Molecular origin of the protein-like dynamical transition in microgels

L. Tavagnacco [a], E. Chiessi [b], M. Zanatta [c], A. Orecchini [d], E. Zaccarelli [a]

[a] CNR-ISC and Department of Physics, Sapienza University of Rome,
Piazzale A. Moro 2, 00185 Rome, Italy
[b] Department of Chemical Sciences and Technologies, University of Rome Tor Vergata,
Via della Ricerca Scientica I, 00133 Rome, Italy
[c] Department of Computer Science, University of Verona, Strada Le Grazie 15, 37138 Verona, Italy
[d] Department of Physics and Geology, University of Perugia and CNR-IOM,
Via A. Pascoli, 06123 Perugia, Italy

e-mail: Letizia.Tavagnacco@roma1.infn.it

Keywords: (protein dynamical transition, molecular dynamics simulations, microgels)

Hydrated proteins start to be biologically active above a temperature of about 220 K which marks also a sudden increase of the protein atomic mobility, a molecular process known as the protein dynamical transition. Indeed, the protein dynamical transition consists in the onset of anharmonic motions which allow proteins to explore conformational substates of functional relevance. Therefore the dynamical transition is associated to the activation of the biological functionality, making it the subject of intensive research. Nonetheless a full understanding of its deepest nature still remains elusive. In particular, the role played by water in the molecular process is widely debated.

Recently, the occurrence of a low temperature dynamical transition was reported also for a non-biological system, such as poly(N-isopropylacrylamide), PNIPAM, microgels [1]. These micrometer particles, characterized by a hydrated cross-linked polymer network, are extensively investigated as smart materials for biological and technological applications because of their stimuli-responsive behaviour. PNIPAM microgels share many features with proteins, because of their extended covalent connectivity and the amphipilic character. In fact, the initial physical-chemical studies on this polymer addressed its behaviour in water, as a synthetic isomer of polypeptides [2].

Here we describe the molecular origin of the low temperature dynamical transition in microgels, as obtained from atomistic molecular dynamics simulations [3]. The study is based on a nanoscale model of a microgel network in water (see Figure 1) which has been previously validated with a direct comparison with elastic incoherent neutron scattering experiments (EINS) [1]. As reported in Figure 2, the polymer network dynamics described by the atomistic model and probed through the mean squared displacements (MSD) of PNIPAM hydrogen atoms quantitatively reproduces neutron scattering experiments and shows a sudden enhancement at about 250 K, the dynamical transition temperature.

In this contribution we show which molecular processes control the dynamics of both the macromolecule and water below the dynamical transition temperature by correlating the information extracted from the analysis of the polymer relaxations times, water self-diffusion coefficients and hydrogen bonding interactions. In particular, we found that below the dynamical transition temperature PNIPAM dynamics is governed by the rotation of the methyl groups belonging to the side chains and that a sudden increase of the polymer segmental dynamics occurs above it. On the other hand, hydrogen bonding interactions determine water dynamics below the dynamical transition temperature. In addition, through a further comparison with the low temperature behaviour of bulk water, we demonstrate that it is primarily the macromolecule-water hydrogen bonding interaction that determines water dynamics below the dynamical transition temperature.

Our study supports the idea that the macromolecule-water coupling is the driving ingredient of the dynamical transition. Therefore this phenomenology should be a general feature of hydrated macromolecular systems able to form hydrogen bonding interactions with water. From the biophysical point of view, the dynamical behaviour of PNIPAM microgels above the dynamical transition temperature can represent a model for the anharmonic motions, involving few repeating units regions, associated to enzyme activity. In this respect, our investigation focuses remarkable correlations between the macromolecule dynamics and that of surrounding water.

[1] M. Zanatta et al., Sci. Adv. 4 eaat5895 (2018).
[2] J. S. Scarpa et al., J. Am. Chem. Soc. (1967), 89, 6024.
[3] L. Tavagnacco et al., J. Phys. Chem. Lett. (2019), 10 (4), 870.

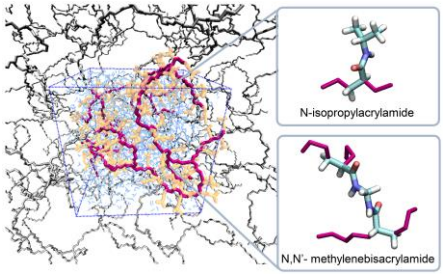

Figure 1. Microgel network model. PNIPAM backbone and side chain atoms are displayed in magenta and yellow, respectively; water molecules and periodic images of the polymer backbone atoms are represented in blue and gray, respectively. The two side-frames displayed on the right show the chemical structure of the repeating unit (top) and the cross-link (bottom).

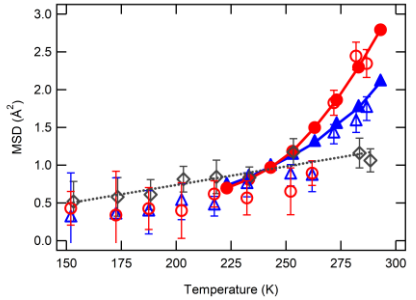

Figure 2. Temperature dependence of MSD obtained from EINS experiments (open symbols) for PNIPAM mass fractions of 43% (circles), 60% (triangles), and 95% (squares) and numerical (filled symbols) MSD, calculated at 150 ps for PNIPAM hydrogen atoms only, for PNIPAM mass fractions of 40% (circles) and 60% (squares). The dotted line is a guide to the eye, suggesting a linear behavior for the dry sample, for which the dynamical transition is suppressed.