

Collagen inspired self aggregating materials.

PhD-fellow: P.J. Skrzyszewska MEng, PDEng (Paulina)
paulina.skrzyszewska@wur.nl
Supervisors: Prof. Dr. M.A. Cohen Stuart (Physical Chemistry and Colloid Science, WU)
Dr. J van der Gucht (Physical Chemistry and Colloid Science)
Dr. F.A. de Wolf (Agrotechnology & Food Innovations)
Sponsors: Dutch Polymer Institute



Introduction

We study the gel networks formed by telechelic polypeptides with end blocks inspired by, and behaving like natural collagen, and a random coil-like middle block rich in hydrophilic aminoacids (Fig.1).

These polypeptides are produced in a fermentation process by genetically modified yeast (*P.pastoris*)¹. They are monodisperse, and have a very well-defined length and aminoacid sequence.

When a solution of these polypeptides is cooled down, the side blocks assemble and form triple helices (see Fig.1), while the middle block maintains a random coil structure. Thus, a physical gel is formed with a node multiplicity of exactly three (see Fig.1).

This **precisely known multiplicity** allowed us to develop an analytical model, which does not require adjustable parameters and accounts for internal gel structure with loops and dangling ends (Fig.1).

With this model we can predict the storage modulus (G_0), viscosity (η) and relaxation time (τ). These are in very good agreement with experimental values.

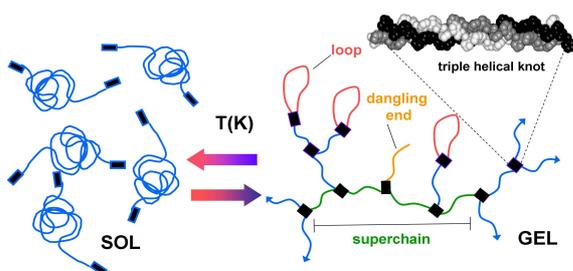


Fig.1

Model development

Each triple helix is formed by association of three end blocks. The equilibrium constant for this process is:

$$K_H = \frac{C_H}{C_F^3}$$

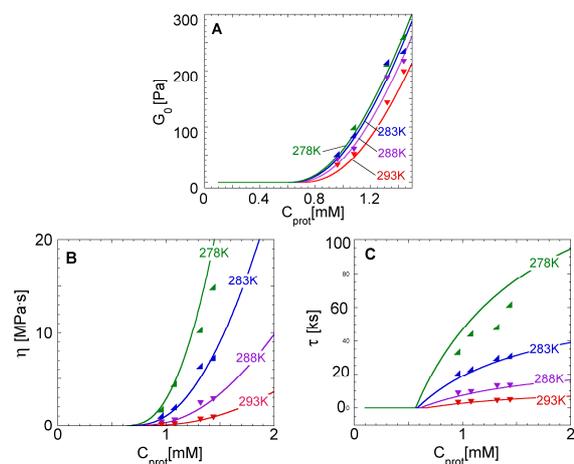
where C_H is the concentration of triple helices and C_F the concentration of free end blocks.

We account for loops and bridges: loops are favored at $C < C^*$ and bridges at $C > C^*$.

The modulus is proportional to the number of elastically active chains where we account for presence of "superchains" (Fig.1).

The temperature dependence of K_H follows with van't Hoff's law and τ follows Arrhenius behavior.

Fig. A,B,C shows storage modulus, viscosity and relaxation time as a function of protein concentration at different temperatures. Solid lines represent model results, while bars experimental data.



References

- 1 Werten, M. W. T.; Teles, H.; Moers, A. P. H. A.; Wolbert, E. J. H.; Eggink, G.; de Wolf, F. A. 2009 submitted.
- 2 Skrzyszewska, P.J.; de Wolf, F. A.; Werten, M.W.T.; Moers, P.H. A.; Cohen Stuart, M.A. and Jasper van der Gucht 2009 submitted