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NMR Study on Polymer-Solvent Interactions during Temperature-Induced Phase Separation in Aqueous Polymer Solutions

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Summary: Some possibilities of NMR spectroscopy (mainly spin-spin relaxation) in investigations of hydration and other polymer-solvent interactions during the temperature-induced phase separation in aqueous polymer solutions are described. A certain portion of water molecules bound in phase-separated mesoglobules was revealed. The residence time of the bound HDO for poly(vinyl methyl ether) (PVME)/D_2O solution ($c = 6$ wt%) is 1.2 ms. With time a slow release of originally bound water from the respective mesoglobules was observed. For highly concentrated PVME/D_2O solutions ($c = 20$–60 wt%), the residence time of bound HDO $\gg 2.7$ ms and fractions of bound water unchanged even for 70 h were found. A similar behaviour as described above for water (HDO) was also found for EtOH molecules in PVME/D_2O/EtOH solutions.

Keywords: hydration; NMR; phase separation; poly(vinyl methyl ether); thermoresponsive polymers

Introduction

It is well known that some acrylamide-based polymers and some other polymers like poly(vinyl methyl ether) (PVME), in aqueous solutions exhibit a lower critical solution temperature (LCST). They are soluble at low temperatures, but heating above the LCST results in phase separation which is shown by turbidity of the solution.[1,2] On molecular level, such phase separation is assumed to be a macroscopic manifestation of a coil-globule transition, as was shown for poly(*N*-isopropylacrylamide) (PIPAAm) in water by light scattering,[2,3] followed by further aggregation and formation of colloidally stable mesoglobules. The phase transition is probably associated with competition between hydrogen bonding and hydrophobic interactions.[2,4,5] Their thermosensitivity makes these systems interesting for possible biomedical and technologival applications. Though these phase transitions were extensively studied by various methods,[2] more recently we have also shown that ^{1}H NMR spectroscopy can be a suitable method in the investigations of temperature-induced phase separation on molecular level.[6,7]

In this work we deal mainly with temperature-induced phase separation in PVME aqueous solutions. We report some new results on hydration and other polymer-solvent interactions as obtained on D_2O solutions of PVME using NMR methods. For completeness some recent results obtained on D_2O solutions of PIPAAm and poly(*N*-isopropylmethacrylamide) (PIPMAAm) are also briefly discussed. For PVME aqueous solutions the LCST is around 308 K, i.e., well above the temperature of the glass transition of PVME in bulk where values in the range $T_g = 191$–251 K are reported.[8] This is in contrast to acrylamide-based polymers in

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aqueous solutions where the LCST is well below the respective T_g. For PIPAAm ($T_g = 403$ K)[8] and PIPMAAm ($T_g = 449$ K)[9] the LCSTs are around 307 and 315 K, respectively.

Experimental Part

Samples

PVME (purchased from Aldrich, supplied as 50 wt% solution in water; molecular weight determined by GPC in THF: $M_w = 60\,500$, $M_w/M_n \cong 3$, tacticity by ^{1}H NMR: 59% of isotactic diads[10]) was used after drying to prepare PVME/D_2O (99.9 % of deuterium) solutions with polymer concentrations in the range c = 0.1–50 wt%. PVME solutions in D_2O/ethanol (EtOH) mixtures were also studied; volume fractions of EtOH in D_2O/EtOH mixtures were in the range 1–20 vol%. All samples of PVME/D_2O and PVME/D_2O/EtOH solutions in 5-mm NMR tubes were degassed and sealed under argon.

NMR Measurements

High-resolution ^{1}H and ^{13}C NMR spectra were recorded with a Bruker Avance 500 spectrometer operating at 500.1 and 75.5 MHz, respectively. The ^{1}H spin-spin relaxation times T_2 of PVME, HDO or EtOH protons were measured using the CPMG[11] pulse sequence 90°_x-(t_d-180°_y-t_d)$_n$-acquisition. In measurements of PVME protons at 309.5 K, $t_d = 0.15$ ms or 0.12 ms; the relaxation delay was 10 s. In measurements of HDO or EtOH protons, $t_d = 5$ ms and the relaxation delay was 80–100 s. All obtained T_2 relaxation curves had the monoexponential character and the fitting process always enabled us to determine the single value of the relaxation time. In all measurements the temperature was maintained constant within $\pm$ 0.2 K using a BVT 3000 temperature unit.

Results and Discussion

Our recent measurements of spin-spin relaxation time T_2 in PVME/D_2O solutions at temperature above the LCST have shown that a very short component ($T_2 <$ 1 ms) dominates the spin-spin relaxation of PVME protons. This short T_2 component, which does not exist at temperatures below the LCST, evidently corresponds to PVME segments forming globular-like structures (mesoglobules).[12] Figure 1 shows the values of the very short component of spin-spin relaxation time T_2, as determined for

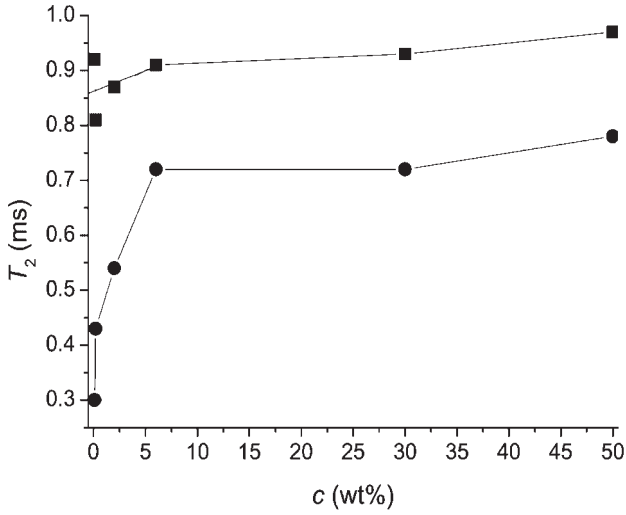

Figure 1.
Concentration dependence of a very short component of spin-spin relaxation time T_2 as determined for $CHOCH_3$ (■) and CH_2 (●) PVME protons in PVME/D_2O solutions at 309.5 K.

$CHOCH_3$ and CH_2 PVME protons in PVME/D_2O solutions at 309.5 K, i.e., at temperature above the phase transition, as a function of polymer concentration in the broad range of concentrations $c =$ 0.1–50 wt%. From Figure 1 it follows that for CH_2 protons T_2 values are virtually constant in the concentration range $c =$6–50 wt%. For lower concentrations, T_2 values decrease with decreasing concentration, showing that mobility of PVME CH_2 protons in mesoglobules formed in dilute solutions is lower in comparison with mobility of these protons in globular-like structures formed in concentrated solutions. This result suggests that globular-like structures are more compact in dilute solutions, compared with semidilute or concentrated solutions, where mesoglobules probably contain a certain amount of water. For $CHOCH_3$ protons (with dominant contribution of CH_3 protons) the T_2 values do not depend on the concentration of the solution, in accord with infrared results[13] showing that most methyl groups of PVME are dehydrated above the LCST.

Figure 2 shows the ^{1}H spin-spin relaxation times T_2 of HDO molecules in PVME/D_2O solutions measured at temperatures below (305 K) and above (309.5 K) the LCST phase transition and plotted as a function of polymer concentration in the range $c = 0.1$–10 wt%. While for dilute solutions ($c = 0.1$ and 0.2 wt%) T_2 values measured at 305 and 309.5 K do not differ too much, for $c \geq 2$ wt% T_2 values at 309.5 K are 1 order of magnitude shorter than those at 305 K. This shows that for polymer concentrations $c \geq 2$ wt% at temperature above the transition there is a portion of HDO molecules that exhibit a restricted mobility; evidently, this portion corresponds to HDO molecules bound in mesoglobules.[12,14] In all cases there was a single line of HDO in ^{1}H NMR spectrum and the T_2 relaxation curves were exponential, indicating a fast exchange between bound and free sites regarding T_2 values (~0.5 s), i.e., the residence time of bound HDO molecules has to be ≤ 50 ms. In such case the observed relaxation time T_{2obs} is given as

$$(T_{2obs})^{-1} = (1-f)(T_{2F})^{-1} + f(T_{2B})^{-1} \quad (1)$$

where subscripts F and B correspond to free and bound states, respectively, and f is the fraction of bound HDO molecules.

There are two most important possible sources of the short T_2 values of HDO observed for PVME/D_2O solutions with $c = 2$–10 wt% at temperature above the LCST transition (cf. Figure 2): (*i*) a lower, spatially restricted mobility; (*ii*) chemical

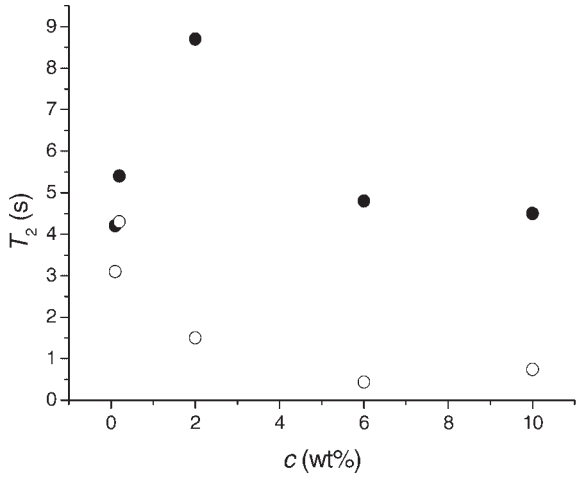

Figure 2.
^{1}H spin-spin relaxation times T_2 of HDO in PVME/D_2O solutions of various polymer concentration, and measured at 305 K (●) and 309.5 K (○).[14]

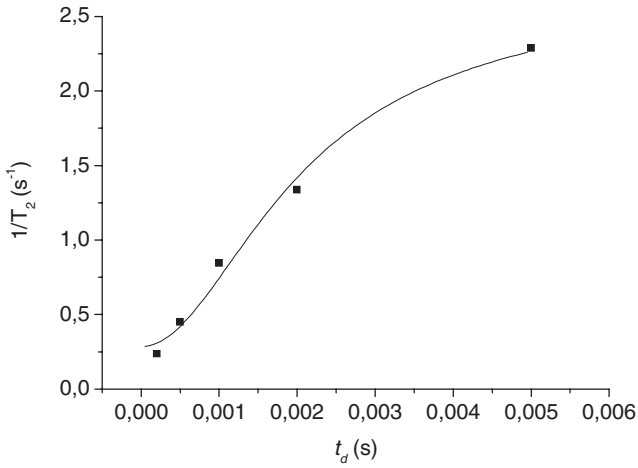

Figure 3.
Dependence of spin-spin relaxation rate $(T_2)^{-1}$ on the interval t_d in CPMG sequence as obtained for HDO protons in PVME/D_2O solution ($c = 6$ wt%) kept at 309.5 K. Solid curve is a fit according eq. (2) with $k_{ex} = 816$ s^{-1} and $(R_2)^0 = 0.284$ s^{-1}.

exchange. Figure 3 shows the dependence of measured spin-spin relaxation rate $(T_2)^{-1}$ on the time interval t_d in CPMG pulse sequence for HDO protons in PVME/D_2O solution ($c = 6$ wt%). Such dependence is often used for characterization of microsecond-millisecond chemical exchange.[15,16] From Figure 3 it follows that contribution of chemical exchange to the spin-spin relaxation rate $(T_2)^{-1}$ is important. Solid curve in this figure shows the best fit as obtained using the equation [16]

$$(T_2)^{-1} = (p_A p_B \Delta^2 \omega^2 / k_{ex}) \times \{1 - [\tanh(k_{ex} t_d)/k_{ex} t_d]\} + (R_2)^0 \quad (2)$$

with $k_{ex} = 816$ s^{-1}. Here k_{ex} is the rate constant for exchange process, $(R_2)^0$ is the spin-spin relaxation rate in the absence of the exchange assumed to be the same in states A and B, p_A and p_B are populations of the states, Δ is the chemical shift difference between the states and ω is the resonance frequency. For PVME/D_2O solution therefore the exchange time (or the residence time of the bound HDO) $\tau_{ex} = 1/k_{ex}$ is $\tau_{ex} = 1.2$ ms.

We were interested in knowing whether the amount of water bound in PVME mesoglobules formed in semidilute and concentrated aqueous solutions is changing with time or not. The time dependence of spin-spin relaxation time T_2 of HDO molecules in PVME/D_2O solution ($c = 6$ wt%) measured at 309.5 K is shown in Figure 4. It follows from Figure 4 that T_2 values of HDO very slowly increase with time, reaching after 24 h a similar value as observed at temperature below the transition. Simultaneously, for the same solution the values of a very short T_2 component of CH_2 protons of PVME slowly decrease with time, reaching after 24 h a similar value as found for dilute solution ($c = 0.1$ wt %).[12] Even after very long time (~days) we did not observe any sedimentation of the polymer-rich phase-separated part in the studied sample. Therefore, these results evidence that water, originally bound in globular-like structures existing in semidilute and concentrated solutions, is with time very slowly released (squeezed out) from these structures. On the contrary, in dilute PVME/D_2O solution ($c = 0.1$ wt%) both T_2 values of the short component of PVME CH_2 protons and HDO protons are time independent showing that dehydration is here rapid.[12]

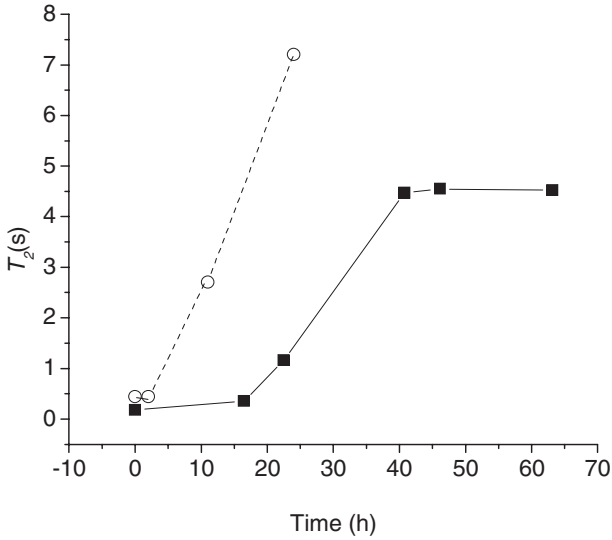

Figure 4.
Time dependence of spin-spin relaxation times T_2 of HDO protons in PVME/D_2O solution ($c = 6$ wt%) at 309.5 K (○, dotted line) and EtOH OH protons in PVME/D_2O/EtOH solution ($c = 6$ wt%, 10 vol% of EtOH in D_2O/EtOH mixture) at 325 K (■, solid line)

Also in D_2O solutions of PIPAAm and PIPMAAm ($c = 5$ wt%) the T_2 values of HDO show that there is a portion of HDO molecules bound in phase-separated globular-like structures with fast exchange between bound and free sites, similarly as reported for PVME/D_2O solutions.[17] When the investigated sample was kept at elevated temperature, then T_2 values of HDO slowly increased with time showing that also in these systems the water originally bound in mesoglobules is with time very slowly released from these structures. Both the time characterizing the exclusion of water from mesoglobules (it is manifested by the increase in T_2 values of HDO), and especially the induction period which precedes the increase in T_2 values, increased in the order PVME<PIPMAAm< PIPAAm.[17] The large differences in the induction period as found for PVME on the one hand and for PIPMAAm and PIPAAm on the other hand are evidently in connection with the fact that while PVME segments exist in rubbery state in mesotglobules, PIPMAAm or PIPAAm segments in mesoglobules are in glassy state.

For D_2O solutions of PIPMAAm/PVME and PIPMAAm/PIPAAm mixtures where two phase transitions were detected,[18–20] a direct connection between the state of globular-like structures (hydrated or dehydrated) formed by the component with lower LCST (PVME, PIPAAm) and the temperatures of the phase transition of the PIPMAAm component was established by NMR spectroscopy.[17] These results corroborate that the temperatures of the phase transition are affected by the arrangement and by the order of water molecules in the investigated system.

From hitherto text it follows that in PVME, PIPAAM and PIPMAAm aqueous solutions with concentrations $c = 2$–10 wt% a certain amount of water is bound in mesoglobules formed at temperatures above the respective LCST and that there is a fast exchange between bound and free water. With time the originally bound water is slowly released from the mesoglobules. A different behaviour we have found for highly concentrated PVME/D_2O solutions. Figure 5 shows ^1H NMR spectra of concentrated PVME/D_2O solutions ($c =$ 20 and 60 wt%) measured at temperature

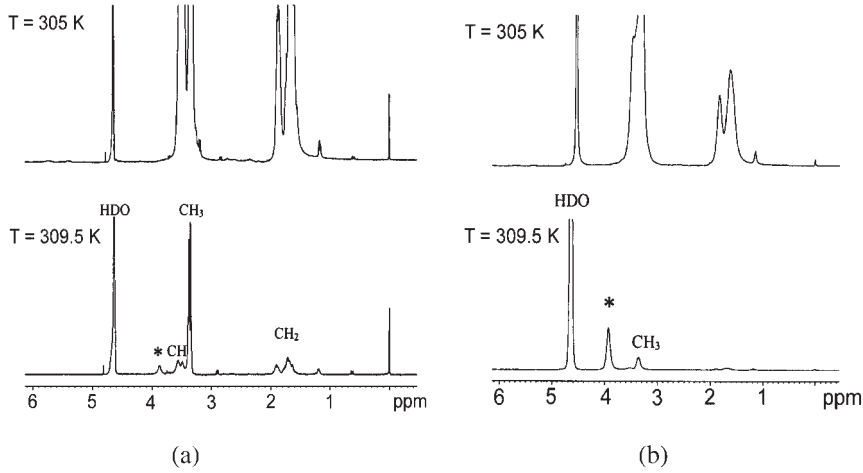

Figure 5.
^{1}H NMR spectra of PVME/D_2O solutions with $c = 20$ wt% (a) and $c = 60$ wt% (b). Line of the bound HDO is marked by asterisk. The spectra were obtained using spin-echo pulse sequence 90°_x-t_d-180°_y-t_d-acquisition with $t_d = 5$ ms to supress the broad lines from protons of phase-separated PVME that exist at 309.5 K.[14]

below the phase transition (305 K) and at temperature above the transition (309.5 K). These spectra were obtained using spin-echo pulse sequence 90°_x-t_d-180°_y-t_d- acquisition with $t_d = 5$ ms to supress the broad lines from fast relaxing protons of phase-separated PVME with $T_2 < 1$ ms (cf. Figure 1) that exist at 309.5 K. A new signal, marked in Figure 5 by asterisk, appears at temperature above the LCST transition. We evidenced that this new signal corresponds to HDO bound in globular-like structures.[14] For HDO in highly concentrated PVME/D_2O solutions therefore there is a slow exchange between bound and free sites; here the term ''slow exchange'' also includes the situation that there is no exchange at all. From the difference of chemical shifts of free and bound HDO in hertz it follows that for the residence time of bound HDO molecules τ it holds $\tau \gg 2.7$ ms. The fact that the chemical shift of the bound HDO does not depend on the polymer concentration and is 0.74 ppm smaller in comparison with the main HDO signal indicates that for the bound HDO the hydrogen bonding is weaker in comparison with that existing in neat water (D_2O) and weaker than hydrogen bonds between water and ether oxygen of PVME at temperatures below the LCST.

The fraction of bound HDO in highly concentrated PVME/D_2O solutions, as determined from ^{1}H NMR spectra, increases with increasing polymer concentration. At the same time, the molar ratio [PVME monomeric unit/bound D_2O] $\cong 2.7$ is constant in the range of concentrations $c =$ 20–60 wt%.[14] Therefore the polymer concentration in polymer-rich phase (mesoglobules) is 89 wt%, in accord with the recently published phase diagram.[21] The fact that spin-spin relaxation time T_2 of PVME CH_2 protons is constant in the range of polymer concentrations $c = 6$-50 wt% (cf. Figure 1) suggests that similar molar ratio [PVME monomeric unit/bound D_2O] and subsequently similar polymer concentration in mesoglobules as in highly concentrated PVME/D_2O solutions one can expect also for the solution with $c = 6$ wt% where is a fast exchange between bound and free water. For highly concentrated PVME/D_2O solutions ($c = 20$–60 wt%) the spin-spin relaxation times T_2 of bound HDO virtually do not depend on the concentration of the solution and are 2 orders of magnitude shorter in comparison with those for ''free'' HDO. Nevertheless, a

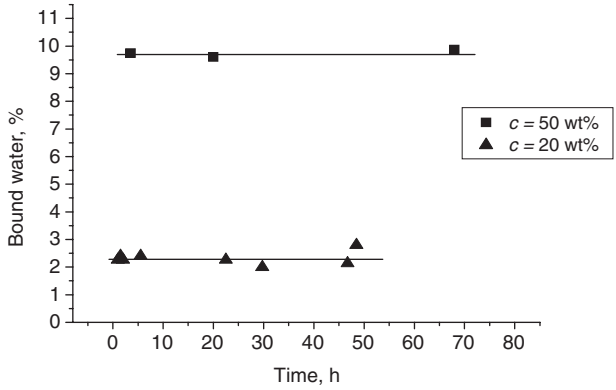

Figure 6.
Fractions of the bound water (HDO) in concentrated PVME/D_2O solutions at 309.5 K as a function of time.

rather small spatial restriction of the motion of bound HDO can be responsible for this difference; the angle which cannot be reached by proton-deuteron internuclear vector is around 3.2°.[14]

Figure 6 shows the fractions of the bound HDO in highly concentrated PVME/D_2O solutions ($c = 20$ and 50 wt%) at 309.5 K as function of time. From this figure it follows that in these cases the fraction of the bound water is constant and no release of the bound water was detected even after 70 h. This is in contrast to lower concentrations where originally bound HDO is slowly released from globular-like structures (cf. Figure 4, dotted line).

A similar behaviour as described above for water (HDO) molecules we also found for ethanol (EtOH) molecules in PVME/D_2O/EtOH solutions.[22] As illustrated in Figure 4 for PVME/D_2O/EtOH solution ($c = 6$ wt%, 10 vol% of EtOH in D_2O/EtOH mixture), at temperature above the transition (325 K) the spin-spin relaxation time T_2 of EtOH OH protons is significantly shortened showing that at this temperature there is a portion of EtOH molecules bound in mesoglobules with fast exchange between bound and free sites, similarly as found for HDO in PVME/D_2O solution of the same concentration. When the sample was kept at 325 K and time dependence of T_2 values of EtOH protons was measured, after 40 h the T_2 significantly increased showing that EtOH molecules originally bound in globular-like structures are with time slowly released from these structures (cf. Figure 4, solid line). From Figure 4 it follows that the releasing process is for EtOH slower in comparison with releasing of originally bound HDO, especially the induction period which precedes the increase in T_2 values is for EtOH significantly longer (17 h). For concentrated PVME/D_2O/EtOH solution ($c = 20$ wt%) the existence of the free and bound EtOH at temperatures above the phase transition is evidenced by their well-separated NMR signals in ^{13}C NMR spectra (Figure 7). From their integrated intensities it follows that in this solution there is 6% of bound EtOH with the residence time $\tau \gg 10$ ms.[22] Interestingly enough, when this sample was kept at 325 K for 4 h, the amount of the bound EtOH decreased to 3% indicating a relatively fast releasing process. This in contrast to the behaviour of the HDO where for highly concentrated PVME/D_2O solutions the fractions of the bound HDO were unchanged even for 70 h (cf. Figure 6).

Conclusion

^1H NMR spin-spin relaxation measurements of both PVME and water (HDO) protons revealed that in D_2O solutions of

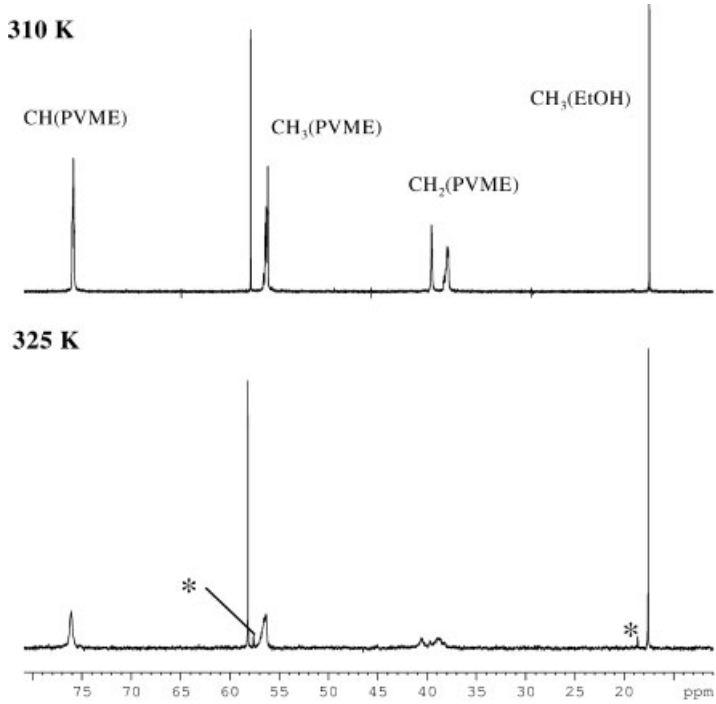

Figure 7.
^{13}C NMR spectra of PVME/D_2O/EtOH solution ($c = 20$ wt%, 5 vol% of EtOH in D_2O/EtOH mixture) measured at 310 K and 325 K. Lines of the bound EtOH CH_2 and CH_3 carbons are marked by asterisks.[22]

PVME ($c = 2$–10 wt%) a certain portion of water molecules is bound in phase-separated globular-like structures (mesoglobules). The residence time of the bound HDO for PVME/D_2O solution ($c = 6$ wt%) is 1.2 ms. Also in D_2O solutions ($c = 5$ wt%) of PIPAAm and PIPMAAm the spin-spin relaxation times T_2 of HDO have shown that above the LCST there is a portion of HDO bound in globular-like structures. With time a slow release of originally bound water from the respective mesoglobules was observed in all cases. For highly concentrated PVME/D_2O solutions ($c = 20$–60 wt%), the residence time of bound HDO $\tau \gg 2.7$ ms and relatively weak hydrogen bonding follow from the position of the separate NMR signal of bound HDO. At the same time the molar ratio [PVME monomeric unit/bound D_2O] $\cong 2.7$ does not depend on the polymer concentration, i.e., the polymer concentration in polymer-rich phase (mesoglobules) is 89 wt%. For highly concentrated PVME/D_2O solutions the fractions of the bound HDO remain unchanged even for 70 h. A similar behaviour as described above for water (HDO) was also found for EtOH molecules in PVME/D_2O/EtOH solutions indicating that the decisive factor in this behaviour is a polar character of these molecules and hydrogen bonding. Nevertheless, some differences in behaviour of water and EtOH exist, especially in the rate of the releasing process.

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[1] H. G. Schild, *Prog. Polym. Sci.* **1992**, *17*, 163.
[2] V. O. Aseyev, H. Tenhu, F. M. Winnik, *Adv. Polym. Sci.* **2006**, *196*, 1.
[3] S. Fujishige, K. Kubota, I. Ando, *J. Phys. Chem.* **1989**, *93*, 3311.

[4] H. Maeda, *J. Polym. Sci.: Part B: Polym. Phys.* **1994**, *32*, 91.
[5] Y. Yang, F. Zeng, X. Xie, Z. Tong, X. Liu, *Polym. J.* **2001**, *33*, 399.
[6] J. Spěváček, L. Hanyková, L. Starovoytova, M. Ilavský, *Acta Electrotechn. Inform.* **2002**, *2*(3), 36.
[7] J. Spěváček, *Macromol. Symp.* **2005**, *222*, 1.
[8] R. J. Andrews, E. A. Grulke, in: ''*Polymer Handbook*'', 4th ed., J. Brandrup,E. H. Immergut,E. A. Grulke, Eds., J. Wiley & Sons, New York **1999**, p. VI-201, 215.
[9] M. Salmerón Sánchez, L. Hanyková, M. Ilavský, M. Monleón Pradas, *Polymer* **2004**, *45*, 4087.
[10] L. Hanykov,áJ. Spěváček, M. Ilavsk,ý *Polymer* **2001**, *42*, 8607.
[11] T. C. Farrar, E. D. Becker, ''*Pulse and Fourier Transform NMR*'', Academic Press, New York **1971**, p. 27.
[12] J. Spěváček, L. Hanyková, L. Starovoytova, *Macromolecules* **2004**, *37*, 7710.
[13] Y. Maeda, *Langmuir* **2001**, *17*, 1737.
[14] J. Spěváček, L. Hanyková, *Macromolecules* **2005**, *38*, 9187.
[15] Z. Luz, S. Meiboom, *J. Chem. Phys.* **1963**, *39*, 366.
[16] D. M. Korzhnev, M. Billeter, A. S. Arseniev, V. Y. Orekhov, *Prog. Nucl. Magn. Reson.* **2001**, *38*, 197.
[17] L. Starovoytova, J. Spěváček, *Polymer* **2006**, *47*, 7329.
[18] E. Djokpé, W. Vogt, *Macromol. Chem. Phys.* **2001**, *202*, 750.
[19] L. Starovoytova, J. Spěváček, L. Hanyková, M. Ilavský, *Polymer* **2004**, *45*, 5905.
[20] L. Starovoytova, J. Spěváček, M. Ilavský, *Polymer* **2005**, *46*, 677.
[21] S. Swier, K. Van Durme, B. Van Mele, *J. Polym. Sci.: Part B: Polym. Phys.* **2003**, *41*, 1824.
[22] L. Hanyková, J. Labuta, J. Spěváček, *Polymer* **2006**, *47*, 6107.

