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HOMOPOLYAMINOACID DYNAMICS IN AQUEOUS SOLUTION

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Water is of fundamental importance in biological systems; nevertheless its role in proteins is still far from being fully understood. Although the coupling between water and protein dynamics has been investigated by means of a variety of experimental techniques, it is not clear if the water fluctuations control the protein dynamics or if both, protein and water dynamics are affected to each other. However, the effects imposed by a protein on water dynamics are very complex, due to the variety of polar and non-polar side chains present in the protein. Thus, to simplify the interaction between protein and water, we have analyzed the response of a simpler homopolyaminoacid, ϵ -Polylysine (ϵ -PLL) which consists of 25–35 L-lysine residues. ϵ -PLL differs from proteins in that the amide linkage is not between the α -amino and carboxyl groups, but between the ϵ -amino and carboxyl group. However, in aqueous solution, ϵ -PLL has a beta-sheet conformation as that found in proteins. In this work we have studied the dynamics of ϵ -PLL in water solution by means of dielectric spectroscopy in a broad frequency (10–2–50 GHz) and temperature range (140–300 K) with the aim to compare it with the dynamics of the single amino acid (L-lysine) [1] as well as with proteins [2]. The dielectric results of ϵ -PLL in aqueous solution show a rich dynamical behavior. Below T_g , three dynamical processes were resolved (P1–3) which can be related to the dynamics of amorphous water. Above T_g , up to 5 dielectric relaxations were observed (P3–7) all of them with a Vogel–Fulcher–Tamman temperature dependence. 1. S. Cerveny; J. Swenson Phys. Chem. Chem. Phys. 2014, 16, 22382. 2. Khodadadi, S.; Sokolov, A. P. Protein Dynamics: From Rattling in a Cage to Structural Relaxation. Soft Matter 2015, 11 (25), 4984–4998