How molecular internal-geometric parameters affect PB-PEO polymersome size in aqueous solution

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ABSTRACT: Amphiphilic polybutadiene polyethylene oxide (PB-PEO) is one of the best known chemistries to form stable vesicular morphologies, stated as polymersomes, in aqueous environment. Mimicking cell membranes, these structures self-assemble in an "amphiphilic window" determined by $0.15 < f < 0.35$ where $f$ is the ratio between the hydrophilic block volume and the entire diblock volume. However the polymersome size distribution also depends on molecular weight ($M_n$) and in order to gain insight on how $f$ and $M_n$ together determine polymersome size, we prepared PB-PEO diblock copolymers with different block lengths and analyzed vesicle morphology via Dynamic light scattering (DLS) and Freeze-fracture transmission electron microscopy (FF-TEM). We found three main regimes: high $f$/low $M_n$ with polymersomes of mixed diameter, high $f$/high $M_n$ with mainly large polymersomes and low $f$, with mainly small polymersomes. In the first region, the polymersomes are highly polydisperse. There is a tendency towards increased diameter with increasing $f$ and $M_n$. Taken together our findings can help to identify how polymersome self-assembly can be controlled to achieve size distribution specificity alleviating the need for subsequent tuning of size via extrusion. This can pave the way for cost-effective upscaling of polymersome production for biomedical and biomimetic applications.

Keywords: PB-PEO, Polymersomes, Self-assembly, Morphologies, Block copolymers
INTRODUCTION

Polymersomes are self-assembled vesicular (hollow spherical) systems based on amphiphilic block copolymers, where the copolymer contains two or more chemically distinct hydrophobic/hydrophilic monomer sequences that are covalently bonded. They are gaining interest due to their colloidal stability, versatile membrane properties and ability to encapsulate or integrate a broad range of drugs and molecules, as artificial cells or matrix compartments for water channel proteins in biomimetic membranes for water separation.

Self-assembly of polymers has been studied extensively theoretically and experimentally. Amphiphilic block copolymers can self-assemble into three main structural categories: bilayers, cylinders, and micelles depending on the interfacial curvature propensity. Thus bilayers form at low interfacial curvature propensity and with increasing interfacial curvature propensity, cylinders and micelles may form. There are two main mechanisms for polymersome formation, see Figure 1. One mechanism involves a closure of bilayer sheets resulting in vesicular shape and occurs when the energy loss due to surface tension is high enough that the vesicle shape is energetically preferable, see Figure 1 mechanism $a$. Another mechanism involves nucleation (formation of semivesicles with a hydrophilic nucleus) with nucleus growth, see Figure 1 mechanism $b$. In mechanism $a$ at thermodynamic equilibrium, the polymersome size is related to a balance between the line tension $\gamma$, which is linearly related to the line energy $E_{\text{disk}}$ of the bilayer sheet rim and the bending modulus $\kappa$, linearly related to the bending energy $E_{\text{bend}}$ (Figure 1) where the polymersome diameter $d_P = \kappa / \gamma$.

For $\kappa$ of 40 kT and $\gamma$ of 1 kT, typical values for block copolymers, the theoretical mean $d_P$ is 160 nm, which is in good agreement with reported experimental data. However, based on experimental data, other factors than $\kappa$ and $\gamma$ can significantly influence polymersome size. These factors can be divided into four groups: internal-chemical factors (block chemistry, functionalization), internal-geometric factors (size, volume, number and distribution of each and both blocks), external-operational factors (conditions of preparation method) and external-environmental factors (temperature, composition and polarity of the solvent and additives). Table 1 lists some factors and their experimentally proven influences with main
Polymersomes can form due to a) bilayer closure to equilibrate out the line tension of the bilayer sheet rim $\gamma$ and the bending modulus $\kappa$ or b) to formation of a semivesicle with interior hydrophilic residues (nucleus) subsequent growth. Focus on internal factors.

Xiao and coworkers recently investigated theoretically, the internal-geometrical factors of polymersome self-assembly. Using dissipative particle dynamics (DPD) simulations of polymersomes formed by self-assembly of triblock copolymers, they modelled the polymersome size distribution with respect to the relationship of the polymersome bilayer thickness $t_P$ and $d_P$ at different $f$. At decreasing $f$, $t_P$ dictates $d_P$ to a higher extent, leading to a transition of large to small $d_P$.

Polybutadiene-polyethylene oxide (PB-PEO) represents a highly promising block copolymer chemistry due to its ability to form robust vesicles in aqueous solution attributable to the low glass transition temperature of 1,2-polybutadiene (PB) of $-10^\circ$C. PB has a close relation to polyprenyl chains found in many animal and plant membranes. PEO is the most commonly used biocompatible polymer, which is important in biomedical/biomimetic applications.

Most of the published experimental PB-PEO assembly studies focused mainly on the general morphology as a function of $f$. The effect of $M_n$ and $f$ on PB-PEO polymersome
Table 1: Main factors influencing polymersome formation. For a given parameter (see abbreviation list for explanation) ↑ indicates an increase and ↓ a decrease.

<table>
<thead>
<tr>
<th>Polymer chemistry</th>
<th>Size range [nm]</th>
<th>Influencing factor</th>
<th>Factor change</th>
<th>Response change</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>PS-PAA</td>
<td>100-500</td>
<td>$I_{mol}$</td>
<td>$I_{mol}$ ↑</td>
<td>$d_P$ ↓</td>
<td>29</td>
</tr>
<tr>
<td>PEE-PEO</td>
<td>N/A</td>
<td>$M_n$</td>
<td>$M_n$ ↑</td>
<td>Stability ↑</td>
<td>30</td>
</tr>
<tr>
<td>PG C</td>
<td>150-550</td>
<td>$M_w$</td>
<td>$M_w$ ↑</td>
<td>$d_P$ ↑</td>
<td>31</td>
</tr>
<tr>
<td>PEE-PEO</td>
<td>~40000</td>
<td>$M_w$</td>
<td>$M_w$ ↑</td>
<td>Fluidity ↓</td>
<td>32</td>
</tr>
<tr>
<td>PDMS-PMOXA</td>
<td>~20000</td>
<td>$M_{n,PDMS}$</td>
<td>$M_{n,PDMS}$ ↑</td>
<td>$D_L$ ↓</td>
<td>33</td>
</tr>
<tr>
<td>PDMS-PMOXA</td>
<td>20-150</td>
<td>$M_{n,PDMS}, f_w$</td>
<td>$M_{n,PDMS} ↑, f_w ↓$</td>
<td>$d_P$ ↑</td>
<td>34</td>
</tr>
<tr>
<td>PS-PAA</td>
<td>30-90</td>
<td>$PDI_{M,M,PAA}$</td>
<td>$PDI_{M,M,PAA} ↑$</td>
<td>$d_P$ ↓</td>
<td>35, 36</td>
</tr>
<tr>
<td>PMPC-PDPA</td>
<td>50-350</td>
<td>$T$</td>
<td>$T$ ↑</td>
<td>$d_P$ ↓</td>
<td>37</td>
</tr>
<tr>
<td>PS-PAA</td>
<td>50-100</td>
<td>$c_{P,wt}$</td>
<td>$c_{P,wt}$ ↑</td>
<td>$d_P$ ↑</td>
<td>38</td>
</tr>
<tr>
<td>PS-PAA</td>
<td>100-500</td>
<td>Additives</td>
<td>NaCl, HCl ↑, NaOH ↓</td>
<td>$d_P$ ↓</td>
<td>29</td>
</tr>
<tr>
<td>PEE-PEO</td>
<td>~25000</td>
<td>Surfactants</td>
<td>Surfactant</td>
<td>Stability ↓</td>
<td>39</td>
</tr>
</tbody>
</table>

bilayer thickness, mechanistic properties, detergent response, mixtures of two PB-PEO polymers or adhesiveness of functionalized PB-PEO polymersomes have also been investigated. However, to our knowledge, no systematic size-distribution study exists for PB-PEO polymersomes, therefore this study focuses on the combined effect of $M_n$ and $f$ on $d_P$ based on PB-PEO polymersome formation in aqueous solution. In this study, $d_P$ and polydispersity of $d_P$ will be determined by using DLS and FF-TEM. For DLS analysis, polydispersity index ($PDI_{DLS}$) is quantified as the ratio:

$$PDI_{DLS} = \frac{\delta^2}{Z_D}$$  \hspace{1cm} (1)

where $\delta$ is the distribution width of $d_P$ and $Z_D$ the intensity-weighted hydrodynamic $d_P$, obtained by DLS cumulant analysis. A related measure of the polydispersity is the variation coefficient:

$$V_{DLS} = \frac{\delta}{\langle d_P \rangle}$$  \hspace{1cm} (2)

where $\langle d_P \rangle$ is the mean value of $d_P$. For analysis using FF-TEM, polydispersity is quantified as:

$$\sigma = \sqrt{\frac{1}{n} \sum_{i=1}^{n} (d_{p(i)} - \langle d_P \rangle)^2}$$  \hspace{1cm} (3)

where $\sigma$ is the standard deviation of the manual $d_P$ measurements from a total of $n$ polymersomes. The FF-TEM derived variation coefficient is defined as:
\[ V_{FF-TEM} = \frac{\sigma}{\langle d_P \rangle} \]  

This knowledge can be very helpful in controlling the polymersome particle size and distribution and thereby circumvent the expensive and time-consuming extrusion process normally employed during production and scale-up of polymersomes for pharmaceutical, biomedical and biomimetic applications.

**EXPERIMENTS**

**Polymer synthesis via one-step approach**

All diblock copolymers except PB_{43-PEO_{32}} and PB_{74-PEO_{60}} were synthesized via one-step ring-opening anionic polymerization according to Förster. Here, butadiene (Bd) and ethylene oxide (EO) monomers were purified and dried via cooling with liquid nitrogen and distilled over \( n \)-dibutylmagnesium (\( n \)-Bu_{2}Mg) and \( n \)-butyl lithium (\( n \)-BuLi) to remove traces of impurities. The synthesis solvent Tetrahydrofuran (THF) was purified and dried via reflux and stirred over sodium in benzophenone and paraffin.

For polymerization of Bd, THF was first introduced in a predried reactor and cooled to \(-40^\circ\)C. Bd was added, followed by \( n \)-BuLi. The reaction was allowed to run for 4h at \(-20^\circ\)C, where the polybutadienyl lithium appeared in a yellow or orange colour. This step was followed by cooling down the mixture to \(-40^\circ\)C and approximately 1ml of EO was added to stop the polymerization, visibly by the disappearance of the yellow colour. The following reaction was left for 1.5 h at \(-40^\circ\)C. A precursor was drawn and analysed via size exclusion chromatography (SEC) on a SIL-10AD (Shimadzu, Kyoto, Japan). The SEC system consisted of a Shimadzu LC-10AD High performance liquid chromatography (HPLC) pump together with a Viscotek Differential Refractometer model 200 differential refractometer followed by the columns 5cm Polymer Laboratories, Guard column 3mm, 30x7.8cm Waters Styragel HMW 6E, and 30x7.5cm Polymer Laboratories, PLgel 5 mm Mixed-D. The columns were kept at room temperature during the measurements. Non-stabilized THF was used as eluent, and the system was calibrated using polystyrene standard samples having very narrow molar mass distributions.
For EO polymerization, remaining EO was added followed by injection of 1-\textit{tert}-Butyl-4,4,4-tris(dimethylamino)-2,2-bis[tris(dimethylamino)-phosphor-anyldenamino]-2\textlambda 5,4\textlambda 5-catenadi-(phosphazene) (tBuP4) in a molar \textit{n}-BuLi-tBuP4 ratio of 1:1 to ensure exact stoichiometry\textsuperscript{56}. This step was followed by heating the reaction to 40°C to start EO chain propagation. Two days later, the reaction was quenched with acetic acid. The polymer was precipitated in cold acetone followed by vacuum drying. Bd-EO stoichiometry was analyzed by nuclear magnetic resonance (NMR) at 300 or 400 MHz. The polydispersity index of the raw polymer ($PDI_M$) was analyzed via SEC. Further details can be found in the supplementary information. The polymer was stored at -20°C until use. All synthesized polymers are list in table 2.

**Polymer synthesis via two-step approach**

PB\textsubscript{43}-PEO\textsubscript{32} and PB\textsubscript{74}-PEO\textsubscript{60} were synthesized following a two-step-approach by\textsuperscript{57}. The Bd was polymerized as mentioned above followed by direct precipitation in cold acetone. This step was followed by vacuum drying of PB that was following an introduction in a predried reactor together with purified THF. This step was followed by titration with potassium naphthalenide into the solution until a slight green color remained for at least 30 min. EO was added and the reaction was allowed to heat to 45°C run for 20 h. The following termination was done with acetic acid. Precipitation, analysis and storage was done like described above.

**Polymersome formation**

For polymer stock solutions, 100 mg was thawed, weighed and dissolved in 10 ml CHCl\textsubscript{3} in order to get a 10 mg/ml solution. This step was followed by a sonication for 5 min. Storage was at -20°C until use. 2.5 ml of the stock solution was injected in a 5 ml round flask, followed by evaporating the CHCl\textsubscript{3} on a rotary evaporator for at least 2 h at room temperature and 2 mbar at a rotation speed of 125 rpm until the polymer remained as a smooth film on the flask wall. This step was followed by a rehydration of the sample with 200 \mu l of tris buffer (10 mM tris pH 8.0, 50 mM NaCl) with 1.3% \textit{n}-octyl-\beta-D-glucoside (OG) to facilitate the release of the film, and the sample was left stirring overnight at 4°C. The sample was diluted with 800 \mu l tris buffer, followed by addition of 20 mg biobeads (Bio-Rad, Hercules, USA) to remove the OG between the polymersome bilayer. The sample was
Table 2: Overview table of all synthesized polymers with $M_n$ (calculated from $^1$H NMR analysis), $PDI_M$ (based on size-exclusion chromatography (SEC) analysis with polystyrene standard calibration) and the hydrophilic volume fraction $f$. PB$_{43}$-PEO$_{32}$, PB$_{74}$-PEO$_{60}$ and PB$_{107}$-PEO$_{22}$ were synthesized with a different synthesis method than the other polymers, starting with the EO-endcapped PB. Calculation of $f$ is given in the supplementary information.

<table>
<thead>
<tr>
<th>Polymer</th>
<th>$M_n$ [kg/mol]</th>
<th>$PDI_M$</th>
<th>$f$</th>
</tr>
</thead>
<tbody>
<tr>
<td>PB$<em>{29}$-PEO$</em>{16}$</td>
<td>2.3</td>
<td>1.076</td>
<td>0.258</td>
</tr>
<tr>
<td>PB$<em>{29}$-PEO$</em>{19}$</td>
<td>2.4</td>
<td>1.086</td>
<td>0.294</td>
</tr>
<tr>
<td>PB$<em>{33}$-PEO$</em>{18}$</td>
<td>2.6</td>
<td>1.087</td>
<td>0.251</td>
</tr>
<tr>
<td>PB$<em>{47}$-PEO$</em>{7}$</td>
<td>2.8</td>
<td>1.109</td>
<td>0.089</td>
</tr>
<tr>
<td>PB$<em>{32}$-PEO$</em>{30}$</td>
<td>3.0</td>
<td>1.094</td>
<td>0.367</td>
</tr>
<tr>
<td>PB$<em>{45}$-PEO$</em>{14}$</td>
<td>3.0</td>
<td>1.078</td>
<td>0.161</td>
</tr>
<tr>
<td>PB$<em>{43}$-PEO$</em>{32}$</td>
<td>3.8</td>
<td>1.110</td>
<td>0.316</td>
</tr>
<tr>
<td>PB$<em>{46}$-PEO$</em>{32}$</td>
<td>3.9</td>
<td>1.080</td>
<td>0.301</td>
</tr>
<tr>
<td>PB$<em>{69}$-PEO$</em>{25}$</td>
<td>4.3</td>
<td>1.080</td>
<td>0.207</td>
</tr>
<tr>
<td>PB$<em>{62}$-PEO$</em>{56}$</td>
<td>5.8</td>
<td>1.081</td>
<td>0.356</td>
</tr>
<tr>
<td>PB$<em>{74}$-PEO$</em>{60}$</td>
<td>6.7</td>
<td>1.081</td>
<td>0.333</td>
</tr>
<tr>
<td>PB$<em>{104}$-PEO$</em>{31}$</td>
<td>7.0</td>
<td>1.244</td>
<td>0.155</td>
</tr>
<tr>
<td>PB$<em>{121}$-PEO$</em>{25}$</td>
<td>7.7</td>
<td>1.092</td>
<td>0.111</td>
</tr>
<tr>
<td>PB$<em>{120}$-PEO$</em>{41}$</td>
<td>8.3</td>
<td>1.072</td>
<td>0.175</td>
</tr>
<tr>
<td>PB$<em>{92}$-PEO$</em>{78}$</td>
<td>8.4</td>
<td>1.167</td>
<td>0.344</td>
</tr>
<tr>
<td>PB$<em>{104}$-PEO$</em>{77}$</td>
<td>9.0</td>
<td>1.130</td>
<td>0.314</td>
</tr>
<tr>
<td>PB$<em>{117}$-PEO$</em>{61}$</td>
<td>9.1</td>
<td>1.204</td>
<td>0.245</td>
</tr>
</tbody>
</table>

left on a shaker with 200 rpm for 3 h at room temperature (RT), followed by addition of another 20 mg of biobeads. The sample was then left overnight shaking with 200 rpm at 4°C.

Analysis of $d_P$ via freeze fracture and transmission electron microscopy (FF-TEM)

FF was performed on a MED020 with EM VCT100 shuttle attached (Leica, Wetzlar, Germany). 1.2 µl sample was injected into a 3 mm aluminium sample carrier at the side with 300 µm depth and covered with another aluminium plate of 200 µm depth side, care was
taken to avoid air bubbles in between. This sandwich was plunged into liquid ethane for 20 s, followed by immediate plunging in liquid N₂. The sample carrier was fixed at the sample holder, followed by introduction in a high vacuum chamber at -140°C. This step was followed by removal of the lower sample carrier, where sample coating was following at the same temperature with 2 nm carbon, followed by 4 nm platinum tilted at 45° and finally with a 19 nm carbon protection layer without tilt. Outside of the chamber, the carrier was thawed for 5 min at RT, followed by carefully replacement in 45° into a 200 μl bath of tris buffer with 10%OG for 5 min for solubilizing the polymersomes. The final step was to place an uncoated TEM copper grid with 400 Mesh at 45° below the replica or single pieces of it. TEM observation was done with a CM100 (Philips, Amsterdam, Netherlands) with an installed Veleta 2k CCD camera (Olympus, Shinjuku, Japan). On a tungsten source, the applied voltage was 80 kV with a 100 μm objective lense aperture. Analysis of $d_P$ on the TEM images was done by manual measurement (after semi-automatic measurement using ImageJ with various plugins failed to work due to too low contrast between polymersomes and background) using the image software Gimp, followed by multiplication of all values with a correction factor of $4/\pi^{58}$.

**Analysis of $d_P$ via DLS**

DLS was done with a Nano Zetasizer (Malvern, Worcestershire, UK). 800 μl sample were injected in a disposable cuvette, followed by three measurements with 6 runs of 10 s per measurement at RT. Raw data of autocorrelation functions of $\text{PB}_{33}$-$\text{PEO}_{18}$, $\text{PB}_{46}$-$\text{PEO}_{32}$ and $\text{PB}_{92}$-$\text{PEO}_{78}$ as examples can be found in the supplementary information.

**RESULTS AND DISCUSSION**

Stable PB-PEO based polymers with $M_n$ ranging from 2.3 – 9.1 kg/mol and $f$ between 0.089 – 0.367 were synthesized as shown in Table 2. Utilizing the film rehydration technique, polymersomes were formulated with the synthesized polymers and characterized using DLS and FF-TEM. First sample preparation will be discussed, in terms of how it can be adopted to ensure minimal external influence on $d_P$, how the analytical methods used (DLS and
FF-TEM) can influence $d_P$ and how one may minimize such influence. Then, results will be compared from DLS and FF-TEM as well as their compatibility or correlation of data generated from them. Finally, the influence of $M_n$ on $d_P$, the influence of $f$ on $d_P$ and the combined effect on $d_P$ of changing both $M_n$ and $f$ will be discussed.

**Issues in experimental determination of polymersome diameter**

**Influence of sample preparation**

During polymersome preparation and analysis, commonly used techniques including centrifugation, dilution and agitation can affect their formation, quality and stability. It is therefore necessary to minimize these external influences as much as possible. In the present study, we prepared all polymersomes with no dilution, centrifugation and minimal agitation during preparation and analysis. To ensure reproducibility, three sample sets are prepared per polymer. Most samples exhibited high turbidity (polymer concentration: 25 mg/ml) throughout the preparation.

**Influence of DLS algorithms**

It is well-known that DLS is biased towards larger particles, because they scatter light more strongly. To minimize this bias, volume size distribution is used instead of the intensity size distribution. The latter is based on Rayleigh scattering that has a intensity-particle-diameter-relationship $I \sim d^6$, where the former is based on Mie scattering that compensates for the strong dependency. Another problem is the polydispersity of samples. The DLS instrument uses two algorithms to measure particle sizes: cumulant analysis and non-negatively constrained least squares (NNLS). Cumulant analysis is more convenient to use, however it assumes only a single particle family (e.g. spheres with narrow size distribution) and is thus not suitable for polydisperse samples. In DLS analysis, polydispersity is quantified as $PDI_{DLS}$ (Equation 1). From previous experiments, we know that the studied polymersomes have a higher $PDI_{DLS}$ than 0.25, where cumulant analysis is not recommended to use. Thus, all values are extracted from the NNLS analysis. NNLS generally introduces several algorithm operators to extract information from the autocorrelation curve generated by DLS. Thus, micelles, different polymersome classes or aggregates can be easier differenti-
ated\textsuperscript{61}. Another issue is the unusually high polymersome concentration (25 mg/ml) leading to high turbidity. The DLS instrument can however compensate highly turbid samples using non-invasive back scattering (NIBS) at 173° detection angle. Thus, laser attenuation as well as measurement position in the cuvette can be adjusted to sample turbidity\textsuperscript{62–64}. However, a potential error source could arise due to strong scattering of highly turbid samples. However, to compare FF-TEM and DLS properly (and minimize influences of external factors) both need to be performed at the same concentration. Lower polymer sample concentrations would however lead to high levels of bad fracturing. We therefore decided to keep 25 mg/ml as fixed concentration throughout all experiments.

**Influence of FF-TEM on \(d_P\)**

FF reveals information about polymersome size as the original shape in aqueous solution is preserved by changing the aggregate state of the solution to the glassy state during quick-freezing without the formation of ice crystals. Compared to negative-staining TEM, there is no labeling with heavy metal derivates that could cause deformation and/or osmotic shrinkage of the polymersomes. Additionally, one can obtain a more 3D-like appearance in contrast to Cryo-TEM. The major drawback is that the polymersomes are not all fractured in the equatorial plane, meaning that the observed diameter is often smaller than \(d_P\). Although we apply a correction factor \((4/\pi)^{58}\), the difference between observed and real diameter remains a source of error for FF-TEM. The advantage of working with the planchet technique (details in the Material & Methods section) is that the smearing effects are minimized, however not completely removed. As the observed \(\langle d_P \rangle\) is larger than the diameter of PB-PEO micellar structures (15-40nm\textsuperscript{49}) and from former Cryo-TEM observations on PB$_{29}$-PEO$_{16}$\textsuperscript{65} we conclude that the majority of spherical structures observed are polymersomes. For the PB-PEO diblock copolymers investigated, FF-TEM revealed highly polydisperse samples that were spread over the whole replica (Figure 2a), distributed in small islands between non-fractured polymersome-free planes (e) or in river-like arrangements (c). All these samples had well-defined edges and clear three-dimensional appearance. Other samples had well-defined edges as well but appeared more planar (Figure 2f). The difference between Figure 2a, g and c could be due to the fact that each polymersome
Figure 2: FF-TEM micrographs of PB-PEO polymersomes of different $M_n$ and $f$, sorted after increasing $M_n$. a)+g) PB$_{29}$-PEO$_{16}$, c)+i) PB$_{29}$-PEO$_{19}$, e)+k) PB$_{33}$-PEO$_{18}$, b) PB$_{60}$-PEO$_{25}$, h) PB$_{45}$-PEO$_{15}$, d)+j) PB$_{74}$-PEO$_{60}$, f)+L) PB$_{92}$-PEO$_{78}$. Scale bar is 1 $\mu$m for a-f and 100 nm for b-L. Polymersomes were spread over larger areas (a), islands (e) or river-like arrangements (c), where they exhibited well-defined edges. At fragile areas of the ends of the replica, the displacement of polymersomes left black rings on the edges (d) complicating the measurement of their $d_P$. Few samples exhibited a more flat (f) or shallow appearance (b), the last is probably not fractured. When observing at higher magnification, all polymersomes had rougher (i+h) or finer (g+k) grains on their surface. The white shadow is generated during platinum shadowing at 45°.
population was at a different position inside the planchet and the presence of air bubbles in the planchet. The possible solution turbulence involved in the vitrification process was probably higher at the edges of the planchet, forcing the polymersomes to accumulate around turbulent areas in the observed river-like arrangements in Figure 2c. The turbulence forces had a less pronounced effect on larger polymersomes consistent with the observation that there were seldom micrometer size polymersomes present in the river-like arrangements. The "islands", observed in Figure 2e, could be due to air bubbles, creating solution-free gaps between both planchets. However, all these factors are not influencing $d_P$ determination per se. A few polymersome samples had less well-defined edges and generally exhibited a more shallow appearance (Figure 2b). These polymersomes were probably not fractured but could be facing the air-water-interface of a captured air bubble. Here, no correction factor would apply as far as no fracture occurred. We rarely observed these structures, thus we assume their influence on $d_P$ to be negligibly small.

Many samples showed black rings around the polymersomes (Figure 2d, j + L). The black-ring polymersomes are probably located at fragile areas at the edges of the replica. Displacement of the original polymersomes will result in low resolution of the most fragile parts of the replica (the polymersome edges) and the thickness of the black ring will affect the precision of $d_P$ determination. The manual measurement was performed from the outer (well-defined) edge of the black ring to ensure reproducible $d_P$ readings. At higher magnification, polymersomes appeared in raspberry-like spherical shapes covered with grains, sometimes revealing an opened inner bilayer (see Figure 2j) or a shadow from the 45° platinum coating (Figure 2i, h and k). Chambon and coworkers observed similar structures of polyglycerol monomethacrylate-polyhydroxypropyl methacrylate-polybenzyl methacrylate (PGMA-PHPMA-PBzMA) triblock copolymers. To avoid any artifacts, $d_P$ measurements are taken at the side without shadow. Due to bad fracturing, there could be small dots at the polymer-some edges (see Figure 2h). However this has only a negligible effect on $d_P$ determination. For each of the triplicates, a minimum of 100 polymersomes is measured, resulting in a minimum of 300 polymersomes per polymer. FF-TEM revealed $d_P$ between 100 nm and 300 nm, where $\sigma$ was often larger than $d_P$ resulting in $V_{FF-TEM} > 1$ (Equation 4). FF-TEM can be biased towards larger polymersomes as well, because these are the ones that
can be observed easiest when screening the TEM grid. So even if there is only one large polymersomes out of 1000 polymersomes, there is a strong bias towards it if there are only 100 polymersomes analyzed per batch. On the other hand it can also lead to false results if they are left out of the analysis even though they have been observed. To overcome this problem, it would require manual measurement of 1000 or more polymersomes per batch, which is beyond the scope of this study. However based on the work of Terreau and coworkers\textsuperscript{36} we are confident that our sampling is sufficient to assess $\langle d_P \rangle$.

**Issues in comparing from DLS versus FF-TEM**

All spherical self-assembled morphologies from a FF-TEM image are measured in terms of $d_P$, regardless if they could be micelles or polymersomes. To be able to compare DLS and FF-TEM, the multi-peak distribution from the DLS NNLS analysis was normalized into one effective peak by performing a weighted average. Comparing the normalized $\langle d_P \rangle$ values from DLS analysis with values from FF-TEM, $\langle d_P \rangle$ values from the DLS analysis were on average 64±39\% higher than values from the FF-TEM analysis. The largest difference was 83.7\% for PB$_{29}$-PEO$_{19}$, the smallest difference 39.5\% for PB$_{46}$-PEO$_{32}$. Even when using volume size distribution, DLS is still highly biased towards larger particles. The $\langle d_P \rangle$ difference between DLS and FF-TEM can thus be to the presence of large aggregates appearing as one particle in DLS analysis, whereas they are left out in FF-TEM analysis. Terrau et al. compared DLS and TEM measurements and also obtained larger $\langle d_P \rangle$ with DLS than with TEM, which they explained by the appearance of aggregates\textsuperscript{36}. The maximal $d_P$ values which we could determine reliably from FF-TEM images were around 1.5µm. Thus effectively all structures larger than this are excluded in the manual FF-TEM analysis of the $d_P$ distribution. We therefore also omitted all morphologies with an apparent $d_P > 1.5$ µm from the DLS analysis corresponding to less than 15\% of the total mass content. After this correction, the difference in $\langle d_P \rangle$ went down to 38±22\%, where the highest difference was 75.8\% observed for PB$_{46}$-PEO$_{32}$ and the smallest was only different by 5.4\% for PB$_{60}$-PEO$_{25}$, for details see supplementary information. A general tendency is that $\langle d_P \rangle$ values of polymersomes with $V_{FF-TEM} > 0.9$ are 50\% larger in DLS analysis compared to FF-TEM. We believe that these corrections (normalization and exclusion of large structures) are sufficient to enable a
comparison of DLS and FF-TEM, although we cannot fully exclude that some of the larger $d_P$ values captured by DLS in fact represent aggregates rather than polymersomes.

Figure 3: Visualization map of the effect of $M_n$ and $f$ on $d_P$ from DLS (a) and FF-TEM (b). $\langle d_P \rangle$ is indicated as full circles (blue and red/orange for DLS and FF-TEM respectively) and the concentric dotted circles indicate $\langle d_P \rangle \pm \delta$ for DLS and $\langle d_P \rangle \pm \sigma$ for FF-TEM. If $\langle d_P \rangle < 400$ nm in (a), the circle color is changed to bright blue in and if $\langle d_P \rangle < 150$nm in (b), the circle color is change to bright red. Three regions are indicated: a region with mixed high/medium/low $d_P$ values (labeled A), a region with medium/high $d_P$ values (labeled B) and a region with medium/low $d_P$ values (labeled C).
The relation between $d_P$ and $M_n$ & $f$

We now analyze how $d_P$ depends on $M_n$ and $f$. The relationship is depicted in Figure 3 where Figure 3a show data from the DLS measurements. $\langle d_P \rangle$ is indicated as full circles (blue and red for DLS and FF-TEM respectively) and the concentric dotted circles indicate $\langle d_P \rangle \pm \delta$ for DLS and $\langle d_P \rangle \pm \sigma$ for FF-TEM. Although the $d_P$ distribution seems to scatter considerably in the $(M_n, f)$ parameter space we can identify three regions: a region with mixed high/medium/low $d_P$ values (labeled A), a region with medium/high $d_P$ values (labeled B) and a region with medium/low $d_P$ values (labeled C). Our finding are on contrast to the findings of Wu et al. who observed a decrease $d_P$ with increasing $f$ for PDMS-PMOXA diblock copolymers\textsuperscript{34}. Hypothetically, this difference could be due to steric repulsion of PMOXA, which may be less pronounced for PEO, as far as the oxazoline ring of PMOXA has a higher steric effect than the PEO monomer.

From the FF-TEM analysis, there was a slight increase in $d_P$ with higher $M_n$ for $f > 0.2$. Bermudez et al. reported an increase in $t_P$ with increasing $M_n$\textsuperscript{51} for PB-PEO polymersomes. From $M_n$ of 3.6 to 5.2 kg/mol, they observed an $t_P$ increase of 1 nm (9.6 to 10.6 nm). Doubling the $M_n$ resulted in an increase in $t_P$ of one third ($M_n$ 10.4 and 20 kg/mol resulted in a $t_P$ of 14.8 and 21 nm respectively). Additionally, Ma et al. reported a linear dependence between $t_P$ and $d_P$ for three out of four polymersomes\textsuperscript{68}. Combining these results a linear relationship between $t_P/M_n$ and $t_P/d_P$ could substantiate the findings of an increased $d_P$ with increasing $M_n$. However the study of Ma et al. was made on PS-PAA polymersomes with $M_n$ between 25 and 55 kg/mol, which complicates a direct comparison. Experimental studies on PS-PAA are generally performed in a mixture of water and organic solvent. This is not the case here where we analyzed PB-PEO with water as the sole solvent. As far as PS is less soluble in water than PB, PS-PAA cannot be made by film rehydration but need to be brought into the aqueous phase by slow solvent exchange\textsuperscript{68, 29}. Thus, the external-environmental factors fundamentally different for PS-PAA compared to PB-PEO which makes a direct comparison difficult.

For both DLS and FF-TEM there is a tendency for $\langle d_P \rangle$ to increase with increasing $f$ (see $f$ vs $d_P$ in the supplementary information). For $f < 0.2$, $\langle d_P \rangle$ was between 100-200 nm,
irrespective of $M_n$. For $f > 0.2$, some $\langle d_P \rangle$ increased up to 200-300 nm but with considerable variation as function of $M_n$. The increase is more pronounced in Figure 3b than in Figure 3a, probably to the issues in obtaining $\langle d_P \rangle$ values from polydisperse samples with DLS. The increase is in agreement with the DPD simulations of Xiao et al. who reported an increase in $\langle d_P \rangle$ with increasing $f^{26}$. They explained this phenomenon with expansion of the hydrophilic blocks in order to maximize the contact with the solvent. The expansion is stronger with increasing $f$ so that larger polymersomes would exhibit more hydrophilic blocks in expanded conformation$^{26}$. On the contrary, Choucair et al. found a decreasing $d_P$ with increasing $f$ on PS-PAA polymersomes$^{29}$. A comparison is hampered by the fundamental differences between PS-PAA and PB-PEO as discussed before.

For $0.17 < f < 0.2$, $\delta$ was minimal with DLS and $\sigma$ was also low with FF-TEM for the polymersomes of $\text{PB}_{45}$-$\text{PEO}_{15}$ ($M_n = 3.1$ kg/mol), $\text{PB}_{60}$-$\text{PEO}_{25}$ ($M_n = 4.3$ kg/mol) and $\text{PB}_{120}$-$\text{PEO}_{41}$ ($M_n = 8.3$ kg/mol). Xiao et al. concluded similarly a minimal $PDI$ with long hydrophobic chain length$^{26}$. They ascribed this to a minimization of energetically unfavorable interactions between the hydrophobic chains and the aqueous solution thus no shielding of the hydrophilic segments was necessary. Ma et al. also experimentally reported an increased $PDI$ with increasing hydrophilic block length$^{68}$, but with PS-PAA polymersomes.

From a thermodynamical point of view, we assume mechanism $a$ from the introduction as the major mechanism since mechanism $b$ applies to more hydrophobic polymers like PDMS$^{26,69}$. Thus, it may be that in regions B and C in the ($M_n$, $f$) parameter space (Figure 3), the equilibrium between $E_{\text{disk}}$, the driving force to keep the bilayer structure open and $E_{\text{bend}}$, the driving force to close the bilayer to vesicular structure, is one broad energetic minimum. For polymers in region B ($M_n$ 5-9 kg/mol and $f$ 0.2-0.4), as well as for polymers in region C ($M_n$ 3-9 kg/mol and $f$ of 0.1-0.2), the bilayer closure or nucleation growth results therefore in one dominant $d_P$. Thus, polymersomes in these regions had less polydispersity than in region A ($M_n$ 2-5 kg/mol and $f$ 0.2-0.4). Here, the energy difference behind bilayer closure/nucleation growth is smaller which likely results in several energetic minima, leading to $d_P$ variation and higher polydispersity.

In order to obtain more insight into how the polydispersity may depend on the characterization method, we analyzed how the variation coefficients $V_{\text{DLS}}$ and $V_{\text{FF-TEM}}$ depend on $M_n$. 
Figure 4: Variation coefficients as function of $M_n$ and $f$ for DLS and FF-TEM analysis. (a) $V_{DLS}$ calculated using Equation 2. (b) $V_{FF-TEM}$ calculated using Equation 4. The color changes from blue to red to yellow with increasing variation coefficient. The regions A, B and C from Figure 3 are also reflected in this map. The variation coefficients are rather low in region B and C, where the are increased and different in region A. The effect is more pronounced for $V_{FF-TEM}$.

and $f$, shown in Figure 4. $V_{DLS}$ is $45\pm22\%$ lower than $V_{FF-TEM}$ (excluding PB$_{32}$-PEO$_{30}$ with the reverse ratio mentioned before). In region B and C, $V_{DLS}$ and $V_{FF-TEM}$ are low, consistent with the obtained $\delta$ and $\sigma$ values, see Figure 3. In region A, the variation coefficients were more different, where the difference between $V_{FF-TEM}$ was higher than in
the case of $V_{DLS}$. The underlying weak energy function in region C is also reflected in the variation coefficients. The resulting randomly $d_P$'s are especially visible in the different $V_{FF-TEM}$s of PB$_{43}$-PEO$_{32}$ and PB$_{46}$-PEO$_{32}$ that have a difference in $M_n$ and $f$ of only 0.1 kg/mol and 0.02 respectively. Xiao revealed as well that samples with lower $f$ assemble to more monodisperse samples$^{26}$.

CONCLUSIONS

In conclusion, polymersomes based on PB-PEO were prepared under identical conditions and analysed via DLS and FF-TEM to determine how $\langle d_P \rangle$ depends on $M_n$ and $f$. Both methods of analysis revealed highly polydisperse samples. We defined three main regions in the $(M_n,f)$ parameter space: A (high $f$/low $M_n$) with mixed high/medium/low $d_P$ and high polydispersity, B (high $f$/high $M_n$) with high/medium $d_P$ and medium polydispersity and C (low $f$) with low/medium $d_P$ and medium polydispersity. There is a tendency towards increased diameter with increasing $f$ and $M_n$. These observations are a first step into the complex and sensitive interplay between block length and morphology at the ”amphiphilic window” between $f 0.15$ and $0.35$ where polymersomes are forming. The understanding of underlying mechanism enables the chemical fine-tuning to achieve desired size distributions for the use of polymersomes as nanoreactors, drug delivery system or matrix compartment for biomimetic membranes.

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ABBREVIATIONS / NOMENCLATURE

Bd - 1,3-Butadiene

\( n\)-BuLi - \( n\)-Butyl lithium

\( n\)-Bu\(_2\)Mg - \( n\)-Dibutylmagnesium

\( c_{P,wt} \) - Polymer weight concentration

\( d_P \) - Polymersome diameter [\( \mu m \)]

\( \langle d_P \rangle \) - Mean \( d_P \)

\( PDI_M \) - Polydispersity index of the polymer length, defined as \( M_w/M_n \)

\( D_L \) - Lateral diffusion coefficient [\( \mu m^2/s \)]

DLS - Dynamic light scattering

\( E_{bend} \) - Bending energy of vesicle

\( E_{disk} \) - Line energy of vesicle bilayer sheet rim

EO - Ethylene oxide

\( f \) - Hydrophilic volume ratio

\( f_{mol} \) - Hydrophilic molar ratio

\( f_w \) - Hydrophilic weight ratio

HPLC - High performance liquid chromatography

\( M_n \) - Number averaged molecular weight

\( M_w \) - Weight averaged molecular weight

NIBS - Non-invasive back scattering

NMR - Nuclear magnetic resonance

NNLS - Non-negatively constrained least squares

OG - \( n\)-octyl-\( \beta\)-D-glucopyranoside

PAA - Polyacrylic acid

PB - 1,2-Polybutadiene

PBzMA - Polybenzyl methacrylate

\( PDI_{DLS} \) - Polydispersity index of \( d_P \) by DLS analysis
PDMS - Polydimethylsiloxane
PDPA - Polydiisopropylaminoethyl methacrylate
PEE - Polyethylene
PEO - Polyethyleneoxide
PGC - Palmitoyl glycol chitosan
PGMA - Polyglycerol monomethacrylate
PHPMA - Polyhydroxpropyl methacrylate
PMOXA - Polymethyloxazoline
PMPC - Polymethacryloyloxyethylphosphorylcholine
PS - Polystyrene
SEC - Size exclusion chromatography
$t_P$ - Polymersome bilayer thickness [nm]
tBuP4 - 1-tert-Butyl-4,4,4-tris(dimethylamino)-2,2-bis[tris(dimethyl-amino)-phosphoranylidenamino]-2λ5,4λ5-catenadi(phosphazene)
TEM - Transmission electron microscopy
THF - Tetrahydrofuran
$V_{DLS}$ - Variation coefficient of DLS analysis
$V_{FF-TEM}$ - Variation coefficient of FF-TEM
$Z_D$ - Intensity-weighted hydrodynamic $d_P$
$\delta$ - Distribution width of $d_P$ measured with DLS
$\gamma$ - Line tension of polymersome bilayer sheet rim
$\kappa$ - Bending modulus of polymersome
$\sigma$ - Standard deviation of FF-TEM $d_P$ measurements

References


