Influence of the size of hydrophilic grafts on the structure of single-chain polymeric nanoparticles: insights from molecular dynamics simulations

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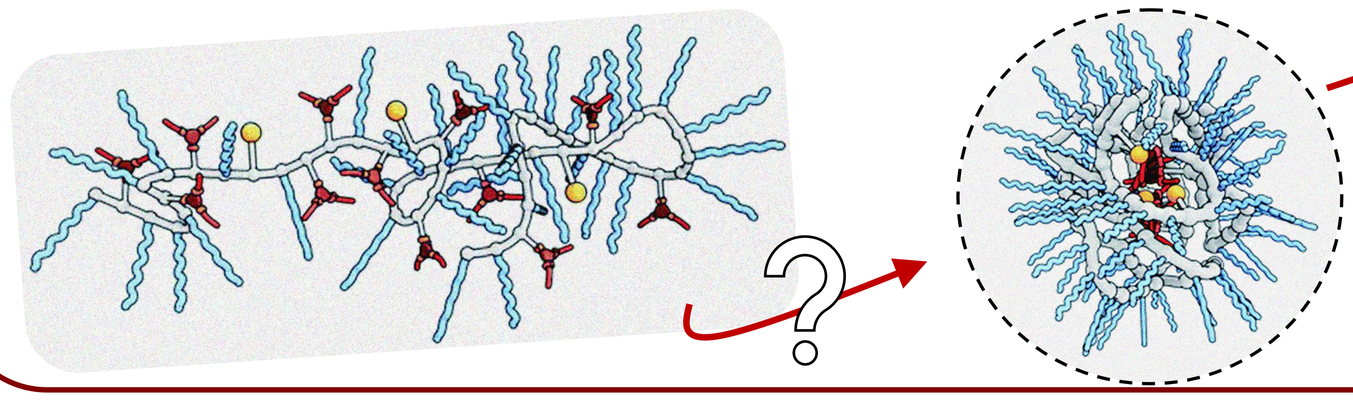
Introduction

Single-Chain Polymeric Nanoparticles **(SCPNs):**
Controlling the collapse of polymer chains to create functional systems[1,2]

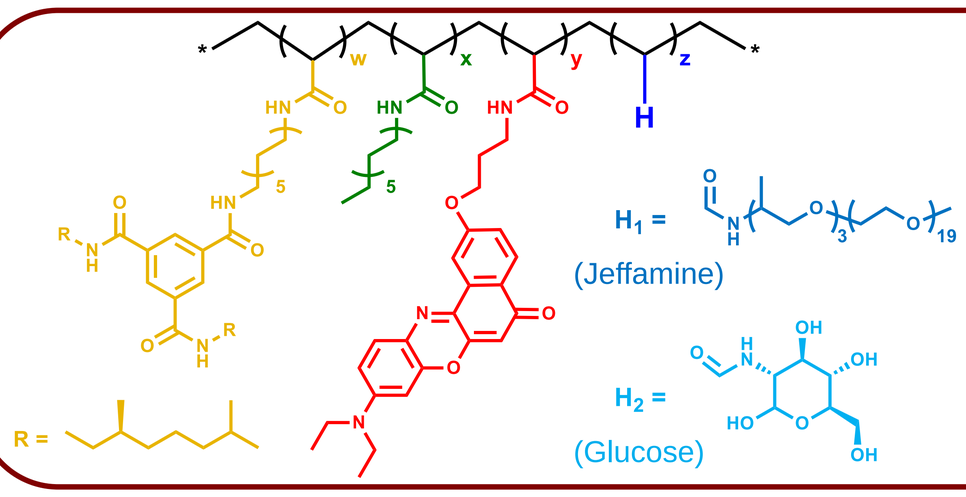


How to predict the folded structure?

Using Molecular Dynamics (MD) simulations!

- AMBER biomolecular simulation programs[3]
- GAFF2 force-field (polymer)
- Explicit solvation with water (OPC water model)
- Microsecond timescale

Chemical structure

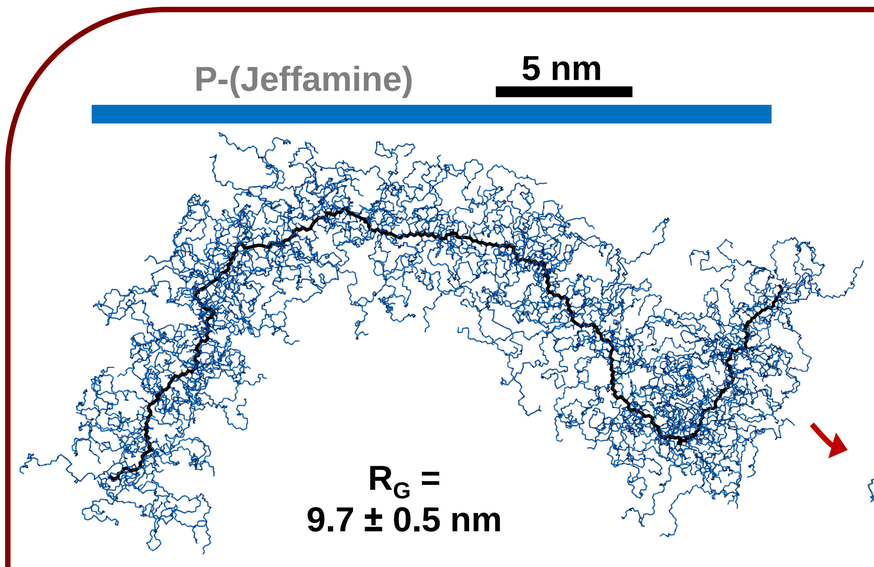


P-(Jeffamine): w = 0.00 x = 0.00 y = 0.00 z = 1.00
P-(Jeffamine-dodecyl-BTA): w = 0.04 x = 0.15 y = 0.00 z = 0.81
DP = 186

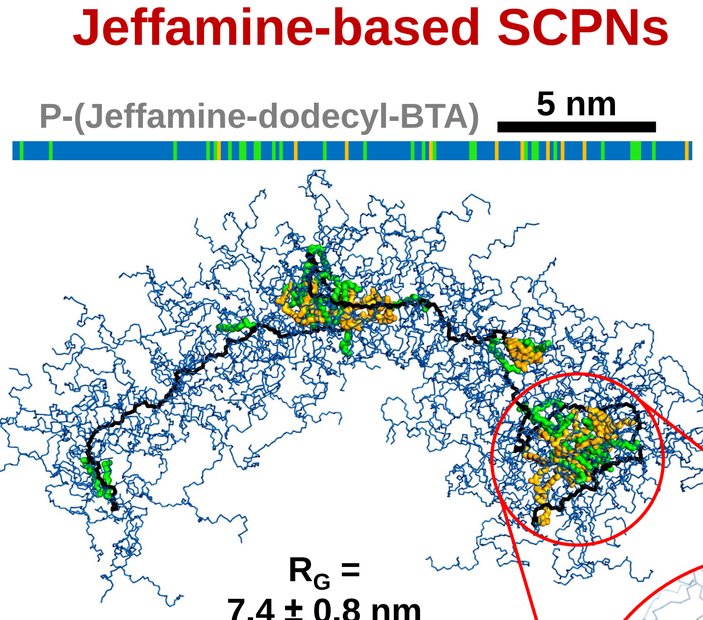
P-(Glucose): w = 0.00 x = 0.00 y = 0.01 z = 0.99
P-(Glucose-dodecyl): w = 0.00 x = 0.15 y = 0.01 z = 0.84
P-(Glucose-BTA): w = 0.05 x = 0.00 y = 0.01 z = 0.94
DP = 103

Hydrophilic units
(long or short)
+
Hydrophobic units
+
Supramolecular units
+
Chromophore

Jeffamine-based SCPNs



R_G = 9.7 ± 0.5 nm

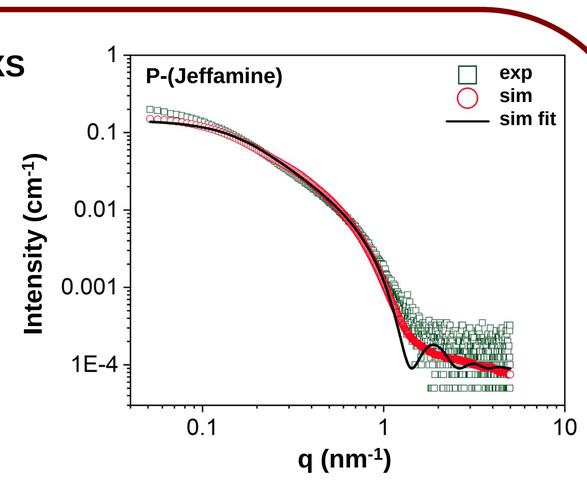


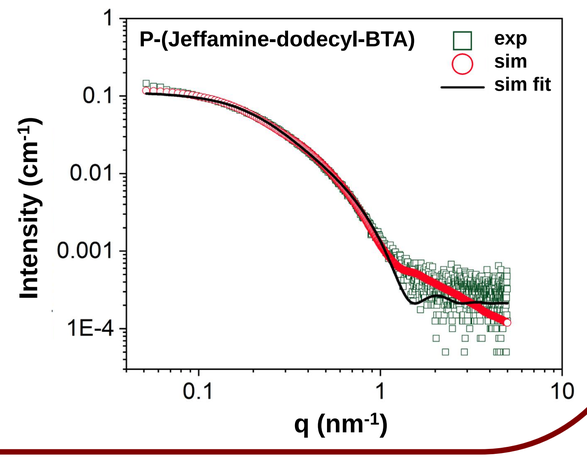
R_G = 7.4 ± 0.8 nm

Simulation of SAXS spectra (with CRYSOL[4])

In collaboration with Stefan Wijker

TU/e EINDHOVEN UNIVERSITY OF TECHNOLOGY





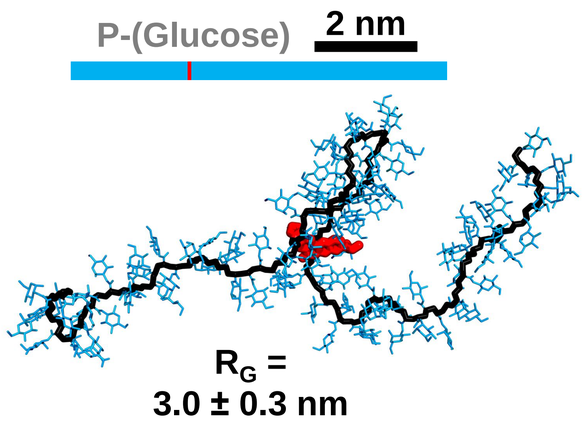
- High steric hindrance from the Jeffamine grafts ➔ No single hydrophobic core
- Monomers far in the sequence ➔ Far in the 3D structure

Jeffamine grafts

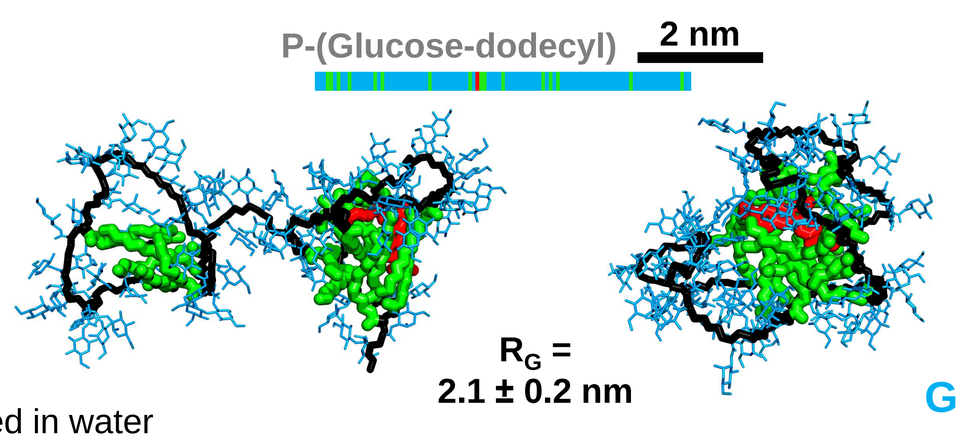
Local hydrophobic clusters

Backbone **Jeffamine** **Glucose** **Dodecyl** **BTA** **Nile Red**

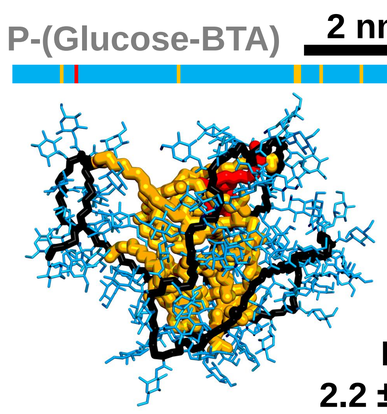
Glucose-based SCPNs



R_G = 3.0 ± 0.3 nm



R_G = 2.1 ± 0.2 nm



R_G = 2.2 ± 0.1 nm

- Fully hydrophilic chain ➔ Remains extended in water
- Amphiphilic systems ➔ Folding into compact, globular nanoparticle

Glucose grafts

One hydrophobic core

Conclusion

- The structure of amphiphilic SCPNs is influenced by the length of hydrophilic grafts:
  - Long grafts **(Jeffamine)** ➔ Local hydrophobic clusters
  - Short grafts **(glucose)** ➔ Full compaction of the chain
- MD simulations, supported by SAXS data, give us an **atomic-scale picture** of the structure of SCPNs

References

1. G. M. ter Huurne et al., *CCS Chem.* **2019**, *1*, 64-82.
2. P. J. M. Stals et al., *Chem. Sci.* **2016**, *7*, 2011-2015.
3. R. Salomon-Ferrer et al., *Wiley Interdiscip. Rev. Comput. Mol. Sci.* **2013**, *3*, 198-210.
4. D. Franke et al., *J. Appl. Crystallogr.* **2017**, *50*, 1212-1225.

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