Volume 29

Number 19

September 19, 1990

Inorganic **Chemistry**

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Communications

Solvent-Dependent Metal Ion-Nucleic Base Recognition. Extent of Macrochelate Formation in the Binary Copper(11) Complexes of Adenosine 5'-Monophosphate (AMP) and Adenosine 5'-Triphosphate (ATP) in Water-Dioxane Mixtures

It is now well established that the "effective" or "equivalent solution" dielectric constants in proteins^{1,2} or active-site cavities of enzymes³ are reduced compared to that in bulk water; i.e., the activity of water is decreased⁴ due to the presence of aliphatic and aromatic amino acid side chains at the protein-water interface. Estimates for the dielectric constants in such locations range from \sim 30 to 70;¹⁻³ hence, by employing aqueous solutions that contain \sim 10-50% 1,4-dioxane,⁵ one may expect to simulate to some degree the situation in active-site cavities.⁶

After study of the stability of complexes of simple phosphate monoester ligands in aqueous solution' and in water-dioxane mixtures,⁸ the position of the intramolecular, concentration-independent equilibrium **1** for Cu(S'-AMP) can now be quantified9

phosphate-ribose-base phosphate $\bar{\bar{M}}^{2*}$ b (1) ō s

in dependence on increasing amounts of dioxane in the aqueous reaction mixture, and be compared with the also varying extent of adenine N-7 back-binding¹⁰⁻¹⁶ in $Cu(5'-ATP)^{2-17}$ the latter

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- (10) With purine-nucleoside 5'-monophosphates¹¹ and 5'-triphosphates,¹² macrochelates may be formed involving oxygen(s) of the phosphate residue and N-7 of the purine moiety;^{13,14} for several complexes of 5'-AMP²⁻ (cf. ref 15) and 5'-ATP⁴⁻ (cf. ref 16) with divalent metal ions, the isomer distribution of **q 1** is established.
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Figure 1. Chemical structures of the adenine-nucleotides (AN), *5'-* $AMP²⁻$ and $5'$ -ATP⁴⁻, in their dominating anti conformation.^{13a,19}

Figure 2. Formation degree of the macrochelates *(eq* 1) in the binary complex systems Cu(5'-AMP) (O) and Cu(5'-ATP)²⁻ (\diamond) as a function of the percentage of 1,4-dioxane added to the aqueous reagent mixtures $(I = 0.1 M (NaNO₃); 25 °C).$

complex being possibly a natural active form of $Cu^{2+}.^{18}$ The results for these Cu²⁺/adenine-nucleotide (AN) systems (Figure

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Table I. Negative Logarithms of the Acidity Constants for the 2-Fold Protonated Adenine Nucleotides (AN) H₂(5'-AMP)[±] and H₂(5'-ATP)²⁻, Comparison of the Measured Log Stability Constants, log $K_{\text{outAN}}^{\text{Cu}}$, of the Cu(AN) Complexes for 5'-AMP²⁻ and 5'-ATP⁴⁻ with the Calculated Stability, log $K_{\text{Cu(AN)}_{\text{Cu(AN)}}}^{\text{Cu(AN)}}$ (See Text), for the Cu(AN) Isomers with Only Cu²⁺-Phosphate Coordination, and Extent of the Intramolecular Macrochelate Formation (Eq 1) in the Cu(AN) Species As Quantified by K_1 (Eq 2) and % Cu(AN)_{cl} (See Text) in Dependence on the Amount of 1,4-Dioxane Added to Water $(I = 0.1 \text{ M } (\text{Na} \text{N} \text{O}_3)$; 25 °C)^{a,b}

$\%$ (v/v) dioxane	mol fract	ϵ^c	$pK_{H_2(AN)}^H$	$pK_{H(AN)}^H{}^a$	$\log K_{\text{Cu(AN)}}^{\text{Cu}}$	$\log K_{\text{Cu(AN)_{\text{on}}}^{\text{Cu}}^{\text{Cu}}$	$log \Delta$	K_{I}	$%$ Cu(AN) _{cl}
0	0	78.5	3.84 ± 0.02	6.21 ± 0.01	3.14 ± 0.01	2.87 ± 0.08	0.27 ± 0.08	0.86 ± 0.35	46 ± 10
20	0.050	61.3	3.58 ± 0.01	6.74 ± 0.01	3.56 ± 0.01	3.49 ± 0.04	0.07 ± 0.04	0.17 ± 0.11	15 ± 8
30	0.083	52.7	3.47 ± 0.02	7.00 ± 0.01	3.86 ± 0.02	3.82 ± 0.03	0.04 ± 0.04	0.10 ± 0.09	9 ± 8
40	0.124	44.1	3.44 ± 0.01	7.31 ± 0.01	4.30 ± 0.02	4.19 ± 0.06	0.11 ± 0.06	0.29 ± 0.19	22 ± 11
50	0.175	35.2	3.42 ± 0.02	7.48 ± 0.01	4.73 ± 0.04	4.45 ± 0.02	0.28 ± 0.04	0.91 ± 0.20	48 ± 5
0	0	78.5	4.01 ± 0.01	6.49 ± 0.01	6.32 ± 0.04	5.83	0.49 ± 0.05	2.09 ± 0.36	68 ± 4
30	0.083	52.7	3.68 ± 0.02	6.82 ± 0.01	6.40 ± 0.05	6.14	0.26 ± 0.05	0.82 ± 0.21	45 ± 6
50	0.175	35.2	3.59 ± 0.02	6.90 ± 0.02	6.34 ± 0.05	6.22	0.12 ± 0.05	0.32 ± 0.15	24 ± 9

^a Definition of equilibrium constants (charges are omitted): $K_{H_1(AN)}^H = [H][H(AN)]/[H_2(AN)], K_{H(AN)}^H = [H][AN]/[H(AN)], K_{CH(AN)}^G = ($ [Cu- $(AN)_{\text{el}}$ + $[Cu(AN)_{\text{op}}]/[Cu][AN]$, and $K_{Cu(AN)_{\text{on}}}^{Cu} = [Cu(AN)_{\text{op}}]/[Cu][AN]$. 3 The error limits for the acidity and stability constants are 3 times the standard error of the mean value or the sum of the probable systematic errors, whichever is larger. The error limits given for log Δ , K_1 , and $\%$ Cu(AN)_{cl} were calculated according to the error propagation after Gauss by using the errors listed in the seventh and eighth column. The data for ATP are from ref 17; here the errors for $log \Delta$, K_1 , and % Cu(ATP)_{cl} are estimates; for the situation in water, see also ref 16. The data for AMP in water are from ref **15.** 'The dielectric constants for the dioxane-water mixtures are interpolated from the data given in ref **5.**

1)13a-i9 are intriguing: macrochelate formation (eq **1)** for Cu- (AMP) passes through a *minimum* with a formation degree of \sim 10% in 30% (v/v) dioxane-water, and \sim 45 and \sim 50% in water and 50% dioxane-water, respectively, while for $Cu(ATP)^{2-}$ it decreases gradually from \sim 70% in water to \sim 25% in 50% dioxane-water.

The experimental data of the potentiometric pH titrations of the Cu2+/AMP systems20 could be fully explained at pH **>3** by taking into account the species H^+ , $H_2(AMP)^{\pm}$, $H(AMP)^{\pm}$, AMP²⁻, Cu²⁺, and Cu(AMP) $[H_3(AMP)^+(cf. ref 19)]$ and Cu- $(H·AMP)^+$ (cf. refs 15,21) are negligible]. The dimensionless equilibrium constant, K_I , of equilibrium 1 is calculated^{9,15} with eq 2, which involves the log stability-constant difference log Δ

$$
K_{\rm I} = \frac{[C_{\rm U}(AMP)_{\rm cl}]}{[C_{\rm U}(AMP)_{\rm op}]} = \frac{K_{\rm Cu(AMP)}^{\rm Cu}(AMP)}{K_{\rm Cu(AMP)_{\infty}}^{\rm Cu} - 1} - 1 = 10^{\log \Delta} - 1 \tag{2}
$$

 $=$ log $K_{\text{Cu(AMP)}}^{\text{Cu}}$ ⁻ log $K_{\text{Cu(AMP)}_0}^{\text{Cu}}$. The overall stability constant $K_{\text{Cu(AMP)}}^{\text{Cu}}$ is experimentally accessible, while the stability constant of the open isomer, $K_{\text{Cu(AMP)}_{2n}}^{\text{Cu}}$, is more difficult to obtain. The latter problem is resolved by constructing $log K_{\text{Cu(R-MP)}}^{\text{Cu}}$ versus $pK_{\text{H(R-MP)}}^{\text{H}}$ plots for the Cu(R-MP) complexes with 4-nitrophenyl phosphate, phenyl phosphate and D-ribose 5'-monophosphate (=R-MP) from the data given in ref 8 for the four mixed solvents employed; the corresponding least-squares regression lines allow calculation of the stability constant of the open isomer for any known acidity constant (p K_a value)^{7,9,15} of a monoprotonated phosphate residue, $H(R-MP)^{-}$. Finally, with K_1 the percentage of the closed or macrochelated form, $Cu(AMP)_{c}$, of eq 1 may be calculated: % Cu(AMP)_{cl} = $100K_1/(1 + K_1)$. All results, including those for $Cu(ATP)^{2-17}$ are summarized in Table I. To facilitate the overview, the percentages of the macrochelated

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 $Cu(AMP)$ and $Cu(ATP)^{2}$ species are also plotted in Figure 2 versus the percentage of dioxane present in the dioxane-water mixtures.

The stability of the $Cu(AMP)$ and $Cu(ATP)^{2-}$ complexes is obviously mainly determined in all solvents by the phosphate-group basicity (Table **I).** However, it is also clear that addition of dioxane to the aqueous solutions of the complexes alters the extent of macrochelate formation considerably and not in a predictable way. A minimum is reached for $Cu(AMP)_{cl}$ in 30% (v/v) dioxane-water, while the extent of $Cu(ATP)_{cl}^{2}$ decreases with increasing dioxane concentrations (Figure **2).** These different influences of dioxane on the formation of the macrochelates must be due to a combination of effects. Among these effects are certainly the alterations of the metal ion affinity of the binding sites due to the decreasing solvent polarity; another aspect is the hydrophobic (lipophilic) solvation of the purine moiety of the nucleotides by the ethylene groups of I,4-dioxane, which may shield a binding site, e.g. N-7, in a certain concentration range of dioxane.

Considering the substrate and product structures in enzymic reactions, the above observations are meaningful, and they are also to be expected for other metal ion-nucleotide complexes: it is evident that at a protein-water interface subtle polarity changes are enough to favor the one or other structure *(eq* **1).6** Moreover, one wonders how far is also metal ion binding to nucleic acids²² affected by changes in the polarity of the surrounding solvent? In this respect, it should be noted that not only the nucleic base residues alter their coordinating properties but also the metal ion affinity of phosphate residues increases drastically with a decreasing solvent polarity as is evident from the data given for phosphate binding in column 8 of Table I. Finally, the influence of solvent changes on the reactivity was already proven²³ for the metal ion facilitated ATP dephosphorylation.

Acknowledgment. We thank Ms. Rita Baumbusch for technical assistance and the Swiss National Science Foundation for a research grant.

⁽²⁴⁾ Work done at the University of Basel during a leave from the A
of Beijing Traditional Medicine, People's Republic of China.

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