gies of binding of the cation to the ionophore, assumed to remain a rigid bracelet-like cage, and the desolvation energies of the cation: the calculated values of the complexation energies are in the order $Na^+ > K^+ > Rb^+ > Cs^+$; the energies required to desolvate the ions decrease in the same order, but the numerical values are such as to bring the balance between the two quantities into the experimentally observed order.

In the case of nonactine, a much more flexible molecule, the computations show that, in the observed preference $K^+ > Na^+$, the complexation energies largely favor Na^+ and that the substraction of the desolvation energies does not suffice to reverse the order of the two cations. In that case the determining factor stems from the intramolecular repulsions between the oxygenated ligands inside the cavity, repulsions appreciably larger in the conformation of the Na^+ cavity than in that of the K^+ cavity, so that the total balance favors K^+. An attempt to account for the preference $NH_4^+ > K^+$ was made, assuming that the conformational changes between the two complexes can be neglected: there, the computed complexations energy largely favors NH_4^+, the preferred cation, and the substraction of the desolvation energy does not modify the order. The optimized computed position for NH_4^+ shows very interesting differences with respect to K^+, confirming some inferences made on the basis of early experimental infrared measurements in solution.

It will also be shown how the notions of molecular electrostatic potential, molecular electrostatic field, and atomic accessibilities can be useful in the domain of cation–ionophore interactions. Two examples will be given: a) the K^+-complex of valinomycine in connection with its ability to fix an anion, and the recently observed K^+–picrate–valinomycine complex; b) the uncomplexed form of valinomycine to propose arguments for a choice between two possible mechanisms recently suggested for initiating the ion capture.

Finally the case of divalent cations will be considered.

B11

Modeling the Molybdenum Sites of the Molybdenum Hydroxylases

J. T. SPENCE* and P. SUBRUMANIAN

Department of Chemistry and Biochemistry, Utah State University, Logan, Utah 84322, U.S.A.

Molybdenum hydroxylases are multicomponent enzymes which catalyze two electron oxidations of purines, aldehydes, formate and sulfite in animals and microorganisms [1]. In addition, eukaryotic nitrate reductase [2] and several as yet poorly characterized molybdenum containing enzymes have properties similar to those of the hydroxylases.

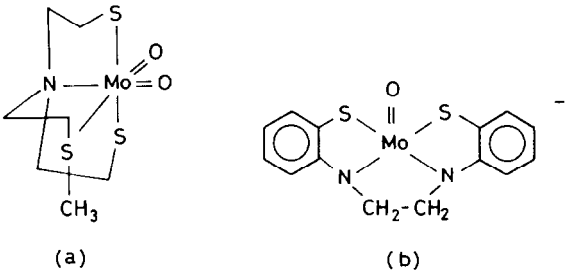


Fig. 1.

Recent EPR and EXAFS investigations indicate the presence of a terminal oxo and a terminal sulfido group on Mo in oxidized (Mo(VI)) xanthine oxidase and xanthine dehydrogenase and two oxo groups in oxidized sulfite oxidase [1, 3]. In the reduced state (Mo(V), (IV)) the sulfido group appears to be converted to SH (xanthine oxidase, xanthine dehydrogenase) or one oxo to OH (sulfite oxidase) [3]. In addition, 2-3 Mo thiolate sulfur ligands are present for both oxidized and reduced enzymes [3]. One or more of the thiolate ligands may be located on a side chain of a reduced pterin proposed to be the cofactor common to all Mo hydroxylases [4]. The reduction potentials of the Mo centers of the hydroxylases have been determined and are found to differ considerably between enzymes (–0.355 V for the Mo(VI)/(V) couple in xanthine oxidase [5], 0.038 V in sulfite oxidase [6], *e.g.*).

Recent model studies have concentrated on synthesis and structural characterization of dioxo-Mo(VI) complexes with N, S donor sets which mimic the EXAFS results [7] (Fig. 1a), on monomeric oxo-Mo(V) complexes having EPR parameters similar to those of the enzymes [8, 9] (Fig. 1b), and on oxo-Mo(VI), (V) and (IV) complexes which mimic the redox behavior of the enzymes [9, 10] (Fig. 1b). These results are briefly reviewed.

Current work in this laboratory is directed towards the synthesis and characterization of dioxo-Mo(VI) complexes with sterically bulky bi-, tri- and tetradentate ligands which may be electrochemically or chemically reduced to monomeric Mo(V)(O)(OH) complexes:

$$\left.\begin{array}{l} MoO_2L_2 \\ MoO_2L'L'' \\ MoO_2L''' \end{array}\right\} \xrightarrow[H^+]{-e^-} \left\{\begin{array}{l} MoO(OH)L_2 \\ MoO(OH)L'L'' \\ MoO(OH)L''' \end{array}\right.$$

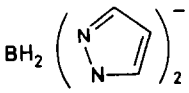
*Author to whom correspondence should be addressed.

Normally, such reductions give oxo bridged Mo(V) dimers; the presence of bulky groups on the ligands, however, inhibits the dimerization.

Representative ligands:

L:

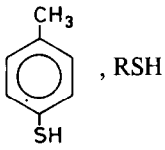
$RNHCH_2C(R')_2SH$
R = Me, Et, Ph, Bz
R′ = Me, Et



L′:

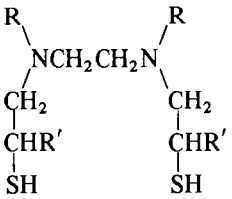
$R_2NCH_2CH_2NHCH_2C(R')_2SH$
R = Me; R′ = Me, Et

L″:

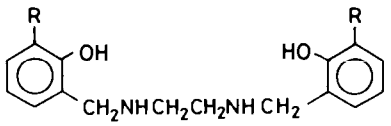


R = i-pr, t-but

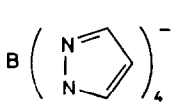
L‴:



R = Me, Et
R′ = Me



R = i-pr, t-but



Synthetic methods for the preparation of the complexes and their properties (IR, electronic and EPR spectra; electrochemistry) are reported. The relationships between EPR and electrochemical parameters and structures of the complexes are explored and the implications for the molybdenum hydroxylases are discussed.

Current problems in modeling the molybdenum centers of the hydroxylases and possible directions for research toward the solution of these problems are presented.

1 R. C. Bray, *Adv. Enzmol. Relat. Areas, 51,* 107 (1980); 'Biological Magnetic Resonance', V. 2, L. G. Berliner and J. Reuben, Eds. Plenum Press, N.Y. (1980) p, 45.
2 E. J. Hewitt, in 'Molybdenum and Molybdenum Containing Enzymes', M. P. Coughlan, Ed., Pergamon Press, N.Y. (1980), p. 273.
3 S. P. Cramer, R. Wahl and K. V. Rajagopalan, *J. Am. Chem. Soc., 103,* 7721 (1981).
4 J. L. Johnson and K. V. Rajagopalan, *Proc. Natl. Acad. Sci. U.S.A., Biochem., 79,* 6856 (1982).
5 R. Cammack, M. J. Barber and R. C. Bray, *Biochem. J., 157,* 469 (1976).
6 S. P. Cramer, H. B. Gray, M. Barber and K. V. Rajagopalan, in 'Molybdenum Chemistry of Biological Significance', W. Newton and S. Otsuka, Eds., Plenum Press, N.Y. (1980), p. 157.
7 J. M. Berg, K. O. Hodgson, S. P. Cramer, J. L. Corbin, A. Elsberry, N. Pariyadath and E. I. Steifel, *J. Am. Chem. Soc., 101,* 2774 (1979).
8 M. I. Scullane, R. D. Taylor, M. Minelli, J. T. Spence, K. Yamanouchi, J. H. Enemark and N. D. Chasteen *Inorg. Chem., 18,* 3213 (1979).
9 J. T. Spence, M. Minelli and P. Kroneck, *J. Am. Chem. Soc., 102,* 4538 (1980).
10 O. A. Rajan, J. T. Spence, C. Leman, M. Minelli, M. Sato, J. H. Enemark, P. M. H. Kroneck and K. Sulger, in the press.

B12

Nickel Containing Hydrogenases

A. V. XAVIER*, M. TEIXEIRA, I. MOURA, J. J. G. MOURA and J. LeGALL

Centro de Química Estrutural, Complexo I, I.S.T., Av. Rovisco Pais, 1000 Lisbon, Portugal, and Department of Biochemistry, University of Georgia, Athens, Ga. 30602, U.S.A.

Hydrogenases have been purified from different biological sources. They are highly diversified enzymes in terms of active centers constitution, although they catalyze the simplest oxidation–reduction process: $H_2 \rightleftharpoons 2H^+ + 2e$.

Hydrogenases have been recognized so far to be iron–sulfur proteins. Generally they contain from four to twelve atoms of non-haem iron arranged in Fe–S clusters representative of the known basic structures, *e.g.*, [2Fe-2S], 3Fe-xS], and [4Fe-4S] [1–7].

Recently, nickel joined the group of transition metals relevant in biological oxidation–reduction