Monte Carlo simulation of Self-assembled Nanogel : Study of Hydrophobic Interaction between Polymers

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What is a Nanogel?

A nanogel is defined as nanoparticle which is three-dimensionally cross-linked hydrogel in any shape with a diameter from 1 to 100nm approximately, so a nanogel has the features of both hydrogel and nanoparticle at the same time.
Nanogel has been used for medical applications, and the study of them has a great interest in the biological field. Nanogel has advantages as transporting large molecules such as drugs or genes to cell membrane because nanoparticles protect them from degradation during cellular uptake process.
Interaction(or bond) that composes monomers of nanogel is categorized into two parts, one is a covalent bond of linked monomers as creating a polymer, and the other is a non-covalent bond between monomers, that is related to agglomeration of nanogel.
Here, we talk about a nanogel based on cholesterol-bearing Xyloglucan(CHXG), a branched polysaccharide with attached cholesterol group by a covalent bond. The driving force of self-assembly, in this case, would be the hydrophobic effect of cholesterol group. [1, 2]

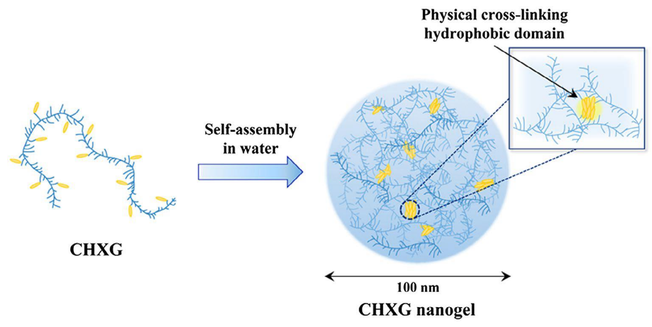

Figure 1. Cholesterol bearing Xyloglucan(CHXG) nanogel and self-assembly effect [1]

Hydrophobicity and Self-assembly

Hydrophobicity is a characteristic of a molecule that repels water molecules, so respectively attracts other molecules which are also hydrophobic. In CHXG(CHolesterol bearing XyloGlucan) molecules, XG is a water-soluble macromolecule, but CH is not. CH has the property of hydrophobicity, and each CH attracts other CH, and this makes the CHXG chain self-assembled in an energetically favorable way.
The potential which drives self-assembly is depicted below as u_{LJ}, and the total potential of the system is depicted as U. [3]

$$U = U_{nonbond} + U_{bond} + U_{ang}$$

$$U_{nonbond} = \sum_{i<j} u_{i,j}(r_{i,j}) + \sum_{k<l} u_{LJ}(r_{k,l})$$

$$u_{LJ}(r_{k,l}) = 4\epsilon\left[(\frac{\sigma}{r})^{12} - \left(\frac{\sigma}{r}\right)^{6}\right]$$

(Lennard–Jones Potential, ϵ =2.48, σ=6.00)

System modelling and simulation

Here, a Coarse-grained(CG) model is used to describing a structure of nanogel. A coarse-grained model is a model describing a system with simplified groups of atoms. The groups of atoms in biomolecules are clustered into new coarse-grained sites with the reduced number of degrees of freedom. A new model of one specific molecule, thus, has fewer sites than real molecules. The information that is reduced for transforming into the coarse-grained model can be emphasized or omitted, but the primary key is which part of a structure should be emphasized or omitted, and how we make it in computation. The simulation package MOLSIM is used to study the conformational behavior of molecules. [5]

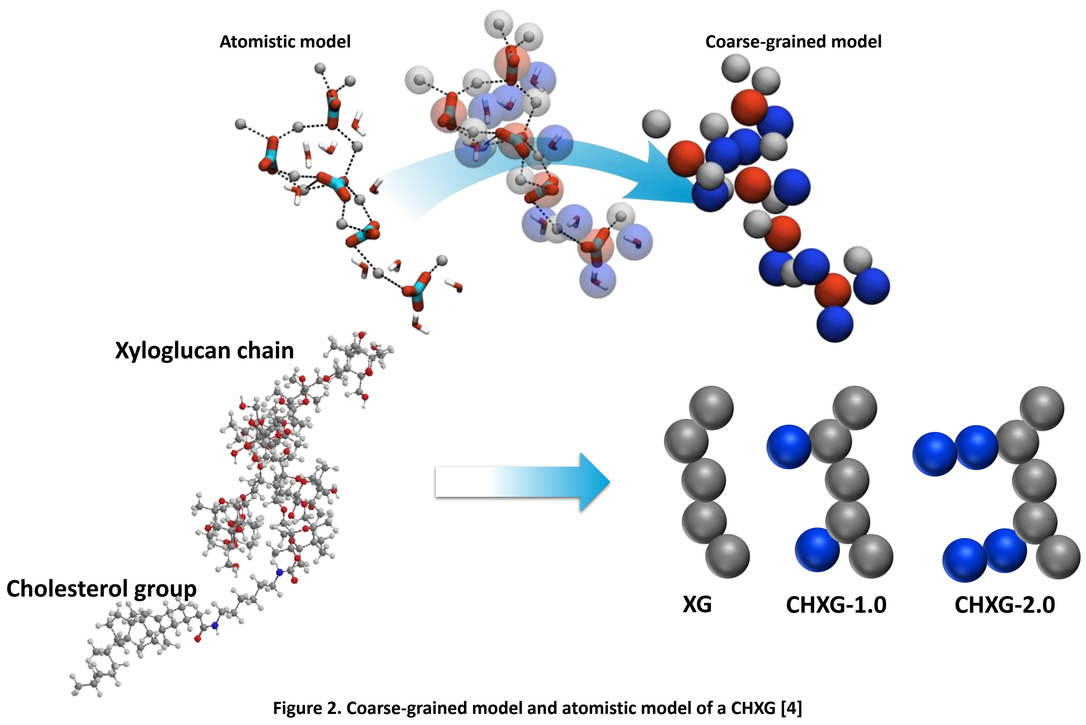

Figure 2. Coarse-grained model and atomistic model of a CHXG [4]

After modeling the system, there are some algorithms that we can calculate a physical property of the system, i.e., the radius of gyration(Rg) and the end-to-end distance(Ree). Here, Monte Carlo method is used for computing the system of Cholesterol bearing Xyloglucan nanogel. A random walk algorithm is attempted for moving each coarse-grained sites, after each microstep. 10,000 microsteps compose one macrostep, and totally ten macrosteps are executed after equilibrium state. (10x10,000 steps) [5]

Snapshots of simullated CHXG nanogel after 10x10,000 steps

As we expected by work of Sawada et al. [1], CH bearing XG has more self-assembly behavior after 10x10,000 steps of random movement. Also, there is a result of comparing the number of CH as CHXG-1.0 and CHXG-2.0. As the names inform, CHXG-2.0 which has the doubled number of CH than CHXG-1.0 shows more agglomeration than CHXG-1.0 and XG in figure 3. The above images of TEM are from Sawada et al. [1], and we can compare two conformation results of simulation and the nanogel particles made by experiment in the lab.

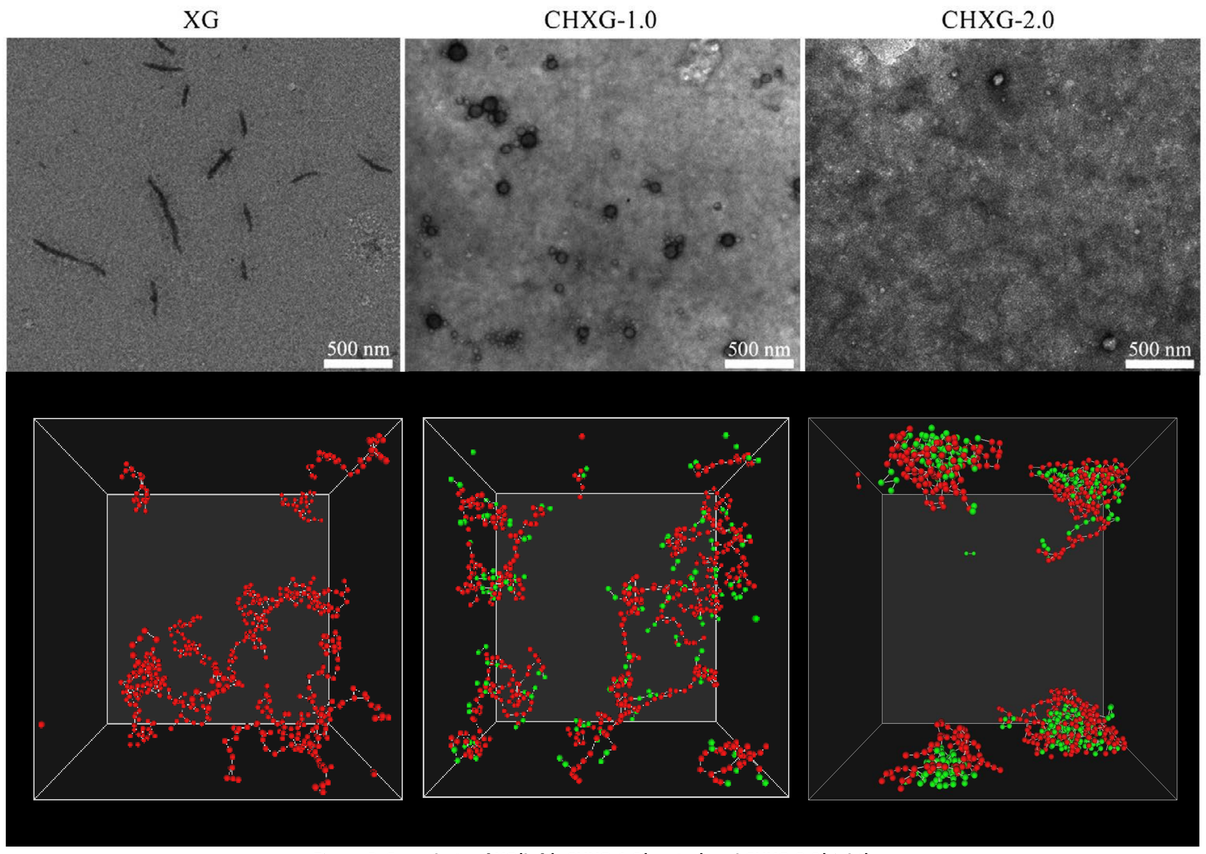

Figure 3. Snapshots of XG(left), CHXG-1.0(center) and CHXG-2.0(right)

Radius of gyration(Rg) and end-to-end distance(Ree)

The snapshots show how nanogel is agglomerated with simulated images. Also, there are two parameters which determine numerically how much self-assembly and agglomeration occurred in three cases of nanogels. One is the radius of gyration(Rg), and the other is the end-to-end distance(Ree). The radius of gyration is a radius of whole agglomerated nanogel, and the end-to-end distance is a distance of the first monomer and the last monomer in one polymer chain.
Therefore, the lower Ree and Rg mean, the higher behavior of self-assembly and agglomeration in a complex.Two plots below(figure 4) show CHXG-2.0 has lower value of Rg and Ree, as we expected in figure 3. However, it can not explain that there is no difference between results from XG and CHXG-1.0.

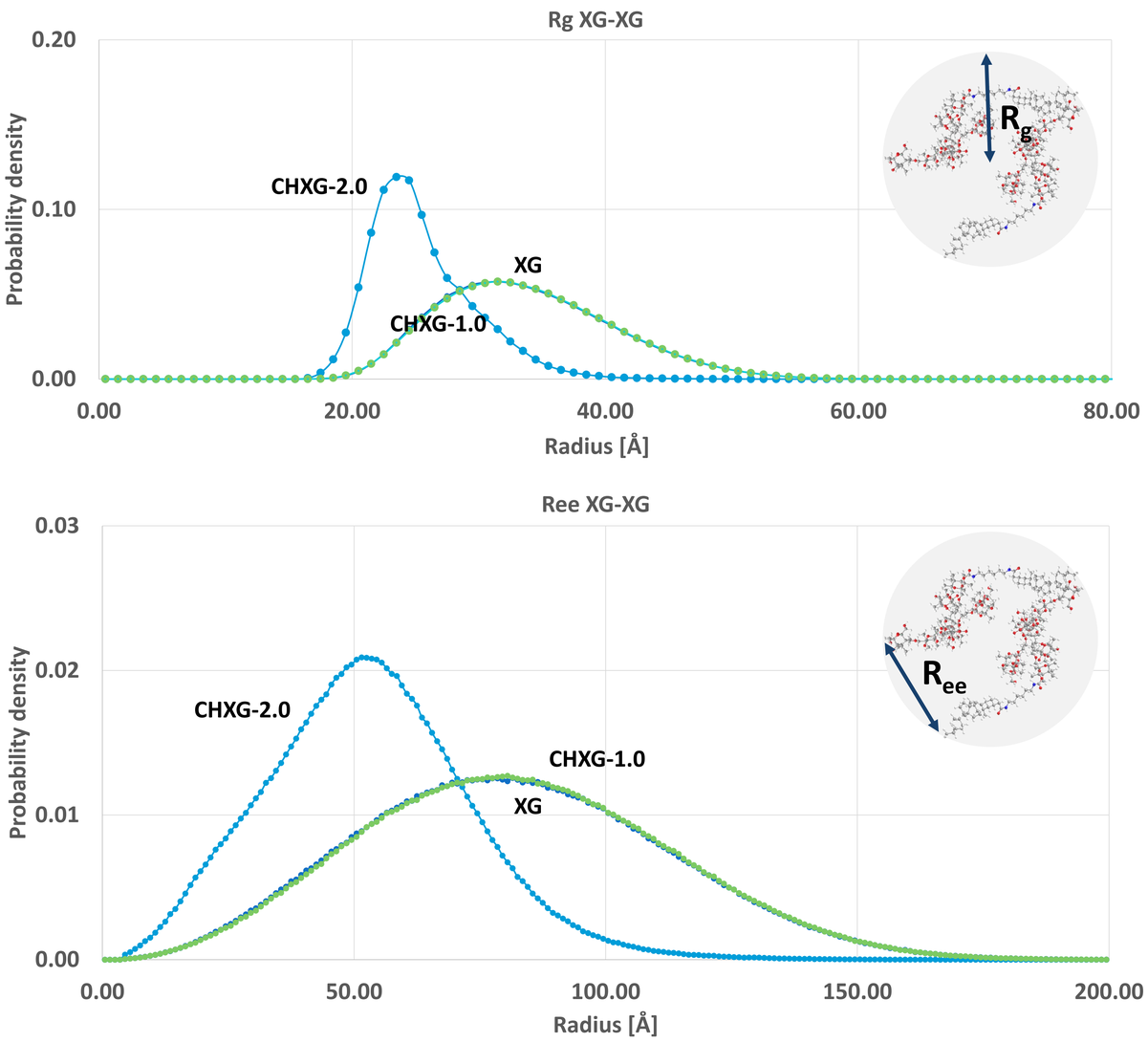

Figure 4. Radius of gyration(Rg) and end-to-end distance(Ree) of XG, CHXG-1.0 and CHXG-2.0 nanogel

Conclusion and Future work

The simulation result is reproduced by basis of the experiment from Sawada et el., and some parts have similarities, for instance, CHXG-2.0 has the highest probability of self-assembly behavior and agglomeration. The next work should be finding a threshold ratio of CH and XG which can decides whether self-assembly occurred or not, and, modeling the system more accurately by other parameters, as radii or masses of molecules.

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