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The Porphinoids – Versatile Biological Catalyst Molecules**

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Bernhard Kräutler was born in November 1946 in Dornbirn, Austria and studied chemistry at the ETH in Zürich; PhD under the guidance of Professor Albert Eschenmoser («An Electrochemical Simulation of the Light-induced A/D-Secocorrin-Corrin Cycloisomerization»); postdoctoral stays with Professors Allen J. Bard (Austin, Texas) and Nicholas J. Turro (Columbia University, New York); at the ETH Zürich since 1979, Oberassistent since 1982. In 1985 habilitation («Concerning the Biological Function of Vitamin B_{12} Derivatives: Relationships between Structure and Reactivity») and venia legendi for organic chemistry; fall 1985: visiting professor at the University of Illinois, Urbana. Lectures at the ETH Zürich on organic electrochemistry, radical chemistry, and natural products chemistry. Werner Prize 1987 of the Swiss Chemical Society.

The natural porphinoids, such as the iron complex heme, the magnesium complex chlorophyll a, the nickel complex coenzyme F430, and the (corrinoid) cobalt complex coenzyme B_{12}, play central roles in all spheres of life, e.g. as cofactors for oxygen or electron transport, for collecting light and transforming energy, and as catalysts in biosynthesis. – How the porphinoid structures developed in nature, how their often unique properties arise from special interactions between the bound metal ions and the macrocyclic ligands, and to which particular chemical reactivities and modes of action the porphinoids owe their specific biological functions – these are central questions to this topic. The latter ones lead ahead to the prospect that such properties might not only be beneficial to the living nature, but could be exploited profitably otherwise, be it by the use of porphinoid compounds as catalysts for synthesis, for the storage and conversion of energy, or for medical treatment. – For these reasons special attention has been given to the porphinoid metal complexes not only from the natural sciences, particularly from (organic and inorganic) chemistry and biology, but recently these molecules attract interest also in the areas of medicine and energy technology.

1. Introduction

The porphinoids[1,2], such as the red pigment of the blood[3] and the green pigments of the plants[4], typically are intensely coloured compounds, indispensable as catalysts in all spheres of life, and therefore have been referred to also as the «pigments of life»[5]. However, their ability to absorb visible light efficiently is not generally linked to their biological function[6], and occasionally is even harmful[7], although indeed exploited, e.g. by the plants and the photosynthesizing bacteria to trap solar irradiation[8]. The colour rather is an indication of the existence of low-lying electronically excited states of the porphinoid molecules[9], and (therefore also) of their readiness to engage in redox chemistry[1,10].

While the unsaturated ligands of the porphinoids themselves display exceptional and biologically important chemistry[11] (e.g. in photosynthesis[9,12]), a second dimension of reactivities arises from the binding of transition metal ions at the center of these ligands[13]. The porphyrin and the related corrin ligands are natural, two-dimensional chelate ligands, that bind metal ions in a kinetically and often thermodynamically inert way[13,14]. In a circular and generally nearly planar array four nucleophilic nitrogens surround a coordination hole with a diameter of ca. 4 Å[15].

The natural porphinoids derive from a common tetrapyrrolic precursor, the porphyrinogen **1** («uroporphyrinogen III»), which, in turn, is formed from the pyrrole porphobilinogen (**2**), itself biosynthesized by condensation of two molecules of δ-aminolevulinic acid (**3**, see Fig. 1)[16,17]. Porphobilinogen (**2**) and related pyrroles also tetramerize selectively under the influence of a weak acid in homogeneous solution[7], to form mixtures of isomeric porphyrinogens, of which, when formed under thermodynamic control, the unsymmetrical **1** indeed is the main constituent[18,19]. Remarkably, the enzymatically controlled assembly of **1** takes up considerable complexity to build up the very same unsym-

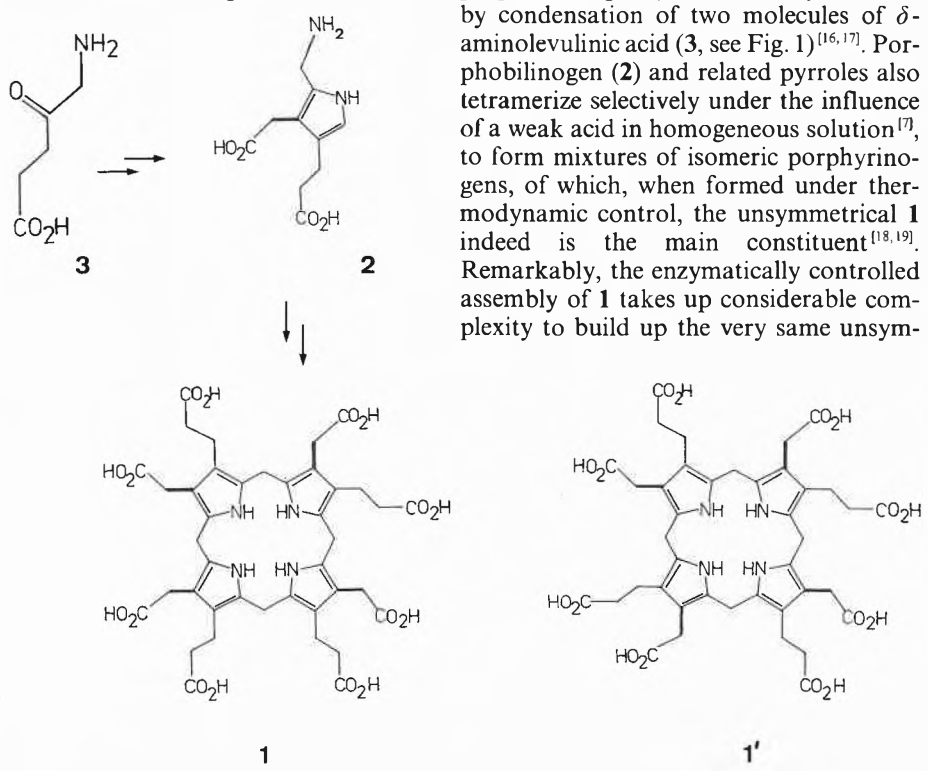

*Fig. 1. Elements of the biosynthesis of uroporphyrinogen III (**1**).*

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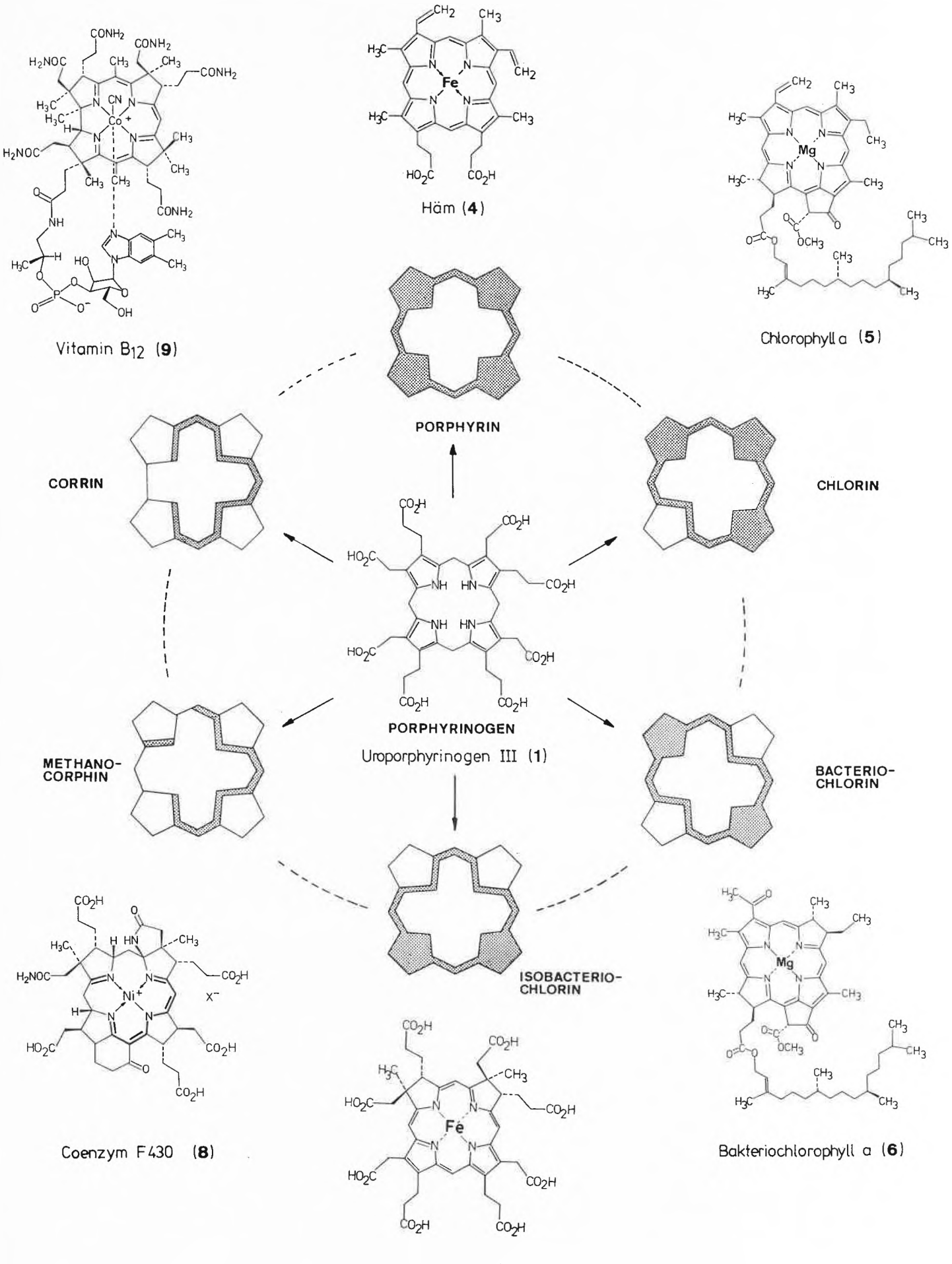

Fig. 2. From uroporphyrinogen III (1) to porphinoids and corrinoids.

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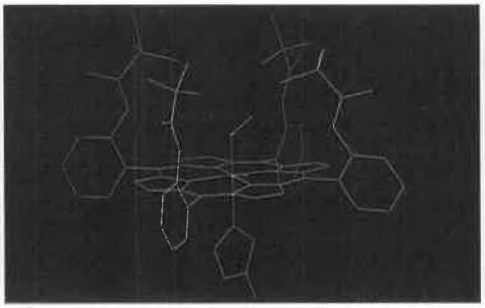

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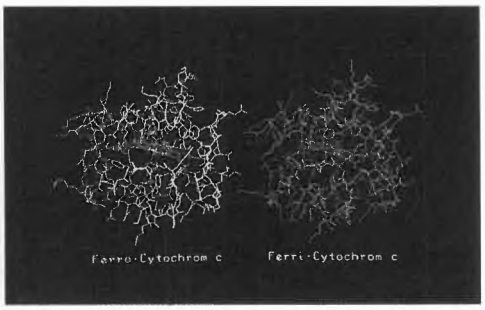

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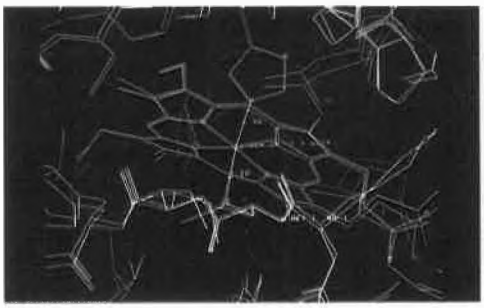

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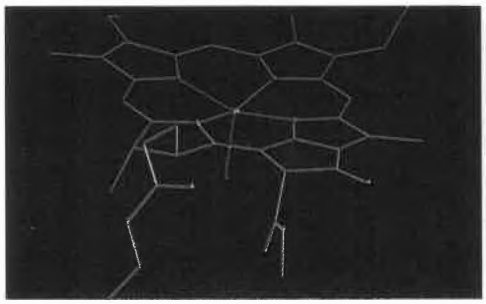

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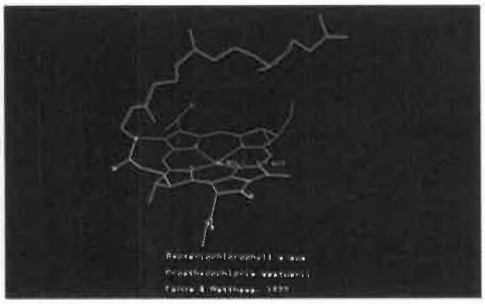

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These images are taken from one [38] of the 400 Evans & Sutherland Computer Graphics Systems installed in Europe.

Typical Configuration:

PS 390 Color Raster System
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Keyboard
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Fig. 11 was generously made available by
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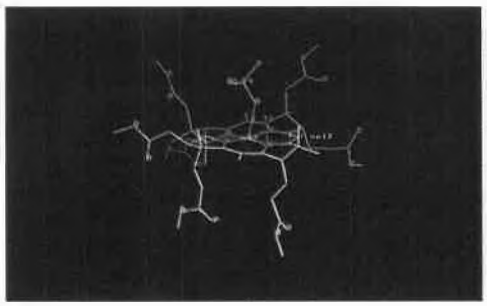

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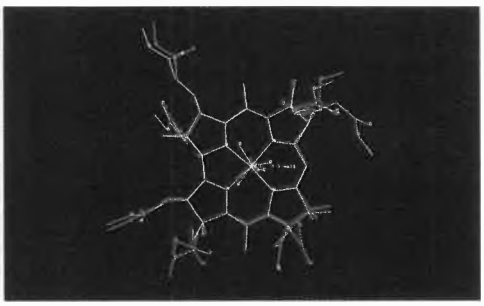

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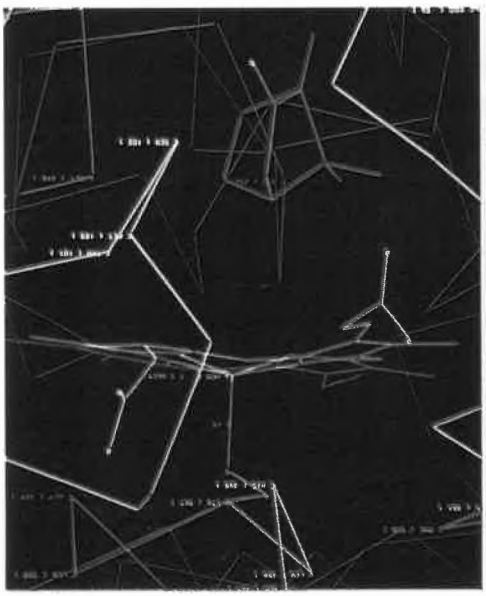

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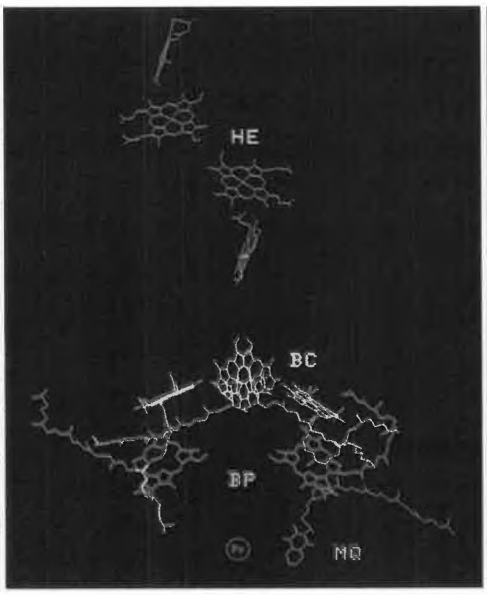

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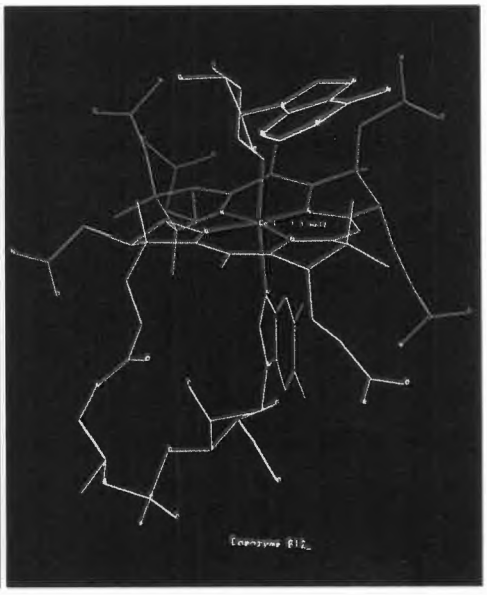

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Fig. 3. Collman's «picket-fence» porphyrin: three-dimensional structures of a) the deoxy form (iron(II)-(2-methylimidazole)-meso-tetra(pivalamido-phenyl)porphyrinate), and b) the oxygenated form (dioxygen-iron(II)-(1-methylimidazole)-meso-tetra(pivalamido-phenyl)porphyrinate) after the X-ray crystal structures [37] [in b) only one of four positions of the «end-on» bound dioxygen is shown].

Fig. 4. Cytochrome c: three-dimensional structures from X-ray analysis [43] of the iron(II)-form (left) and iron(III)-form (right) of the enzyme from tuna hearts: The heme prosthetic group is coordinated at iron by a histidine and a methionine residue, as well as at the porphyrin periphery via two sulfide bridges to cysteine residues.

Fig. 5. Comparison of three-dimensional structures of the active site of tuna ferrocytochrome c (blue/yellow) and of ferricytochrome c (red/green) based on the X-ray data [43] (covalent sulfide bonds to the heme were omitted).

Fig. 7. Cytochrome P-450 from Pseudomonas putida: three-dimensional structure based on the X-ray data from Poulos et al. [51]; a) integral ferri-form of the camphor binding enzyme (of the protein, the peptide backbone only is shown); b) active site segment with thiolate-bound heme (red/yellow) and camphor (dark blue).

Fig. 8. Three-dimensional molecular structures, as obtained from X-ray crystal data a) of ethyl chlorophyllide a (left) [63] and b) of bacteriochlorophyll a (right, taken from the analysis of the light-harvesting protein of the green photosynthesizing bacterium Prosthecochloris aestuarii; the axial ligand of the Mg^{II}-ion is a histidine-imidazole from the peptide envelope of the protein) [65].

Fig. 11. The reaction center chromophores of the purple photosynthesizing bacterium Rhodopseudomonas viridis: three-dimensional structure, as revealed by high resolution X-ray analysis [80] [colour code: bacteriochlorophyll b (BC) = yellow, bacteriopheophytin b (BP) = blue, hemes (HE) = brown, menaquinone (MQ) = purple, and an iron ion (FE) = red]; from the «special pair», in the center, two nearly symmetry-equivalent branches of BC and BP chromophores extend downward, but only the side that terminates with the quinone MQ is involved in light-induced electron transfer.

*Fig. 17b. Three-dimensional structure of coenzyme B_{12} (**17**), based on the X-ray crystal data [38,110c]; see also Fig. 17a (on p. 287).*

*Fig. 19b. The molecular structure of «Co^{II}-cobester» (**21**, Co_{β}-perchlorato-heptamethylcob(II)yrinate). a Co^{II}-corrinate derived from vitamin B_{12} [117]; see also Fig. 19a (on p. 288).*

*Fig. 20. Structural comparison between the Co^{III}-cobyrinate «cobester» (**22**) [38,118b] and its Co^{II}-derivative «Co^{II}-cobester» (**21**) [117]: Superposition of **21** (red) and **22** (blue); axial view.*

metrical **1** specifically, and not the chemically equal and more regular isomeric uroporphyrinogen I (**1'**)[16,17]: this has been pointed out as a striking indication of the preenzymatic origin of the structures of the porphinoid coenzymes[19,20].

The unsymmetric uroporphyrinogen III (**1**) is biological precursor of (inter alia) the iron porphyrinate heme (**4**), the magnesium chlorinate chlorophyll a (**5**), the magnesium bacteriochlorinate bacteriochlorophyll a (**6**), the iron isobacteriochlorinate siroheme (**7**), and the nickel corphinate coenzyme F430 (**8**), as well as of the cobalt corrinate vitamin B_{12} (**9**) (see Fig. 2)[16]. In comparison to the hexahydroporphinoid mother compound **1**, with 8 double bonds, the ligands of the porphyrins (such as **4**) and of the chlorophyll derivatives (such as **5** and **6**) are more highly oxidized, whereas the ligands of the corrin **9** and of the nickel corphinate **8** are more highly saturated and only contain 6 and 5 double bonds, respectively: In this way the degree of oxidation of the porphinoid ligand of the biosynthetic offspring of **1** apparently correlates with the evolutionary position of the organism that biosynthesizes it[20]. Furthermore, the hypothesis[20] has been experimentally verified[19] that appropriate simple precursors derived from HCN ($+NH_3$ + cyanoacetylene) can assemble in non-enzymatic reactions to porphyrinogens related to **1**. Remarkably, from there the other complex tetrapyrroles are postulated to be accessible in pre-enzymatic reactions also, even «protocobyric acid», an unmethylated forerunner of the corrin part of vitamin B_{12} (*Eschenmoser*[20,21]).

The structure of the macrocyclic tetrapyrroles allows for sufficient variability and gives access to such unparalleled, biologically important redox-, photo-, and coordination chemistry in the porphinoid (metal)complexes[1], that they have taken up central roles and are reproduced in all spheres of life[1,22]. Recently the view has been expanded that due to their stability and their readiness to form without enzymatic catalysis[19-21], porphinoid and corrinoid metal complexes represent «first hour» catalysts[19,23]. Their basic reactivities indeed need not be altered in the protein-bound state of porphinoid enzymes, but merely modulated to function optimally under physiological conditions[24]: for transport and storage of molecular oxygen, of electrons, and of methyl groups, in photosynthesis etc. as delineated in the following.

2. Porphinoid Iron Complexes

For a long time the red body fluid, blood, has been an object of scientific interest[25]. At the beginning of this century, the chemical nature of the organic part of heme (**4**), the red pigment of the blood, was more closely examined. An original structural suggestion by *Küster*[26] of a macrocyclic tetrapyrrole at first was refused[27], due to the presumed strain in such a large ring, but finally the basic structure of porphyrins was established by synthesis in *Hans Fischer*'s laboratory[28]. There also hemin was made available by total synthesis in 1928[29], mainly to provide proof of its earlier suggested structure of an iron complex of protoporphyrin[28].

Which are the special properties of iron porphyrins that enable them to play the role of cofactors in oxygen-carrying enzymes in humans, mammals, and other organisms? This question could not be answered easily at first, since in fluid solution molecular oxygen rapidly oxidizes Fe^{II}-porphyrins, such as heme (**4**), to the corresponding Fe^{III}-porphyrins[30]. To elucidate the structure of the heme proteins as oxygen carriers, pioneering X-ray crystallographic investigations were taken up around the middle of this century: the monomeric heme protein myoglobin yielded first (in 1960) to accurate X-ray analysis in *Kendrew*'s laboratory[31], followed by that of hemoglobin itself in *Perutz*'s[32]. Without going into the details of these studies, meanwhile treated in textbooks[33], I should like to return to the examination of the structural properties of the iron porphyrins themselves as potential carriers of molecular oxygen[30,34]. Amongst a series of attempts in the last three to four decades to find conditions where an iron porphyrin would function reversibly as oxygen carrier at room temperature in fluid solution, the first particular successful one was that of *Collman*[35]. In his laboratory the «picket-fence» porphyrin was synthesized[36], the iron complex of which could be reversibly oxygenated at room temperature in solution and whose oxygen-free high-spin and oxygenated diamagnetic Fe^{II}-forms could be crystallized. Their X-ray analyses show at high resolution pentacoordinate, square-pyramidal and hexacoordinate pseudo-octahedral Fe^{II}-centers, respectively (see Fig. 3)[37,38], qualitatively found similarly for the prosthetic groups in the heme proteins[39]. In the «picket-fence» porphyrin the sterically demanding pivalamide residues block one face of the iron porphyrin, still allowing the nearly unperturbed «end-on» binding[39c] of molecular oxygen, but leave room for the ligation of one imidazole ligand to the other axial site. Heme and similar Fe^{II}- (and Co^{II}-)porphyrins thus are inherently able to reversibly bind molecular oxygen to the porphyrin-bound metal center, and the most elementary function of the protein in oxygen-carrying heme proteins is now recognized to be the inhibition of the detrimental oxidation via μ-peroxo-Fe^{III}-porphyrin dimers[40].

The second important function of heme proteins is that of one-electron storage and transfer by the so-called cytochromes, e.g. in the respiratory chain, in photosynthesis, etc.[41]. The cytochromes c are the best studied ones, that have an electron-relay function in the respiratory chain (together with other cytochromes, labeled a, a_3, b, and c_1)[42]. The cytochromes c exist either in a diamagnetic Fe^{II}- or in a low-spin Fe^{III}-form. Independent of its oxidation state, the porphyrin-coordinated iron center is hexacoordinate, in pseudooctahedral environment, with axially binding histidine and methionine residues[41d] (see Fig. 4)[38,43]. The porphinoid prosthetic group is located at the periphery of the protein and is also covalently linked to the peptide via two cystein thiol groups. The one-electron redox process that interconverts the oxidized and the reduced forms of cytochrome c, is accompanied by only small geometrical changes at the iron center, of the porphyrin cofactor and even of the protein structure in the vicinity of the active site (see Fig. 5[41d,43]). According to the considerations of the Marcus theory on electron transfer reactions in solution[44] this could be a structural prerequisite for the rapid electron transfer observed[41c,44]. The one-electron redox properties of the cytochromes are those of the protein-bound heme, and are similar to those of other iron porphyrins[41,45]: the protein provides, among other factors, the axial ligation and the medium to modify thermodynamically and kinetically those of the prosthetic group, heme[45].

A third function of basic relevance of heme proteins arises from their ability to reductively activate coordinated oxygen for oxygenation reactions in oxygenating enzymes, such as monooxygenases and dioxygenases (as well as peroxidases)[46]. These widely distributed enzymes use molecular oxygen (or peroxides) to produce highly electrophilic oxygen species. Of them, the cytochromes P-450[47] are monooxygenases (i.e. enzymes that incorporate one oxygen atom from molecular oxygen) that have been particularly well studied. By introducing oxygen functions in «unactivated» hydrocarbon positions (e.g. in steroid biosynthesis) they have central roles as catalysts in metabolism[22]. The cytochrome P-450 from *Pseudomonas putida*[48] hydroxylates camphor with a striking regio- and stereo-selectivity at the 5-*exo* position, consuming molecular oxygen and the reducing equivalents of nicotinamide-adenine dinucleotide (NADH)[49]. Spectroscopic and kinetic investigations have provided evidence for the following mechanistic picture concerning the hydroxylation of camphor, catalyzed by the cytochrome P-450 camphor hydroxylase from *Ps. putida* (see Fig. 6)[49]: The resting state of the enzyme with a low-spin porphyrin-bound hexacoordinate Fe^{III}-center (A) is converted by the incorporation of a molecule of camphor into the high-spin state B, with pentacoordinate Fe^{III}. This activates the prosthetic group for the subsequent one-electron reduction by the iron-sulfur protein putidaredoxin to the ferroheme C, that coordinates one molecule of oxygen (D). A second one-electron reduction and a protonation lead to a hydroperoxo-Fe^{III}-porphyrin (E). Heterolysis (presumably induced by an electrophilic

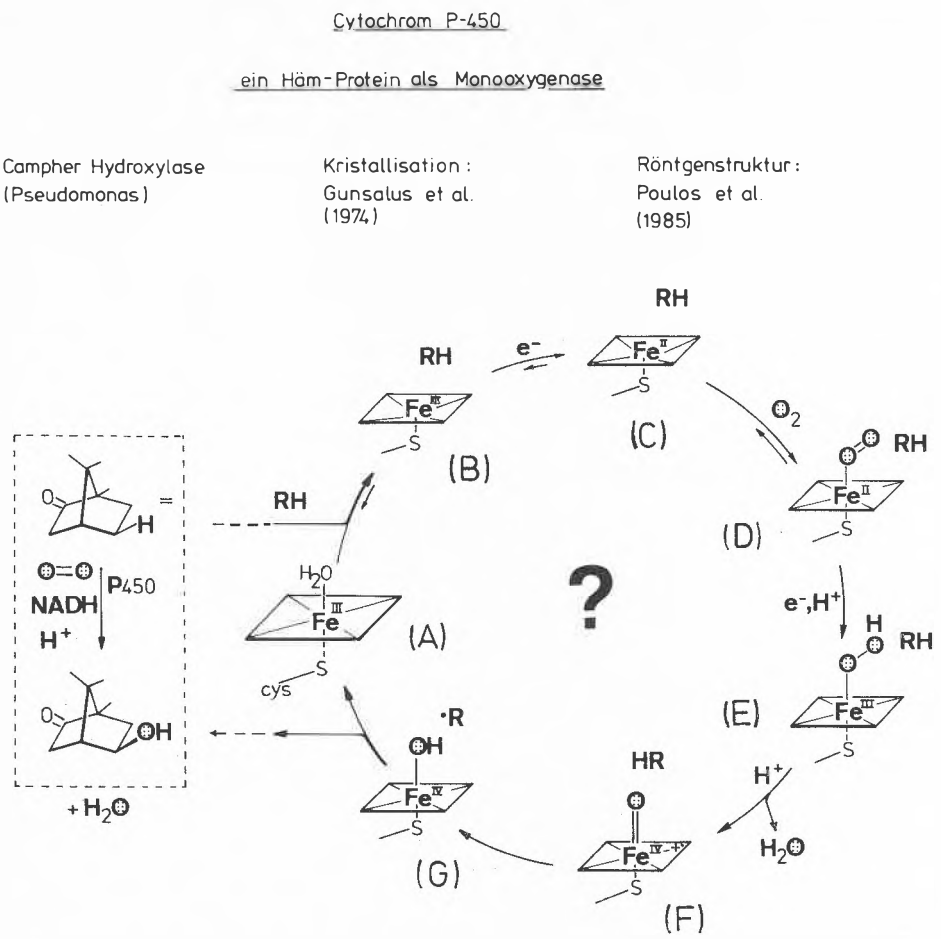


Fig. 6. The camphor hydroxylating cytochrome P-450 from Pseudomonas putida: Possible sequence of events in the enzyme-catalyzed hydroxylation of camphor in a schematic illustration [49].

species, such as a proton) produces the activated oxygenated species, to which the structure of the ferryl-porphyrin cation radical F is ascribed [50]. The electrophilic «oxenoid» oxygen ligand bound axially to the oxidized iron center (formal oxidation state + IV) abstracts the 5-*exo* hydrogen atom from the enzyme-bound substrate (→G). The 5-camphoryl radical, fleetingly formed by the stereoselective hydrogen abstraction [49b], in turn abstracts the iron-bound hydroxy group of G to give the hydroxylation product.

Due to high resolution X-ray determinations of the structure of camphor hydroxylase from *Ps. putida* by *Poulos* et al. [51], some of the unusual features of this cytochrome P-450 could be clarified (see Fig. 7): in the substrate binding high-spin Fe^{III}-form a molecule of camphor is bound inside the protein and properly oriented. The prosthetic group is bound, as had previously been suggested on the basis of UV/VIS spectra [52], via axial ligation of a cysteinyl thiol(ate) group to the pentacoordinate, square-pyramidal iron center. The 5-*exo* hydrogen atom of the substrate is oriented close to the position expected for an oxygen atom, axially bound to the free face of the iron center. The incorporation of the camphor molecule occurs without significant reorganization of the protein, as is shown by comparison with the structure of the substrate-free enzyme [51b]: In the latter (the enzyme in its resting state), water takes up the space otherwise occupied by the camphor molecule and provides the sixth ligand for the low-spin Fe^{III}-center.

Experiments with iron porphyrins, based on the *meso*-tetraphenylporphyrin skeleton, but also with e.g. chromium and manganese analogs, meanwhile have reproduced the basic reactivities of the cytochromes P-450, their ability to hydroxylate alkanes, to epoxidize alkenes, to reduce alkyl halides, etc. [50, 53]. While unusual regio- and stereo-selectivities have been achieved using sterically hindered metalloporphyrins [54], the selectivities and the efficiencies of the cytochromes P-450 are far from being reproduced. For these, the mutual orientation of the incorporated substrate and the iron-bound oxygen of the prosthetic group appear responsible, as recognized in the X-ray structures of the cytochrome from *Ps. putida* [51]. Another question to be solved with more apt model compounds concerns the role of the unusual and characteristic thiolate ligand of the protein-bound heme prosthetic group in the cytochromes P-450 [52, 55].

In the heme proteins, the iron-porphyrin prosthetic groups function as carriers of molecular oxygen and of electrons, and in concert with these two properties, they activate molecular oxygen in mono-oxygenation reactions. Related functions of the cofactor heme to that in the cytochromes P-450 appear in the cytochrome peroxidases, the peroxidases, the myeloperoxidases, and the catalases [56]. Still less investigated are the more recently discovered (and presumably mechanistically related) enzyme activities involving iron-porphinoid cofactors in nitrite and sulfite reducing bacteria, such as the siroheme **7** [57], and hemes d and d_1 [58].

3. Porphinoid Magnesium Complexes and Metal-Free Porphinoids

The second important role of porphinoid molecules in nature, which was early recognized, is commonly associated with the green pigments in the plants mainly. They participate in the conversion of the energy of solar irradiation into «chemical» energy, in «photosynthesis» [12, 59]. For this task, the basis for the production of «biomass» with the help of sunlight, plants, and photosynthesizing microbes make use of porphinoid pigments, that absorb visible light in the long wavelength range and which often are green coloured. The best known of these pigments, chlorophyll a (**5**), was isolated at the beginning of this century by *Willstätter* [60] and prepared by total synthesis, in 1960, by *Woodward* [61]. Chlorophyll a (**5**) is the magnesium complex of the dihydroporphyrin pheophorbide a, a chlorin in which the peripheral 17,18-positions of ring D are saturated. A fundamental consequence of the chlorin ligand structure is its ability to absorb low energy visible light: In a polar solvent chlorophyll a exhibits an absorbtion maximum at $\lambda = 660$ nm, near the wavelength of highest intensity of the solar spectrum [12, 62]. X-ray analysis of crystalline ethyl chlorophyllide a (in which the phytyl rest of **5** has been replaced by an ethyl group, see Fig. 8a) [63] informed on the detailed molecular structure and revealed in particular the specific intermolecular association that arranges the chlorophyll molecules in stacks, via axial coordination of a water molecule at the Mg^{II}-center.

In (green and purple) phototrophic bacteria, the related bacteriochlorophylls are the main pigments of the photosynthetic units. Bacteriochlorophyll a (**6**) is the magnesium complex of the tetrahydroporphyrin bacteriopheophorbide, a bacteriochlorin in which opposite rings B and D are saturated at the periphery; **6** absorbs at still longer wavelengths than chlorophyll a, namely at $\lambda = 770$ nm [64]. The three-dimensional structure of **6** can also be visualized due to X-ray analysis, which indicated a similar coordination of an axial ligand at the Mg^{II}-center, as with **5** (see Fig. 8b) [65].

The photosynthesizing machinery of bacteria is much simpler and meanwhile better known than that of the more noticed

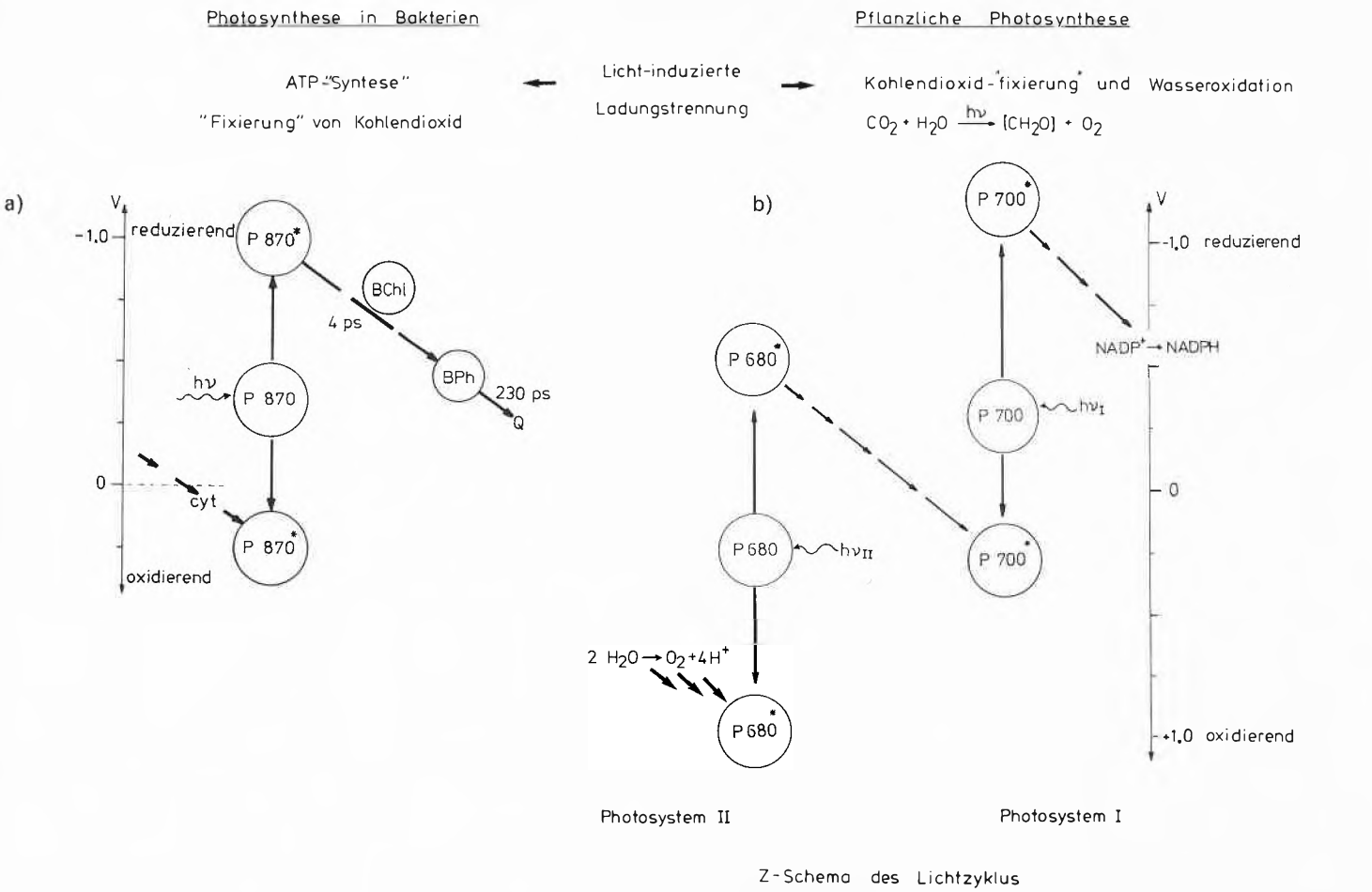


Fig. 9. The «first nanoseconds» of photosynthesis: light-induced charge separation in a) the reaction center of the purple bacterium Rhodopseudomonas spheroides [70] *[P870 = reaction center pigment («special pair»), BChl = bacteriochlorophyll a, BPh = bacteriopheophytin a, Q = ubiquinone, cyt = cytochrome]; b) Z-scheme of the photosynthesis in plants* [72]*: two reaction centers with photosystem I (special pigment P700) and photosystem II (special pigment P680) cooperate in photoinduced electron transfer reactions to oxidize water to molecular oxygen, and to produce reducing equivalents for the reduction of NADP to NADPH.*

plants[66]. Above all it has the task to transform the energy of the absorbed light into chemical energy, stored in adenosine triphosphate (ATP), and to a lesser extent (presumably only in green photosynthesizing bacteria[67a]), to induce the reduction of nicotinamide adenosine dinucleotide (NAD(P)) to the hydride NAD(P)H[67b].

Two important chemical phenomena come into play here[44]:

- Electronically excited pigments, such as the chlorophylls, are kinetically and thermodynamically efficient oxidizing and reducing agents[68].
- In contrast to the usual situation in organic chemistry (where more exergonic processes usually are more rapid) a «rate inversion» occurs with highly exergonic transitions from electronically excited states[69]: Deactivation from the excited state then generally occurs more rapidly via such paths (e.g. via electron transfer processes) that are accompanied by little transformation of electronic energy into thermal energy, rather than via those that cross over, with large structural changes, to a vibrationally highly excited electronic ground state.

Fig. 9a shall illustrate this, which schematically depicts the primary processes of the light-excited bacterial photoreaction center, as studied with the phototrophic purple bacterium *Rhodopseudomonas spheroides*[70]: The pigment P870 is a «special» bacteriochlorophyll whose structure will be analyzed below, that absorbs maximally at $\lambda = 870$ nm. Direct light excitation, or electronic energy transfer from the accessory pigments of the light-harvesting machinery, produce the excited pigment P870*, which donates an electron within 4 picoseconds to a (metal-free) bacteriopheophytin (BPh). In this process, a neighbouring bacteriochlorophyll (BChl) probably functions as a mediator[70c]. With a time constant of ca. 230 ps the reduced $BPh^{\ominus}$ delivers an electron to an ubiquinone molecule (Q). This rapid cascade of slightly exergonic electron transfer steps far outruns the seemingly energetically more favourable return to the ground state: the rereduction of the now oxidized $P870^{\oplus}$ by the reduced $BPh^{\ominus}$ or the quinone $Q^{\ominus}$ occur with time constants of only ca. 15 ns or ca. 70 ms, respectively. This amount of time is more than enough to have $P870^{\oplus}$ oxidize one (the nearest) of the hemes of the reaction center cytochrome (time constant 270 ns). In this way a charge-separated state is built up, with an oxidized heme and a reduced quinone.

Similar in organization, however more complex and less understood in detail, are the light-induced primary processes of the photoreaction center of the plants and cyanobacteria («blue-green algae»)[59d]. The photosynthesis of plants serves the light-driven reduction of NADP to NADPH mainly, for the «fixation» of carbon dioxide[71a], but also for the («photo»)-phosphorylation of ADP[71b]. Molecular oxygen thereby is liberated from the uncommon reducing agent water. To achieve this, two consecutive light-driven electron transfer sequences are needed, as illustrated in the «Z-scheme» (Fig. 9b)[72]. Two photosynthesis systems, PSI and PSII, act concertedly and following the same physical principles as seen with the bacterial photoreaction[70,73]. They contain the reaction center pigments P700 and P680, again named according to their light absorption characteristics. Again very rapid, slightly exergonic electron transfer processes, following the electronic excitation, induce and perpetuate the light-induced charge

separation. Indirect result of the cycle of light-induced processes is the reduction of NADP, and the oxidation of water with liberation of molecular oxygen. In a second, dark phase, the actual «CO_2-fixation» takes place, based on the reducing power of NADPH mainly[71b].

To date, in particular the structure and molecular function of the water oxidizing machinery supporting **PSII** is still unknown[74]. The nature of the central pigments P700 und P680 also still requires clarification: although different in their light absorption, redox, and ESR characteristics etc. in the intact photoreaction centers, apparently they are made up of «ordinary» chlorophyll a only. Work of *Katz* et al.[75], who studied association phenomena of chlorophylls in solution, helped uncover a unexpected structural model for the reaction center pigments: Based on the observed red shift of such associates in solution, as similarly known for the PSI pigment P700, they proposed the latter to be a pair of closely associated chlorophyll molecules (see Fig. 10)[75b,c]. In these «special pairs», the interactions in the electronically excited state should cause the red shift of the absorption maximum. Secondly, the enhanced oxidizability of P700 (compared to monomeric chlorophylls), as well as the ESR data, could also be rationalized by the distribution of the defect electron on two identical molecules in the «special pairs».

According to most of the presently available information the «special pair» model explains best the physicochemical properties of the pigment P700 and probably also of the other reaction center pigments of plants and phototrophic bacteria, such as P680, P870, etc.[75,76]: A series of experiments in *Katz*'s laboratory, as well as by *Closs* and *Boxer* and other groups, with covalently joined chlorophyll dimers, confirmed the ability of the «special pair» models to simulate the spectral and electrochemical properties of P700[77], as well as, furthermore, to undergo light-induced oxidation in the presence of suitable acceptor molecules[78].

A dramatic confirmation of the «special pair» model for the P870 in the reaction center of purple bacteria, and a general breakthrough in research on photosynthesis came about recently, when the intact reaction center protein of *Rhodopseudomonas viridis* ($M_r \approx 150000$) could be crystallized by *Michel*[79] and its structure determined by high resolution X-ray analysis with *Deisenhofer* and *Huber* (see Fig. 11)[80]: At the heart of the reaction center protein from this bacterium a «special pair», of bacteriochlorophyll b molecules is indeed found, flanked on each side by a second bacteriochlorophyll b (BC) and a bacteriopheophytin b (BP) molecule. The BP leads down to the acceptor quinone (MQ, a menaquinone) and an iron ion. From the central «special pair», a chain of four hemes extends into the opposite direction. According to the model, the quinone

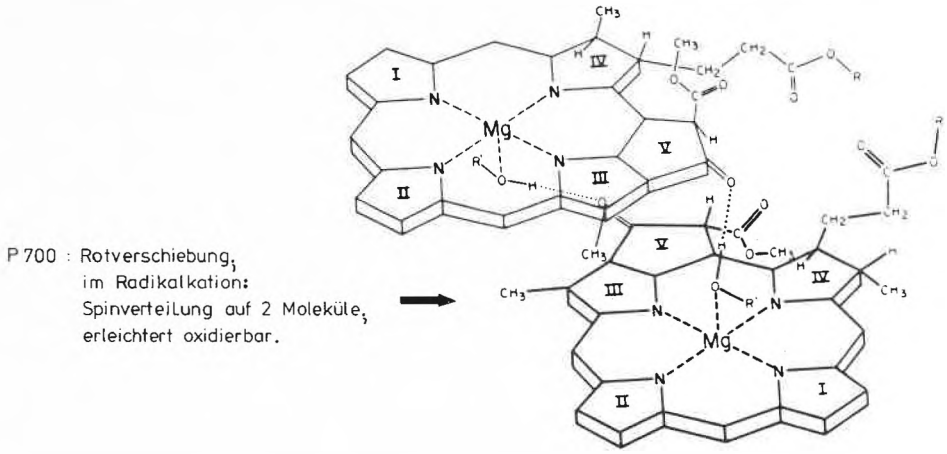


Fig. 10. The «special pair» model by Katz et al.[75] *for the reaction center pigment P700: via hydrogen bonds, two chlorophyll a molecules form a C_2-symmetric dimer.*

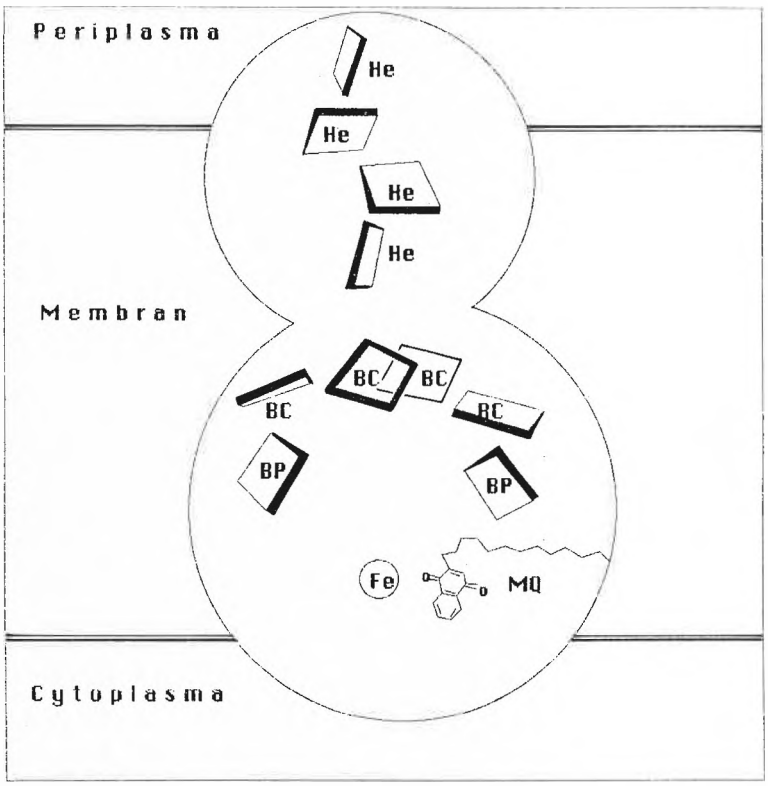


Fig. 12. Illustration of the presumed location of the reaction center chromophores of Rhodopseudomonas viridis in the photosynthetic membrane[80]*: The photoexcited «special pair» of BC-molecules is oxidized by BP with (a time constant of) 4 ps; the reduced BP reduces MQ with 230 ps; the hemes (He) finally furnish an electron to the oxidized BC-pair (with 270 ns); the role of the iron ion is not yet clear.*

is located at the outer surface of the photosynthetic membrane, while the terminal one of the four hemes presumably resides close to the inner membrane boundary (see Fig. 12)[67,80]. Except for the «special pair», the remaining porphinoid chromophores are all held by the surrounding protein in such a mutual orientation that the planes of neighbouring porphyrin units are nearly orthogonal.

In this manner, now also visualized structurally for the photoreaction center from *Rps. viridis*[80], the light-induced processes terminate with a charge separation across the photosynthetic membrane[67,70]. As a consequence of this and of the resulting perturbation of the acid-base equilibria, a gradient of proton activity is built up across the membrane. This is discharged via the membrane-bound ATP-synthetase complex with phosphorylation of ADP to ATP[81].

The structure determination of the reaction center of *Rps. viridis*[80], a milestone that stands out in the context of research on bacterial and plant photosynthesis,

(and lately also that of *Rps. spheroides*[82]) should help to understand the consequences of the spatial arrangement of the porphinoid chromophores on the rates of electron transfer. This is a current problem, not only in biological research on photosynthesis[59,83], but a general one in biological electron transfer[44,84]. Secondly, it represents an example, after which to model artificial systems for photosynthesis, of interest also as a means to use solar energy for the synthesis of «useful» chemicals («fuels»)[85]. Research concerned with such photoreactors can afford to center mostly around the problem of «supramolecular» organization, and can rely on the suitability of the (porphinoid) pigments for the purpose of photosynthesis. Indeed, it appears that the evolution of photosynthesis and the molecular photo(redox)reactivity of metal-free and magnesium-containing porphinoids are intimately mutually linked[86,87].

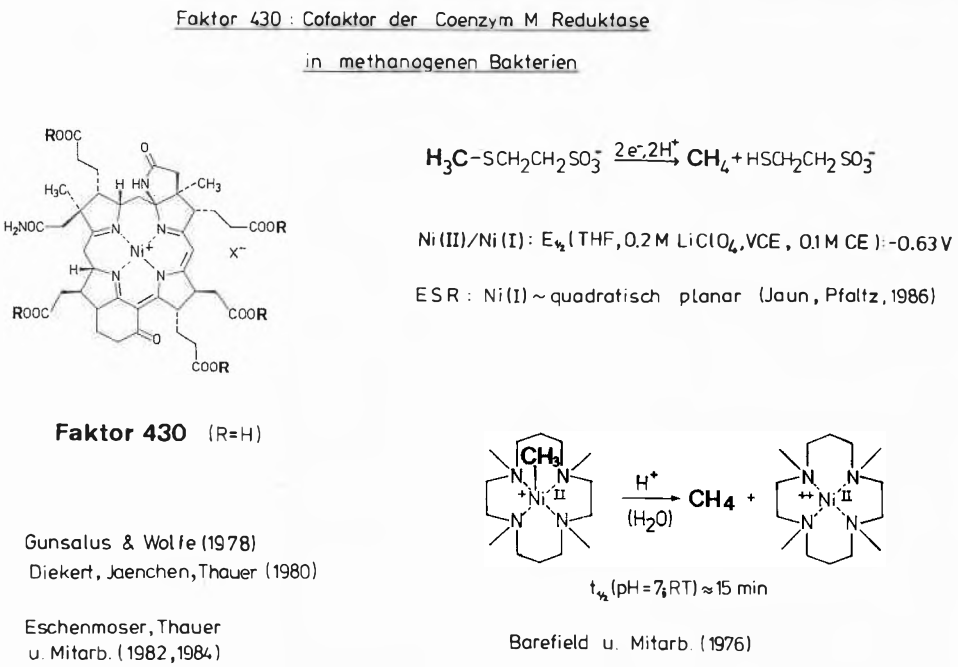
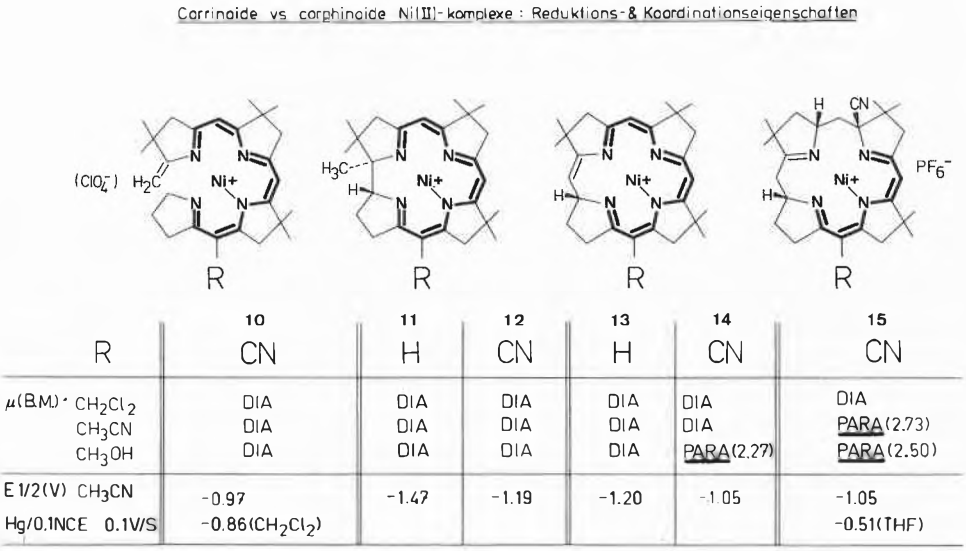


Fig. 13. Coenzyme F430: structure (left)[93], *enzymatic function*[95] *and redox properties*[99-101] *(right, top), and a reaction of potential model character (right, bottom)*[98].

4. Porphinoid Nickel Complexes

A new chapter on the chemistry of porphinoids was introduced only some five years ago, when the newly discovered yellow pigment factor 430[90] from methanogenic bacteria[91] was shown by *Thauer* et al.[92] to be a nickel-containing tetrapyrrol, and was structurally characterized by *Eschenmoser, Thauer, Pfaltz, Jaun* and others[93] as the Ni^{II}-tetrahydrocorphinate **8** (the pentamethylester **8M** was analyzed originally[93a], see Fig. 13). Factor 430 is the cofactor of one out of several newly discovered nickel-dependent enzymes[94] from the «primitive» methanogenic bacteria[91]. It could be identified in *Wolfe*'s group[95] as the coenzyme for the enzymatic cleavage of methyl coenzyme M (2-(methylthio)-ethanesulfonate) to methane (see Fig. 13). In this role in the central energy yielding process in methanogens[94,96] the cobalt methylated derivatives of vitamin B_{12} had been suspected earlier[97]. However, apparently the corrins are not unrivalled in metabolically important, organometallic chemistry: A new candidate for this unexplored area would appear on the scene with F430 (**8**). Indeed experiments with simple macrocylic tetraazanickel complexes have indicated their methyl-nickel derivatives to be demethylated easily in protic solvents with liberation of methane[98]. They could be taken as experimental examples hinting at the appropriate reactivity of the methyl-nickel(II) derivative of **8** as an intermediate in the reductive liberation of methane from methyl coenzyme M[98b].

To date, many of the particular chemical reactivities, that distinguish **8** for its biological role, remain to be clarified experimentally, however. Of the ones uncovered already at the ETH Zürich[99-101], the ease of the electrochemical one-electron reduction of the Ni^{II}-complex **8M** is noteworthy, which occurs at a half-wave potential of



	10	11	12	13	14	15
R	CN	H	CN	H	CN	CN
μ(B.M.) · CH_2Cl_2	DIA	DIA	DIA	DIA	DIA	DIA
CH_3CN	DIA	DIA	DIA	DIA	DIA	PARA(2.73)
CH_3OH	DIA	DIA	DIA	DIA	PARA(2.27)	PARA(2.50)
E 1/2(V) CH_3CN	-0.97	-1.47	-1.19	-1.20	-1.05	-1.05
Hg/0.1NCE 0.1V/S	-0.86(CH_2Cl_2)					-0.51(THF)

Fig. 14. Magnetic and electrochemical properties of the (seco)corrinoid Ni^{II}-complexes **10**, **11** *and* **12**, *of the Ni^{II}-dihydrocorphinates* **13** *and* **14**, *and of the Ni^{II}-tetrahydrocorphinate* **15**, *a model for coenzyme F430*[99,103].

$E_{½} = -0.63$ V (vs. 0.1 N calomel electrode); secondly, the high axial electrophilicity of the d^8 nickel(II)-center in **8**, which has a high tendency to bind solvent molecules axially[99]. Together with ESR-spectroscopic studies by *Jaun*[101], that confirmed the one-electron reduction product of **8M** in tetrahydrofuran to have the structure of a tetracoordinate Ni^{I}-complex, the low reduction potential reflects the electrophilicity of the metal center and its correspondingly expected high tendency for reduction. The ease of such a presumably rather nucleophilic metal center to come about by reduction of **8** and to become methylated at nickel could at present be understood as the most relevant reactivities for the coenzymic activity of factor 430.

A series of experiments from this laboratory with model compounds of **8**[93b,102], that originally were designed to help establish the nature of the chromophoric unit of F430, revealed the exceptional redox and coordination chemistry of such nickel complexes (see Fig. 14)[99,102]. There, the size of the coordination hole provided by the cyclic ligand, was found to have a profound influence in these respects: The 16-membered ligands in the hydroporphinoid nickel complexes **8** and its models provide a weak equatorial ligand field only, which results in an easily reduced nickel(II)-center, with high-spin electronic configuration in methanol, due to the axial coordination of solvent molecules. In contrast, the stronger ligand field of the 15-membered

corrin ligand, or the flexible secocorrin ligand of **10** saturate the coordination tendencies of Ni^{II} in such a way, that it has little demand to bind ligands axially: in all solvents investigated, diamagnetic complexes are found. The ease and the site of the one-electron reduction of such Ni^{II}-complexes correspondingly depends on the nature of the equatorial ligand in a remarkable way: in contrast to the easily reduced nickel tetrahydrocorphinates **8** and **15**, the corresponding corrinates **11** and **12** take up an electron at more negative electrode potentials (and possibly not at the central metal, but into the ligand π-system)[103]. Secondly, as exemplified by the behaviour of the synthetic compounds with a cyano substituent at C-15[99,103], the electrophilic and unusual cyclic-ketone function at the same position in **8** would help to decrease further the already weak equatorial ligand field of the large hydroporphinoid ligand of F430.

X-ray analyses by *Kratky* (Graz) have beautifully helped to visualize the misfit of the size of the coordination hole of the decahydroporphinoid ligand of **8** and of the ionic radius of the low-spin Ni^{II}-ion (ca. 1.88 Å): The tetracoordinate low-spin Ni^{II}-center in the model **16** is equatorially surrounded by a contracted, strongly ruffled ligand, with short metal-nitrogen bonds (average 1.90 Å). In the roughly corresponding high-spin complex **15** (hexacoordinate and dimeric in the crystal), the axial ligation apparently blows up the ionic radius of the metal ion, so that the longer Ni–N bonds (2.09 Å) correspond rather better to the hole of the unstrained, flat ligand (see Fig. 15)[99]. In the low-spin form of **8**, the strain induced by the misfit of the tetrahydrocorphin ligand to the metal center, makes it behave as a «loaded spring». Unlike the situation in Ni^{II}-corrins (such as **11** and **12**), that contain an axially rather «sterile» metal center, in **8** therefore axial reactivity is provided by the drive to match by ligation, the ionic radius of the (then high-spin) Ni^{II}-center to that of the equatorial ligand.

The crucial mutual adaptation of the coordination radii of the central metal and

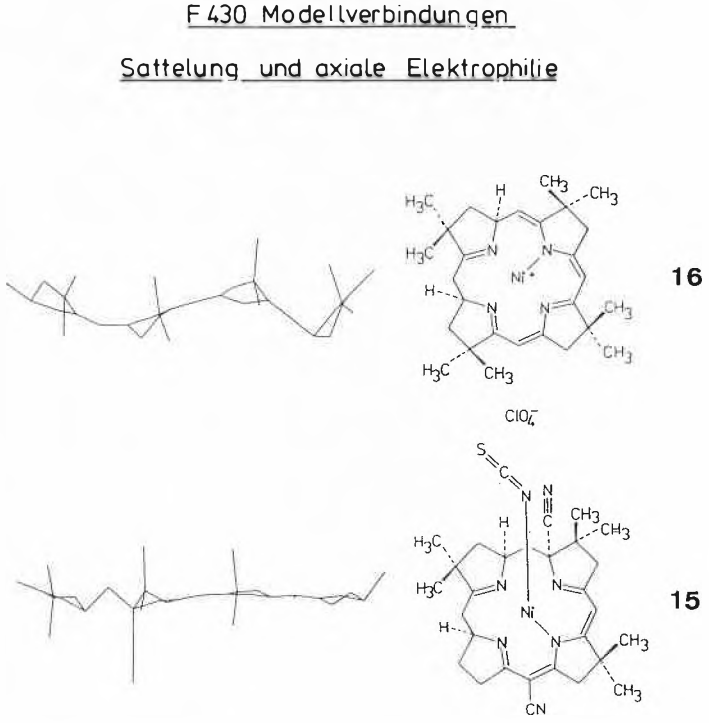


Fig. 15. Effect of high-spin/low-spin transition on the ligand pucker of Ni^{II}-tetrahydrocorphins, models for coenzyme F430: Cylindrical projections of the ligand in the low-spin Ni^{II}-complex **16** *and the high-spin Ni^{II}-complex* **15**[99].

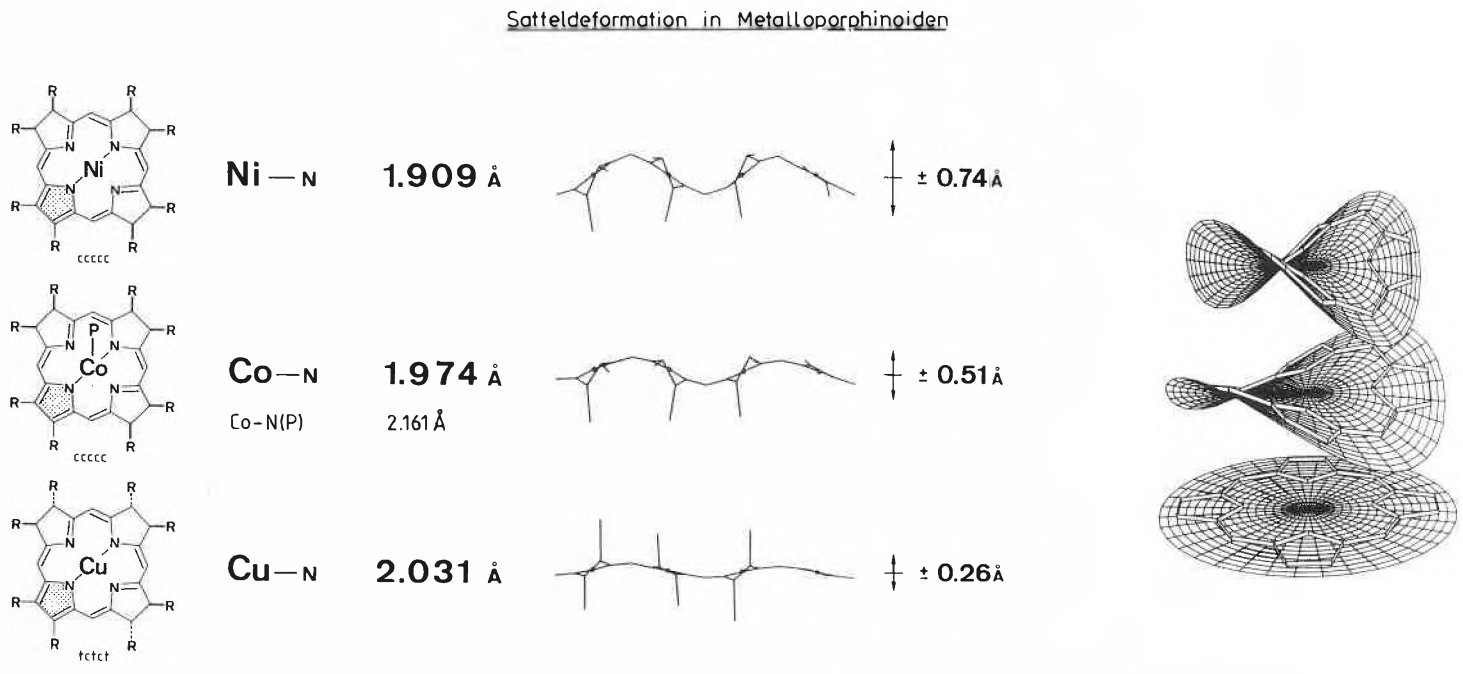


Fig. 16. Saddle-deformation due to ligand contraction in Cu^{II}-, Co^{II}-, and low-spin Ni^{II}-complexes of the hexahydroporphyrin pyrrocorphin; a correlation between the equatorial metal-nitrogen bond lengths and the ligand pucker, based on X-ray crystal data and visualized by cylindrical projections[100,104].

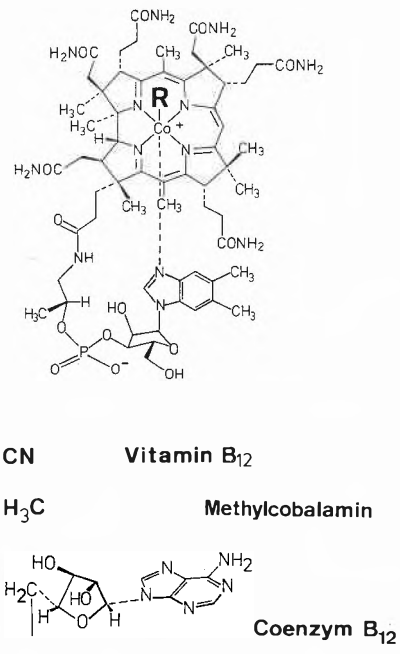


*Fig. 17a. Structural formulae of vitamin B_{12} (**9**), coenzyme B_{12} (**17**), and methylcobalamin (**23**).*

the (hydro)porphinoid ligands has been systematically investigated at the ETH Zürich, in cooperation with the group in Graz[100,104]: In the consistent series of the Cu^{II}-, Co^{II}-, and low-spin Ni^{II}-complexes of the hexahydroporphinoid pyrrocorphin ligand, the decreasing radius of the metal ion is paralleled by a successive increase of the nonplanarity of the ligand, as revealed by X-ray analyses (see Fig. 16). The observed deformation towards a saddle-shaped ligand can be traced back to a contraction of the metal-nitrogen bonds in the equatorial plane, a basic mode of deformation of porphinoid ligands, according to a factor analysis[105].

In this way, the (mis)fit of the coordination tendencies of the metal and the central hole of the nearly two-dimensional cyclic porphinoid ligands can induce conformationally controlled ruffling of the ligand and exerts (stereo)electronic and steric control in the axial direction. At the end of such a development, from the porphinoids the more complex corrinoids are accessible by ligand contraction[21,100] and, along with that, a step further into the third dimension.

5. Corrinoid Cobalt Complexes

About 40 years ago, the red cobalt complex vitamin B_{12} (**9**) was discovered[106], as the «antipernicious» factor in liver. Its structure was determined some 7 years later, largely by X-ray analysis in the laboratory of *Hodgkin*[107]. In it the novel corrin ligand was discovered and the unique intramolecularly coordinating nucleotide loop, that together form a three-dimensional frame to hold the Co^{III}-center of the vitamin. About 10 years ago, also the conquest of the structure of **9** by total synthesis in the laboratories of *Eschenmoser* and of *Woodward* was accomplished in a joint effort[108,109].

A coenzyme form of vitamin B_{12}, coenzyme B_{12} (**17**), was isolated in 1959 and proved (again by X-ray analysis, see Fig. 17)[110] to carry a cobalt-bound 5'-deoxyadenosyl group, thus to be an organometallic compound, that remarkably does not hydrolyze under physiological conditions. Coenzyme B_{12} catalyzes a series of complex enzymatic rearrangement reactions[111a] and a form of ribonucleotide reduction[111b]. One of these, that is essential in the human metabolism also, is the isomerization of (*R*)-methylmalonyl-CoA (**18**) to succinyl-CoA (**19**, see Fig. 18)[112]. In this rearrangement, a hydrogen atom of the methyl group and the thioester function of **18** exchange their positions in a pseudointramolecular fashion and with formation of **19**[113]. The mechanism of this rearrangement is not known, but the experimental information accumulated so far supports the hypothesis that it occurs via a radical reaction, induced by the protein-bound coenzyme **17**[111a,112,114].

The 5'-deoxyadenosyl radical, liberated from **17** by homolysis of the Co–C bond, is believed to trigger the rearrangement reactions by hydrogen atom abstraction from the substrate. The relevant reactivity of the coenzyme **17** for this function apparently then is its ability to homolytically cleave its unique organometallic bond, in particular when activated to do so when bound to the apoenzyme in presence of the substrate[115]. Experiments in aqueous solution indeed indicate **17** to cleave readily into the organic radical and cob(II)alamin (**20**), with a bond dissociation energy of only ca. 30 kcal/mol[116]. However, the enzyme-catalyzed process proceeds at a rate at room temperature, that exceeds the rate of the homolysis in homogeneous solution by a factor of $\geqslant 10^{10}$. The question thus remains, of how the Co–C bond homolysis can be accelerated that much under the influence of the protein[116]. The factors that help to stabilize the state with enzyme-bound homolysis products, compared to that before Co–C bond cleavage, should be of relevance in this respect. Therefore, knowledge of the structure of the cob(II)-alamin fragment **20** would be welcome.

A contribution to this question we could recently furnish by crystallizing the Co^{II}-corrin **21** and by elucidating the crystal

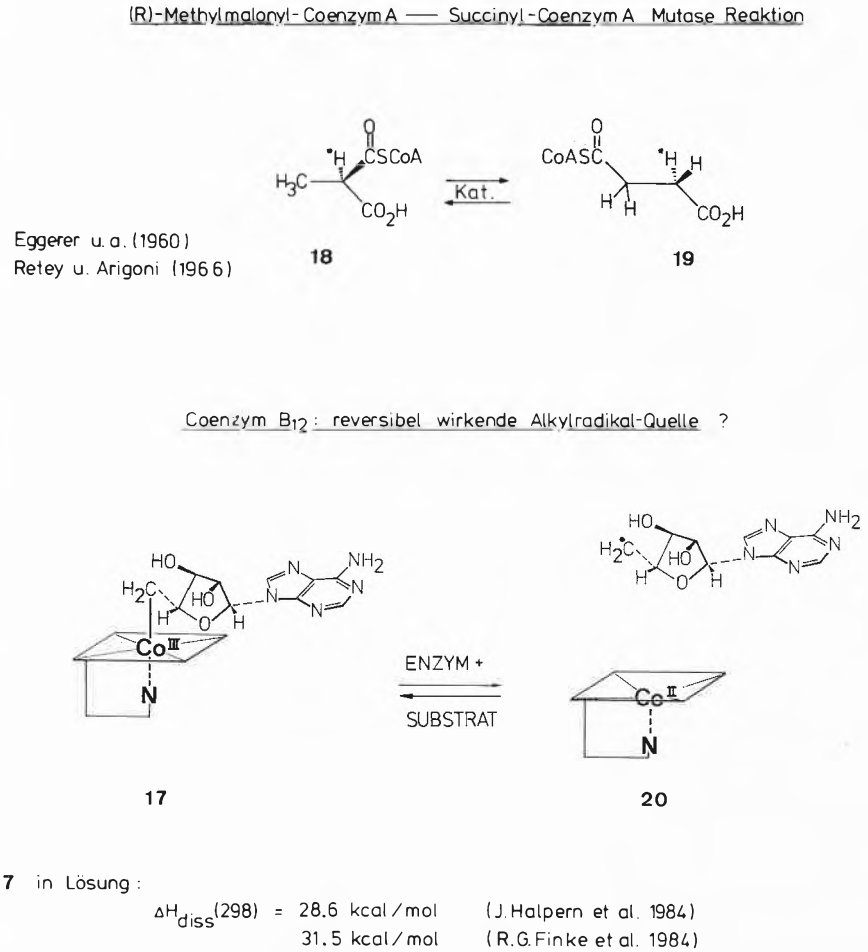


Fig. 18. Top: the (R)-methylmalonyl-coenzyme A to succinyl-coenzyme A rearrangement, a coenzyme B_{12} catalyzed isomerization[113]; bottom: the Co–C bond homolysis as biologically relevant reactivity of coenzyme B_{12}[114–116].

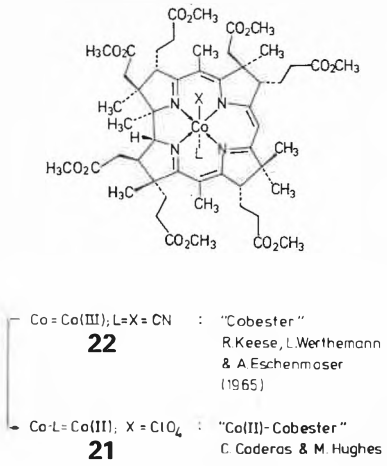


Fig. 19a. Structural formula of «Co^{II}-cobester» **21**.

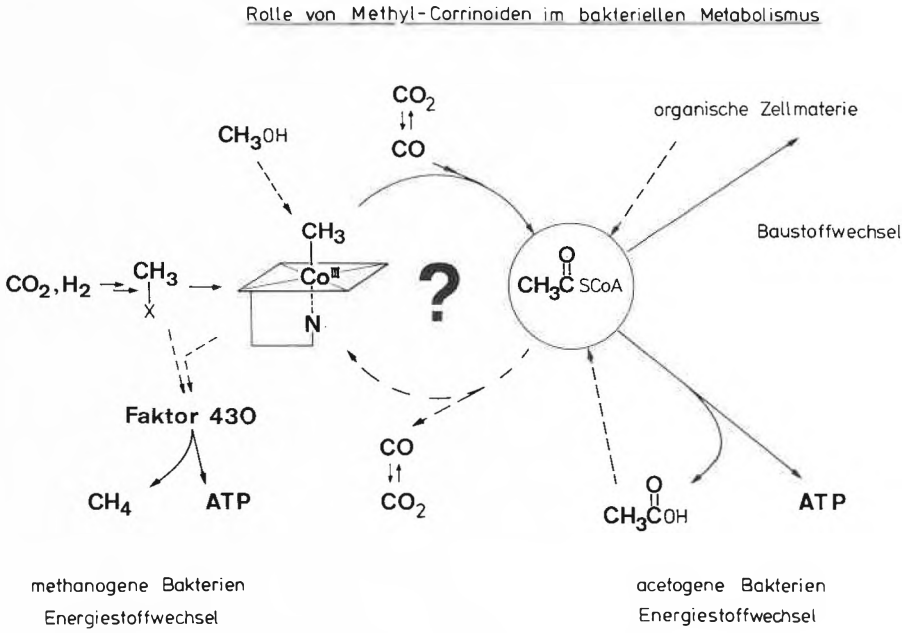


Fig. 21. Methyl-corrinoids in bacterial metabolism: Their hypothetical central role in the C–C bond forming step of the CO_2-fixation via acetyl-coenzyme A and in the C–C cleavage of acetate catabolism (degradation to methane) in methanogens supplied with acetic acid.

structure of it due to a collaboration with *Kratky*'s group in Graz (see Fig. 19)[117]. The cob(II)yrinate **21**, that crystallized as the perchlorate salt, could be obtained by reduction of the vitamin B_{12} methanolysis product «cobester» (**22**, dicyano-heptamethylcobyrinate)[118] with formic acid[119]. The X-ray analysis confirmed our earlier assumption[119] that in Co^{II}-corrins lacking the nucleotide function of the coenzyme **17**, such as **21**, the presumably pentacoordinate Co^{II}-center may preferentially carry the fifth ligand on the upper of the two diastereotopic faces. This is of interest, since in cob(II)alamin (**20**), in all probability, the intramolecularly coordinating nucleotide function would coordinate from the bottom face. Furthermore the X-ray analysis of **21** indicates, that the transition Co^{III}→Co^{II} hardly affects the cobalt-corrin portion of the molecule (in-plane binding of the pentacoordinate Co^{II}-center approximately conserved, length of the equatorial Co–N bonds not changed), as is shown by a comparison of the structures of the Co^{III}-corrin **22** and its reduction product **21** (see Fig. 20). Such a conservation of the geometry of the cobalt-corrin fragment would presumably be a factor in support of particularly low activation barriers in radical bond formation and cleavage reactions at cobalt. Except for by a change of bond lengths of the axially binding ligand(s), on the other hand, the information from the X-ray analysis does not help to visualize how steric deformations[120] should contribute to the presumed enhancement of the rate of Co–C bond homolysis[116] of the protein-bound coenzyme **17** in the enzyme-catalyzed reactions.

A second organometallic B_{12} derivative methylcob(III)alamin (**23**)[121], with a cobalt-bound methyl group (see Fig. 17), was isolated from natural sources about 25 years ago[122a], shortly after having become available (as the simplest organometallic derivative of vitamin B_{12}) by partial synthesis[122b,c]. Methyl-corrinoids, such as **23**, hold several fundamental functions in human, animal, and bacterial metabolism[123]: Firstly, **23** serves in the human metabolism (also) as an intermediate stage in the methylation of homocysteine to methionine and (on the occasion) demethylation of N^5-methyl-tetrahydrofolate[124]. Secondly, methyl-corrinoids, such as **23**, are involved in methyl group transport in methanogenic bacteria, indirectly therefore in the synthesis of methane[125,126]. Thirdly, methyl-corrinoids, such as **23**, are intermediate stages in the bacterial fixation of carbon dioxide via acetyl-coenzyme A (see Fig. 21)[127]. In the central metabolic C–C bond forming step, the cobalt-bound methyl group of **23** is incorporated intact into the methyl group of acetyl-CoA, via an as yet unknown carbonylation reaction[128]. A direct carbonylation of **23**[94a,128] was shown to be feasible chemically by assembly of the acetyl group via a radical reaction[123b,129,130].

Methyl-corrinoids thus have fundamental biological importance in the transport of methyl groups. Interestingly, the methyl group transport from methyl-tetrahydrofolate to homocysteine formally involves a «$CH_3^{\oplus}$», the methyl group abstraction by electrophiles a «$CH_3^{\ominus}$», and a radicaloid formation[129] of the acetyl group a «$CH_3^{\odot}$». Formal examples for the three types of transport of the cobalt-bound methyl group of **23** could be examined[131] with the corresponding nucleotide-free Co^{I}- and Co^{II}-cobinamides **25a** and **25b**, respectively, as CH_3-acceptors (and supplemented with the result of a study[132] with the cob(III)inamide **25c**): At room temperature, the cobalt-bound methyl group rapidly equilibrates between the cobalamins and the nucleotide-free cobinamides in deaerated aqueous solution (see Fig. 22)[131b]. In addition, from the analysis of the equilibria of such methyl group transfers, the influence of the nucleotide function on the Co–CH_3 bond strengths can be determined[131]. This appeared of particular interest, as the nucleotide functionality in the corrinoids is unique in nature, which has come up with considerable structural variety for it (see next paragraph). Clearly the nucleotide coordination in **23** strengthens the Co–CH_3 bond against methyl abstraction (formally as $CH_3^{\oplus}$) by the nucleophilic Co^{I}-corrin **25a**, hardly influences the Co–CH_3 bond in a homolytic abstraction (by **25b**), and weakens[132] it for the transfer (formally as $CH_3^{\ominus}$) to an electrophilic acceptor (such as **25c**). These considerable («trans») effects of the nucleotide coordination on the homolytic and heterolytic Co–C bond dissociation energies in methylcobalamin can in turn be correlated with the strength of the nucleotide coordination at cobalt[131]. Likewise, in coenzyme B_{12} the nucleotide coordination can be analyzed to slightly weaken the Co–C bond towards homolysis[131b], while in related organocobalamins carrying more bulky alkyl groups it causes a rate enhancement of $> 10^3$[133].

As concerns the variety of nucleotide bases[123,134] of natural corrinoids, the B_{12}-content of a series of bacteria has been examined with *Stupperich*'s group (Ulm) (see Fig. 23)[134b]. The information obtained at present shows that, e.g. among the methanogenic bacteria (apparently specific to each bacterial genus), the corrinoids (analog B_{12}) differ by the constitution of the nucleotide function (e.g. 5-hydroxybenzimidazole and adenine). Such a structural variation of a central cofactor is unusual, in particular since the corrinoids presum-

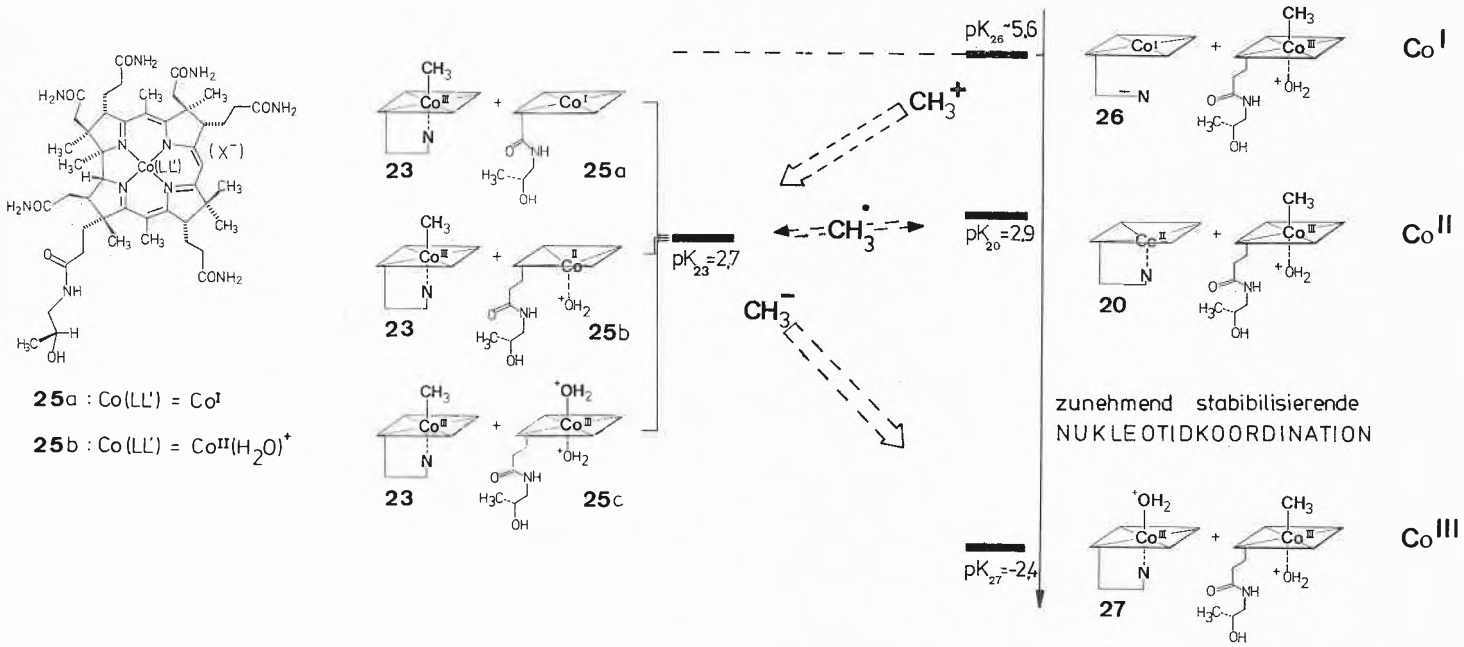


*Fig. 22. Effect of the nucleotide coordination in methylcobalamin (**23**) on homolytic and heterolytic Co–C bond dissociation energies [131]; methyl-transfer equilibria involving cobalamins and cobinamides.*

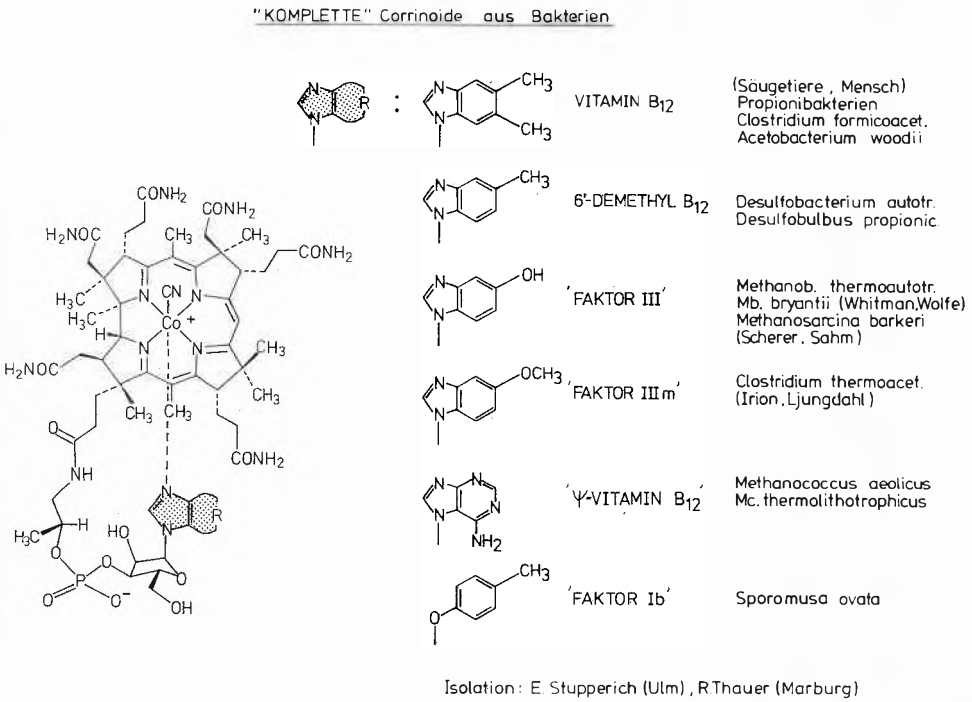


Fig. 23. Variability of the nucleotide portion of «complete» corrinoids from bacteria (as analyzed via Co$_\beta$-cyano complexes) [134].

ably have similar function(s), not only in methanogens, but also in acetogenic bacteria[127].

The corrins hold a special place in nature as biosynthesis catalysts. As they are synthesized by (the «primitive») microbes only, higher organisms have depended on these for their supply of the «vitamins». Apparently the organometallic properties of the corrins provide an unparalleled series of biologically important reactivities: Organocorrins (such as **17**) are stable towards physiological Brønsted acids (unlike organonickel complexes), but act as a source of organic radicals; the Co^{II}-corrins (as **20**) are excellent radical traps, and the Co^{I}-corrins highly nucleophilic (and nucleofugic) metal complexes (as well as possibly[126] one-electron reducing agents).

In the nucleotide containing (i.e. «complete») corrinoids (such as **9**, **17**, **23**, etc.), the unique structure of the ring-contracted, reduced corrin ligand is combined with an intramolecularly coordinating nucleotide function in an unparalleled way for low molecular weight natural products[135]. While considerable effects of the nucleotide coordination on the organometallic and redox properties of corrins have been determined (see e.g.[131–133]), the particular corresponding consequences of the corrin ligand remain to be clarified. Indeed, in contrast to the presumed flexibility[120] of the corrin ring (as opposed e.g. to that of the porphyrin ring, see also ref.[136]), the X-ray structure of the Co^{II}-corrin **21** fails to reveal considerable structural deformation of the Co^{II}-corrin fragment[117].

The example of the simplest organisms, which apparently learned to make use of the complex corrinoids and (reduced) metalloporphinoids already available before the advent of enzymatic catalysis[19–21] («first hour catalysts»[23]), could be a lesson to the modern chemist. This has been pointed out already by *Scheffold*[23,137] in particular, as well as by *Fischli*[138], who have set out impressingly to explore the potential of corrinoids as chiral organometallic catalysts in organic synthesis.

6. Prospects

Interest from several areas of chemistry for the porphinoid metal complexes originates first of all from their range of important properties in nature. These reactivities come about in stable, low molecular weight entities, which are used as catalyst centers in enzymes, where they are adapted

for a variety of functions by appropriate incorporation in proteins. The porphyrin macrocycle does not represent a single solution of nature to capture and transform solar irradiation[66a], nor by far to contain transition metal centers and to direct their reactivity[139], but it appears to be an especially well developed one, that is synthesized and profitably used in all spheres of life. The ongoing research in isolation and structural characterization of new porphinoid natural products[58,140] lets anticipate the discovery of still unknown reactivities in nature.

The porphinoid metal complexes promise potential as catalysts in synthesis, for the storage and conversion of energy, or as sensors in analytical chemistry and active components in medical treatment. The organometallic chemistry of porphinoid metal complexes is still largely unexplored in synthesis, not only with «natural» Fe, Co, and Ni ions, but also with other metal centers, such as Rh, Ir, Ru, Os ions etc.[141]. Unusual reactivities of monomeric and dimeroid[142] or other, «superstructured» porphyrins[143] should considerably expand the application in catalysis. Phthalocyanins and other porphinoid metal complexes that are easily accessible synthetically[144] are explored as catalysts[53,54,137], as are even vitamin B_{12} derivatives[138].

In surface-bound form in particular, (even more complex forms of) such metal complexes are considered useful as electrocatalysts for synthesis[145] or for energy conversion[146]. «Tuning» of the redox properties of (metallo)porphyrins by the choice of the metal center, the axial ligands, or the porphyrin and substituent structure, offers a potential for optimization[147]. Recent interest in varying the basic skeleton of the tetrapyrrole ring, has led to the synthesis of a series of porphyrin analogs, such as the pentapyrrol «pentaphyrin»[148], the porphyrin isomer «porphycen»[149], or porphyrin homologs with expanded perimeter[150].

The examination of porphinoid materials in liquid crystals[151] and in conducting polymers[152], the synthesis and examination of «functional porphyrin assemblies»[85b] and of microheterogeneous, porphyrin containing structures[153] are all of interest in information storage, in energy research, and particularly in the field of solar energy conversion[85,154].

Due to their exceptional coordination chemistry at the metal center, lipophilic B_{12}-derivatives and metal porphinoids also promise application as carriers in ion selective sensors[155]. Last, phototherapy, used e.g. in the treatment of neonatal jaundice[7], develops into a new method in medicine, by which the tissue of tumors is photooxydatively degraded, with metal-free porphinoids as photosensitizers[7,156].

Obviously, from the exceptional properties of the porphinoids as low molecular weight catalysts not only nature should profit, but also human technology and medicine.

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