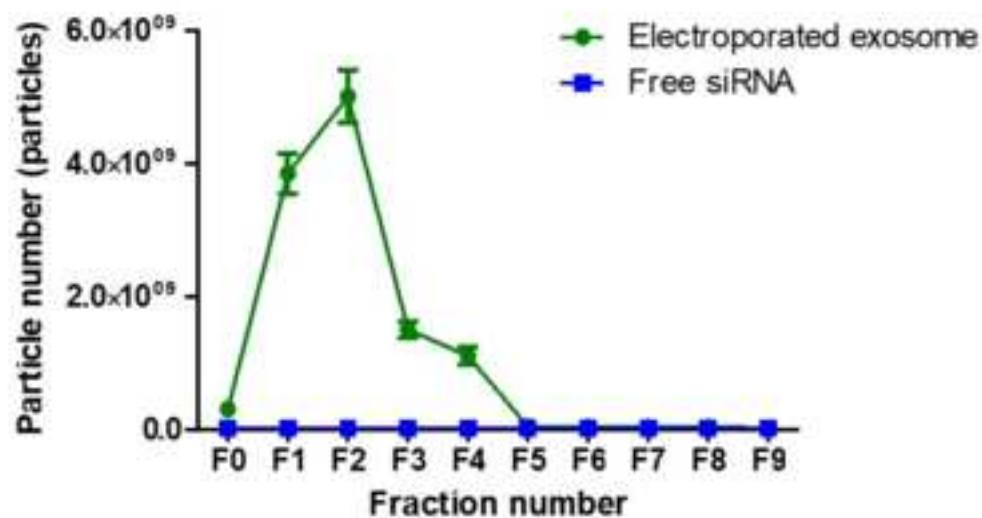
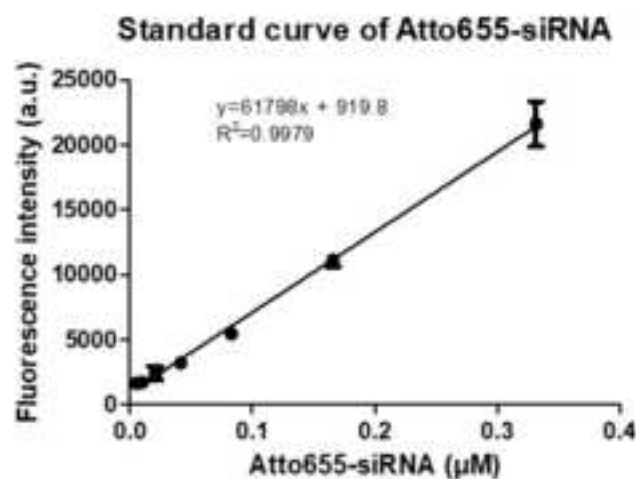
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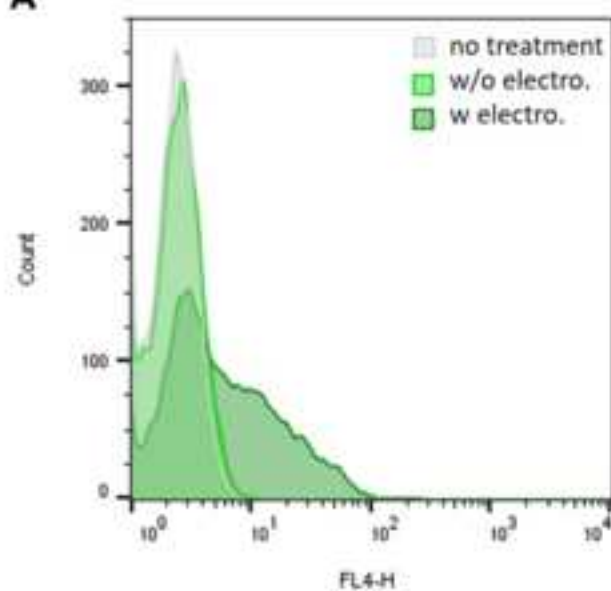
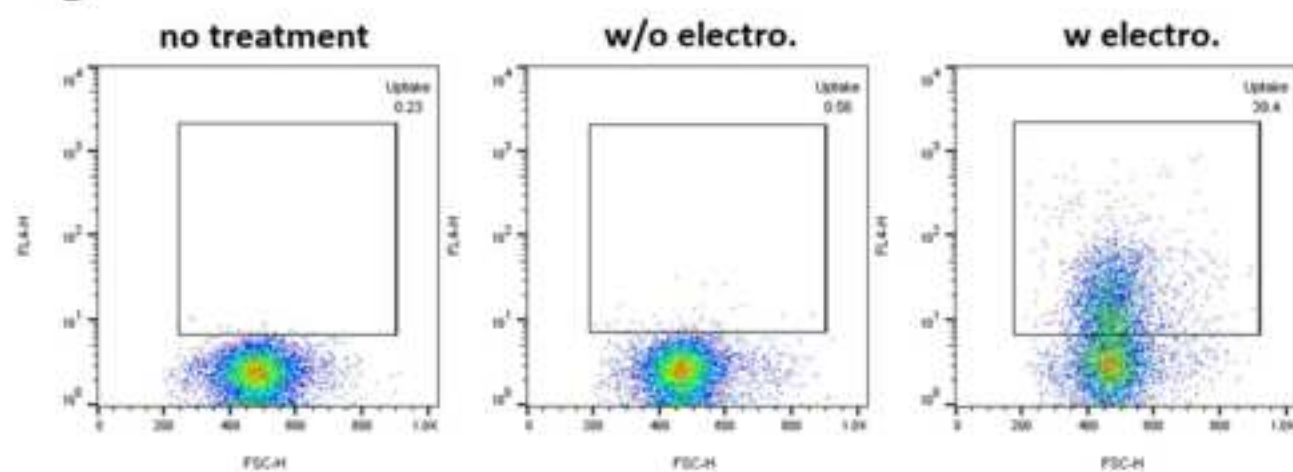
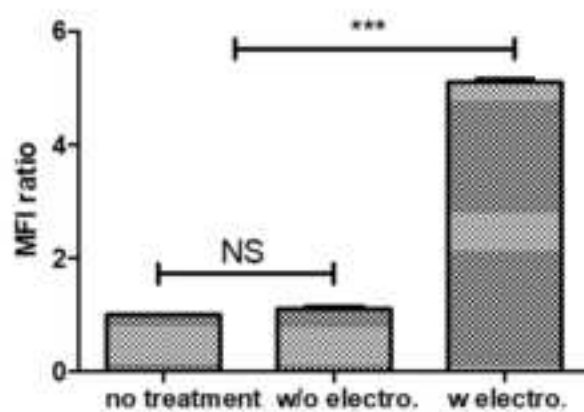
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A**B****C**

A**B****C**

Exosome	Size ^{1,2} (nm)	Yield ^{1,2,3} (p/mL)	[Protein] ^{2,4} (µg/mL)	Particle-to-protein (P:P) ratio ⁵ (p/µg)
HEK-293	107.0 ± 8.2	6.99 ± 0.22 x 10 ¹²	84.3 ± 9.8	8.3 ± 1.7 x 10 ¹⁰

- 1 Measured using nanoparticle tracking analysis (NTA instrument)
- 2 Values are expressed as mean ± SD, where n=3
- 3 Yield was obtained by cell-conditioned medium pooled from 2 rounds of harvesting from bioreactor flasks (~24 mL)
- 4 Measured using a protein assay kit
- 5 Value obtained by using formula: P:P ratio = Yield / [Protein]



Name of the Material	Company	Catalog number	Comments/Description
Sterile Newborn Calf Serum Heat Inactivated	First Link	08-05-850	500 ml
EMEM medium	Thermo Fisher Scientific	11090081	500 ml
Penicillin/Streptomycin	Thermo Fisher Scientific	15140-122	100 ml
GlutaMax	Thermo Fisher Scientific	35050-038	100 ml
Sucrose	Fisher Scientific	S/8600/60	1 kg
Deuterium oxide (D ₂ O)	Sigma-Aldrich	151882	250 g
1X Phosphate Buffered Saline	Thermo Fisher Scientific	10010015	500 ml
Glycine	VWR Chemicals	101196X	1 kg
Sepharose CL-2B	GE Healthcare Life Sciences	17-0140-01	1 L; Particle Size 60 µm-200 µm
Trypsin-EDTA 0.05%	Thermo Fisher Scientific	25300096	100 ml
Aldehyde/sulfate latex beads	Thermo Fisher Scientific	A37304	4% w/v, 4 µm, 15 ml
MicroBCA kit	Thermo Fisher Scientific	23235	
CD81 antibody (APC)	Thermo Fisher Scientific	17-0819-42	Lot: E15950-104, RRID: AB_11150235, 1:10 dilution in 50 µl sample
CD81 isotype (APC)	Thermo Fisher Scientific	17-4714-81	Lot: 4291563, RRID: AB_763650, 1:10 dilution in 50 µl sample
CD9 antibody (FITC)	Thermo Fisher Scientific	11-0098-41	Lot: 4345870, RRID: AB_10698007, 1:10 dilution in 50 µl sample
CD9 isotype (FITC)	Thermo Fisher Scientific	11-4714-41	Lot: 4299784, RRID: AB_10598647, 1:10 dilution in 50 µl sample
CD63 antibody (PE)	Thermo Fisher Scientific	12-0639-41	Lot: 1930435, RRID: AB_2572564, 1:10 dilution in 50 µl sample
CD63 isotype (PE)	Thermo Fisher Scientific	12-4714-81	Lot: 1937696, RRID: AB_470059, 1:10 dilution in 50 µl sample
Atto655-siRNA	Eurogentec	SQ-SIRNA	(Labelled-S) UGC-GCU-ACG-AUC-GAC-GAC-GAU-G55; (Unlabelled-AS) CAU-CGU-CGA-UCG-UAG-CGC-A55.

Name of the Equipment	Company	Catalog number / model	Comments/Description
Millex-GP Syringe Filter Unit 0.22 µm	Millipore	SLGP033RS	
CELLine AD1000 bioreactor flasks	Wheaton	WCL1000ad	
Ultracentrifuge	Beckman Coulter	Optima XPN-80	
Swing-out rotor	Beckman Coulter	SW45 Ti	
Fixed-angle rotor	Beckman Coulter	Type 70 Ti	
Ultracentrifuge tubes	Beckman Coulter	355631	Polycarbonate. Max. fill 32 ml
Ultracentrifuge bottles	Beckman Coulter	355618	Polycarbonate. Min. fill 16 ml, max. fill 25 ml
NanoSight	Malvern	LM10	Software: NanoSight NTA v3.2
Flow Cytometer	BD Biosciences	FACSCalibur	
Centrifuge	Eppendorf	5810R	
Plate reader	BMG Labtech	FLUOstar Omega	
Flow cytometry tubes	BD Biosciences, Falcon	352052	
Microfuge tubes	Starlab	S1615-5500	1.5 ml
Cell culture flasks	Fisher Scientific	156499	75 cm ²
Transmission electron microscope	FEI Electron Optics	Philips CM 12	with Tungsten filament and a Veleta - 2k × 2k side-mounted TEM CCD Camera (Olympus, Japan)
Amaxa Nucleofector I	Lonza	Nucleofector I	with Amaxa's Nucleofector Kits
24-well flat-bottom plates	Corning	Costar	
Blunt fill needle	BD Biosciences	305180	18G x 1 1/2" (1.2 mm x 40 mm)
Glass pipettes	Fisher Scientific	1156-6963	

Name of reagents			Composition
Normal medium			Eagle's Minimum Essential Medium supplemented with 10% foetal bovine serum (FBS), 1% penicillin/streptomycin and 1% GlutaMax.
Exosome-depleted medium			Eagle's Minimum Essential Medium supplemented with 10% exosome-depleted FBS (see below), 1% penicillin/streptomycin and 1% GlutaMax.
Exosome-depleted FBS			Subject FBS to ultracentrifugation at 100,000 g for 18 h at 4°C. The FBS supernatant post-centrifugation was collected and sterile-filtered using 0.22 µm filters.
25% w/w sucrose cushion			Add 1.9 g (± 0.001 g) of sucrose in a universal tube, and top up with D ₂ O until the weight reaches 7.6 g (± 0.001 g). This makes ~6ml of the 25% w/w sucrose cushion.
3% FBS/PBS			Add 1.5 ml exosome-depleted FBS to 48.5 ml 1X PBS to prepare 50 ml of 3% FBS/PBS.
100 µM BSA solution			Prepare 1mM BSA solution by adding 0.3325 g to 50 ml PBS. Make 1:10 dilution of this stock to obtain 100 µM BSA solution. Make 5-10 µl aliquots of this 100 µM BSA solution (for single use) and store them at -20°C. All BSA solution should be stored at -20°C, and discard solutions that have undergone ≥2 freeze-thaw cycles.
100 mM glycine solution			Add 0.375 g of glycine to 50 ml PBS to obtain 100 mM glycine solution, store at 4°C.
Citric acid buffer with EDTA			Mix 0.1954 g citric acid and 0.2087 g disodium phosphate in 50 mL of deionised water. Add EDTA to 0.1 mM. Adjust pH to 4.4.
Fixing solution			Prepare formaldehyde/glutaraldehyde, 2.5% (w/v) each in 0.1 M sodium cacodylate buffer, and adjust pH to 7.4.

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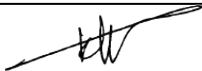
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Changes to be made by the Author(s) regarding the manuscript:

1. Please take this opportunity to thoroughly proofread the manuscript to ensure that there are no spelling or grammar issues.

Done to the best of our ability.

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This figure is adopted from another manuscript prepared by the authors, which is currently being revised to address reviewers' comments from another journal. Since this figure is more relevant and critical to this manuscript, this figure will be removed from the other manuscript and put in this manuscript instead.

4. Keywords: Please provide at least 6 keywords or phrases.

Added.

5. Please use SI abbreviations for all units: L, mL, μ L, h, min, s, etc.

Corrected.

6. Please include a space between all numerical values and their corresponding units: 15 mL, 37 °C, 60 s; etc.

Corrected.

7. Please use centrifugal force (x g) for centrifuge speeds.

Corrected.

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Corrected.

9. Please add more details to your protocol steps. There should be enough detail in each step to supplement the actions seen in the video so that viewers can easily replicate the protocol. Please

ensure you answer the “how” question, i.e., how is the step performed? Alternatively, add references to published material specifying how to perform the protocol action. Some examples:
1.1: Please specify the culture conditions.

Added

4.2, 4.3: Please describe how to measure size distribution and concentration.

Added

5.1: Please ensure that the protocol here can stand alone. As currently written, users must refer to another commercial protocol in order to complete this protocol.

Added

7.1: What concentration is considered to be proper?

Added.

10.2: Please provide more details here.

Corrected.

10.6: What volume of sterile PBS is used to wash?

Added.

10. 7.4: Please write this step in the imperative tense.

Modified.

11. Please include single-line spaces between all paragraphs, headings, steps, etc.

Included.

12. After you have made all the recommended changes to your protocol (listed above), please highlight 2.75 pages or less of the Protocol (including headings and spacing) that identifies the essential steps of the protocol for the video, i.e., the steps that should be visualized to tell the most cohesive story of the Protocol.

Highlighted in yellow.

13. Please highlight complete sentences (not parts of sentences). Please ensure that the highlighted part of the step includes at least one action that is written in imperative tense.

Done.

14. Please include all relevant details that are required to perform the step in the highlighting. For example: If step 2.5 is highlighted for filming and the details of how to perform the step are given in steps 2.5.1 and 2.5.2, then the sub-steps where the details are provided must be highlighted.

Done.

15. Please reference Figure 1 and Figure 2 in the protocol.

Figure 1 is originally drawn by the author. For Figure 2, please see comment on (3) above.

16. Figure 1 and Table 1: Please change “ml” to “mL”.

Changed.

17. Figure 2: Please use “x g” instead of “g” for centrifugation force (i.e., 2000 x g, 500 x g). Please include a space between the number and temperature unit (i.e., 4 °C). In panel D, please only capitalize the first word of a phrase (i.e., Exosome characterization, Protein quantification, etc.).

Corrected

18. Figure 5: Please revise to refer to the treatment in a consistent manner. For instance, panel A uses w/ electro while panel c uses w electro.

Corrected.

19. Table 1: Please upload Table 1 to your Editorial Manager account as an .xls or .xlsx file.

Corrected.

20. Line 343: Please convert the reference to a superscripted numbered reference.

Corrected.

21. Table of Equipment and Materials: Please remove trademark (™) and registered (®) symbols. Please provide lot numbers and RRIDs of antibodies, if available.

Symbols have been removed. Lot numbers and RRIDs of antibodies have been listed in table of materials.

22. For in-text references, the corresponding reference numbers should appear as superscripts after the appropriate statement(s) in the text (before punctuation but after closed parenthesis). The references should be numbered in order of appearance.

Corrected.

23. Please ensure that the references appear as the following: [Lastname, F.I., LastName, F.I., LastName, F.I. Article Title. Source. Volume (Issue), FirstPage – LastPage (YEAR).] For more than 6 authors, list only the first author then et al.

Corrected.

Reviewers' comments:

Reviewer #1:

Manuscript Summary:

This is a well-written manuscript detailing exosome isolation from tissue culture media, characterization of the exosomes, and loading of the exosomes with siRNAs. The methodology is clear and the figures supportive of the text.

Minor Concerns:

Some additional clarifications would aid the researcher attempting to follow this protocol in the laboratory.

Is deuterium oxide required for the preparation of the sucrose? Many protocols use standard sucrose preparations thus comments on the advantages of this method are appropriate.

[This is already discussed in the manuscript \(lines 531-533\).](#)

Details on the nucleofection kit used as well as the program used for electroporation of exosomes.

[The nucleofection kit is purchased. The detailed product information is provided in the table of materials.](#)

The size of the sepharose columns used is not provided.

[The column size is 2.9 cm \(H\) x 1.3 cm \(W\). This has been added to the manuscript.](#)

Reviewer #2:

Manuscript Summary:

The manuscript #JoVE58814, entitled "Isolation and characterisation of exosomes for siRNA delivery to cancer cells" by Faruqu et al., demonstrated that basis protocols of isolated cell-secreted exosomes could be used as the gene delivery carrier. Procedures including cell culture, exosome isolation and purification, as well as exosome characterization and formulation have been presented in details.

Major Concerns:

1. It is doubtful if the bioreactor flask is properly used for cell culture and media collection to produce high amounts of exosome. Please clarify if exosomes could pass across the semipermeable membrane of bioreactor. Do concentrated media with the high amount of exosomes have effect on the continuous release of exosomes in cells? Another concern is cell morphology and confluency in the bioreactor flask. As the authored discussed, "it can be assumed that the cells in the bioreactor flask are not growing in a monolayer like the regular cell culture," it is questionable if this culture would also impact on the exosome release. Have any studies reported that cells in the bioreactor is growing closer to physiological conditions compared to regulation culture flask?

- [The semi-permeable membrane MWCO is 10 kDa, so exosomes would not be able to pass through \(supplier's manual and reference 40\)](#)
- [The exosomes are harvested on a weekly basis, so this avoids the excessive accumulation of exosomes in the culture supernatant that can potentially harm/influence the exosome production. This has been demonstrated in a study \(reference 40\) that shows consistent high yield of](#)

exosomes from prolonged culture in the bioreactor flask for up to 1 year, suggesting there is no negative feedback mechanism that reduces exosome production by the cells in an exosome-rich milieu.

- Weekly harvesting of the culture supernatant also will remove dead/loosely attaching cells (i.e. less viable) so this prevents the build-up of materials on the semi permeable that can adversely affect the exchange of gas, nutrients or waste products (reference 40)
- There hasn't been a study that looked on how the cells in the bioreactor flask are growing closer to physiological conditions, this is the authors' speculation. However, one study (reference 40) demonstrated that exosomes produced from the bioreactor flasks have similar morphology, phenotype and immunomodulatory functions as those sourced from regular culture flasks.

2. Is it useful for the yield rate per ml of exosomes from concentrated media? As more cells grow in the flask, more exosomes will be released. The later collected media are supposed to have more exosomes, right?

The p/mL unit used to express the exosome yield in Table 1 refers to p/mL of PBS the exosomes were resuspended in at the final stage of the isolation, and not the volume of conditioned-medium that was initially used for isolation. The exosomes are always harvested after 7 days, and are always resuspended in 400 μ L of PBS at the final step of the isolation, so exosome yield between different harvests can be directly comparable.

3. High amount of exosomes could easily come from large volume of cell culture media using more and/or larger conventional flasks. While more times are needed to concentrate media in the exosome isolation, variability related to exosome quality and quantity could be minimized in the cell growth, cell morphology, exosome release, and exosome yield. The authors should have valuable discussion and insights on the related issues in the manuscript.

Added to Discussions – Significance to other method.

4. List detailed information about siRNA. What are the target and sequence of siRNA? Is the label step of siRNA missing?

The detailed information including sequence of siRNA and catalogue number are added in the table of materials. The labelling step is conducted by the company. The siRNA used in this protocol is a negative siRNA.

5. Provide more studies of exosome delivered siRNA in the cancer cells such as downstream knockdowns of target RNA and protein levels using PCR, ELISA and western blotting. As the labeled Atto665 may be dissociated, a fake positive result could be observed in the cellular uptake. This is a good question. The proposed protocol provides a general methodology of using exosome for siRNA delivery to cancer cells *in vitro*. We used negative control siRNA for an example. As for the knockdown efficacy of a specific siRNA, we strongly suggest readers to investigate thoroughly using techniques such as PCR, ELISA, and western blotting.

Minor Concerns:

The manuscript is poorly written. There are lot of unprofessional expression and writing inconsistently. For example,

Equipment resources: some are provided and some not.

The table of materials and equipments have been updated.

Delete steps 10.2 and 10.3 as they were presented in the steps 8 and 9.

The description of these two steps are simplified and detailed information are pointed out to refer to Steps 8 and 9.

Table 1: Yield ($\times 10^{12}$ p/ml), 6.99 ± 0.22 ; P:P ratio ($\times 10^{10}$ p/ μ g), $8.3 \pm ?$
Added.

Figure 4, provide SD in the 4A and 4B
Provided.

Figure 5, treatments are named improperly
Corrected.

Provide statistical analysis method.
Added statistical analysis method in Figure legends.