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Dynamics of the Hydration of Amino Alcohols and Diamines in Aqueous Solution

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The ^{17}O NMR spin–lattice relaxation times (T_1) of solvent water molecules in aqueous solutions of amino alcohols (AA), charged amino alcohols (AA$^+$), and charged diamines (DA^{2+}) were determined as a function of concentration at 298 K. The values of the dynamic hydration number, $n_{\mathrm{DHN}} = n_{\mathrm{h}}(\tau_c{}^{\mathrm{h}}/\tau_c{}^0 - 1)$, were determined from the concentration dependence of T_1. The ratios ($\tau_c{}^{\mathrm{h}}/\tau_c{}^0$) of the rotational correlation times ($\tau_c{}^{\mathrm{h}}$) of the water molecules around each solute molecule in the aqueous solutions to that of pure water ($\tau_c{}^0$) were obtained from the n_{DHN} and the hydration number (n_{h}), which was calculated from the water accessible surface area (ASA) of the solute molecule. The hydrophobic hydration is disturbed by the adjacent polar groups. The effect of disturbance decreases in the following order: $NH_3{}^+ > OH > NH_2$. The ASA dependence of the $\tau_c{}^{\mathrm{h}}/\tau_c{}^0$ value for diamines (DA), AA, and diols decreases in the following order: DA > AA > diols. When DA and AA are in a charged state, this order is reversed, namely, diols > AA$^+$ > DA^{2+}. The thermodynamic quantities of hydration for AA and AA$^+$ are linearly dependent on their n_{DHN} values.

A series of compounds with polar groups at both ends of an alkyl group show the behavior of key importance in an aqueous environment in biochemical and physiological processes. For instance, the diamines induce the B- to A-type transmission of DNA[1] and increase its thermal stability.[2] The diols stabilize or destabilize the structure of a protein depending on the length of the alkyl group and affect the transport of water in aquaporin 3.[3] Glycine and γ-aminobutyric acid inhibit the neurotransmission.[4]

The specific interactions of solutes with biopolymers are found to closely correlate with the characteristics of their hydrations.[5–7] However, there remains some ambiguity about the role of the water–solute interactions.

For attaining a better understanding of the role of water–solute interactions, one should study the effects of the alkyl and polar groups on solute hydrations from the viewpoint of dynamics. The $H_2{}^{17}O$ NMR spectrometry is most suitable for investigating solute hydration dynamics in aqueous solution, since the ^{17}O relaxation is not affected by the proton exchange between the hydrophobic group and water molecules.

We have measured the spin–lattice relaxation time, T_1, of the ^{17}O nuclei of water in aqueous solutions of amino acids,[8] amines and diamines,[9] alcohols, and diols,[10] and have obtained the dynamic hydration number, n_{DHN}, which represents the dynamic characteristics of hydration. Hertz et al.[11] emphasized the importance of the B-coefficient in Eq. 1 ($= n_{\mathrm{DHN}}/55.5$) as an indicator for hydration. In these investigations, we found that the hydrophobic hydration of an alkyl group is disturbed by the adjacent hydrophilic groups, and the degree of disturbance is a major factor in determining the total hydration of a solute.[8–10]

The thermodynamic characteristics of hydration of homologues are generally studied by using various key parameters: for example, the number of carbons or methylene groups, the number of polar groups, or the accessible surface area (ASA) is used. The selection of these parameters is arbitrary depending on the homologues. Moreover, one cannot explain the differences in hydration of given isomers, since these parameters have about the same value for the isomers. It is therefore very difficult to compare the thermodynamic hydration characteristics of one homologue with those others, if different parameters are adopted for these homologues. A universal parameter is necessary to compare the hydration of various kinds of homologues, and to clarify the effect of their hydration on the interaction between the homologues and the biopolymers. We showed that there are linear correlations between the n_{DHN} and the thermodynamic properties of the homologues.[8,12]

It is a subject of considerable interest to investigate the inter-relations of hydration behaviors among diamine, diol, and amino alcohol, since amino alcohol has the NH_2 and OH groups. It is also of particular interest to clarify the effect of uncharged and charged groups on hydrophobic hydration since an amino group can bear either an uncharged or a charged state. To date, however, few reports have appeared concerning thermodynamic data of amino alcohols.[13,14]

In the present paper, we report the results of T_1 measurements of ^{17}O nuclei in aqueous solution of amino alcohols, amino alcohol hydrochlorides and diamine hydrochlorides at 298 K. We determined the n_{DHN} of these compounds, and calculated the water-accessible surface area (ASA) and the hydration number (n_{h}). The ratio of the rotational correlation time ($\tau_c{}^{\mathrm{h}}/\tau_c{}^0$) was derived from the n_{DHN}.

The effects of OH, NH_2, and $NH_3{}^+$ groups on hydrophobic hydration will be discussed. We describe the relations between the thermodynamic properties and the n_{DHN} of these compounds.

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Method

The T_1 of $H_2{}^{17}O$ in aqueous solutions is adequately represented by an empirical equation of the form

$$T_1{}^0/T_1 = 1 + Bm. \tag{1}$$

Where $T_1{}^0$ is the spin–lattice relaxation time of $H_2{}^{17}O$ in pure water and m is the molality of the solute.

In the extreme motional narrowing condition, the ^{17}O relaxation rate is given by the relation[15]

$$1/T_1 = (3/125)(1 + \eta^2/3)(e^2qQ/\hbar)\tau_c \tag{2}$$

where η is an asymmetric parameter of the electrical field gradient, $e^2qQ/\hbar$ is the quadrupole coupling constant (^{17}OQCC), and τ_c is the correlation time of reorientation. The contribution of η will be omitted in the following discussion, since this value is usually small.[16]

In aqueous solutions, the ^{17}O nuclei of water molecules are distributed between two motional states with different intrinsic relaxation rates. Since the exchange of water molecules between the hydration water (mole fraction x_h) and the bulk water is fast, the following relation is obtained:[16]

$$1/T_1 = (1 - x_h)/T_1{}^0 + x_h/T_{1h} \tag{3}$$

where T_{1h} is the relaxation time of hydration water, $x_h = n_h m/55.5$, and n_h is the hydration number.

Combining Eqs. 2 and 3, we obtain

$$\begin{aligned} T_1{}^0/T_1 &= 1 + n_h(\tau_c{}^h/\tau_c{}^0 - 1)(m/55.5) \\ &= 1 + n_{DHN} \cdot x/(1 - x) \end{aligned} \tag{4}$$

where x is the mole fraction of the solute.

We define the dynamic hydration number, n_{DHN}, as follows:[8,17]

$$n_{DHN} = 55.5B = n_h(\tau_c{}^h/\tau_c{}^0 - 1) \tag{5}$$

where $\tau_c{}^h$ and $\tau_c{}^0$ are the rotational correlation times of water molecules in the hydration sphere and those in the bulk water state, respectively.

In aqueous solutions, it can be assumed that the value of ^{17}OQCC for hydration water is equal to that for bulk water.[18] In the case of the hydrochlorides of amino alcohols and diamines, Eq. 5 is expressed as[9]

$$\begin{aligned} n_{DHN} &= n_h{}^+(\tau_c{}^{h+}/\tau_c{}^0 - 1) + \nu_i n_h{}^-(\tau_c{}^{h-}/\tau_c{}^0 - 1) \\ &= n_{DHN}(M(NH_3{}^+)_i) + \nu_i n_{DHN}(Cl^-) \end{aligned} \tag{6}$$

where $M(NH_3{}^+)_i$ represents the charged amino alcohols ($i = 1$, $\nu_i = 1$) or diamines ($i = 2$, $\nu_i = 2$).

Consider a hypothetical molecule of the same size and shape as the solute molecule, that interacts with water in the same manner as would be the case in a water–water interaction. Then the n_{DHN} represents a difference in the dynamic states of water molecules in the hydration spheres of the solute and of the hypothetical molecule.

Since it is very difficult to obtain the n_h values experimentally, the values have been determined from the ASAs of the solute molecules.[9,10] We calculated the ASAs by drawing spheres with a radius of $(r_v + r_w)$ around each atom, where r_v is the van der Waals radius of each atom in a solute molecule and r_w is the radius of a water molecule ($r_w = 1.5$ Å). The computer program QCPE No. QCMP 132 was used for the ASA calculation. Taking account of the packing density of water molecules in the hydration sphere, we calculated the n_h value from the ASA.

The calculated values of the ASA and n_h for amino alcohols and charged diamines are shown in the 3rd and 4th columns of Table 1.

Experimental

Amino alcohols and diamines were purchased from Wako. All of the compounds were of GR grade and were used without additional purification.

The solutions of charged amino alcohols (AA$^+$) and diamines (DA^{2+}) were prepared by adding the equivalent amounts of hydrochloric acid to those of the uncharged amino alcohols (AA) and diamines (DA). All aqueous solutions were prepared in deionized and ultrafiltered water.

All natural-abundance ^{17}O NMR experiments were performed using a JUN EX-270 spectrometer operating at 36.63 MHz. The T_1 of nuclei was measured with an error of ±3% at 298 K by using the inversion recovery sequence. The temperature was maintained within the variation range of ±0.5 K by means of gas-thermostating.

Table 1. Hydration Characteristics of Amino Alcohols and Changed Diamines in Aqueous Solution at 298 K

No	Compounds	ASA /Å^2	n_h	n_{DHN}	$\tau_c{}^h/\tau_c{}^0$	$\overline{V^0}$ /cm^3·mol^{-1}	$\overline{C_p^0}$ b) /J·K^{-1}·mol^{-1}
1	$HO(CH_2)_2NH_2$	227.2	16	8.4	1.51	59.25	146.5
2	$HO(CH_2)_3NH_2$	258.6	19	13.9	1.75	75.21	237.7
3	$HO(CH_2)_4NH_2$	289.6	21	16.8	1.80	91.21 a)	328.9
4	$HO(CH_2)_5NH_2$	320.7	23	23.2	2.00	107.21 a)	420.1
5	$HO(CH_2)_2NH_3{}^+$	227.2	16	6.1	1.37	53.07	108
6	$HO(CH_2)_3NH_3{}^+$	258.6	19	9.2	1.49	69.57	199.2
7	$HO(CH_2)_4NH_3{}^+$	289.6	21	13.9	1.67	86.07 a)	290.4
8	$HO(CH_2)_5NH_3{}^+$	320.7	23	18	1.78	102.57 a)	381.6
9	$NH_3{}^+(CH_2)_2NH_3{}^+$	235.3	17	4.8	1.28		
10	$NH_3{}^+(CH_2)_3NH_3{}^+$	266.4	19	8.1	1.42		
11	$NH_3{}^+(CH_2)_4NH_3{}^+$	297.5	22	12.5	1.58		
12	$NH_3{}^+(CH_2)_5NH_3{}^+$	328.9	24	16.2	1.68		
13	$NH_3{}^+(CH_2)_6NH_3{}^+$	359.5	26	21.2	1.82		

a, b) Calculated values. For details of calculations, see text.

Results and Discussion

The values of $T_1{}^0/T_1$ for $H_2{}^{17}O$ in aqueous solutions as a function of solute concentration at 298 K are shown in Figs. 1, 2, and 3 for amino alcohols, amino alcohol hydrochlorides, and diamine hydrochlorides, respectively. The straight lines in the three figures were drawn through calculation by the least-squares method. The slopes of these straight lines correspond to the values of n_{DHN} from Eq. 4.

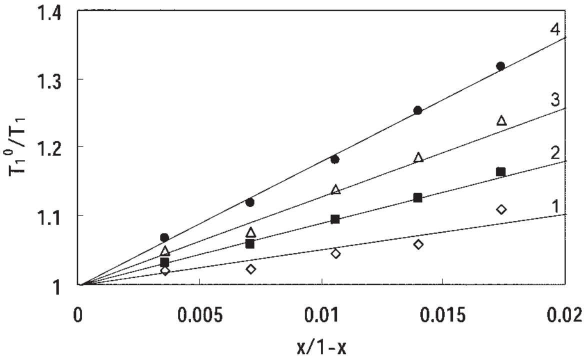

Fig. 1. $T_1{}^0/T_1$ for $H_2{}^{17}O$ in the aqueous solutions of amino alcohols as a function of the solute concentration at 298 K. The numbers in this figure denote the compounds having the same numbers in Table 1.

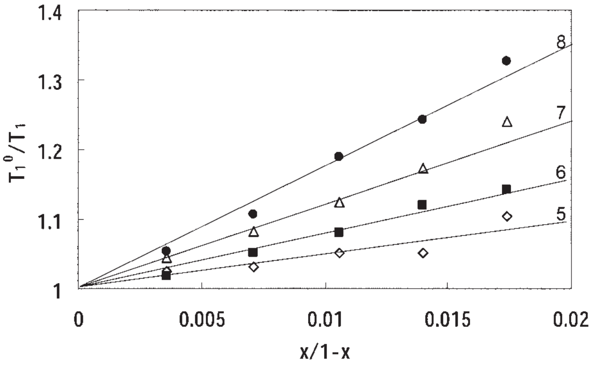

Fig. 2. $T_1{}^0/T_1$ for $H_2{}^{17}O$ in the aqueous solutions of amino alcohol hydrochlorides as a function of the solute concentration at 298 K. The numbers in this figure denote the compounds having the same numbers in Table 1.

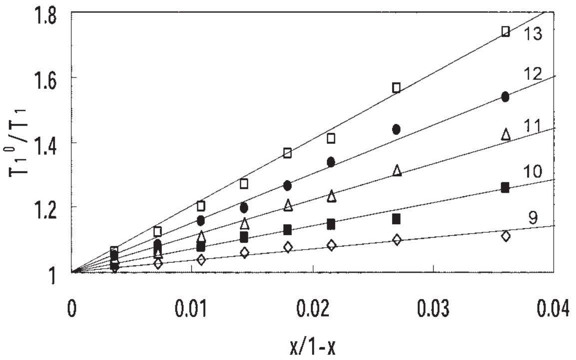

Fig. 3. $T_1{}^0/T_1$ for $H_2{}^{17}O$ in the aqueous solutions of diamine hydrochlorides as a function of the solute concentration at 298 K. The numbers in this figure denote the compounds having the same numbers in Table 1.

The values of $\tau_c{}^h/\tau_c{}^0$ for AA were calculated using Eq. 5 regarding n_{DHN} and n_h. The values of n_{DHN} and $\tau_c{}^h/\tau_c{}^0$ for AA^+ and DA^{2+} were calculated from Eq. 6, taking $n_{\mathrm{DHN}}(Cl^-) = -1.21$ into account.[19]

The values of n_{DHN} and $\tau_c{}^h/\tau_c{}^0$ for AA, AA^+, and DA^{2+} are presented in the 5th and 6th columns of Table 1.

As indicated in Table 1, for all the amino alcohols and charged diamines, $n_{\mathrm{DHN}} > 0$ and $\tau_c{}^h/\tau_c{}^0 > 1$. These results signify that the thermal motion of water molecules around these solutes is more inhibited than that in bulk water. Although the values of $\tau_c{}^h/\tau_c{}^0$ increase, on the whole, with an increase in chain length, the values depend on the kind and the charged state of the polar group.

The values of $\tau_c{}^h/\tau_c{}^0$ for AA, AA^+, and DA^{2+} having an equal number of carbon atoms decrease in the following order, as shown in Table 1:

$$AA > AA^+ > DA^{2+}. \tag{7}$$

We will then examine these results and the inter-relations of the dynamic hydration among amino alcohols, diamines, and diols.

Dynamics of Hydration. Since the rotational correlation time of water molecules in the hydration shell differs for different local environments such as alkyl and polar groups, the $\tau_c{}^h$ is an average over the hydration number. It reflects the effects of these groups on the thermal motion of water molecules around the solute.

Water molecules in the hydration shell of a hydrophobic group form a local cage-like hydrogen bonding structure, in which water–water interactions are slightly stronger than those in bulk water.[20] As a result, the thermal motion of solvating water molecules is more inhibited.

The hydrophilic groups directly interact with water molecules, and disturb the arrangement in the hydration shell of any hydrophobic group near them. The disturbing effect of the hydrophilic groups results in a decrease in the $\tau_c{}^h/\tau_c{}^0$ value.[8–10,21]

The $\tau_c{}^h/\tau_c{}^0$ values for 1,2-ethanediol and 1,3-propanediol are 1.36 and 1.56, respectively[10] (see Fig. 4). These values are smaller than those for neutral 2-aminoethanol and 3-aminopropanol as shown in Table 1. The $\tau_c{}^h/\tau_c{}^0$ values for *n*-alcohols are also slightly smaller than those for *n*-amines.[9,10] Hence, the OH group disturbs more strongly the hydrophobic hydration near it than the NH_2 group.

Since the $NH_3{}^+$ group interacts electrostatically with water molecules, its effect on the arrangement of solvating water molecules is stronger than that of the NH_2 group. The hydrophobic hydration shell around an alkyl group is more strongly disturbed by the adjacent $NH_3{}^+$ group. As a result, the $\tau_c{}^h/\tau_c{}^0$ values for AA are larger than those for AA^+.

Cabani et al.[13] obtained the volume changes associated with solute–solvent interactions for bifunctional compounds such as amino alcohols and diamines. They suggested that the effect of the $NH_3{}^+$ group on hydrophobic hydration is larger than that of the NH_2 group. Their suggestion is in accord with our concluded results.

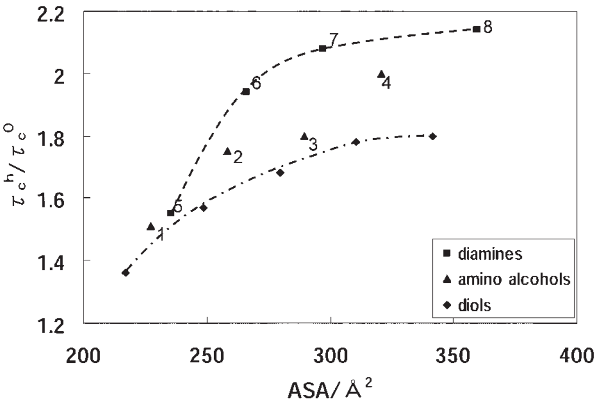

Fig. 4. Relationship between $\tau_c{}^h/\tau_c{}^0$ and ASA of the neutral diamines, neutral amino alcohols, and diols. The numbers in this figure denote the compounds having the same numbers in Table 1, but the $\tau_c{}^h/\tau_c{}^0$ values for diols (—◆—) are not numbered. The data for diols were cited from Ref. 10.

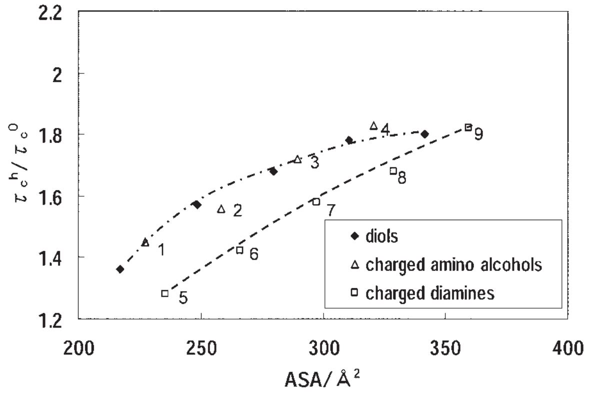

Fig. 5. Relationship between $\tau_c{}^h/\tau_c{}^0$ and ASA of the charged diamines, charged amino alcohols, and diols. The numbers in this figure denote the compounds having the same numbers in Table 1, but the $\tau_c{}^h/\tau_c{}^0$ values for diols (—◆—) are not numbered. The data for diols were cited from Ref. 10.

By the comparison of the $\tau_c{}^h/\tau_c{}^0$ values for AA, AA^+, and DA^{2+}, it can be defined that the effect of the polar group on hydrophobic hydration decreases in the following order:

$$NH_3{}^+ > OH > NH_2. \tag{8}$$

Inter-relations of Hydration between Amino Alcohols, Diamines, and Diols. In order to make clear the hydration behavior of amino alcohols, diamines, and diols, the plots of the $\tau_c{}^h/\tau_c{}^0$ values versus ASA for AA, DA, and diols, and for AA^+, DA^{2+}, and diols are shown in Figs. 4 and 5, respectively. As indicated in Figs. 4 and 5, the $\tau_c{}^h/\tau_c{}^0$ values for solutes approach a constant level after a steep increase with increasing ASA. These results are explained as follows. In the dilution process of a solute molecule into water, a rearrangement of the water molecules occurs around the solute molecule. In the case of a large solute particle, however, the rearrangement of water molecules is insufficient to maintain the same degree of hydrogen bonding, i.e., hydrogen bonds between the water molecules are destroyed.[20] Kjellender and Marcelja[22] showed that close to large hydrophobic surface, the number of hydrogen bonds between water molecules decreases. Lazaridis and Paulaitis[23] showed by Monte Carlo simulations that the orientational correlation entropy of water molecules in the hydration shell increases with solute size and then decreases slightly for larger solutes.

Therefore, the particle which is too large is less restricted than that around a molecule of a certain size. Namely, the $\tau_c{}^h/\tau_c{}^0$ value increases with ASA and then levels off. The value of ASA, (ASAc), at which the $\tau_c{}^h/\tau_c{}^0$ value approaches constant is different for different homologues. For the different homologues with the same size of alkane group, the value of ASAc depends on the kind and the number of the polar group.

The $\tau_c{}^h/\tau_c{}^0$ values decrease in the following order, as shown in Fig. 4:

$$\text{DA} > \text{AA} > \text{diols}. \tag{9}$$

The $\tau_c{}^h/\tau_c{}^0$ values for AA are approximately equal to the mean values of those for DA and diols. This means that the dynamic hydration property of AA is intermediate between those of DA and of diols.

In the case of charged amino alcohols and diamines, the $\tau_c{}^h/\tau_c{}^0$ values decrease in the following order, as shown in Fig. 5:

$$\text{diols} > AA^+ > DA^{2+}. \tag{10}$$

That is, the inter-relation of the dynamic hydration behavior of these compounds is strikingly affected depending on whether the amino group is in an uncharged or charged state. These results suggest that the interactions between amino alcohols and biopolymers can be made clearer by comparison with diols.

Relationship between Thermodynamic Properties and n_{DHN}. We found that the thermodynamic hydration properties of various homologues such as polyols,[7] amino acids,[8] alcohols,[10] and carbohydrates[17] depend linearly on their n_{DHN}. Consequently, the n_{DHN} can be regarded as the universal key parameter which connects the thermodynamic hydration properties with the dynamic behavior of hydration water.

Only for ethanolamine, 3-aminopropanol, and their hydrochlorides, the values of the partial molar volumes V^0 have been reported by Cabani et al.[13] The V^0 values of charged 2-aminoethanol and 3-aminopropanol were calculated from those of their hydrochlorides, taking into account $V^0(Cl^-) = 17.83\ cm^3\cdot mol^{-1}$.[24]

Cabani et al. estimated the contributions of methylene groups to the limiting partial molar volume in a homologous series of compounds. We calculated the V^0 values of amino alcohols (Nos. 3, 4, 7, and 8 in Table 1) using the values of $V^0(CH_2)^2$: 16.0 and 16.5 $cm^3\cdot mol^{-1}$ for AA and AA^+, respectively.

Makhatadze and Privalov[25] have reported the partial molar heat capacities $C_p{}^0$ of a homologous series of compounds such as n-alcohols, amino acids, and amines, and have estimated the $C_p{}^0$ value: 91.2, −3.6, −32.3, and −70.8 $J\,K^{-1}\,mol^{-1}$ for CH_2, OH, NH_2, and $NH_3{}^+$, respectively. By using their $C_p{}^0$, we calculated the $C_p{}^0$ values of the neutral and charged amino alcohols.

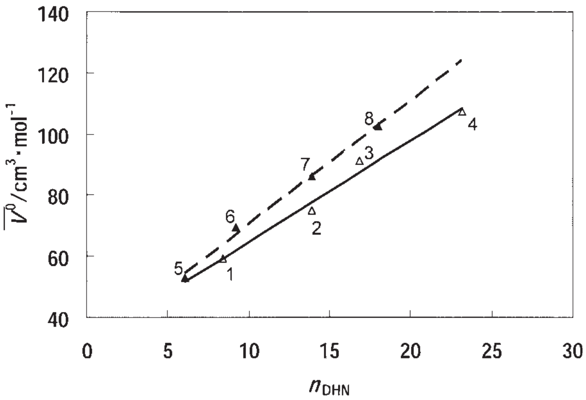

Fig. 6. Relationship between n_{DHN} and V^0 for AA and AA^+. The numbers in this figure denote the compounds having the same numbers in Table 1.

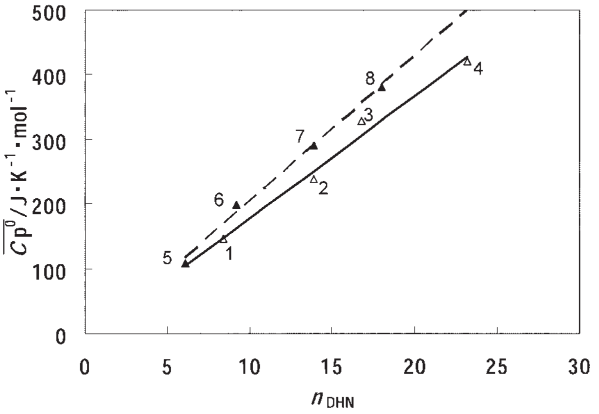

Fig. 7. Relationship between n_{DHN} and $C_p{}^0$ for AA and AA^+. The numbers in this figure denote the compounds having the same numbers in Table 1.

The values of V^0 and $C_p{}^0$ are listed in the 7th and 8th columns of Table 1. These thermodynamic quantities for AA and AA^+ are plotted as a function of their n_{DHN} in Figs. 6 and 7, respectively.

The V^0 are expressed by the following linear equations: for AA

$$V^0 = 31.53 + 3.32n_{\mathrm{DHN}} \tag{11}$$

for AA^+

$$V^0 = 29.92 + 4.06n_{\mathrm{DHN}}. \tag{12}$$

The $C_p{}^0$ are expressed by the following linear equations: for AA

$$C_p{}^0 = -11.57 + 18.93n_{\mathrm{DHN}} \tag{13}$$

for AA^+

$$C_p{}^0 = -19.98 + 22.44n_{\mathrm{DHN}}. \tag{14}$$

The limiting thermodynamic quantity approximately consists of the intrinsic quantity of the solute molecule and the contribution from the solute–water interaction. From the definition of n_{DHN}, the n_{DHN} depends on the size of the solute molecule and the rotational motion of hydration water. The intrinsic quantity is proportional to the molecule size, and the rotational motion of hydration water is affected by the solute–water interaction. It is, therefore, reasonable that V^0 and $C_p{}^0$ linearly correlate with n_{DHN}.

Conclusion

The $\tau_c{}^h/\tau_c{}^0$ values for AA, AA^+, and DA^{2+} confirm that the hydrophobic hydration is disturbed by the adjacent polar groups and that the degree of disturbance depends largely on the kinds of polar groups at both ends of the alkyl group. The effect decreases in the following order: $NH_3{}^+ > OH > NH_2$. The ASA dependence of the $\tau_c{}^h/\tau_c{}^0$ value for DA, AA, and diols decreases in the following order: DA > AA > diols. When DA and AA are in a charged state, this order is reversed, namely, diols > AA^+ > DA^{2+}. The thermodynamic quantities of hydration for AA and AA^+ are expressed by a linear equation of n_{DHN}.

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