Coordination Chemistry Reviews 255 (2011) 2378–2387

Contents lists available at ScienceDirect

Coordination Chemistry Reviews

journal homepage: www.elsevier.com/locate/ccr

Chiral and supramolecular model complexes for vanadium haloperoxidases: Host–guest systems and hydrogen bonding relays for vanadate species

Winfried Plass*

Lehrstuhl für Anorganische Chemie II, Institut für Anorganische und Analytische Chemie, Friedrich-Schiller-Universität Jena, Humboldtstr. 8, 07743 Jena, Germany

Contents

ARTICLE INFO

Article history:
Received 22 March 2011
Accepted 28 April 2011
Available online 7 May 2011

Keywords:
Vanadium complexes
Cyclodextrins
Haloperoxidases
Hydrogen bonding
Inclusion compounds
Carbohydrates
Sulfoxidation

ABSTRACT

Supramolecular interactions and hydrogen bonding play a fundamental role in determining both structure and function of vanadate in enzymatic systems and in particular for the active site of vanadium haloperoxidases. Vanadium complexes with *N*-salicylidene hydrazide ligands provide a versatile approach towards molecular model systems with hydrogen bonding interactions. The variation of the side chains within these hydrazone ligands provides the ability to introduce chirality in molecular model complexes by the utilization of appropriate carbohydrate fragments. Moreover, the synthetic potential and the transformation reactions found for dioxidovanadium(V) complexes with *N*-salicylidene hydrazide ligands are reminiscent of what is usually observed for carboxylates and can therefore be regarded as their inorganic counterpart. The anisotropy effect of the oxido groups in vanadium complexes is a valuable tool that allows for the configurational and conformational analysis of structures with corresponding chelate rings. Utilizing appropriate vanadium complexes it is possible to generate inclusion compounds with cyclodextrins. The dependence of solid state and solution structures on the ring size of the cyclodextrin is discussed.

1. Introduction

There is continuous interest in the coordination chemistry of vanadium due to the biological and catalytic properties of relevant systems [1–8]. Besides the discovery of the insulin-like effect of vanadium compounds, this is related to the presence of vanadium in certain haloperoxidases [9] and nitrogenases [10,11]. Vanadium haloperoxidases are enzymes that catalyze different oxidation reactions like the oxidation of halides to corresponding hypohalous acids and the oxidation of organic sulfides to sulfoxides [12–14]. Particularly the latter reaction is of current interest, as sulfoxides are valuable products in synthetic organic chemistry [15–17], which are accessible through catalysis promoted by various transition metals [18–23]. The active site species in vanadium-dependent haloperoxidases is a vanadate moiety with proposed trigonal-bipyramidal geometry which is covalently linked to a histidine residue. However, their reactivity can be attributed to the presence

* Tel.: +49 03641 948130; fax: +49 03641 948132.
E-mail address: sekr.plass@uni-jena.de
URL: http://www.plass.uni-jena.de.

0010-8545/$ – see front matter © 2011 Elsevier B.V. All rights reserved.
doi:10.1016/j.ccr.2011.04.014

of an extensive hydrogen-bonding network [24], which seems to be a more general feature in the understanding of the biological and catalytic action of vanadium compounds [25]. Model complexes with chiral ligand systems are of interest with respect to their catalytic properties, as such systems can basically exhibit enantioselectivity [26]. Of particular current interest in this context are systems containing chiral sugar-based ligand systems [27].

Host–guest systems are attractive alternatives to provide supramolecular environments for relevant complex moieties. Utilizing cyclodextrins (CDs) it is possible to generate inclusion compounds with various apolar groups, that are included partially or completely in the hydrophobic cavity [28–30]. On the other hand, CDs form hydrogen-bonds due to their free hydroxy groups. For the parts of the guest molecules protruding out of the CD ring opening this can lead to relevant hydrogen-bonding interactions. Moreover, CDs as well as their substituted derivatives are attractive components of artificial enzymes due to their ability to act as catalysts for several asymmetric reactions, like oxidations, hydrolyses and separation of racemates [31–33]. Even though CDs are well-known hosts to encapsulate metal complexes containing aromatic constituents leading to assemblies which often exhibit markedly different physical and chemical properties, only very few examples of such inclusion compounds have been successfully characterized by single-crystal X-ray diffraction [34–41].

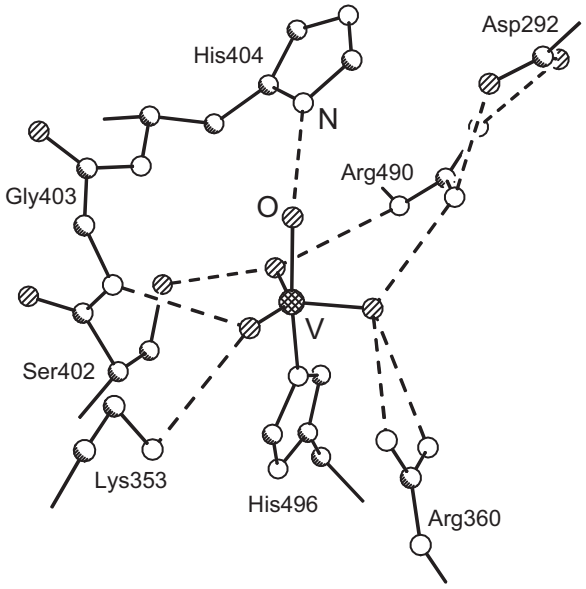


Fig. 1. Structural representation of the supramolecular environment of the active site of vanadium-dependent chloroperoxidase from *C. inaequalis*; hydrogen bonds depicted as broken lines [4].

2. Vanadate and supramolecular interactions

2.1. Vanadium haloperoxidases as supramolecular hosts

Key features for the basic role of vanadium in biological systems are associated with the chemical analogy between vanadates and phosphates [4] and the supramolecular interactions through hydrogen bonding [42]. Both features are closely related with the biological systems of vanadium-dependent haloperoxidases which have been found in marine algae as well as in some fungi and lichens. For some of these systems the structures have been determined by X-ray crystallography, namely for the vanadium-dependent chloroperoxidase (V-CPO) isolated from the terrestrial fungus *Curvularia inaequalis* [43] and the bromoperoxidases (V-BPOs) isolated from the brown algae *Ascophyllum nodosum* [44] and the red algae *Corallina officinalis* [45]. The active site structure of the V-CPO and the V-BPOs are similar as the first interaction sphere is concerned. Moreover, the overall structure seems to be rather rigid as the comparison with the structures of the apoprotein and the vanadate and tungstate derivatives of V-CPO suggests [46]. The representative schematic structure of the V-CPO active site derived from *C. inaequalis* is depicted in Fig. 1.

Although vanadate as the active site species in this class of enzymes is covalently linked to a histidine residue, their reactivity is determined by the presence of an extensive hydrogen-bonding network [24]. A considerable number of experimental [47–50] and theoretical [25,51–53] studies have led to a significant advance in the understanding of the catalytic mechanism of these enzymes. However, there are still important issues that are unresolved, which are closely related with the molecular structure of the vanadate moiety in the active site, including its protonation state and the actual protonation sites [25]. Of particular interest in this context is the role of the hydrogen-bonding network given by the protein matrix on structure and mode of action of the vanadate cofactor [42].

2.2. Molecular models based on N-salicylidene hydrazide ligands

In contrast to the enzymatic system, functional and structural model compounds for vanadium-dependent haloperoxidases generally neglect the influence of supramolecular interactions present in the protein matrix. As these interactions are most certainly a basic feature governing structural aspects as well as the mode of action of such enzymes, it is necessary to investigate supramolecular interactions of vanadium complexes with appropriate ligand systems [42,54]. Vanadium complexes with *N*-salicylidene hydrazide ligands containing a variety of functional groups attached to the ligand core provide to be a versatile tool to generate relevant model systems [23,55–59]. These ligands are derived from salicylaldehyd and carbonic acid hydrazides and can coordinate as tridentate chelate ligands in either their mono- or dianionic form. The ligand synthesis as well as the substitution pattern employed thus far in our ongoing studies are depicted in Scheme 1.

Utilizing the phenyl substituted derivative H_2salhyph the versatility of this ligand system could be shown towards both the ability to support oxido and dioxidovanadium(V) complexes as well as the generation of a mono- and dianionic ligand moiety [60]. The reaction with potassium metavanadate in methanol solution yields the potassium salt of the corresponding anionic *cis*-dioxidovanadium(V) complex K[VO_2(salhyph)]. Upon protonation in aqueous solution this complex can be converted to the corresponding neutral complex [VO_2(Hsalhyph)], which is protonated at the ligand backbone and not at the dioxidovanadium(V) moiety. The structure depicted in Fig. 2 is characterized by the presence of a square pyramidal *cis*-dioxidovanadium(V) moiety. The protonation results in significant changes within the molecular structure which are consistent with the formation of the keto form of the amide functionality [60].

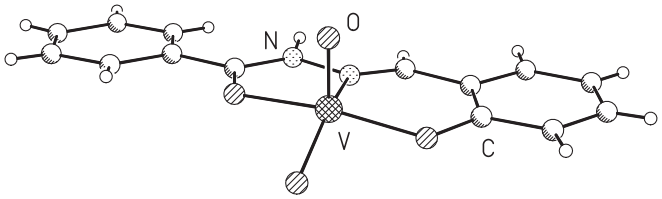
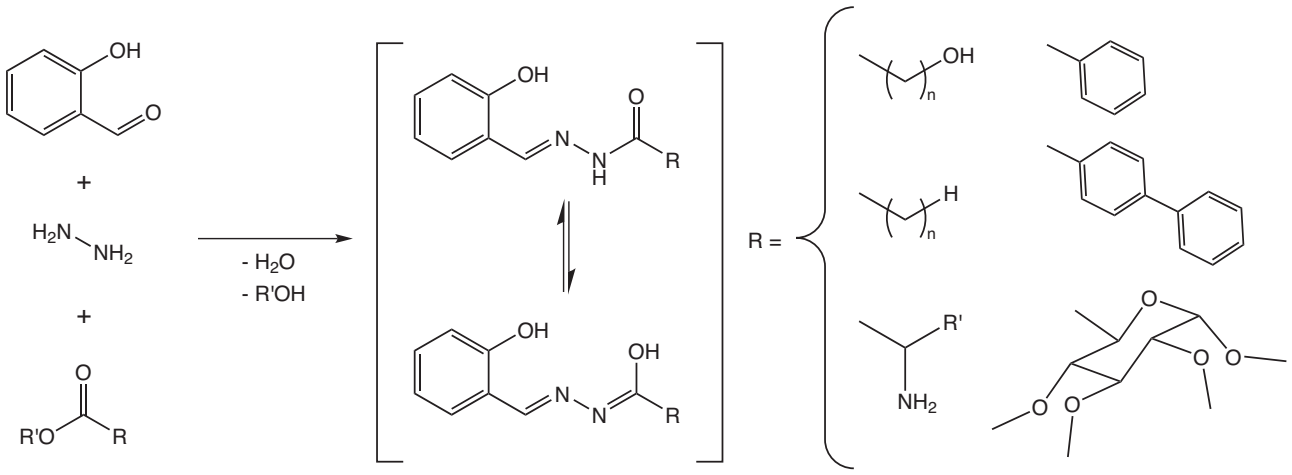


Fig. 2. Molecular structure of the neutral dioxidovanadium(V) complex [VO_2(Hsalhyph)] [60].



Scheme 1. Synthesis and substitution pattern of *N*-salicylidene hydrazide ligand systems.

When ammonium metavanadate is used as vanadium precursor for the synthesis in aprotic solvents the ammonium salt of the anionic *cis*-dioxidovanadium(V) complex $NH_4[VO_2(salhyph)]$ can be isolated [61]. The reaction of this ammonium salt with an excess of water leads to the formation of the neutral complex $[VO_2(Hsalhyph)]$. The reconversion can be achieved by deprotonation of the neutral complex in liquid ammonia. The molecular structure of $NH_4[VO_2(salhyph)]$ depicted in Fig. 3 is embedded in an extended hydrogen-bonding network established by the ammonium cations that solely interact with the four oxygen atoms of the central vanadium moiety.

The synthetic potential and the transformation reactions found for dioxidovanadium(V) complexes with the H_2salhyph ligand are reminiscent of what is usually observed for carboxylates and these complexes can therefore be regarded as inorganic counterparts (see Scheme 2). Under appropriate reaction conditions anionic dioxidovanadium(V) complexes can be converted into their esters $[VO(OR)(salhyph)]$ and anhydrides $[V_2O_3(salhyph)_2]$. With the appropriate alcohol component (e.g. 8-hydroxyquinoline or ethane-1,2-diol) the corresponding mixed ligand esters $[VO(OR)(salhyph)]$ [56,57,60] and $[VO(OR)_2(OMe)]$ [62] are accessible. However, it has to be noted that a free acid with a protonated oxido group is not observed for this system, as protonation leads to the neutral complex $[VO_2(Hsalhyph)]$ (see Fig. 2). This is in contrast to earlier reports on a so-called free acid with an oxidohydroxido core, *viz.* $[VO(OH)]^{2+}$, which has been described for a bis(8-quinolinato)vanadium(V) complex [63].

Since this ligand system can easily be modified (Scheme 1), it allows one to introduce additional functional groups in the vicinity of the central vanadium atom, which in the case of ω-hydroxy substituted side chains leads to intramolecular assemblies [64–66]. A relevant example $NH_4[VO_2(salhyhp)]$ with a medium chain length is depicted in Fig. 4. Moreover, it is interesting to note here that a

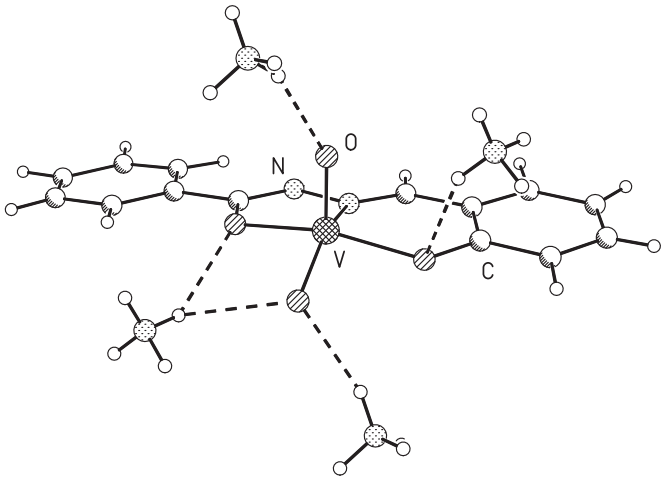
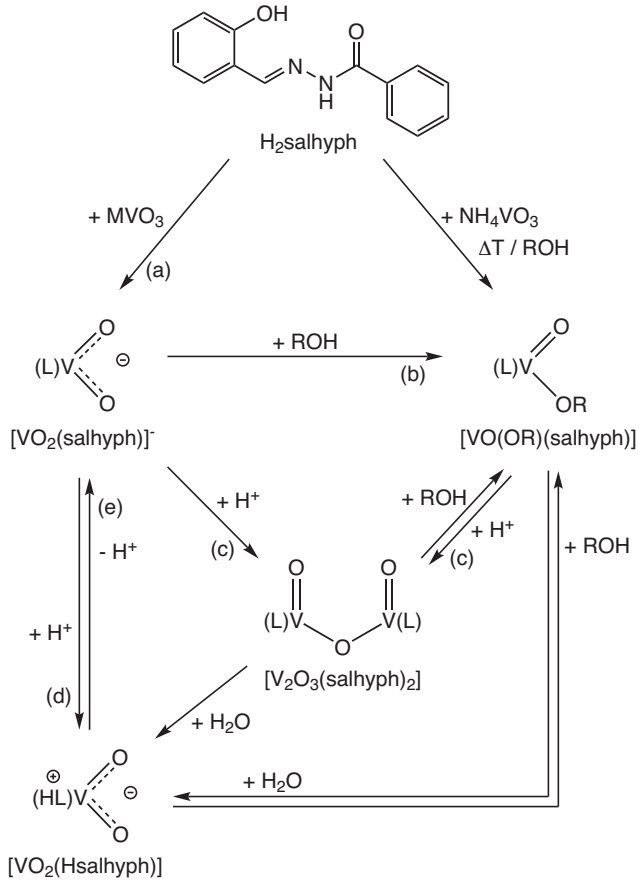


Fig. 3. Molecular structure of $NH_4[VO_2(salhyph)]$; hydrogen bonds depicted as broken lines [61].



Scheme 2. Syntheses and transformations of vanadium complexes with H_2salhyph ligand: (a) M = NH_4^+: DMF, ΔT; M = K^+: MeOH, ΔT; (b) M = NH_4^+: ROH, ΔT; (c) $(t\text{-BuO})_2PO(OH)$, THF; (d) M = NH_4^+: H_2O, ΔT; M = K^+: $HClO_4$, H_2O; (e) M = NH_4^+: liquid NH_3 [60,61].

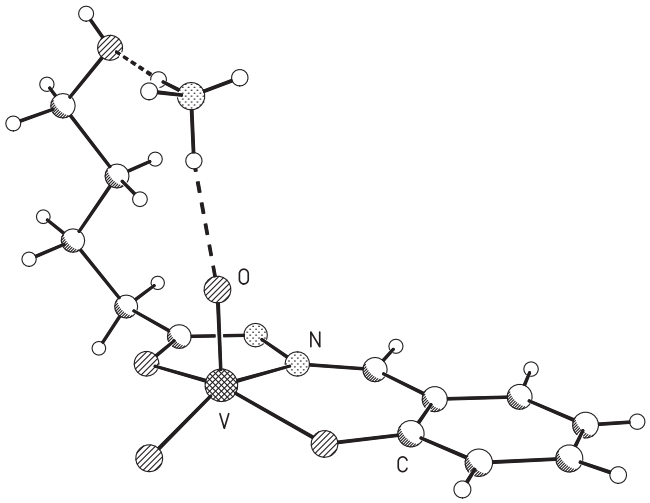


Fig. 4. Molecular structure of $NH_4[VO_2(salhyhp)]$ containing a hydroxy alkyl side chain (see Scheme 1, $n = 4$); hydrogen bonds depicted as broken lines [65].

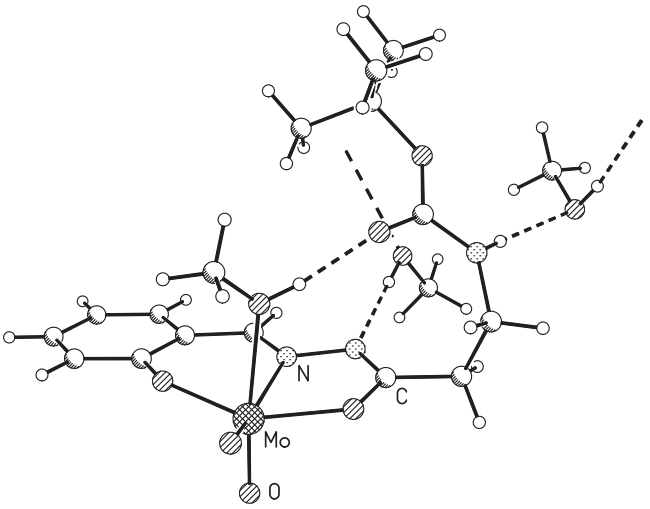


Fig. 6. Molecular structure of the dioxidomolybdenum(VI) complex $[MoO_2(salhy\beta alaBoc)(MeOH)]\cdot 2MeOH$ containing a BOC protected β-alanine side chain; hydrogen bonds depicted as broken lines [23].

variation of the chain length is not changing the basic structure, as the ammonium cation is in all cases involved in a hydrogen bonding relay between the hydroxyl side chain and the oxidovanadium(V) moiety. For these and other systems ^{51}V solid state NMR is a powerful tool in order to gain insight into structural features of model complexes leading to valuable correlations with spectroscopic parameters [67,68], which particularly includes ionic interactions and supramolecular environments.

Such hydrogen bonding relays can also be used to model interactions of vanadium moieties with peroxo groups as depicted in Fig. 5 [64]. Similar interactions are also discussed for the supramolecular interactions observed for the peroxo form of the V-CPO enzyme, which has been proposed as an intermediate in the catalytic cycle of these enzymes [69]. The oxidoperoxovanadium(V) complex $[VO(O_2)(salhyhb)(H_2O)]$ has been active towards both the haloperoxidase and sulfoxidation reactions.

Intramolecular hydrogen bonding interactions with relays established by protic solvent molecules have also been observed for a related molybdenum(VI) complex based on a Boc-protected β-alanine derivative depicted in Fig. 6 [23]. This complex is a remarkably efficient catalyst for the peroxidic oxidation of sulfides, but does not show any enantioselectivity.

Besides the generation of supramolecular interactions and hydrogen bonding relays, the *N*-salicylidene hydrazide ligand system also allows the introduction of centers of chirality next to the vanadium moiety. This feature is found for model complexes with ligands containing a side chain derived from 1,2,3,4-tetra-*O*-methyl-α-D-glucopyranuronic acid. As an example the dioxidovanadium(V) complex $K[VO_2(salhyglcpaOMe)]$ is given in Scheme 3 [55]. This complex also exhibits catalytic activity towards sulfoxidation reactions. However, no enantioselectivity could be observed, which might be attributed to the rather large distance of the chiral sugar side chain from the catalytically active vanadium center.

3. Vanadium complexes with carbohydrate-derived Schiff-base ligands

Carbohydrates have been frequently utilized as auxiliary ligands in systems for applications in asymmetric catalysis [27,70–72]. Moreover, also the vast biological relevance of carbohydrates and their interactions with metal ions has led to an intensive exploration of the complexation properties of relevant ligand systems where the sugar backbone has been functionalized with amides, amines, imines, and carboxylic groups [73–80]. Of particular interest in this context have been Schiff-base ligands due to their common availability via condensation of appropriate amino sugars with aldehyde components [81–90]. Although the interaction of carbohydrates with vanadium species is of great interest for vanadium biochemistry [91,92], vanadium(V) complexes with carbohydrate-based Schiff-base ligands are rather limited [87,93]. Moreover, such ligands have only scarcely been employed as chiral auxiliaries in vanadium-promoted enantioselective catalysis,

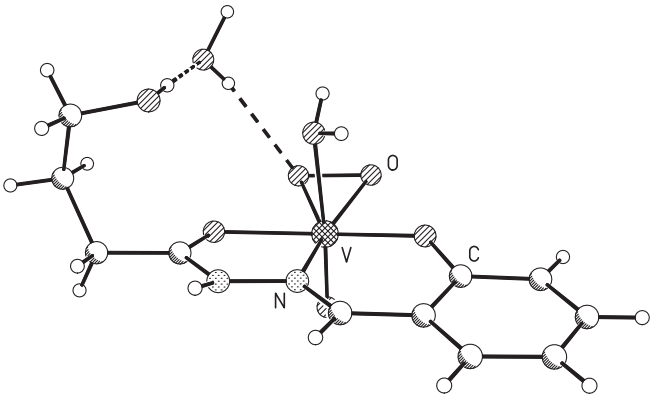
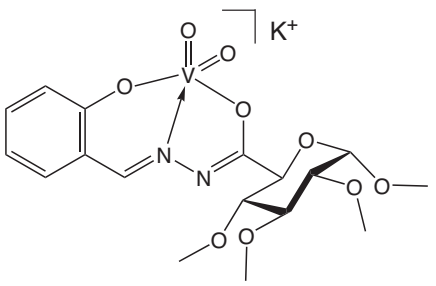
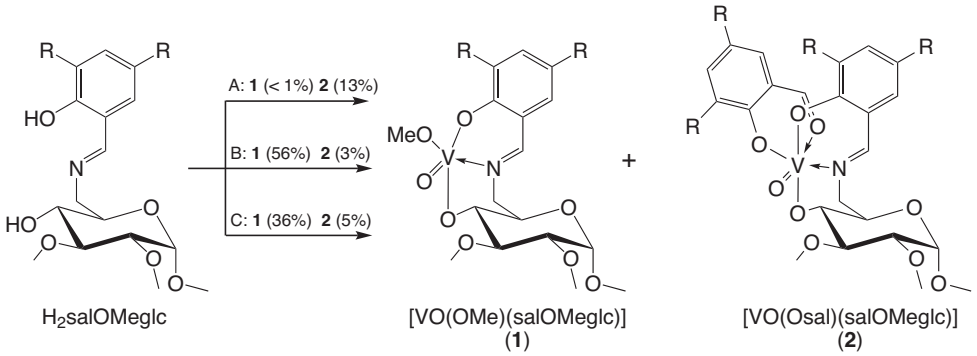


Fig. 5. Molecular structure of the oxidoperoxovanadium(V) complex $[VO(O_2)(salhyhb)(H_2O)]\cdot H_2O$ containing a hydroxy alkyl side chain (see Scheme 1, $n = 3$); hydrogen bonds depicted as broken lines [64].



Scheme 3. Dioxidovanadium(V) complex $K[VO_2(salhyglcpaOMe)]$ derived from 1,2,3,4-tetra-*O*-methyl-α-D-glucopyranuronic acid salicylidene hydrazide (see Scheme 1) [55].



Scheme 4. Synthesis of oxidovanadium(V) complexes with Schiff-base ligand H_2salOMeglc derived from 6-amino-6-deoxy-1,2,3-tri-O-methyl-α-D-glucopyranoside: (A) (i): NH_4VO_3/MeOH, 6d, 65 °C (ii): ethylene glycol/MeOH, 3d, 65 °C; (B) NH_4VO_3, ethylene glycol/MeOH, 2d, 65 °C; (C) $VO(iPrO)_3$/Et_2O (under argon), RT, redissolved in dry methanol [86,95].

which utilizes corresponding ligands based on 2-aminoglucose [94].

3.1. Complexes with 6-amino-6-deoxyglucopyranoside-derived Schiff-base ligands

If the ligand H_2salOMeglc derived from Schiff-base condensation of the aminosugar 6-amino-6-deoxy-1,2,3-tri-*O*-methyl-α-D-glucopyranoside and 3,5-di-*tert*-butylsalicylaldehyde [86] is utilized, two chiral oxidovanadium(V) complexes [VO(OMe)(salOMeglc)] and [VO(Osal)(salOMeglc)] can be synthesized according Scheme 4. The synthetic approach is based on two different routes starting from either ammonium metavanadate or tris(isopropoxy)oxovanadium(V) [95].

Along with the methanolate of the oxidovanadium(V) compound [VO(OMe)(salOMeglc)] also the complex [VO(Osal)(salOMeglc)] with a diprotonated salicylaldehyde (Osal = salicylaldehydato) as a bidentate coligand is formed, the latter being formed by partial hydrolysis of the utilized Schiff-base ligand. Moreover, under certain reaction conditions the methaolate complex [VO(OMe)(salOMeglc)] itself is prone to hydrolysis yielding the corresponding dioxidovanadium(V) complex [VO_2(HOMe)(HsalOMeglc)]. The molecular structure of the five-coordinate methanolate complex [VO(OMe)(salOMeglc)] is depicted in Fig. 7, for which a distorted trigonal bipyramidal geometry is observed for the vanadium center.

As compared to the dioxidovanadium(V) complex K[VO_2(salhyglcpaOMe)] (see Scheme 3) the centers of chirality are much closer to the vanadium atom in the case of the methanolate complex [VO(OMe)(salOMeglc)]. Therefore the latter complexe

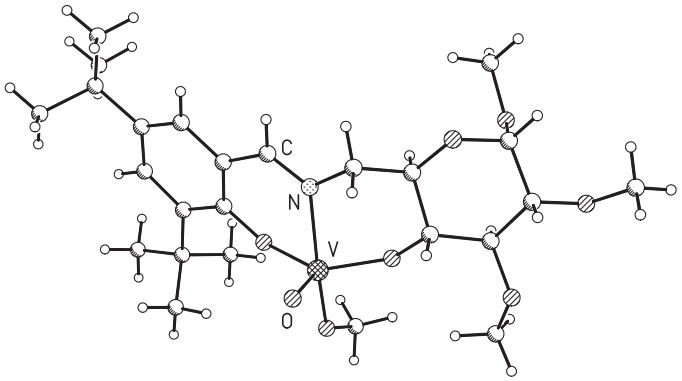
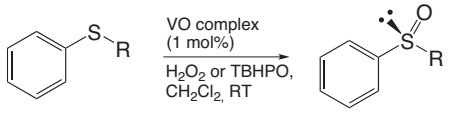


Fig. 7. Molecular structure of the oxidovanadium(V) complex [VO(OMe)(salOMeglc)] with a 6-aminoglucose-based Schiff-base ligand (see Scheme 4) [95].



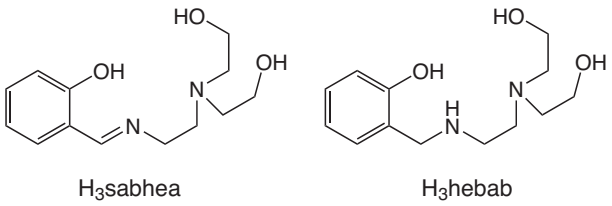
Scheme 5. Sulfoxidation catalysis with oxidovanadium(V) complexes.

has been tested for its capability in enantioselective sulfoxidation reactions (see Scheme 5) [95]. If [VO(OMe)(salOMeglc)] is utilized, moderate enantiomeric excess can be achieved depending on the substrate and the employed oxidant. For methyl phenyl sulfide as substrate and hydrogen peroxide as oxidant after reaction times of 2 h an overall conversion of 91% with 26% ee is observed. However, the presence of the bulky salicylaldehydato coligand leads to a considerable loss of activity (120 h: 61% conversion) and no enantioselectivity is observed.

3.2. Structural assignment of chelate rings in oxidovanadium complexes

It has been shown that ^{51}V NMR is an efficient tool to examine structures of vanadium complexes both in solution as well as in solid state [96]. This has been of particular interest related to the speciation in relevant vanadate systems [97,98]. An important issue here is the assignment of solution structures for catalytically active vanadium(V) complexes, which commonly contain supporting chelate ligands [99,100].

Based on oxidovanadium(V) complexes derived from the pentadentate chelate ligands H_3sabhea [101] and H_3hebab [102] depicted in Scheme 6 it has been possible to show that ^1H and ^{13}C NMR are valuable tools for the assignment of both the relative orientation of chelate rings as well as there conformations with respect to the oxido group [103]. The complex [VO(sabhea)] contains a pentadentate Schiff-base ligand with rigid backbone, leading to an unusual equatorial orientation of the chelate rings with respect to the oxido group in both solid state and solution (see Fig. 8). Whereas for complex [VO(hebab)] containing the flexible



Scheme 6. Pentadentate chelate ligands with rigid (H_3sabhea) and flexible (H_3hebab) backbone [101,102].

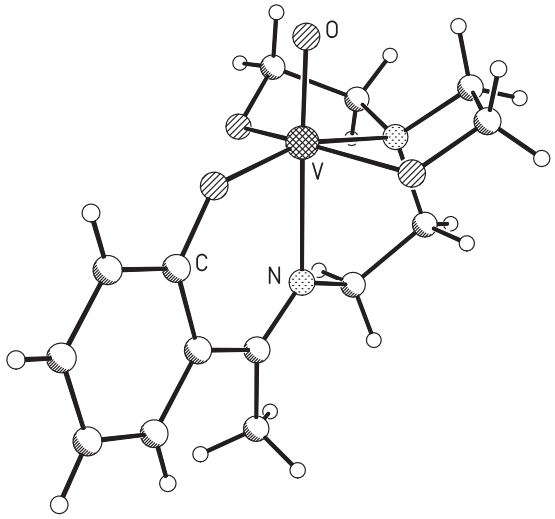


Fig. 8. Molecular structure of the oxidovanadium(V) complex [VO(sabhea)] with the rigid pentadentate H_3sabhea ligand (cf. Scheme 6) [101].

ligand the corresponding chelate rings in solid state are in an axial orientation with respect to the oxido group (see Fig. 9). However, in solution an equilibrium between the two possible chelate ring configurations is observed for complex [VO(hebab)], corresponding to a meridional and facial arrangement of the phenolate and ethylene diamine donor atoms as depicted in Scheme 7.

Comparison of the ^{1}H and ^{13}C NMR spectra for the complexes [VO(sabhea)] and [VO(hebab)] clearly shows that these data can be utilized to assign the relative position of hydrogen and carbon atoms in chelate rings attached to oxidovanadium(V) moieties as indicated in Scheme 8. Generally, for resonances of nuclei in equatorial positions a considerably more pronounced downfield shift is observed. Moreover, this also allows one to distinguish between different conformations of the corresponding chelate rings, as the resonances of hydrogen atoms attached to carbon atoms in equatorial chelate rings experience a characteristic shift, based on their axial or equatorial conformation and consequently their proximity to the anisotropic electrostatic field generated by the oxidovanadium(V) moiety [103]. This tool has already been proven to be a valuable tool for the conformational analysis of chelate rings in solution structures [104].

The oxidovanadium(V) complex [VO(OMe)(salOMeglc)] (cf. Fig. 7) is an interesting case with a sugar-based ligand system for which it is possible to assign the solution structure based on the anisotropic shielding effect of the $\{V{=}O^{3+}\}$ group. The typical coordination-induced shift (CIS) of the relevant resonances is observed for [VO(OMe)(salOMeglc)] [105,106]. In particular the CIS values for the ^{13}C resonances of the carbon atoms C-4 and C-6 of the sugar chelate ring at the vanadium center with about 25 and 6.5 ppm, respectively, are in the expected range for an equatorial chelate ring at the oxidovanadium(V) moiety. This is consistent with the large CIS value for the ^{1}H resonance of the H-4 proton of the sugar backbone of 1.6 ppm, which is clearly indicative for its cisoid orientation. Moreover, this is further corroborated by the distinct differences of about 0.8 ppm for the two methylene protons at the C-6 carbon atom of the sugar backbone, with H-6ax showing up more downfield. The resulting conformation of the sugar-based chelate ring for the solution structure is depicted in Scheme 9. A similar assignment results for the hexa-coordinate complex [VO(Osal)(salOMeglc)] with an additional bidentate coligand replacing the methanolate group.

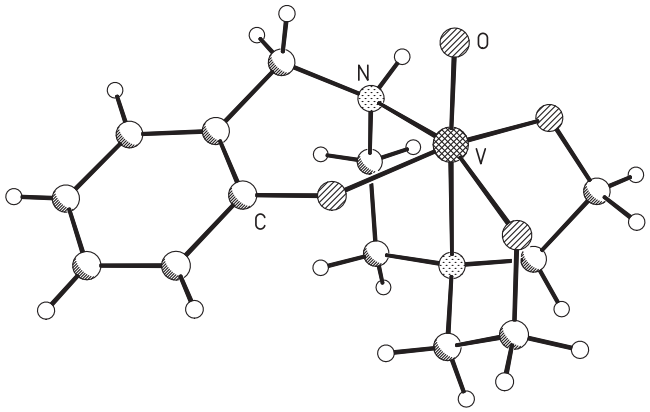
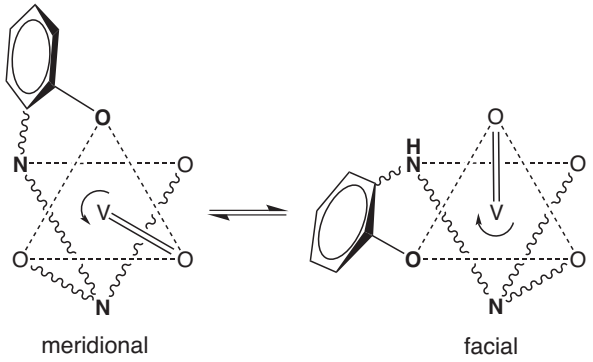
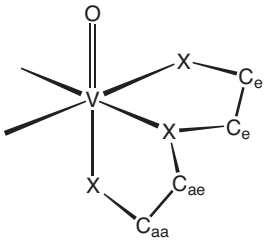


Fig. 9. Molecular structure of the oxidovanadium(V) complex [VO(hebab)] with the flexible pentadentate H_3hebab ligand (cf. Scheme 6) [102].



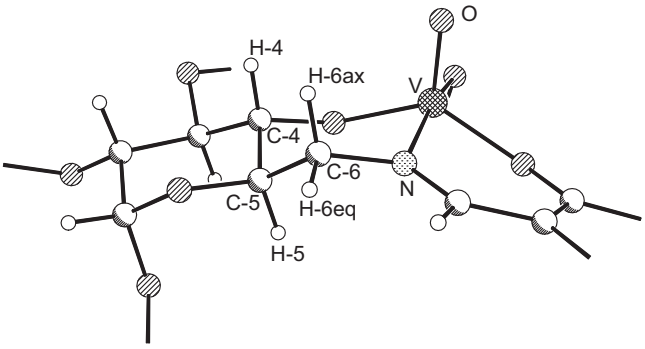
Scheme 7. Isomerization between the meridional and facial arrangement of the oxidovanadium(V) complex [VO(hebab)] by rotation about a pseudo C_3 axis; phenolate (O) and ethylene diamine (NH, N) donor atoms are marked in bold; methylene and ethylene bridges are depicted as wiggly lines; octahedral geometry is indicated by broken lines; bonds of the chelate ligand towards the vanadium are omitted for clarity; for complex structure see Fig. 9 and cf. Scheme 6 [103].



Scheme 8. Possible configurations of chelate rings in an octahedral environment at an oxidovanadium $\{V{=}O\}^{3+}$ moiety: C_e denotes a position oriented in the equatorial plane; C_{ae} and C_{aa} denote positions oriented in an axial plane with the second subscript descriptor indicating the position either adjacent to an equatorial or axial heteroatom X [103].

4. Cyclodextrin inclusion compounds

Host–guest compounds based on cyclodextrins (CDs) are unique systems which allow one to combine properties of different components and facilitate an attractive alternative to generate supramolecular environments for relevant complex moieties. This includes the introduction of chirality and hydrogen bonding relays. The latter is particularly evident for parts of the guest molecules protruding out of the hydrophobic CD cavity [29]. Consequently, host–guest compounds based on CDs and their derivatives are attractive systems due to their capability to be utilized as catalysts for a variety of applications including asymmetric and oxidation reactions [31].

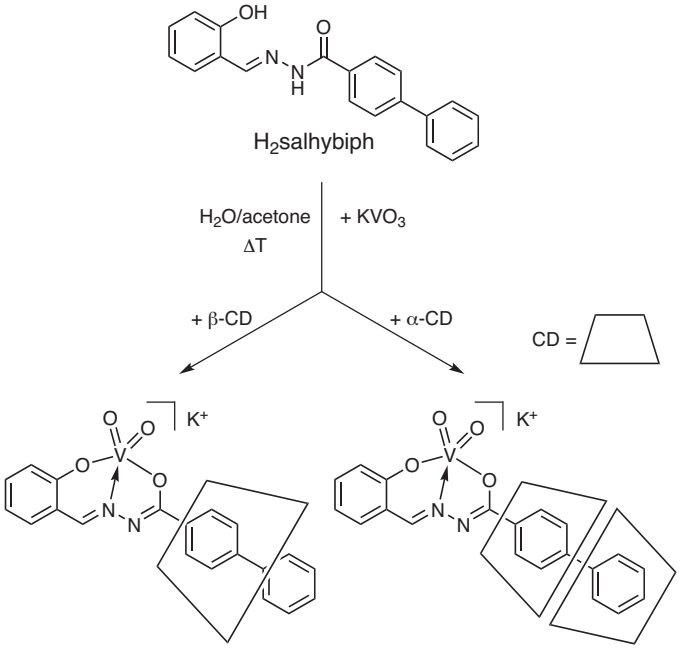


Scheme 9. Configuration of the sugar ligand and chelate backbone in the oxidovanadium(V) complex [VO(OMe)(salOMeglc)] (see Fig. 7); numbering scheme is according conventional carbohydrate nomenclature.

4.1. Synthetic design

Given the basic properties of CD hosts with an hydrophobic inner cavity, appropriate guest complexes can be derived from the versatile ligand approach utilizing *N*-salicylidene hydrazide ligand system which allows to generate vanadium complexes with apolar anchoring groups (cf. Scheme 1). If a biphenyl side chain is employed, appropriate inclusion compounds can be derived depending on the variation of the rings size of the CD host system. As shown in Scheme 10, the one pot reaction of potassium vanadate with the H_2salhybiph ligand leads the CD inclusion compounds. Interestingly the constitution of the resulting inclusion compound depends on the ring size of the employed CD. For β-CD a 1:1 inclusion compound is obtained with the potassium salt of the dioxidovanadium(V) complex K[VO_2(salhybiph)] [34], whereas for the smaller α-CD host a 2:1 ratio is observed [35].

Notably, it has been observed that the analogous route based on ammonium vanadate is less promising to generate such inclusion compounds, as the resulting vanadium(V) complexes lead to a variety of different species including the very sparingly soluble neutral complex [VO_2(Hsalhybiph)] (cf. Scheme 2 and Section 2.2). However, utilizing the potassium salts the formation of inclusion compounds is possible for both pre-synthesized and *in situ* generated vanadium complexes as guest molecules.



Scheme 10. Synthesis of cyclodextrin (CD) inclusion compounds with K[VO_2(salhybiph)] guest.

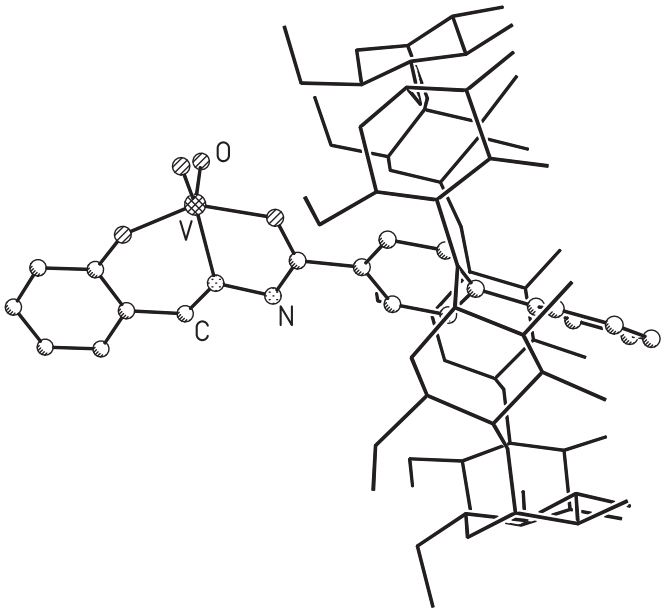


Fig. 10. Molecular structure of the anion of the inclusion compound K[VO_2(salhybiph)@β-CD] (cf. Scheme 10) [34].

4.2. Solid state structures

The crystallographic characterization for the inclusion compounds of the potassium salt K[VO_2(salhybiph) with α-CD and β-CD hosts revealed that the guest complexes exhibit structural parameters consistent with those usually observed for this class of vanadium(V) complexes with similar *N*-salicylidene hydrazide ligands (cf. Section 2.2) [60,61,64,65]. The molecular structure of K[VO_2(salhybiph)@β-CD], the 1:1 inclusion compound with β-CD, is shown in Fig. 10 [34]. Based on its rigid rod-like shape the guest complex anion clearly protrudes from the β-CD host. Moreover, the rather large size of the host allows for a considerable tilting of the guest anion within the cavity.

Head-to-head dimers are formed for the inclusion compound K[VO_2(salhybiph)@β-CD] by hydrogen bonding between the secondary hydroxyl sides of both β-CD hosts as depicted in Fig. 11. Together with the tilted arrangement of the guest molecules within the cavities this leads to a π-π stacking interaction of the biphenyl side chains.

The molecular structure of the 2:1 host–guest assembly for the α-CD inclusion compound K[VO_2(salhybiph)@(α-CD)$_2$] is depicted in Fig. 12 [35]. In this case a hydrogen bonded head-to-head dimer

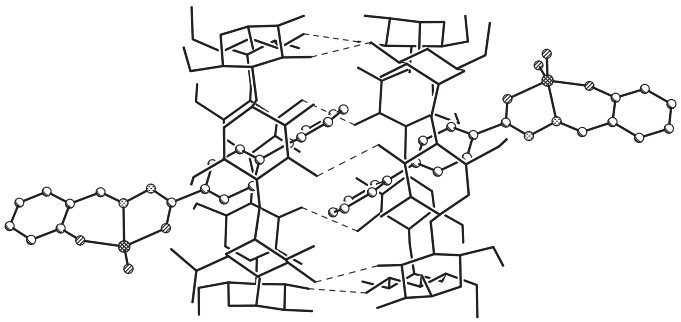


Fig. 11. Head-to-head dimer formation for the inclusion compound K[VO_2(salhybiph)@β-CD] in the solid state [34].

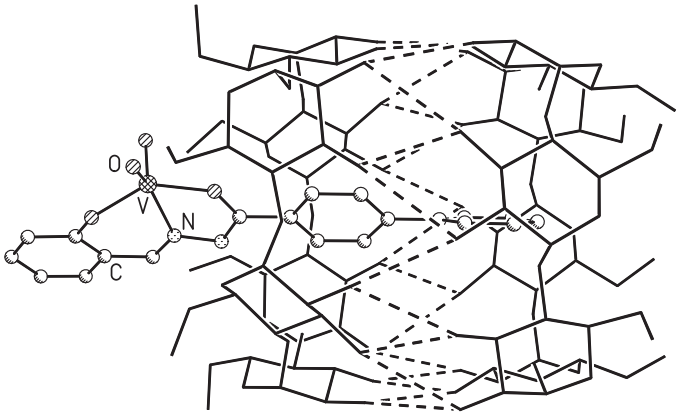


Fig. 12. Molecular structure of the anion of the inclusion compound K[VO_2(salhybiph)@(α-CD)$_2$] (cf. Scheme 10) [35].

of two α-CDs forms the host cavity, with the axes of this cavity and the biphenyl side chain of the guest anion being virtually collinear, which might be attributed to the smaller ring size of the α-CD. As a consequence the biphenyl side chain is completely located within the hydrophobic cavity of the dimeric host, whereas the remaining polar part of the complex anion is protruding from the cavity at the periphery of the primary hydroxy side of one of the α-CD rings. This leads to an extensive hydrogen bonding which includes the dioxidovanadium(V) moiety of the complex guest anion.

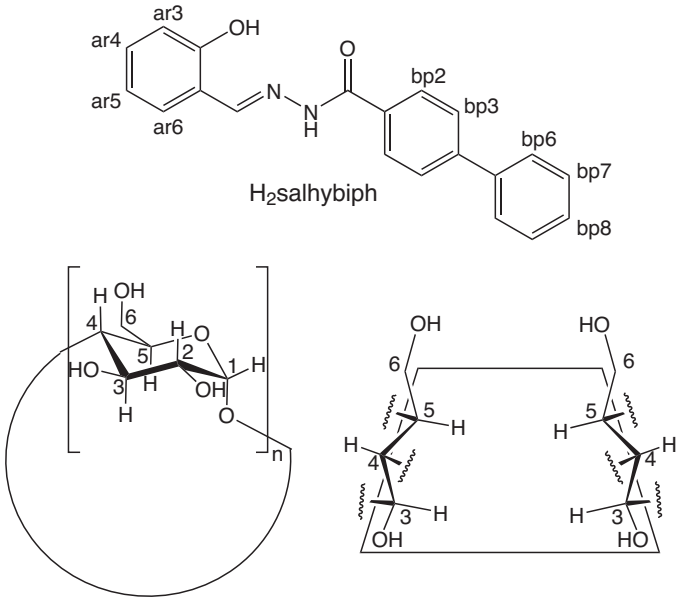
For both α-CD and β-CD the formation of head-to-head dimers by hydrogen bonding seems to be a general feature in the solid state structures. However, the variation in size not only leads to different host–guest arrangements, but also results in an alteration of the observed host–guest ratio for the inclusion compounds, with 2:1 for the α-CD and 1:1 for the larger β-CD.

4.3. Solution structures

Whether or not the structures observed in the solid state are inherent to properties of the host–guest compounds or driven by intermolecular interactions and packing effects cannot be answered by crystallography. However, this can be addressed by elucidating the relevant structural features in solution utilizing NMR spectroscopy. For the inclusion compounds K[VO_2(salhybiph)@β-CD] and K[VO_2(salhybiph)@(α-CD)$_2$] proton diffusion-ordered NMR spectroscopy (DOSY) clearly proves the integrity of the assemblies in solution, as only one species can be detected for both systems [34,35]. Based on the orientation of the H-3 and H-5 protons of the CD host towards the inside of the hydrophobic cavity as depicted in Scheme 11, the detection of through space interactions with the protons of the guest molecule should allow for clearer structural assignments of the assemblies.

The NOESY NMR spectrum for K[VO_2(salhybiph)@β-CD] depicted in Fig. 13 exhibits cross-peaks between the relevant biphenyl side chain proton signals of the vanadium guest complex and the β-CD host [34]. The penetration of the guest from the primary hydroxyl side of the β-CD into the cavity is confirmed by the absence of cross-peaks between the H-5 protons of the β-CD and the bp7 and bp8 protons of the biphenyl side chain of the guest complex. Moreover, this is consistent with intense cross-peaks observed between the H-6 protons of the β-CD host and the bp2 and bp3 protons of the biphenyl side chain. It should be noted here, that the spectra neither showed any evidence for interactions of the salicylidene moiety with the β-CD host nor for the formation of head-to-head dimers in solution.

Also for K[VO_2(salhybiph)@(α-CD)$_2$] the ROESY NMR spectrum depicted in Fig. 14 shows cross-peaks between the proton sig-



Scheme 11. Labeling scheme for host and guest of the inclusion compounds together with the orientation of the hydrogen atoms of the cyclodextrin backbone with respect to the established cavity.

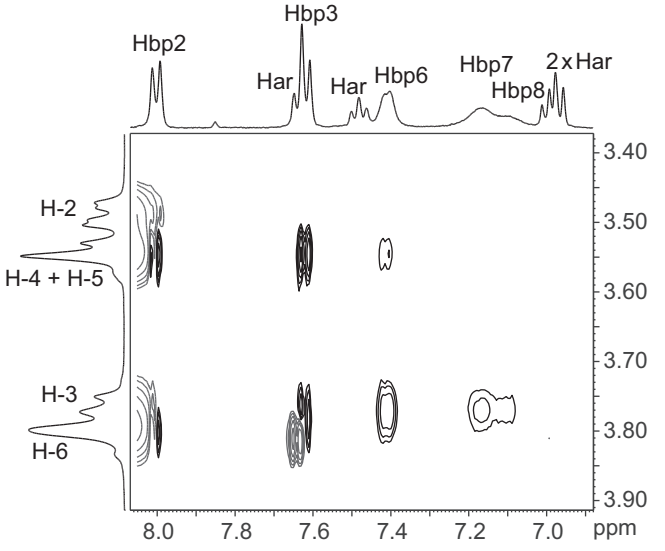


Fig. 13. NOESY spectrum for K[VO_2(salhybiph)@β-CD] in D_2O indicating host–guest interactions (for labeling cf. Scheme 11) [34].

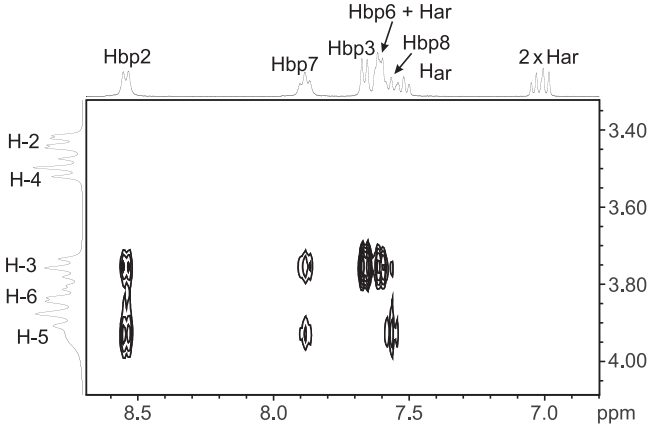


Fig. 14. ROESY spectrum for K[VO_2(salhybiph)@(α-CD)$_2$] in D_2O indicating host–guest interactions (for labeling cf. Scheme 11) [35].

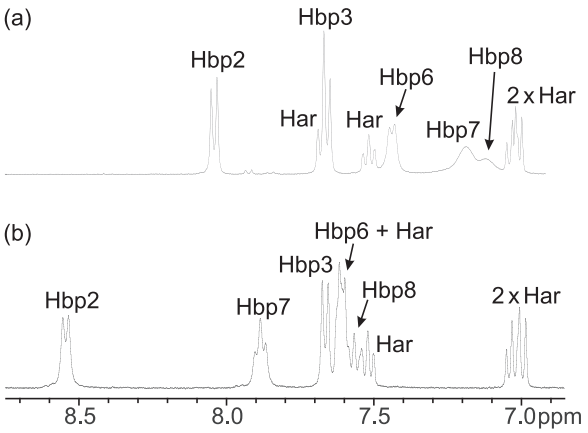


Fig. 15. Comparison of the downfield regions of the ^{1}H NMR spectra of (a) K[VO_2(salhybiph)@β-CD] and (b) K[VO_2(salhybiph)@(α-CD)$_2$] (for labeling cf. Scheme 11) [34,35].

nals relevant for supramolecular interactions within the host–guest assembly [35]. Nevertheless, since the overlapping proton resonances of the two α-CD rings cannot be assigned to individual moieties, the question arises whether a head-to-head dimer hosts the guest molecule similar to the solid state (see Fig. 12), or just a single α-CD ring is threaded on the biphenyl side chain with either orientation of the primary hydroxy side.

However, the presence of strong cross peaks between the proton signals of H-5 and bp2 as well as bp7 and bp8 clearly shows that a head-to-head arrangement of two α-CD rings must be present, with the biphenyl side chain of the guest molecule fully embedded in the host. This not only confirms the presence of a 1:2 inclusion compound in solution, but also shows the clear preference of the biphenyl side chain vs. the salicylidene moiety of the vanadium(V) complex to interact with the α-CD host cavity.

The concluded differences for the solution structure of the host–guest assemblies can further be corroborated by comparison of the ^{1}H NMR spectra of the inclusion compounds of K[VO_2(salhybiph)] with α-CD and β-CD depicted in Fig. 15 [35]. As expected for the resonances of the aromatic protons of the salicylidene moiety are unaffected, due to the absence of any interaction with the CD hosts. However, a notable difference is observed for the resonances of the protons located at both ends of the biphenyl side chain (bp2, bp7, and bp8), which are shifted far downfield for the α-CD inclusion compound K[VO_2(salhybiph)@(α-CD)$_2$]. This can be related to the difference in length of the two host cavities of the α-CD and β-CD inclusion compound and consistent with the presence of a head-to-head dimer host in the α-CD based assembly.

5. Conclusions

Vanadium(V) complexes based on the versatile *N*-salicylidene hydrazide ligand allow for the synthesis of a series of systems exhibiting hydrogen bonding interactions with vanadate species. This particularly includes the generation of appropriate hydrogen bonding relays for such systems. It should be noted here, that the observed transformation reactions for dioxidovanadium(V) complexes with *N*-salicylidene hydrazide ligands are somewhat reminiscent of what is usually observed for organic carboxylates. Therefore dioxidovandium(V) complexes can be regarded as their inorganic counterpart. Moreover, this approach also facilitates the design of host–guest compounds based on cyclodextrin (CD) giving access to supramolecular assemblies relevant for the modeling of vanadate in biological and potentially chiral matrices. The assignment of both the solution and the solid state structures is possible for such CD inclusion compounds, indicating preferences based on the utilized ring size of the CD. Whereas for the α-CD compound a host–guest ratio of 2:1 is observed with a head-to-head dimer of the host, a 1:1 stoichiometry is found for the β-CD case. An alternative variant to introduce chirality is given by the use of appropriate ligand scaffolds based on carbohydrates. Based on 6-aminoglucose it is possible to generate chiral vanadium(V) complexes which proof to be efficient sulfoxidation catalysts, but with only moderate enantioselectivity. Furthermore, the anisotropy effect of oxido groups on NMR chemical shifts for vanadium(V) complexes has been demonstrated to be an efficient tool to analyze configurations and conformations of chelate rings. This can be exemplified utilizing a vanadium(V) complex with a 6-aminoglucose-based Schiff-base ligand. In principle, this orientation dependence of the relevant coordination induced shifts is a versatile tool for solution structure assignments of oxidovanadium(V) complexes and possibly also other types of oxido metal complexes.

Acknowledgments

The generous support of this research initiative by the Deutsche Forschungsgemeinschaft is gratefully acknowledged. The results presented in this review are based on the engagement and outstanding skills of many co-workers which are named in the relevant literature citations.

References

[1] H. Sigel, A.E. Sigel (Eds.), Metal Ions in Biological Systems, vol. 31, Vanadium and its Role in Life, Marcel Dekker, New York, 1995.
[2] K. Kustin, J. Costa Pessoa, D.C. Crans (Eds.), Vanadium: The Versatile Metal, ACS Symposium Series 974, American Chemical Society, Washington, DC, 2007.
[3] D.C. Crans, J.J. Smee, E. Gaidamauskas, L. Yang, Chem. Rev. 104 (2004) 849.
[4] W. Plass, Angew. Chem. Int. Ed. Engl. 38 (1999) 909.
[5] M.V. Kirillova, M.L. Kuznetsov, J.A.L. da Silva, M.F.C.G. da Silva, J.J.R.F. da Silva, A.J.L. Pombeiro, Chem. Eur. J. 14 (2008) 1828.
[6] K.H. Thompson, J.H. McNeill, C. Orvig, Chem. Rev. 99 (1999) 2561.
[7] T. Hirao, Pure Appl. Chem. 77 (2005) 1539.
[8] J. Hartung, Pure Appl. Chem. 77 (2005) 1559.
[9] R. Wever, W. Hemrika, A. Messerschmidt, R. Huber, T. Poulos, K. Wieghardt, Handbook of Metalloproteins, vol. 2, Wiley, Chichester, 2001, p. 1417.
[10] R.R. Eady, Chem. Rev. 96 (1996) 3013.
[11] W. Plass, J. Mol. Struct. (THEOCHEM) 121 (1994) 53.
[12] M. Andersson, A. Willetts, S. Allenmark, J. Org. Chem. 62 (1997) 8455.
[13] H.B. ten Brink, H.E. Schoemaker, R. Wever, Eur. J. Biochem. 268 (2001) 132.
[14] V. Trevisan, M. Signoretto, S. Colonna, V. Pironti, G. Strukul, Angew. Chem. Int. Ed. 43 (2004) 4097.
[15] E. Wojaczyńska, J. Wojaczyński, Chem. Rev. 110 (2010) 4303.
[16] I. Fernández, N. Khiar, Chem. Rev. 103 (2003) 3651.
[17] M.C. Carreno, Chem. Rev. 95 (1995) 1717.
[18] T. Katsuki, Adv. Synth. Catal. 344 (2002) 131.
[19] S.A. Blum, R.G. Bergman, J.A. Ellman, J. Org. Chem. 68 (2003) 150.
[20] A. Korte, J. Legros, C. Bolm, Synlett (2004) 2397.
[21] C.O. Kinen, L.I. Rossi, R.H. de Rossi, Appl. Catal. A.: Gen. 312 (2006) 120.
[22] K.P. Bryliakov, E.P. Talsi, Chem. Eur. J. 13 (2007) 8045.
[23] M. Mancka, W. Plass, Inorg. Chem. Comm. 10 (2007) 677.
[24] W. Plass, Pure Appl. Chem. 81 (2009) 1229.
[25] W. Plass, M. Bangesh, S. Nica, A. Buchholz, ACS Symp. Ser. 974 (2007) 163.
[26] C. Bolm, Coord. Chem. Rev. 237 (2003) 245.
[27] S. Woodward, M. Diéguez, O. Pàmies, Coord. Chem. Rev. 254 (2010) 2007.
[28] P. Bortolus, G. Marconi, S. Monti, B. Mayer, G. Köhler, G. Grabner, Chem. Eur. J. 6 (2000) 1578.
[29] J. Szejtli, Chem. Rev. 98 (1998) 1743.
[30] K. Harata, Chem. Rev. 89 (1998) 1803.
[31] R. Breslow, S.D. Dong, Chem. Rev. 98 (1998) 1997.
[32] H. Sakuraba, H. Maekawa, J. Incl. Phenom. Macrocycl. Chem. 54 (2006) 41.
[33] F. Kramer, W. Dietsche, Chem. Ber. 92 (1959) 1739.
[34] I. Lippold, H. Görls, W. Plass, Eur. J. Inorg. Chem. (2007) 1487.
[35] I. Lippold, K. Vlay, H. Görls, W. Plass, J. Inorg. Biochem. 103 (2009) 480.
[36] Y. Liu, R.Q. Zhong, H.Y. Zhang, H.B. Song, Chem. Commun. (2005) 2211.
[37] G. Meister, H. Stoeckli-Evans, G. Süss-Fink, J. Organomet. Chem. 453 (1993) 249.
[38] B. Klingert, G. Rihs, J. Chem. Soc. Dalton Trans. (1991) 2749.
[39] Y. Odagaki, K. Hirotsu, T. Higuchi, A. Harada, S. Takahashi, J. Chem. Soc. Perkin Trans. 1 (1990) 1230.
[40] B. Klingert, G. Rihs, Organometallics 9 (1990) 1135.
[41] D.R. Alston, A.M.Z. Slawin, J.F. Stoddart, D.J. Williams, Angew. Chem. Int. Ed. Engl. 24 (1985) 786.
[42] W. Plass, Coord. Chem. Rev. 237 (2003) 205.

[43] A. Messerschmidt, R. Wever, Proc. Natl. Acad. Sci. U.S.A. 93 (1996) 392.
[44] M. Weyand, H.J. Hecht, M. Kiess, M.F. Liaud, H. Vilter, D. Schomburg, J. Mol. Biol. 293 (1999) 595.
[45] M.N. Isupov, A.R. Dalby, A.A. Brindley, Y. Izumi, T. Tanabe, G.N. Murshudov, J.A. Littlechild, J. Mol. Biol. 299 (2000) 1035.
[46] A. Messerschmidt, R. Wever, Inorg. Chim. Acta 273 (1998) 160.
[47] R. Renirie, W. Hemrika, S.R. Piersma, R. Wever, Biochemistry 39 (2000) 1133.
[48] C. Kimblin, X.H. Bu, A. Butler, Inorg. Chem. 41 (2002) 161.
[49] N. Tanaka, Z. Hasan, R. Wever, Inorg. Chim. Acta 356 (2003) 288.
[50] Z. Hasan, R. Renirie, R. Kerkman, H.J. Ruijssenaars, A.F. Hartog, R. Wever, J. Biol. Chem. 281 (2006) 9738.
[51] M. Bangesh, W. Plass, J. Mol. Struct. (THEOCHEM) 725 (2005) 163.
[52] J.Y. Kravitz, V.L. Pecoraro, Pure Appl. Chem. 77 (2005) 1595.
[53] S. Raugei, P. Carloni, J. Phys. Chem. B 110 (2006) 3747.
[54] X.-A. Zhang, M. Meuwly, W.-D. Woggon, J. Inorg. Biochem. 98 (2004) 1967.
[55] J. Becher, I. Seidel, W. Plass, D. Klemm, Tetrahedron 62 (2006) 5675.
[56] S. Nica, M. Rudolph, H. Görls, W. Plass, Inorg. Chim. Acta 360 (2007) 1743.
[57] S. Nica, A. Buchholz, M. Rudolph, A. Schweitzer, M. Wächtler, H. Breitzke, G. Buntkowsky, W. Plass, Eur. J. Inorg. Chem. (2008) 2350.
[58] A. Schweitzer, T. Gutmann, M. Wächtler, H. Breitzke, A. Buchholz, W. Plass, G. Buntkowsky, Solid State Nucl. Magn. Reson. 34 (2008) 52.
[59] R. Debel, A. Buchholz, W. Plass, Z. Anorg. Allg. Chem. 634 (2008) 2291.
[60] W. Plass, A. Pohlmann, H.-P. Yozgatli, J. Inorg. Biochem. 80 (2000) 181.
[61] W. Plass, H.-P. Yozgatli, Z. Anorg. Allg. Chem. 629 (2003) 65.
[62] S. Nica, A. Pohlmann, H. Görls, W. Plass, Acta Cryst. E63 (2007) m1450.
[63] A. Giacomelli, C. Floriani, A.O. de Souza Duarte, A. Chiesi-Villa, C. Guastini, Inorg. Chem. 21 (1982) 3310.
[64] S. Nica, A. Pohlmann, W. Plass, Eur. J. Inorg. Chem. (2005) 2032.
[65] A. Pohlmann, S. Nica, T.K.K. Luong, W. Plass, Inorg. Chem. Commun. 8 (2005) 289.
[66] A. Pohlmann, W. Plass, J. Inorg. Biochem. 86 (2001) 381.
[67] T. Gutmann, A. Schweitzer, M. Wächtler, H. Breitzke, A. Buchholz, W. Plass, G. Buntkowsky, Z. Phys. Chem. 222 (2008) 1389.
[68] A. Fenn, M. Wächtler, T. Gutmann, H. Breitzke, A. Buchholz, I. Lippold, W. Plass, G. Buntkowsky, Solid State NMR 36 (2009) 192.
[69] A. Messerschmidt, L. Prade, R. Wever, Biol. Chem. 378 (1997) 309.
[70] M. Diéguez, O. Pàmies, A. Ruiz, Y. Díaz, S. Castillón, C. Claver, Coord. Chem. Rev. 248 (2004) 2165.
[71] M. Diéguez, C. Claver, O. Pàmies, Eur. J. Org. Chem. (2007) 4621.
[72] S.A. Johannesen, B.O. Petersen, J.Ø. Duus, T. Skrydstrup, Inorg. Chem. 46 (2007) 4326.
[73] S. Yano, Coord. Chem. Rev. 92 (1988) 113.
[74] D. Steinborn, H. Junicke, Chem. Rev. 100 (2000) 4283.
[75] Y. Alexeev, I.S. Vasilchenko, B.I. Kharisov, L.M. Blanco, A.D. Garnovskii, Y. Zhdanov, J. Coord. Chem. 57 (2004) 1447.
[76] A. Roth, D. Koth, M. Gottschaldt, W. Plass, Cryst. Growth Des. 6 (2006) 2655.
[77] A. Burkhardt, W. Plass, Inorg. Chem. Commun. 11 (2008) 303.
[78] A. Burkhardt, H. Görls, W. Plass, Carbohydr. Res. 343 (2008) 1266.
[79] A. Burkhardt, E.T. Spielberg, S. Simon, H. Görls, A. Buchholz, W. Plass, Chem. Eur. J. 15 (2009) 1261.
[80] W. Plass, Coord. Chem. Rev. 253 (2009) 2286.
[81] J.C. Irvine, J.C. Earl, J. Chem. Soc. 121 (1922) 2376.
[82] A. Fragoso, M.L. Kahn, A. Castiñeiras, J.-P. Sutter, O. Kahn, R. Cao, Chem. Commun. (2000) 1547.
[83] J. Zhao, X. Zhou, A.M. Santos, E. Herdtweck, C.C. Romão, F.E. Kühn, Dalton Trans. (2003) 3736.
[84] A.K. Sah, T. Tanase, M. Mikuriya, Inorg. Chem. 45 (2006) 2083.
[85] A. Burkhardt, A. Buchholz, H. Görls, W. Plass, Eur. J. Inorg. Chem. (2006) 3400.
[86] A. Roth, J. Becher, C. Herrmann, H. Görls, G. Vaughan, M. Reiher, D. Klemm, W. Plass, Inorg. Chem. 45 (2006) 10066.
[87] A.K. Sah, C.P. Rao, P.K. Saarenketo, E. Wegelius, E. Kolehmainen, K. Rissanen, Eur. J. Inorg. Chem. (2001) 2773.
[88] A. Burkhardt, A. Buchholz, H. Görls, W. Plass, Acta Cryst. E63 (2007) 2527.
[89] A. Burkhardt, A. Buchholz, H. Görls, W. Plass, Acta Cryst. E63 (2007) 2994.
[90] A. Burkhardt, E.T. Spielberg, H. Görls, W. Plass, Inorg. Chem. 47 (2008) 2485.
[91] A.C.F. Ribeiro, A.J.M. Valente, V.M.M. Lobo, E.F.G. Azevedo, A.M. Amado, A.M.A. da Costa, M.L. Ramos, H.D. Burrows, J. Mol. Struct 703 (2004) 93.
[92] E.J. Baran, J. Inorg. Biochem. 103 (2009) 547.
[93] J. Costa Pessoa, I. Tomaz, R.T. Henriques, Inorg. Chim. Acta 356 (2003) 121.
[94] M.E. Cucciolito, R. Del Litto, G. Roviello, F. Ruffo, J. Mol. Catal. A: Chem. 236 (2005) 176.
[95] I. Lippold, J. Becher, D. Klemm, W. Plass, J. Mol. Catal. A: Chem 299 (2009) 12.
[96] D. Rehder, T. Polenova, M. Bühl, Annu. Rep. NMR Spectrosc. 62 (2007) 49.
[97] L. Pettersson, I. Andersson, A. Gorzsás, Coord. Chem. Rev. 237 (2003) 77.
[98] A.S. Tracey, Coord. Chem. Rev. 237 (2003) 113.
[99] J. Hartung, S. Drees, M. Greb, P. Schmidt, I. Svoboda, H. Fuess, A. Murso, D. Stalke, Eur. J. Org. Chem. (2003) 2388.
[100] C. Wikete, P. Wu, G. Zampella, L. De Gioia, G. Licini, D. Rehder, Inorg. Chem. 46 (2007) 196.
[101] W. Plass, Z. Anorg. Allg. Chem. 620 (1994) 1635.
[102] W. Plass, Inorg. Chim. Acta 244 (1996) 221.
[103] W. Plass, Z. Anorg. Allg. Chem. 623 (1997) 461.
[104] M. Schulz, R. Debel, H. Görls, W. Plass, M. Westerhausen, Inorg. Chim. Acta 365 (2011) 349.
[105] D.C. Crans, K.P. Shin, J. Am. Chem. Soc. 116 (1994) 1305.
[106] W. Plass, Eur. J. Inorg. Chem. (1998) 799.