Stabilized α-Helix Structure of Poly(L-lysine)-*block*-poly(ethylene glycol) in Aqueous Medium through Supramolecular Assembly

Atsushi Harada,[†,‡] Sandrine Cammas,[‡,§,||] and Kazunori Kataoka*[,†,‡]

Department of Materials Science and Technology, Science University of Tokyo, Yamazaki 2641, Noda, Chiba 278, Japan, International Center for Biomaterials Science, Research Institute for Biosciences, Science University of Tokyo, Yamazaki 2669, Noda, Chiba 278, Japan, and Institute of Biomedical Engineering, Tokyo Women's Medical College, 8-1 Kawada, Shinjuku, Tokyo 162, Japan

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ABSTRACT: Stabilization of the α-helix structure of the poly(L-lysine) segment in a poly(ethylene glycol)−poly(L-lysine) block copolymer was evidenced in aqueous medium through circular dichroism (CD), ^{1}H-NMR, and static light scattering (SLS) measurements. It was revealed that poly(L-lysine) oligomers (M_w = 2450), which themselves cannot form an α-helix structure due to substantially lower molecular weight, form an α-helix structure under high-pH condition when they are conjugated with poly(ethylene glycol). Moreover, it has been suggested by static light scattering that the block copolymer under high-pH condition exists as a dimer with α-helical poly(L-lysine) segments. The α-helix content in the block copolymer gradually decreased in a linear manner with the addition of urea, which is in sharp contrast to the high molecular weight poly(L-lysine) (M_w = 170 000), showing a steep transition from an α-helix structure to a random coil at a critical urea concentration (1.0 M). To completely shift the conformation of the block copolymer to a random coil, 3.0 M urea is needed, suggesting a substantial significance of the stabilization effect. From 2D-NOESY ^{1}H-NMR and static light scattering measurement, it was suggested that the block copolymers selectively form dimers with a micelle-like structure: a poly(ethylene glycol) shell segregates the poly(L-lysine) segment from the aqueous medium to stabilize the α-helix structure.

Introduction

It is well-known that the tertiary structure of protein molecules is strongly dependent upon the formation of secondary structures including an α-helix and a *β*-sheet in the molecule. The conformation of a protein is determined by its domain structure. In this context, simple poly(amino acid)s with particular secondary structures have been used as models to analyze complicated features of proteins, in attempt to gain insight into the details of their conformations.[1−6] Zimm and Bragg showed that the molecular weight of a poly(amino acid) is an important factor in the formation of a stable helical structure.[7] According to their theory, the transition from a random coil to an α-helix structure depends on two parameters, the formation and the growth of a helical nucleus. It is believed that the initial helical nucleus forms statistically in the region of the random coil and spreads to vicinal residues. They demonstrated by statistical analysis that the probability of observing a helical nucleus was lower at the region near the ends of the polymer chain compared to the middle of the polymer chain. Consequently, a critical molecular weight to induce a helix−coil transition was observed.[8,9] The Zimm−Bragg theory can also be applied to copolymers of amino acids. One approach to increase the stability of the helical state of a particular poly(amino acid) segment is block copolymerization with different poly(amino acid) segments. Stabilization of the α-helix structure was indeed observed for several block copolymers in organic solvents,[10,11] yet not in aqueous solution, as far as we know. On the other hand, block copolymers containing a poly(amino acid) segment have recently been considered as functional materials, and their molecular design has been investigated extensively.[12] In such cases, the influence of the second segment on the conformation of the poly(amino acid) segment should be one of the important parameters to determine the properties of the material. From the viewpoint of a biomedical application, poly(ethylene glycol) has received considerable attention as a segment conjugated with a poly(amino acid) segment. It is known to have low toxicity and to be nonimmunogenic. Its injection *in vivo* does not lead to the formation of antibodies.[13,14] Due to these interesting characteristics, block copolymers composed of poly(ethylene glycol) and poly(amino acid) were studied with regard to their application in the field of biomedical materials and drug delivery systems. Particularly, we have focused on polymeric micelles formed by intermolecular association of poly(ethylene glycol)−poly(amino acid) block copolymers in aqueous medium as a carrier system in drug targeting.[15,16] In the course of these studies, we have found that, by conjugation with poly(ethylene glycol), poly(L-lysine) with relatively low molecular weight (M_w = 2450) was able to show a pH-induced helix−coil transition in aqueous medium. In this paper, we demonstrate the substantial contribution of the poly(ethylene glycol) segment to the stabilization of the α-helix structure of the poly(L-lysine) segment through the formation of a dimer with a micelle-like structure.

Experimental Section

Materials. α-Methoxy-*ω*-aminopoly(ethylene glycol) (M_w = 4300 and 5900) was a kind gift from Nippon Oil & Fats Co., Ltd., Japan. *ϵ*-(Benzyloxycarbonyl)-L-lysine *N*-carboxyanhydride was synthesized from *ϵ*-(benzyloxycarbonyl)-L-lysine by the Fuchs−Farthing method using triphosgene.[17]

* To whom correspondence should be addressed.
† Department of Materials Science and Technology, Science University of Tokyo.
‡ International Center for Biomaterials Science, Research Institute for Biosciences, Science University of Tokyo.
§ Institute of Biomedical Engineering, Tokyo Women's Medical College.
|| Present address: Laboratoire de Physico-Chimie des Biopolymères (LPCB), UMR 27 CNRS, Université Paris XII, 2à8 rue Henry Dunant, 94320 Thiais, France.
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The poly(L-lysine hydrobromide)s having different molecular weights (M_w = 170 000 and 2400 in the nonionized state) were purchased from Sigma and used without further purification.

HCl (0.01 N) and NaOH (0.01 N) (titration grade) were purchased from Wako Pure Chemical Industries, Ltd., Japan.

Synthesis of Poly(ethylene glycol)−Poly(L-lysine) Block Copolymer (PEG-P(Lys)). PEG-P(Lys) was synthesized according to the procedure previously reported.[17] Briefly, poly(ethylene glycol)−poly(ϵ-(benzyloxycarbonyl)-L-lysine) block copolymers (PEG-P(Lys(Z))) were obtained by the ring-opening polymerization of ϵ-(benzyloxycarbonyl)-L-lysine *N*-carboxyanhydride using α-methoxy-ω-aminopoly(ethylene glycol) as an initiator in DMF at 40 °C. ^{1}H-NMR measurement in DMSO-d_6 (EX400, JEOL) at 80 °C for the obtained PEG-P(Lys(Z)) was carried out to determine the relative composition. From the peak intensity ratio of the methylene protons of PEG (OCH_2CH_2: δ = 3.5 ppm) and the phenyl protons of the ϵ-(benzyloxycarbonyl) group ($CH_2C_6H_5$: δ = 7.3 ppm), the polymerization degree of the Lys(Z) unit was calculated to be 19 for poly(ethylene glycol) M_w = 4300 (43−19) and 18 for poly(ethylene glycol) M_w = 5900 (59−18). PEG-P(Lys(Z))s were deprotected by trifluoroacetic acid and methanesulfonic acid to obtain PEG-P(Lys) methanesulfonates. The counterion (methanesulfonate) of PEG-P(Lys) was then removed by using an anion exchange column (Amberlite IR-402, Organo Co., Ltd.), followed by freeze-drying to obtain PEG-P(Lys). The PEG-P(Lys) thus obtained was confirmed to have 19 units of L-lysine for 43−19 and 18 units of L-lysine for 59−18 by ^{1}H-NMR spectroscopy in D_2O (EX400, JEOL). The deprotection of the ϵ-(benzyloxycarbonyl) group as well as the removal of methanesulfonic acid were also confirmed by ^{1}H-NMR in D_2O based on the disappearance of peaks corresponding to the phenyl protons of the ϵ-(benzyloxycarbonyl) group ($CH_2C_6H_5$: δ = 7.3 ppm) and the methyl protons of methanesulfonic acid (CH_3SO_3H: δ = 2.8 ppm), respectively.

Potential Titration. PEG-P(Lys) (70 mg) was dissolved in 30 mL of 0.01 N HCl and titrated with 0.01 N NaOH. An automatic titrator (DL-25, Mettler) was used, and the dissociation degree at a given pH was then determined from the obtained titration curve. The titrant was added in 0.01 mL quantities at 12−120 s intervals. In a manner similar to that described above, 30 mg quantities of poly(L-lysine) homopolymers having different molecular weights were dissolved in 30 mL of 0.01 N HCl and titrated with 0.01 N NaOH.

Circular Dichroism Measurements. Circular dichroism (CD) measurements were carried out using a 1 mm cell (GL Science Co., Ltd.) and a J-600 spectropolarimeter (JASCO). All samples were prepared to have 0.01 wt % of lysine, and the pH was adjusted with 0.01 N HCl and 0.01 N NaOH.

2D-NOESY ^{1}H-NMR Measurements. PEG-P(Lys) was dissolved in D_2O including NaOD or DCl. 2D-NOESY ^{1}H-NMR spectra were measured using an EX400 spectrometer (400 MHz, JEOL). 2D-NOESY ^{1}H-NMR spectra were recorded at 400 MHz with a sweep width of 4000 Hz into 1024 data points. The pulse sequence used is the following: 90°−t_1−90°−Δ−90°−FID, where Δ is the mixing time. The first pulse was 11.6 ms; the relaxation delay was 0.455 ms (t_1). The second 90° pulse was also 11.6 ms; the mixing time was 20 ms (Δ). After a third 90° pulse of 11.6 ms, FID was recorded with 8 scans.

Static Light Scattering Measurements. Static light scattering measurements (SLS) were carried out using a DLS-700 spectrophotometer (Otuka Electronics Co., Ltd.). Vertically polarized light of λ_0 = 488 nm wavelength from an Ar ion laser (15 mW) was used as the incident beam. All measurements were performed at 23.5 °C. All solutions were purified by passage through a 0.1 μm filter (Millex-VV, Millipore).

In order to obtain Zimm plots, light scattering measurements were taken at 12 angles from 40° to 150° for the solvent and each block copolymer solution. The light scattered by a dilute polymer solution may be expressed as

$$Kc/\Delta R(\theta) = 1/M_w[1 + (16\pi^2 n_0^2 R_G^2/3\lambda_0^2)\sin^2(\theta/2) + ...] + 2A_2c + ...$$

where K is an optical constant, c is the polymer concentration, $\Delta R(\theta)$ is the difference between the Rayleigh ratio of the solution and that of the solvent, M_w is the weight-average molar mass, R_G^2 is the mean square radius of gyration, n_0 is the solvent refractive index, λ_0 is the wavelength of the incident beam, and A_2 is the second virial coefficient.

To estimate M_w and R_G, it is necessary to know the refractive index increments, dn/dc. The refractive index increments of the block copolymer solutions were measured using a DRM-1020 double-beam differential refractometer (Otuka Electronics Co., Ltd.).

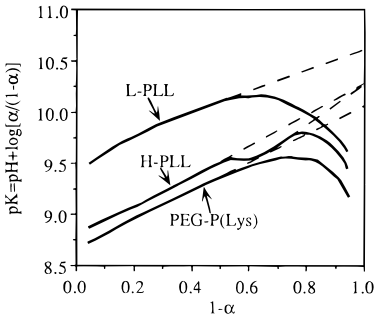

Figure 1. Modified curves of the potential titration for PEG-P(Lys)(43−19), H-PLL, and L-PLL (temperature: 25 °C).

Table 1. pK_a, pK_0, and ΔG Values Obtained from the Modified Curves

	pK_a	pK_0	ΔG (kJ/mol)
H-PLL	9.51	10.28	58.72
L-PLL	10.11	10.62	60.66
PEG-P(Lys)[a]	9.37	10.07	57.52

[a] PEG-P(Lys)(43−19) was used in this experiment.

Results and Discussion

Potential Titration. For pH-induced helix−coil transitions of poly(L-lysine), potential titration is one of the useful methods, and the standard free energy change of the deprotonation process, ΔG, can be determined from the relationship between pK (=pH + log[α/(1 − α)]) and 1 − α, where K is the effective dissociation constant and α is the protonation degree.[18−24]

Figure 1 shows the modified curves of the potential titration for PEG-P(Lys)(43−19) and two poly(L-lysine) homopolymers (H-PLL: M_w = 170 000; L-PLL: M_w = 2400) with different molecular weights. In the case of H-PLL, two linear ranges ($1 - \alpha < 0.5$ and $0.6 < 1 - \alpha < 0.75$) were observed due to two deprotonation processes, i.e., the random coil state and the α-helical state, suggesting that the transition occurred around α = 0.5. However, one linear range was observed for the modified curves of both PEG-P(Lys) and L-PLL. Worth noticing is a substantial decrease in the apparent pK_a for PEG-P(Lys) compared with both H-PLL and L-PLL, indicating a facilitated proton release in the block copolymer.

Table 1 shows the pK_a, pK_0, and ΔG values obtained from the modified curves, where pK_0 is the pK value at α = 0. The ΔG value was obtained from pK_0, based on the following equation[18]

$$\Delta G = pK_0 RT/0.434$$

where R is the gas constant and T is the absolute temperature. L-PLL has higher pK_a and ΔG values than H-PLL, indicating that the nonprotonated form of L-lysine units is more stable in H-PLL compared to L-PLL. This is due to the helix−coil transition of H-PLL: H-PLL adopts an α-helix structure at high pH through intramolecular hydrogen bonding, which facili-

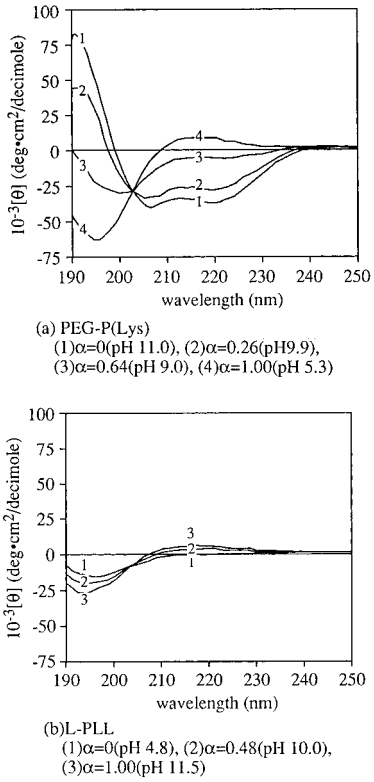

Figure 2. Circular dichroism spectra of PEG-P(Lys)(43−19) (a) and L-PLL (b) as a function of the protonation degree (pH) (concentration of lysine, 0.01 wt %; cell length, 1 mm; room temperature).

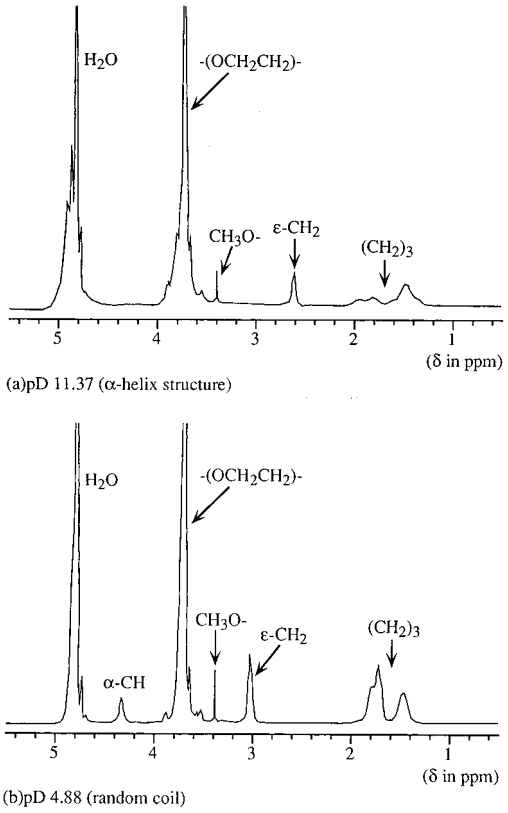

Figure 3. ^{1}H-NMR spectra of PEG-P(Lys)(43−19) at high pD (pD = 11.37, α-helical state) (a) and low pD (pD = 4.88, random coil state) (b).

tates the proton release to decrease the pK_a value. On the other hand, L-PLL does not undergo a helix−coil transition because its molecular weight is lower than the critical molecular weight to induce the transition. Worth mentioning is that the pK_a value of PEG-P(Lys) was even lower than that of H-PLL, although the poly(L-lysine) segment in PEG-P(Lys) had a lower molecular weight than in L-PLL. This result indicates that the nonprotonated form of L-lysine units is considerably stabilized through block copolymerization of poly(L-lysine) with poly(ethylene glycol). Indeed, in line with this lowered pK_a, the helix−coil transition of the poly(L-lysine) segment in PEG-P(Lys) was confirmed as described below.

Helix−Coil Transition of PEG-P(Lys) and Poly(L-lysine). The helix−coil transition was monitored by a pH-dependent change in circular dichroism (CD) spectra. Figure 2 shows the change in the CD spectra of PEG-P(Lys) and L-PLL with protonation degree (pH). A considerable change in the CD spectra of PEG-P(Lys) dependent on pH was observed. This change in the CD spectra is in good accordance with data reported for helix−coil transitions of poly(L-lysine) with a sufficiently high degree of polymerization.[25] The α-helix structure was characterized by a maximum at 191 nm and two minima at 210 and 222 nm. The helix−coil transition of PEG-P(Lys) was also confirmed by ^{1}H-NMR measurements. Figure 3 shows the ^{1}H-NMR spectra obtained for PEG-P(Lys) at high and low pD, i.e., helical and random coil states, respectively. A shift in the ϵ-CH$_2$ of the poly(L-lysine) segment was observed from 3.0 to 2.6 ppm due to the deprotonation of amino groups. A loss and a broadening of peaks corresponding to α-CH and (CH$_2$)$_3$ of the poly(L-lysine) segment were also observed, indicating a decreased mobility of these groups. These phenomena are in line with the results

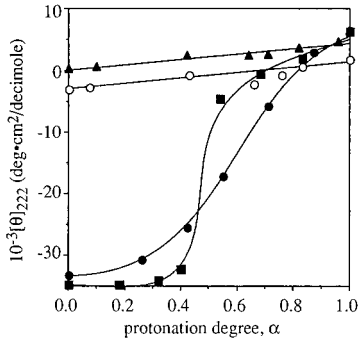

Figure 4. Variation in $[\theta]_{222}$ with protonation degree for PEG-P(Lys)(43−19) (●), H-PLL (■), L-PLL (▲), and a mixture of poly(ethylene glycol) (M_w = 8500) and L-PLL (○) (concentration of lysine, 0.01 wt %; cell length, 1 mm; room temperature).

already reported for helix−coil transitions of poly(L-lysine).[26] On the other hand, L-PLL having a molecular weight similar to that of the poly(L-lysine) segment in the block copolymer was confirmed to form no α-helix structure as indicated in the CD spectra. Its structure remains a random coil over the measured pH range as shown in Figure 2b, indicating the essential role of poly(ethylene glycol) conjugation for the induction of a helix−coil transition. In Figure 4, the mean residual ellipticity at 222 nm ($[\theta]_{222}$), characterizing an α-helix structure, was plotted against the protonation degree determined by potential titration. The $[\theta]_{222}$ values of L-PLL were unchanged through the whole pH range, indicating that L-PLL undertakes no helix−coil transition and remains as a random coil. In contrast, the $[\theta]_{222}$ values for PEG-P(Lys) and H-PLL decreased with a decrease in the protonation degree due to the transition from the random coil to the α-helix structure. In the case of H-PLL, the $[\theta]_{222}$ values steeply changed

around α = 0.5, reflecting cooperative transition. On the other hand, the change in the $[\theta]_{222}$ values for PEG-P(Lys) was gradual with α, suggesting an equilibrium between the α-helical state and the random coil state depending on pH. These observations were in good agreement with the profile of the modified curves shown in Figure 1: the curve having two linear ranges for H-PLL in contrast to a monotonic change for PEG-P(Lys). The $[\theta]_{222}$ values for the mixture solution of poly(ethylene glycol) and L-PLL are constant regardless of the protonation degree, excluding the possibility of a simple additive effect of poly(ethylene glycol) to alter the solvent properties.

Estimation of the Spatial Arrangement of the Block Copolymer by 2D-NOESY ^{1}H-NMR. The spatial arrangement of poly(ethylene glycol) and poly(L-lysine) segments of the block copolymer was estimated by a 2D-NOESY measurement under high pD (pD = 11.21) for an α-helix structure and low pD (pD = 4.92) for a random coil, respectively (Figure 5). Obviously, a correlation between the methylene groups of the poly(ethylene glycol) segment (δ = 3.7 ppm) and the ϵ-CH_2 groups of the poly(L-lysine) segment (δ = 2.6 ppm) was observed for the high-pD solution in which the poly(L-lysine) segment forms an α-helix structure. This result indicates that two segments locate close to each other under this condition. On the other hand, this correlation was not observed at a low pD where the poly(L-lysine) segment forms a random coil. Correlation in the 2D-NOESY spectrum at the α-helix state suggests that increased hydrophobicity of the poly(L-lysine) segment through deprotonation facilitates its segregation from the aqueous medium surrounded by the poly(ethylene glycol) segment as an outer shell. Stabilization through site association of two segments by short-range interactions (dipole−dipole interaction, hydrogen bonding) may also be assumed.

Estimation of the Micelle-like Structure in the α-Helical State of PEG-P(Lys). In order to confirm the formation of a micelle-like structure, the SLS measurements of the block copolymer were performed for the α-helical (pH 11.2) and random coil (pH 4.1) states. The Zimm plots were linear both in angle and concentration (data not shown). The M_w value was determined from the intercept of the $Kc/\Delta R(\theta)$ value for $c \rightarrow 0$ and $\theta \rightarrow 0$, the R_G value was determined from the slope of the $Kc/\Delta R(\theta)$ value for $c \rightarrow 0$, and the A_2 value was determined from the slope of the $Kc/\Delta R(\theta)$ value for $\theta \rightarrow 0$. However, in the case of block copolymer, the M_w value is an apparent one ($M_{w,app}$) due to the chemical heterogeneity of the copolymer.[27] Table 2 summarizes the $M_{w,app}$, R_G, and A_2 values obtained from the Zimm plots. The $M_{w,app}$ value (8596 g/mol) for the random coil state agreed well with the calculated value (8225 g/mol) determined from ^{1}H-NMR measurements, suggesting that the $M_{w,app}$ value represents the real M_w value. The $M_{w,app}$ value (16 502 g/mol) for the α-helical state was twice the value calculated, indicating the dimer formation. On the other hand, the R_G value (36.1 Å) for the α-helical state was smaller than that of the random coil state (51.1 Å), although the $M_{w,app}$ value increased due to the formation of associates. This indicates the effective compartmentalization of constituent polymer chains in the associates. In line with a decreased R_G value, the A_2 value also decreased with the formation of associates, because the A_2 value reflects interactions between a polymer and a low molecular weight solvent. The dissymmetric factor (Z_{45}), which is the value of

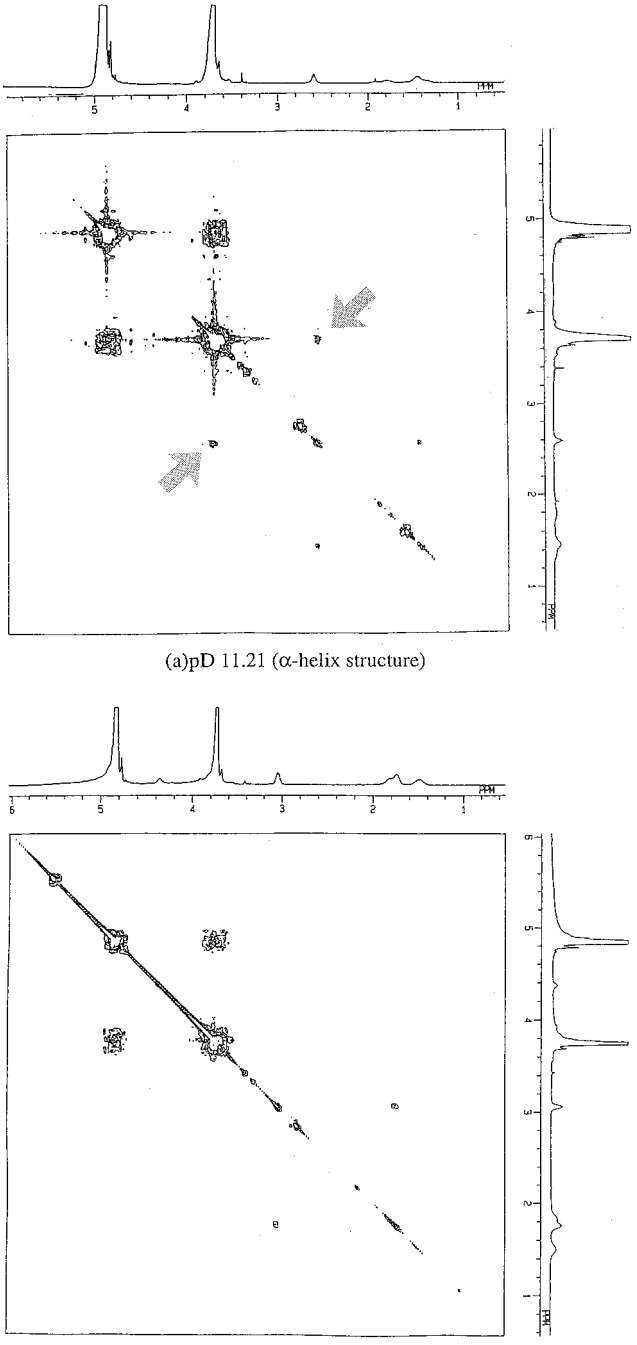

Figure 5. 2D-NOESY ^{1}H-NMR spectra for PEG-P(Lys)(43−19) at high pD (pD = 11.21, α-helical state) (a) and low pD (pD = 4.92, random coil state) (b).

Table 2. $M_{w,app}$, R_G, and A_2 Obtained from Zimm Plots of SLS[a]

pH	urea (5.0 M)	conformation	$M_{w,app}$ (g/mol)	R_G (Å)	A_2 (mol·mL/g^2)
4.1	−	random coil	8596	51.1	9.24×10^{-3}
11.2	−	α-helix	16502	36.1	0.14×10^{-3}
11.2	+	random coil	8712	55.3	8.61×10^{-3}

[a] PEG-P(Lys)(59−18) was used in this experiment.

$\Delta R(45°)/\Delta R(135°)$ for $c \rightarrow 0$, was also obtained from the SLS measurement. The theoretical Z_{45} value for a sphere is unity. In the case of ellipsoids or rods, the Z_{45} value increases with increasing dissymmetry.[28,29] The Z_{45} value of α-helical PEG-P(Lys) (1.0160) was close to unity, suggesting that the associate may have a spherical shape.

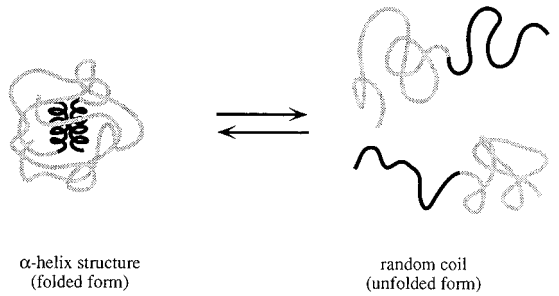

Figure 6. Schematic model of helix−coil equilibrium for PEG-P(Lys).

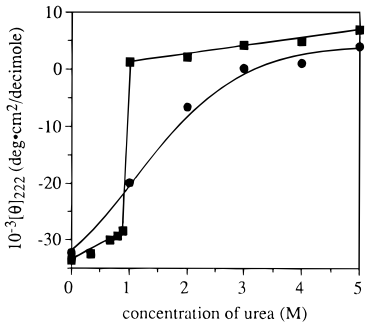

Figure 7. Influence of urea upon stability of the α-helix structure for PEG-P(Lys)(43−19) (●) and H-PLL (■) (concentration of lysine, 0.01 wt %; pH 11.0; room temperature).

It is known that, in a helical poly(amino acid), the amino acid residue expands over 1.5 Å.[9,30] In the case of poly(L-lysine) (polymerization degree of lysine = 18), the helical end-to-end distance was calculated to be 27.0 Å. On the other hand, several reports are available regarding the end-to-end distance of poly(ethylene glycol) in different conformations, as fully extended, meander, and random coil.[31] In the case of poly(ethylene glycol) with M_w of 5900, the estimated chain length for the fully extended, meander, and randon coil models are 469.3, 241.4−268.2, and 40.5 Å, respectively. Considering the end-to-end distance (27.0 Å) of helical poly(L-lysine) with a degree of polymerization of 18 for lysine and taking into account the correlation between the two segments in the 2D-NOESY spectrum, it is safe to assume that the α-helical poly(L-lysine) segment is surrounded by the poly(ethylene glycol) segment to form a spherical micelle-like structure as schematically shown in Figure 6. At present, there is no direct information on the orientation of α-helical poly(L-lysine) segments in the micelle, yet it may be plausible to consider that two poly(L-lysine) segments may associate side-by-side in antiparallel manner so as to compensate a dipole moment of the helix. This inference is consistent with end-to-end distances of the both segments and the R_G value of the associate obtained from Zimm plots. In this way, the poly(L-lysine) segment is compartmentalized into the domain of poly(ethylene glycol), which may have a lower dielectric constant than the outer aqueous medium. A decrease in the local dielectric constant should certainly contribute to stabilizing the α-helix structure of poly(L-lysine).

A gradual pH-induced helix−coil transition in the PEG-P(Lys) system shown in Figure 4 is in line with micelle formation, as schematically shown in Figure 6. The micellar form with an α-helical poly(L-lysine) segment (folded form) is likely to be in an equilibrium with the unfolded form of the block copolymer exhibiting a random coil conformation. By increasing the pH, this equilibrium should shift to the micellar (folded) form, resulting in an increase in $[\theta]_{222}$ of the CD spectrum.

Stability of the α-Helix Structure. The stability of the α-helix structure at pH 11.0 for H-PLL and PEG-P(Lys) was investigated by adding varying concentrations of urea, a strong breaker of hydrogen bonding as well as a disruptor of hydrophobic interactions. Figure 7 shows the dependence of the $[\theta]_{222}$ values on the concentration of urea. In the case of H-PLL, the $[\theta]_{222}$ values increase drastically between 0.9 and 1.0 M of urea because the intramolecular hydrogen bonding between peptide bonds is broken to induce a random coil conformation. On the other hand, the $[\theta]_{222}$ values for PEG-P(Lys) increase gradually with urea addition in the range from 0 to 3.0 M of urea, indicating a gradual shift of equilibrium to an unfolded, random coil conformation. It is worth noticing that, in the region of higher concentration of urea (1.0 M), the α-helix structure of H-PLL was completely destroyed, whereas a considerable portion of poly(L-lysine) in PEG-P(Lys) still kept its α-helix structure. This result strongly suggests that the poly(ethylene glycol) chain surrounding the α-helical poly(L-lysine) segment contributes greatly to the stabilization of the α-helix structure even in the presence of excess urea.

In order to confirm the relationship between the stability of the micelle-like structure and the stability of the α-helix structure of PEG-P(Lys), SLS measurements were performed for α-helical PEG-P(Lys) solutions including 5.0 M urea at pH 11.2, in which the α-helix structure was destroyed as shown in Figure 7. Table 2 shows the $M_{w,app}$, R_G, and A_2 values obtained from the Zimm plots of the SLS measurement. The $M_{w,app}$, R_G, and A_2 values after adding urea to the system agreed with the values obtained for the random coil state. With the addition of urea, the α-helix structure of PEG-P(Lys) was destroyed and the micelle-like structure was also dissociated, even though the poly(L-lysine) segment was in the deprotonated form. This result demonstrates that the formation of a dimer with a micelle-like structure was strongly correlated with the formation of an α-helix structure of PEG-P(Lys).

Conclusion

In this study, we have found that poly(L-lysine) of low molecular weight (M_w = 2400) can form a stable α-helix structure in an aqueous medium when this polymer is conjugated with poly(ethylene glycol). This pH-induced helix−coil change for PEG-P(Lys) is proposed to be due to an equilibrium between a micellar dimer with an α-helical poly(L-lysine) segment (folded form) and an unfolded form of the block copolymer, a random coil. It was demonstrated by urea addition that the α-helix structure in PEG-P(Lys) has an even higher resistance to urea than that in the poly(L-lysine) homopolymer with considerably higher molecular weight (M_w = 170 000). This effective stabilization of the α-helix structure seems to be due to the formation of a protective layer of poly(ethylene glycol) surrounding the core of poly(L-lysine) segments. This novel type of supramolecular assembly of the block copolymer with a particular conformation may have potential utility as elements for constructing higher ordered assemblies of macromolecules.

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