BULLETIN OF THE CHEMICAL SOCIETY OF JAPAN, VOL. 46, 335—336 (1973)

## A Fluorescence Study of a β-Structural 1-Dimethylaminonaphthalene-5-sulfonyl Poly-L-lysine Conjugate

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An  $\alpha$ -helical poly-L-lysine (PLy) is irreversibly transformed in its conformation to a  $\beta$ -structure when the temperature of the solution is raised to  $50^{\circ}\text{C.}^{1}$  It is agreed that the  $\beta$ -structure is stabilized by the hydrophobic bond between the side chains in addition to the hydrogen bond between the main-chain peptide groups. The intensity of the observed emission light of the 1-dimethylaminonaphthalene-5-sulfonate (DNS) bound to PLy is increased as the conformation of the DNS-PLy conjugate is changed from the  $\alpha$ -helix to the  $\beta$ -structure (Fig. 1). On the other hand, the optical

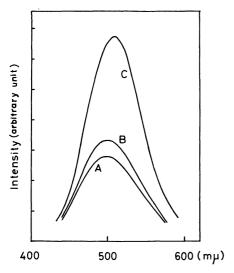


Fig. 1. Observed emission spectra of DNS-PLy conjugate in 0.01n KCl solutions at 20°C. Wavelength of excitation light was 350 m $\mu$ . A: Random coil (pH 5.8), B:  $\alpha$ -Helix (pH 12.4), C:  $\beta$ -Structure (after heating the  $\alpha$ -helical solution at 50°C for 30 min, then cooled to 20°C).

density of the conjugate at the wavelength of the excitation light scarcely changes during the conformational transition. The increase in the relative fluorescence intensity in the  $\beta$ -structural conjugate may be a reflection of the change in the environment around the DNS group. The DNS group may come in contact with the solvent molecules in the case of the  $\alpha$ -helix; on the other hand, it may be incorporated in the hydrophobic region and surrounded by the hydrophobic residues when the conjugate takes the  $\beta$ -structure. As a support to this conclusion, we can offer the fact that the quantum yield of DNS is increased from 0.29 to 0.71 when the solvent is changed from water to n-butanol at  $20^{\circ}\text{C.}^{2}$ 

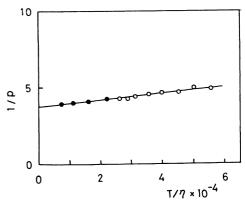


Fig. 2. Depolarization curve of  $\beta$ -structural DNS-PLy conjugate in 0.01n KCl (open circles) and in mixture of water and glycerine containing 0.01n KCl at 20°C (filled circles). Wavelength of excitation light and that of emission light were 350 m $\mu$  and 500 m $\mu$ , respectively.

We desire to obtain information on the rotational motion of the DNS group which is incorporated into the hydrophobic region. This information can be obtained from the depolarization curve<sup>3,4)</sup> of the  $\beta$ -structural conjugate (Fig. 2). The isothermal plot (filled circle) and the heating plot (open circle) give the same straight line. From this plot, we can obtain the rotational relaxation time ( $\rho_h$ ) at a particular temperature (T) of the DNS group bound to the  $\beta$ -structural PLy according to Eq. (1);

$$\rho_{\mathbf{h}} = \left(\frac{1}{p_0} - \frac{1}{3}\right) \cdot \frac{3\tau}{\text{the slope}} \cdot \left(\frac{\eta}{T}\right)_{\mathbf{T}} \tag{1}$$

where  $p_0$  is an intrinsic polarization,  $\tau$  is the lifetime of the lowest excited state of the DNS group, and  $\eta$  is the viscosity of the solvent. The  $\tau$  value is proportional to the relative fluorescence intensity,<sup>5)</sup> so the  $\tau$  value is obtained according to Eq. (2);

$$\tau_{\beta} = \tau_{\text{coil}} \cdot \frac{F_{\beta}}{F_{\text{coil}}} \cdot \frac{OD_{\text{coil}}}{OD_{\beta}}$$
 (2)

where F is the fluorescence intensity and OD is the optical density of the conjugate at the wavelength of the excitation light. The magnitude of F is calculated as follows: the corrected emission spectra which is obtained by calibrating the observed emission spectra (Fig. 1) for the detector system is plotted on graph paper, and the magnitude of F is determined by calculating the area beneath the curve. As the  $\tau_{\rm coil}$  value, we adopt  $1.2 \times 10^{-8}$  sec, this value is an average

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<sup>3)</sup> F. Perrin, J. Phys. Radium., 7, 390 (1926).

<sup>4)</sup> G. Weber, Adv. Protein Chem., 8, 415 (1953).

<sup>5)</sup> J. R. Laurence, "Physical Methods in Macromolecular Chemistry," ed. by B. Carroll, Marcel Dekker, New York (1969), p. 275.

of the measurements of three different DNS-protein conjugates in the neutral pH region.<sup>6)</sup> The  $\tau$  value for the  $\beta$ -structural conjugate is determined as  $2.7 \times 10^{-8}$  sec. Then we obtained  $\rho_h = 38.2 \times 10^{-8}$  sec for the  $\beta$ -structural conjugate at  $20^{\circ}\mathrm{C}$ ; this value is larger than that of the conjugate in the other conformations (see Ref. 7). The large value of  $\rho_h$  means that the rotational motion of the DNS group in the  $\beta$ -structural conjugate is extremely suppressed. The value of  $\rho_h = 38.2 \times 10^{-8}$  sec corresponds to the rotational relaxation time of a sphere with a radius of 50 Å, showing that the DNS group is incorporated in a very large  $\beta$ -structural region.

In the course of this experiment, we found a very interesting fact: the 1/p value of the  $\beta$ -structural conjugate do not depend on the wavelength of the excita-

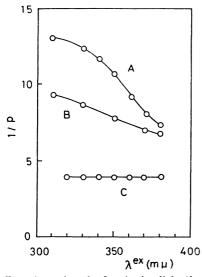


Fig. 3. Effect of wavelength of excitation light  $(\lambda^{\rm ex})$  on degree of polarization (p) of 500 m $\mu$  emission light in DNS-PLy conjugate. Measurements were performed in 0.01n KCl at 20°C. Slit width for excitation light was 6 m $\mu$ . Marks are the same as Fig. 1.

tion light  $(\lambda^{ex})$ . On the contrary, the 1/p values of the conjugate in the other conformations depend on the  $\lambda^{ex}$  value (Fig. 3). The DNS-protein conjugates show the same  $1/p - \lambda^{ex}$  relationship as do the  $\alpha$ -helical and random coiled conjugates.<sup>8)</sup> The reason for these results is unknown at this stage; we wish to leave it for future investigation.

## Experimental

DNS-Cl was bound to PLy (molecular weight, 30000) according to the method reported by Weber.<sup>9)</sup> The molar ratio of the bound DNS to the L-lysyl residue was 1: 48.5. All the fluorescence measurements were performed in a concentration of  $3.5 \times 10^{-6}$  mmol of DNS per ml. The fluorescence spectra and polarization of fluorescence were measured with a grating-type Hitachi Fluorescence Spectrophotometer MPF-2A. The degree of polarization (p) was calculated according to Eq. (3):

$$P = \frac{I_{\rm vv} - GI_{\rm hv}}{I_{\rm vv} + GI_{\rm hv}} \tag{3}$$

where  $I_{\rm vv}$  and  $I_{\rm hv}$  are, respectively the fluorescence intensity of vertically-polarized light and that of horizontally-polarized light when the solution is excited with vertically-polarized light, and where  $G = I_{\rm vh}/I_{\rm hh}$  is a correction factor which is needed when the P value is measured using a grating-type fluorometer; here  $I_{\rm vh}$  and  $I_{\rm hh}$  are, respectively the fluorescence intensity of vertically-polarized light and that of horizontally-polarized light when the solution is excited with horizontally-polarized light. The depolarization curve was obtained by plotting the reciprocal of the polarization of the fluorescence (1/p) as a function of the temperature divided by viscosity  $(T/\eta)$  in degree poise -1.

The author wishes to express very many thanks to Dr. K. Mihashi, and Dr. Y. Kawasaki (Nagoya University) and to Dr. S. Takahashi (Kyoto University) for their encouragement and discussions.

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