

Microbial Siderophores

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1. Introduction

Iron is of great importance for many metabolic processes since the redox potential between its two valence states Fe^{2+} and Fe^{3+} lies within the range of physiological processes. Actually, iron is not a rare element, it is fourth in abundance in the earth crust, but it is not readily available for microorganisms. In the soil ferric oxide hydrates are formed at pH values around seven and the concentration of free Fe^{3+} is at best 10^{-17} mol/dm³ while about 10^{-6} mol/dm³ would be needed. In living organisms iron is usually strongly bound to peptidic substances such as transferrins. To increase the supply of soluble iron microorganisms other than those living in an acidic habitat may circumvent the problem by reduction of Fe^{3+} to Fe^{2+} (182), which seems to be of major importance for marine phytoplankton (151); see also amphiphilic marine bacteria (Sect. 2.8) and Fe^{2+} binding ligands (Sect. 7) below. An important alternative is the production of Fe^{3+} chelating compounds, so-called siderophores. Siderophores are secondary metabolites with masses below 2,000 Da and a high affinity to Fe^{3+} . Small iron-siderophore complexes can enter the cell via unspecific porins, larger ones need a transport system that recognizes the ferri-siderophore at the cell surface. In the cell, iron is released mostly by reduction to the less strongly bound Fe^{2+} state (137), and the free siderophore is re-exported (“shuttle mechanism”); for a modified shuttle system see pyoverdins (Sect. 2.1) and amonabactins (Sect. 2.7). Rarely the siderophore is degraded in the periplasmatic space as, e.g. enterobactin (Sect. 2.7). Alternatively Fe^{3+} is transferred at the cell surface from the ferri-siderophore to a trans-membrane transport system (“taxi mechanism”). A probably archaic and unspecific variety of the taxi mechanism comprises the reduction of Fe^{3+} at the cell surface (see ferrichrome A, Sect. 2.6 (99, 105)). The terms “shuttle” and “taxi mechanism” were coined by *Raymond* and *Carrano* (296).

A microbial strain may produce more than one siderophore. There are variations in fatty acid chains of a lipophilic part or in the amino acids making up the backbone, as well as released intermediates of the biosynthetic chain. These variations belong all to the same structural pattern. However, there is also the possibility that so-called secondary siderophores are encountered. They constitute a different structural type, usually less complex in their constitution but also less efficient in binding Fe^{3+} than the primary ones. Secondary siderophores will be produced when the demand for iron is not so severe or in case there is a genetic defect impeding the production of the primary ones. Examples will be found throughout the review.

Obviously siderophores can be potent virulence factors of pathogenic bacteria. Siderophores in many cases have elaborate structures providing recognition only by the receptor site of the producing species. This renders a pirating by competing microorganisms more difficult. The structural specificities of siderophores have been used for classification purposes of bacterial species (see especially pyoverdins, Sect. 2.1).

Whether a Fe^{3+} binding metabolite is actually involved in the iron transport has not always been established firmly. Criteria are the pronounced production under iron starvation and growth after feeding, or labeling studies (at best simultaneously of Fe^{3+} and of the ligand, see, e.g. parabactin, Sect. 3.2, and schizokinen, Sect. 4.1). Chelators whose function is uncertain will be included in this review with an explanatory remark. Incompletely characterized siderophores will be mentioned when at least some structural elements have been identified. However, the mere statement that color reactions for catecholates (8a) or hydroxamates (9a) were positive will not be sufficient. Not included will be the sideromycins, conjugates of siderophores with antibioticly active residues, produced mainly by *Streptomyces* spp., which use the iron transport paths for “Trojan Horse” strategies. For further references see (34, 97, 187).

Due to its high charge density, small ion radius, and low polarizability, Fe^{3+} is a hard *Lewis* acid and can bind strongly to hard *Lewis* bases such as oxide ions. It forms octahedral d^5 high spin complexes providing six coordination sites, which can accommodate three bidentate ligands. The major ligands types are catecholates, hydroxamates, and α -hydroxy carboxylates; other ligands are encountered occasionally. Siderophores containing different ligand types are not uncommon. Three bidentate ligands are often connected by aliphatic segments keeping them in place for complexation. This results in an entropic advantage over three non-connected ligands. Siderophores containing only two binding sites form either $(\text{Fe}^{3+})_2\text{Lig}_3$ complexes or the remaining two octahedral loci accommodate some external ligand (see, e.g. pyochelin, Sect. 5). For $(\text{Fe}^{3+})_2\text{Lig}_3$ structures with three bridges or with one bridging ligand have been discussed. The latter variety has been proven for alcaligin (Sect. 3.3). Three bidentate ligands can be arranged around the Fe^{3+} nucleus in two ways forming a left-handed or a right-handed screw, designated as Λ or Δ . Three identical ligands can point all in the same direction (*cis*) or one of them is reversed (*trans*). The chiral arrangement of the Fe^{3+} complex can be determined by X-ray analysis or can be deduced from the sign of the broad CD extremum at ca. 500 nm correlated with the metal-to-ligand charge transfer band. A positive $\Delta\epsilon$ indicates a Λ configuration.

Ga^{3+} complexes are frequently analyzed for two reasons. Ga^{3+} also forms octahedral structures and it has almost the same ion radius as Fe^{3+} (62 vs. 65 pm). In contrast to Fe^{3+} it is diamagnetic and its complexes are therefore amenable to NMR analysis. Also in contrast to Fe^{3+} it cannot be reduced and therefore it is used for uptake studies interested in the fate of the complex in the cell.

Siderophores can be classified by different criteria. In this review related structural types will be grouped together. Some arbitrariness cannot be avoided due to the occurrence of “mixed types”. Cross-references will then be given. Trivial names

have either been given to the free ligands or to their iron complexes. In the latter case the free ligands are referred to as “desferri” or “deferri” (sometimes in a shortened form as “desferrioxamines” for “desferriferrioxamines”) or as “pro” (see Sect. 3.3). Occasionally the name applied originally to the iron complex was used later for the free ligand (*e.g.* ferriactins, Sect. 2.1). These variations should be kept in mind when literature search programs are used.

For earlier compilations of siderophores see (97, 255a, 276), specifically for fungal siderophores (157a, 300, 383), and for biosynthesis pathways (19, 63, 403). Reviews for specific classes of siderophores will be mentioned where applicable.

2. Peptide Siderophores

In this group the ligands are incorporated in a peptide chain usually containing both D- (underlined in the structural formulas below) and L-configured amino acids. Frequently the two ends of the peptide chain are blocked by the formation of cyclic structures or otherwise. This prevents the degradation by proteolytic enzymes. Non-proteinogenic amino acids are encountered (homoserine, Hse; ornithine, Orn; 2,4-diaminobutyric acid, Dab; 2,3-dehydrobutyric acid, Dhb), lysine and ornithine may be incorporated in the chain by their ϵ/δ - rather than by their α -amino group, and amino acids may be modified to form ligand sites (3-hydroxy-aspartic acid, OHAsp; 3-hydroxy-histidine, OHHis; N^5 -acyl- N^5 -hydroxy-ornithine, acylOHOrn; N -hydroxy-*cyclo*-ornithine, *i.e.* 3-amino-1-hydroxy-piperidone-2, cOHOrn). Diaminobutyric acid frequently condenses with the preceding amino acid (Chart 1) giving a tetrahydropyrimidine ring (116). These condensation products are indicated below by a parenthesis as *e.g.* (Hse-Dab) in azoverdin (Sect. 2.2).

2.1. Pyoverdins and Related Siderophores from *Pseudomonas spp.*

The most thoroughly investigated representatives are the pyoverdins, also spelled pyoverdines and occasionally named pseudobactins (353), produced by the fluorescent members of the genus *Pseudomonas*. For reviews see (44, 231); for a detailed

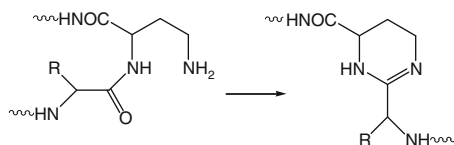


Chart 1. Condensation of a Dab residue with the preceding amino acid residue

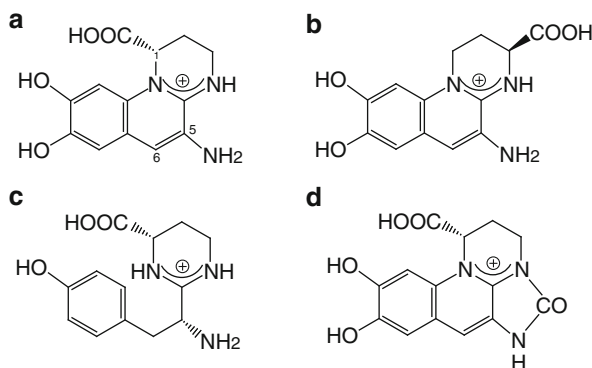


Fig. 1. Chromophore types: (a) pyoverdinin, (b) isopyoverdinin, (c) ferribactin, (d) azotobactin

study of the siderophores of this genus (37). Pyoverdins consist of three distinct structural parts, a chromophore (Chra) (Fig. 1, a), a peptide chain comprising six to twelve amino acids, and a dicarboxylic acid (succinic acid – Suc-, malic, glutamic, and 2-oxoglutaric acid) or monoamides (succinamide, malamide). For glutamic and 2-oxoglutaric acid the binding to the chromophore by their γ -carboxyl groups has been established by chemical degradation (124). For malic acid some not really convincing and partially contradictory NMR arguments have been advanced (319) for the binding by the carboxyl group neighboring the CH_2 group. Recently mass spectrometric arguments were reported suggesting a binding *via* the other carboxyl group (45).

The about fifty pyoverdins for which structures have been proposed can be divided into three structural types exemplified by the three pyoverdins of *Pseudomonas aeruginosa* (234) (Fig. 2), *viz.* pyoverdins (a) with a C-terminal tri- or tetra-cyclopeptidic substructure (lactam formation between the C-terminal carboxyl group and an in-chain lysine or ornithine), *e.g.* ATCC 15692 (PAO1) (1), (b) with a C-terminal cOHOrn, *e.g.* ATCC 27853 (2), and (c) with a C-terminal free carboxyl group, *e.g.* Pa6 (R) (3). The free carboxyl group is probably the hydrolysis product of a depsipeptidic substructure (ester formation between the C-terminal carboxyl group and an in-chain serine or threonine). In several cases both the cyclic and the hydrolyzed open-chain form were found (*e.g.* (50)). Binding sites for Fe^{3+} are the catecholate part of the chromophore Chra and two units in the peptide chain, hydroxamate (acylOHOrn, cOHOrn) and/or α -hydroxycarboxylate (OHAsp, OHHis).

Complete structural analysis requires mass spectral and NMR data as well as chemical degradation and analysis of the chirality of the constituent amino acids, determination of the mode of linkage of lysine (α - or ϵ -), the size of the cyclopeptide or cyclodepsipeptide ring, *etc.* (37). In some cases structures have been proposed based only on mass spectral data. Difficulties arising in this approach were discussed (44). To determine the three-dimensional structure an X-ray

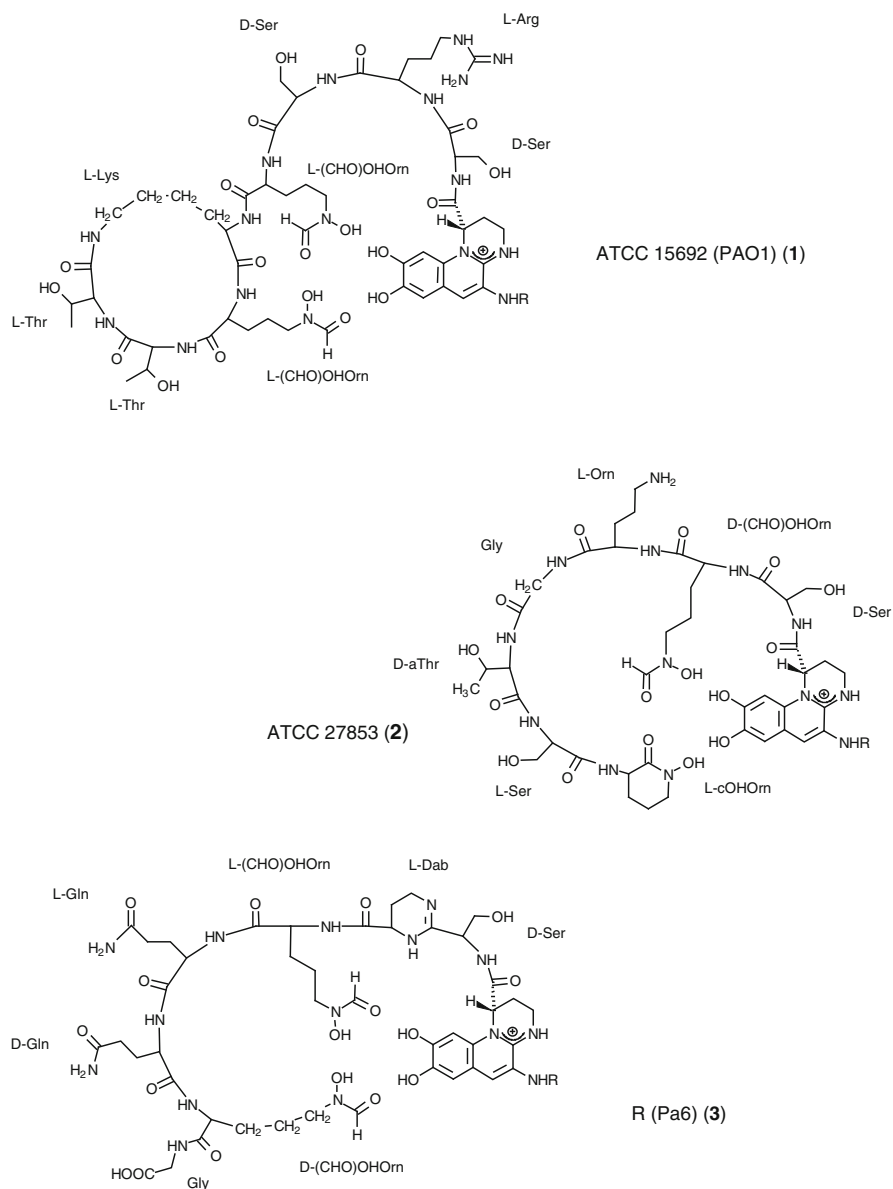


Fig. 2. Pyoverdins from *Pseudomonas aeruginosa* representing the three structural types

analysis (Plate 1) so far only of the Fe^{3+} complex of the pyoverdin B10 (4) was performed (353).

4 Suc-Chra- ϵ Lys-OHAsp-Ala- α Thr-Ala-cOHOrn

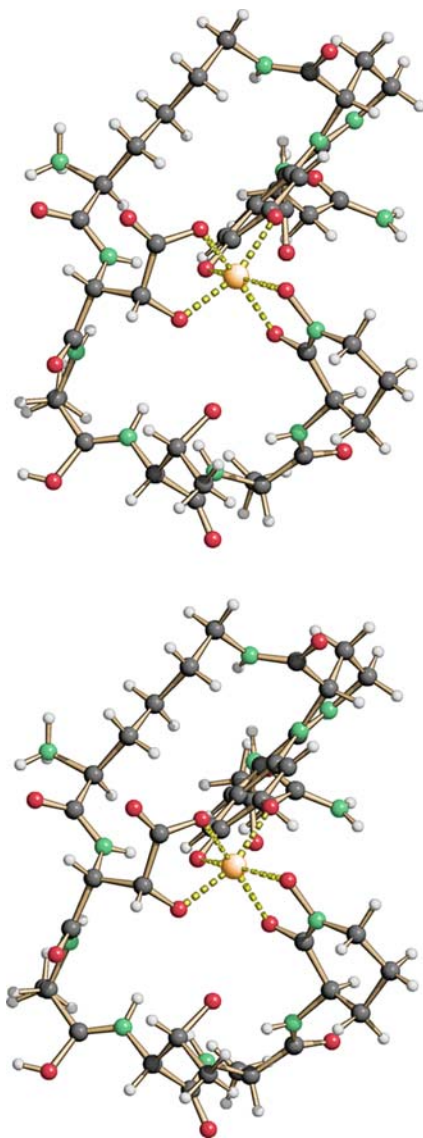


Plate 1. X-ray structure (stereo view) of ferri-pyoverdinin B10 (ferri-4)

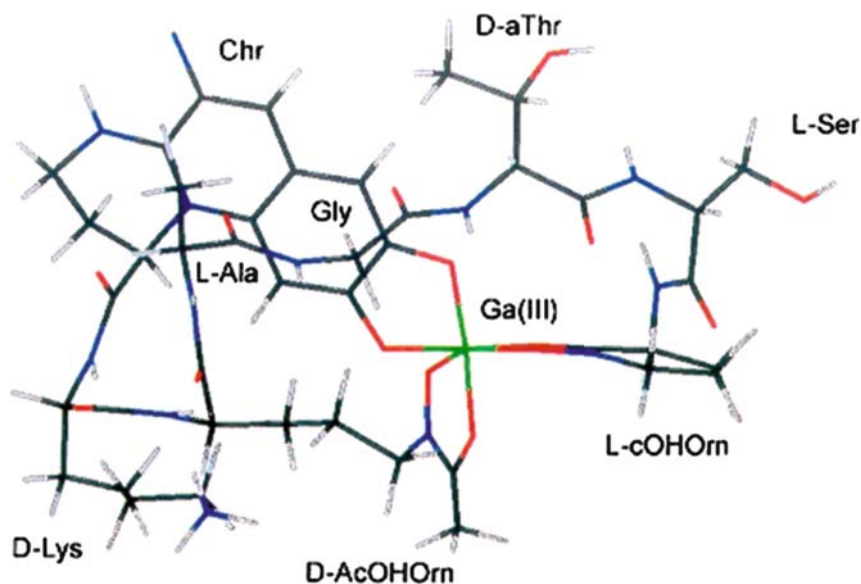


Plate 2. Calculated three-dimensional structure of the Ga^{3+} -complex of pyoverdine PL8 (without side chain) Chr-Lys-acetylOHOrn-Ala-Gly-aThr-Ser-cOHOrn

As an alternative strategy the investigation of the isomorphous Ga^{3+} complexes by NMR analysis was developed (241) for the pyoverdine GM-II (5) and extended to other pyoverdins, e.g. PL8 (16) (Plate 2) (H. Budzikiewicz, unpublished).

5 Suc-Chr-Ala-Lys-Gly-Gly-OHAsp-Gln-Ser -Ala-Ala-Ala-Ala-cOHOrn

In all cases the metal ion was found to lie at the surface of the complex. This facilitates its uptake and release. For the pyoverdins both Λ and Δ arrangements have been reported (37).

Iron transport through the cell membrane follows a modified shuttle mechanism. Evidence has been presented that the iron-free siderophore of *P. aeruginosa* PAO1 (1, Fig. 2) binds strongly to the receptor protein (67, 314a). This suggests two scenarios for the subsequent steps of iron transfer, an exchange of the ligands or a transfer of Fe^{3+} between them. By ^3H - and ^{55}Fe -labeling as well as fluorescence studies it was shown that an exchange between the approaching ferri-pyoverdine and the bound iron-free pyoverdine occurs and that the former one enters the cell, i.e. that no Fe^{3+} exchange between the two ligands takes place (314b). Model studies with *Aeromonas* (Sect. 2.7) demonstrated there the iron-exchange variety. Binding of the iron-free siderophore to the receptor protein seems to be a common feature of the transport systems of *P. aeruginosa* and *Escherichia coli* (145a).

The peptide chains of the pyoverdins are responsible for the recognition of the ferri-siderophore at the cell surface of the producing species. It is usually highly strain specific. Cross-recognition between two strains is only observed when structurally closely related pyoverdins are produced (125, 233). An exception seems to be *P. aeruginosa* ATCC 15692, which besides its own ferripyoverdin (Fe-1), accepts several foreign ones (128a).

Without going into structural details, the pyoverdins stemming from the saprophytic group *Pseudomonas aeruginosa/fluorescens/putida* contain either two hydroxamic acid units or one hydroxamic and one α -hydroxycarboxylic acid, and those from the phytopathogens *P. syringae* etc. two α -hydroxycarboxylic acids. Structural differences of pyoverdins have been used recently to characterize species newly defined by breaking up the classical cluster of *P. fluorescens/putida* (e.g. (229, 231)). A listing of all pyoverdins from *Pseudomonas* spp. for which structural data have been published up to December 2009 is contained in the Appendix.

Pyoverdin-like siderophores with other chromophores have also been observed (see Fig. 1) (45). The 5,6-dihydropyoverdins (Chra without the 5,6-double bond) and the ferribactins (Chrc) are considered to be biogenetic precursors of the pyoverdins (318) (the term “ferribactin” was originally used for the Fe^{3+} complex (221) and later for the free ligand). An azotobactin chromophore (Chrd, see also below Sect. 2.2) is occasionally found in *Pseudomonas* isolates (e.g. (146)). Siderophores produced by a specific *Pseudomonas* strain but differing in the chromophore always have identical peptide chains.

Isopyoverdins contain the siderophore Fig. 1, Chrb with aspartic acid as the first amino acid. They have been encountered so far only in isolates from *Pseudomonas putida* strains, e.g. BTP1 (168) (6).

6 Glu-Chrb-Asp-Ala-Asp-acetylOHOrn-Ser-cOHOm

2.2. *Azomonas* and *Azotobacter* Siderophores

For a detailed discussion of this class of compounds see (37).

Azomonas macrozytogenes produces a siderophore with an isopyoverdin chromophore, azoverdin, but with a peptide chain 7 related to those of azotobactins, viz. (236).

7 Suc-Chrb-Hse-(Hse-Dab)-acetylOHOrn-Ser-acetylOHOrn

The three-dimensional structure of the Ga^{3+} complex was determined by NMR techniques as outlined above. Also here the metal ion lies at the surface of the complex (377).

From *Azotobacter vinelandii* the structures of two siderophores were elucidated. They contain the chromophore Chrd (Fig. 1) and Hse units: azotobactin 87-I (8) (from the three Hse in this sequence two are L and one D configured) from the strain ATCC 12837 (314), and azotobactin D (9) (76) from the strain CCM 289.

8 Chrd-Ser-Ser-Hse-Gly-OHAsp-Hse-Hse-Hse

- β -hydroxybutyrylOHOrn-Hse

9 Chrd-Asp-Ser-Hse-Gly-OHAsp-Ser-Cit-Hse-acetylOHOrn-Hse

Both of them are accompanied by compounds where the C-terminal Hse forms a γ -lactone ring (azotobactin 87-II and δ). An azotobactin O for which also a structure had been proposed (120) was shown later to be identical with azotobactin D (272). For secondary metabolites see protochelin and its constituents (Sect. 3.2).

Azotobacter chroococcum produces ornithine-containing hydroxamate siderophores with molecular masses 800 and 844 Da (difference of one carboxyl group?) of unknown structure (115a).

2.3. Anachelin

Cyanobacteria were probably the first organisms to perform oxygenic photosynthesis resulting eventually in the oxidation of environmental Fe^{2+} to Fe^{3+} with all its consequences. To cope with this problem the production of siderophores was initiated. Not much is known about the siderophores of cyanobacteria. Schizokinen (see below under citrate siderophores, Sect. 4.1) (326) found to be produced by several bacterial species may have been acquired by gene transfer; see however also the citrate siderophores synechobactins.

Certainly of genuine origin is anachelin, a strange compound whose biosynthesis requires *inter alia* steps from the peptide and polyketide paths. It exists in an open (anachelin H, Fig. 3, (10)) and two cyclic forms arising from an interaction of the carbonyl group of the salicylic acid residue with one of the neighboring

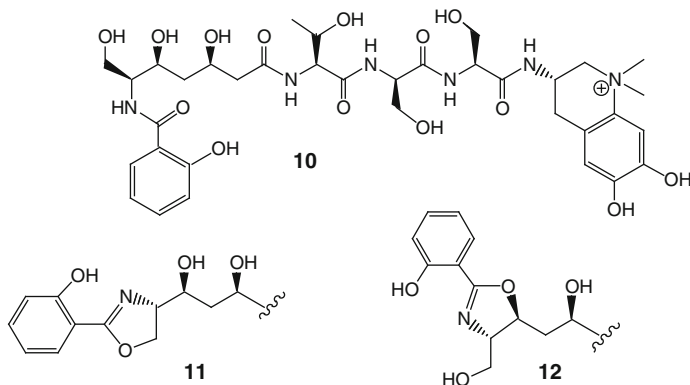


Fig. 3. Anachelin H (10), anachelin 1 (11), anachelin 2 (12)

hydroxy groups (anachelin 1 and 2, Fig. 3, (11) and (12)) (22, 167). The relative and absolute stereochemistry of all chiral centers was established (22, 166) and confirmed by synthesis (121) (see Sect. 8.1). In solution anachelin forms a β -turn arrangement (122). Mass spectrometric analysis of the Fe^{3+} complex suggests a 1:1 ratio.

2.4. Actinomycetal Metabolites

Desferrimaduraferrin is a Fe^{3+} complexing metabolite of *Actinomadura madurae* (185). It consists of salicylic acid, β -Ala, Gly, L-Ser and N^5 -hydroxy- N^2 -methyl-L-Orn, with the latter incorporated in a heterocyclic system (Fig. 4, 13). From the same species the madurastatin group was obtained (136). The main representative **A1** shows the sequence salicylic acid, D-azaridine carboxylic acid, L-Ala, β -Ala, N^5 -hydroxy- N^2 -methyl-Orn, L-cOHOrn (Fig. 4, 14). In **A2** the azaridine ring is opened giving a Ser residue, **A3** is an isomer of the open form with the salicylic acid bound to the hydroxy group of Ser. **B1** and **B2** are the precursors N -salicyloyl-azaridine carboxylic acid and N -salicyloyl-Ser. The madurastatin species **A1** forms a 1:1 Fe^{3+} complex as shown by mass spectrometry.

Asterobactin from *Nocardia asteroides* (257) contains salicylic, 2,3-dihydroxypropionic, and 2-methyl-3-hydroxyundecanoic acid as well as derivatized Orn and Arg residues (Fig. 4, 15). It forms a Fe^{3+} complex. The stereochemistry of the various centers was not determined but L-configuration is proposed for Orn and Arg for biosynthetic reasons (general amino acid pool) and a negative $[\alpha]_D^{25}$ of asterobactin. Whether the three compounds are involved in metal transport has not been investigated.

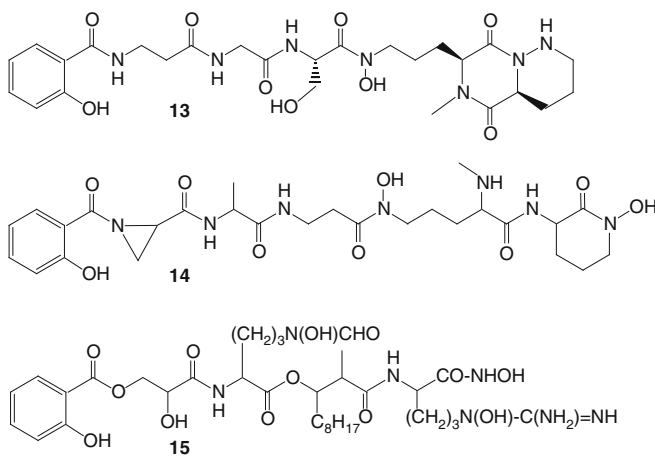


Fig. 4. Desferrimaduraferrin (13), madurastatin A1 (14), asterobactin (15)

2.5. Bacterial Hydroxamate Siderophores

Exochelins (322, 323) are peptidic siderophores from *Mycobacterium* spp. (see also below mycobactins). Exochelin MS (16) from *M. smegmatis* comprises β -Ala and three N^5 -OHOrn units, which are linked by their N^5 atoms to acyl groups thus forming hydroxamic acids.



Exochelin MN (17) from *M. neoaurum* contains N^2 -methyl- N^5 -hydroxy-Orn linked by its N^5 to β -Ala and by its carboxyl group to N^2 of Orn, which in turn is bound amidically to cOHOrn; all amino acids are L configured.



The Fe^{3+} chelating properties of exochelin MN (17) were investigated in detail (pK_a values, chelation constants, redox equilibria, etc.) (87). In one publication (128) siderophores from *Mycobacterium tuberculosis* otherwise referred to as carboxymycobactins (see below Sect. 2.8) were also named exochelins.

Vicibactin (18) (previously called hydroxamate K (61a) from *Rhizobium leguminosarum* is a macrocyclic trilactone consisting of N^2 -acetyl- N^5 -hydroxy-D-Orn and (*R*)-3-hydroxybutyric acid (91).



Vicibactin 7101 from a mutant strain lacks the N-acetyl groups but shows comparable siderophore activity as demonstrated by $^{55}\text{Fe}^{3+}$ uptake studies (91). The answer to the question why vicibactin is biosynthesized if vicibactin 7101 is as efficient in iron sequestering may be the greater stability of the acetylated compound (*cf.* fusarinines, Sect. 2.6). Vicibactin is identical with neurosporin produced by the fungus *Neurospora crassa* for which X-ray data of the Fe^{3+} complex are available. CD spectroscopy indicates a Λ -*cis* configuration both for crystals and for solution (108).

A hydroxamate siderophore from *Salmonella typhimurium* is described as containing isoleucine/leucine, phenylalanine and valine, but not serine and lysine. Further details are not given (290a). For other *Salmonella* siderophores see Sect. 2.7.

2.6. Fungal L-Ornithine-Based Hydroxamate Siderophores

For other fungal siderophores see neurosporin above, pistilarin (a spermidine derivative, Sect. 3.2) and rhizoferrin (a citrate siderophore, Sect. 4.4); siderophores

produced by marine fungi are treated in (147). The siderophores to be discussed here can be divided in three groups, the fusarinines, the ferrichromes, and the coprogens, all based on N^5 -hydroxy- N^5 -acyl-L-Orn. There exist some earlier reviews (204, 300, 383); for the early days see also (395). Lists of siderophores and the producing fungi have been assembled (384, 385) to which the marine yeast *Aureobasidium pullulans* may be added (374a); see also (139). Chromatographic separation techniques were established (175, 192). For a number of siderophores and their Fe^{3+} complexes X-ray and other structural analyses are reported (366). In the text and the figures, the desferri ligands will be presented without adding the prefix “desferri” to their names.

Fusarinines (19) produced by several fungal genera comprise the acyl unit (*Z*)-5-hydroxy-3-methyl-pent-2-enoic acid (anhydromevalonic acid) (Fig. 5, a) bound to N^5 -hydroxy-L-ornithine. They can be a linear monomer, dimer (fusarinine A) or trimer (fusarinine B) (the monomer can also be (*E*)-configured) (172). Fusarinine B is possibly identical with coprogen C (89).



The trimer by forming an ester bond between the two terminal functions results in a lactone ring (fusarinine C or fusigen) (88, 313). Since the fusarinines are rather labile it is not clear whether the open forms are genuine siderophores, precursors of fusigen or just hydrolysis products (204). The monomers (*Z*)- and (*E*)-fusarinine form in aqueous solution at neutral pH (Fe^{3+})Lig₃ complexes, which are mixtures of Λ and Δ isomers (172).

The free α -amino groups of the ornithine units were also found in an acetylated form (90, 243). Since triacetylfusigen is resistant to hydrolysis, formation of the acetylated mono-, di-, and trimeric linear acetylfusarinines is assumed to be effected by enzymatic cleavage (103a, 243). X-ray and CD data of the Fe^{3+} complex of triacetylfusigen have been obtained (152). Depending on the solvent used for crystallization the crystals show Λ -*cis* or Δ -*cis* configuration, while in solution Δ -*cis* prevails.

The members of the ferrichrome group are cyclohexapeptides with the general structure $[-(N^5\text{-acyl-}N^5\text{-hydroxy-L-Orn})_3\text{-A-B-Gly-}]$ where A and B can be Gly, Ala, or Ser (Table 1); the various acyl groups are depicted in Fig. 5. Exceptions are tetraglycyferrichrome, a cycloheptapeptide with four Gly units in sequence and three acetyl residues in the Orn part (ferrichrome with an additional Gly) (82), and des(diserylglycyl)ferrirhodin, a linear tripeptide containing only the three Orn units

- | | |
|---|---|
| a. (<i>Z</i>)-CO-CH=CCH ₃ -(CH ₂) ₂ -OH | f. (<i>E</i>)-CO-CH=CCH ₃ -CH ₂ -COOH |
| b. (<i>E</i>)-CO-CH=CCH ₃ -(CH ₂) ₂ -OH | g. CO-CH ₂ -COOH |
| c. (<i>E</i>)-CO-CH=CCH ₃ -CHOH-CH ₂ OH | h. CO-(CH ₂) ₁₄ -CH ₃ |
| d. (<i>E</i>)-CO-CH=CCH ₃ -(CH ₂) ₂ -OCOCH ₃ | i. COCH ₃ |
| e. CO-CH ₂ -CH(CH ₃)OH-(CH ₂) ₂ -OH | |

Fig. 5. Acyl residues encountered in fungal hydroxamate siderophores

Table 1. The ferrichrome family^a

$$\sim\text{NH}-\underset{\substack{| \\ (\text{CH}_3)_3 \\ | \\ \text{HO}-\text{N}-\text{Ac}^1}}{\text{CH}}-\text{CO}-\text{NH}-\underset{\substack{| \\ (\text{CH}_2)_3 \\ | \\ \text{HO}-\text{N}-\text{Ac}^2}}{\text{CH}}-\text{CO}-\text{NH}-\underset{\substack{| \\ (\text{CH}_2)_3 \\ | \\ \text{HO}-\text{N}-\text{Ac}^3}}{\text{CH}}-\text{CO}-\text{A}-\text{B}-\text{Gly}\sim$$

Name	A	B	Ac ¹	Ac ²	Ac ³	References
ferrichrome	Gly	Gly	i	i	i	(106)
ferrichrome A	Ser	Ser	f	f	f	(106, 383, 396)
ferrichrome C	Gly	Ala	i	i	i	(209, 383)
ferrichrysin	Ser	Ser	i	i	i	(170, 174, 184, 383)
ferricrocin	Gly	Ser	i	i	i	(184, 383)
ferrirubin	Ser	Ser	b	b	b	(170, 174, 383)
ferrirhodin	Ser	Ser	a	a	a	(383)
malonichrome	(Gly	Ala)	g	g	g	(104)
sake colorant A	Ser	Ala	i	i	i	(209)
asperochrome A	Ser	Ala	b	b	b	(155, 174)
asperochrome B ₁	Ser	Ser	i	b	b	(170, 174)
asperochrome B ₂	Ser	Ser	b	(b	i)	(170, 174)
asperochrome B ₃	Ser	Ser	b	(b	i)	(170)
asperochrome C	Ser	Ser	(b	b	d)	(174)
asperochrome D ₁	Ser	Ser	b	i	i	(170, 174)
asperochrome D ₂	Ser	Ser	i	(b	i)	(170, 174)
asperochrome D ₃	Ser	Ser	i	(b	i)	(170, 174)
asperochrome E	Ser	Ser	(a	b	b)	(177)
asperochrome F ₁	Ser	Ser	(b	b	e)	(177)
asperochrome F ₂	Ser	Ser	(b	b	e)	(177)
asperochrome F ₃	Ser	Ser	(b	b	e)	(177)

^aParentheses indicate that the position of the residues is not certain. For the designation of the acyl residues see Fig. 5. Where the chirality of Ala or Ser was determined it was found to be L.

of ferrirhodin (169). One of the members of this group, ferricrocin was identified as an intra- and intercellular iron transporter for *Aspergillus fumigatus* (374).

Ferrichrome (as do also at least the members of the group for which structural data are available ((366) and references noted in Table 1) shows Λ-, synthetic *enantio*-ferrichrome based on D-Orn Δ-configuration (253). Uptake studies performed with *Ustilago sphaerogena* (103) using ⁵⁹Fe³⁺ and [¹⁴C]-ferrichrome under optimal conditions (30°C, pH 7) showed rapid resorption of both labels during the first 30 min. The uptake of ⁵⁹Fe³⁺ continued for further 30 min, then the level of radioactivity stayed constant, while the level of ¹⁴C dropped to a lower constant value. Desferri-[¹⁴C]-ferrichrome is not taken up or even bound to the cell surface. These findings are in agreement with shuttle mechanism and re-export of the ligand after detachment of iron. See also analogous experiments with parabactin (Sect. 3.2) and with schizokinen (Sect. 4.1). In contrast, ferrichrome A does not enter the cell. Fe³⁺ is rather reduced and given off at the cell surface and subsequently transported into the cell (99, 105). ⁵⁵Fe uptake studies performed with *Neurospora crassa* showed the same incorporation rate for ferrichrome and tetraglycylferrichrome indicating that the peptide ring size is of minor importance for the acceptance by the transport system (82).

The third group comprises the coprogen family. Their characteristic element is a diketopiperazine ring formed by the head-to-head condensation of two N^5 -acyl- N^5 -hydroxy-L-Orn units. Rhodotorulic acid (**20**) first isolated from the yeast *Rhodotorula pilimanae* and subsequently found to be produced by many yeasts (*9a*) contains two acetyl groups (Fig. 6) (**9**), and dimerum acid (**21**) from *Fusarium dimerum* (*89*) and other fungi (*172*) two (*E*)-anhydromevalonyl residues (Fig. 6). An acetyl-dimerum acid of unknown structure has been encountered (*157b*). In the coprogens a third variously substituted (*E*)-fusarinine unit is added by means of an ester bond (Table 2) (*300*). Rhodotorulic and dimerum acid form $(\text{Fe}^{3+})_2\text{Lig}_3$ complexes, but also a mixed 1:1:1 complex of Fe^{3+} with dimerum acid and (*Z*)-fusarinine was observed. Various coprogens were shown to yield 1:1 complexes with Fe^{3+} (*60*, *153*, *172*). The CD-spectra of the coprogen and neocoprogen I/II Fe^{3+} complexes demonstrate Δ -configuration for the solutions and for the crystals of neocoprogen I

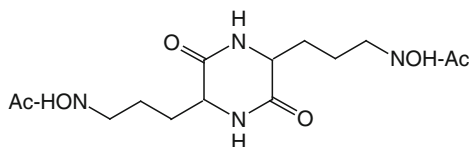


Fig. 6. Rhodotorulic acid (Ac = Fig. 5, i) (**20**) and dimerum acid (Ac = Fig. 5, b) (**21**)

Table 2. The coprogen family^{a,b}

$\text{Ac}^2 = \text{CO-CH=C}(\text{CH}_3)\text{-(CH}_2)_2\text{-O-CO-CH}(\text{NR}^1\text{R}^2)\text{-(CH}_2)_3\text{-NOH-Ac}^3$

Name	Ac ¹	Ac ³	R ¹	R ²	References
coprogen	b	b	COCH ₃	H	(117, 184a)
coprogen B	b	b	H	H	(89)
triornicin (isoneocoprogen I)	b	i	COCH ₃	H	(117)
isotriornicin (neocoprogen I)	i	b	COCH ₃	H	(118, 153)
neocoprogen II	i	i	COCH ₃	H	(153)
<i>N</i> ² -methyl coprogen B	b	b	CH ₃	H	(30c, 157b)
<i>N</i> ² -dimethyl coprogen	b	b	CH ₃	CH ₃	(173)
<i>N</i> ² -dimethyl neocoprogen I	i	b	CH ₃	CH ₃	(173)
<i>N</i> ² -dimethyl isoneocoprogen I	b	i	CH ₃	CH ₃	(173)
hydroxycoprogen	b	c	COCH ₃	H	(176)
hydroxyneocoprogen I	i	c	COCH ₃	H	(176)
hydroxyisoneocoprogen I	c	i	COCH ₃	H	(176)
palmitoylcoprogen	b	b	h	H	(5)

^aFor the designation of the acyl residues see Fig. 5

^bCoprogen C is possibly identical with fusarinine B (*89*)

(153). Palmitoylcoprogen (Table 2 last entry) from *Trichoderma* spp. is retained in the fungal mycelium and may therefore be considered as a candidate for an iron uptake taxi mechanism (5).

Relationships between the structure of the siderophores and the iron transport were investigated for the fungus *Neurospora crassa* (160, 160a). Apparently two different receptors exist for ferrichromes and for coprogens. For the recognition and the binding to the cell surface the iron configuration and the nature of the acyl chains is of importance. However, the transport system seems to be the same for both siderophore types dependent on the peptide part of the molecules.

2.7. Catecholate Siderophores

For other catecholate siderophores see di-/tri-aminoalkane (Sect. 3.2) and citric acid (Sect. 4.3) derivatives below; for a review see (38).

2,3-Dihydroxybenzoic acid is produced by a series of microorganisms, viz. *Aerobacter aerogenes* (291), *Azotobacter vinelandii* (70, 273), *Bacillus subtilis* (282), *Escherichia coli* (261, 291), *Klebsiella oxytoca* (196), *Micrococcus denitificans* (347), *Nocardia asteroides* (112), *Rhizobium* sp. (74), and *Salmonella typhimurium* (290), 3,4-dihydroxybenzoic acid by a mutant of *Aerobacter aerogenes* (291), *Azomonas macrocytogenes* (380), *Bacillus anthracis* (123), *Escherichia coli* (291), *Magnetospirillum magneticum* (54), and *Mycobacterium smegmatis* (291). Both dihydroxybenzoic acids can act as siderophores.

Condensation products of DHB (which usually is found also in the fermentation broth) with amino acids were reported, viz. with glycine from *Bacillus subtilis* (164) named subsequently itoic acid (282); with serine from *Escherichia coli* (261) and *Klebsiella oxytoca* (196); with threonine from *Klebsiella oxytoca* (196) and *Rhizobium* spp. (275, 327); with arginine from *Pseudomonas stutzeri* (62); with glycine and threonine from *Rhizobium* sp. (240); with threonine and lysine as well as with leucine and lysine from *Azospirillum lipoferum* (312, 320). In most cases the isolate (sometimes designated as being a siderophore) was hydrolyzed and the constituents were determined by paper chromatography. The relative amounts of the constituents, the chiralities of the amino acids and the molecular mass of the isolate have not been determined. Hence it is not known whether condensation products of the enterobactin type exist.

Ideally suited for Fe^{3+} complexation – exemplified by the extremely high complexing constant of 10^{49} (originally estimated as 10^{52}) (210) – is enterobactin (enterochelin) first isolated from *Salmonella typhimurium* (286) and *Escherichia coli* as well as from *Aerobacter aerogenes* (261) and recently from *Enterobacter cloacae* (368). It is a cyclic trilactone of *N*-2,3-dihydroxybenzoyl-L-serine (DHB-Ser) (Fig. 7, 22). Syntheses have been reported (71, 321). DHB-Ser by itself can act as a siderophore. In the culture medium degradation products of enterobactin also were found, and are open-chain compounds comprising two or three constitutional units. Iron release in the cell is effected by degradation of

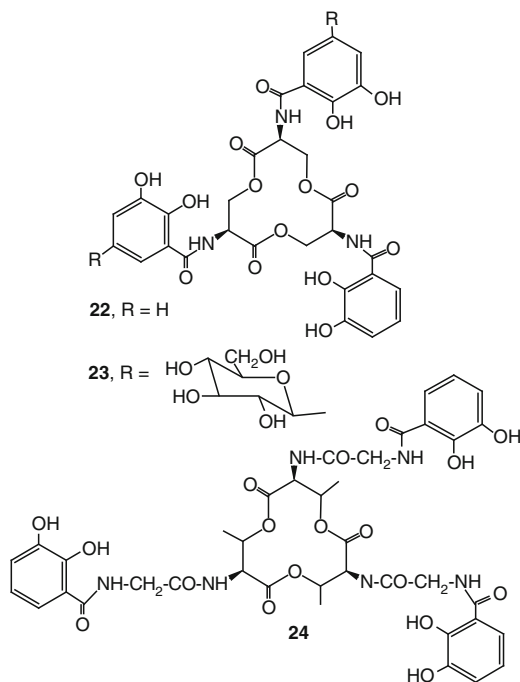


Fig. 7. Enterobactin (**22**), salmochelin S4 (**23**), corynebactin (**24**)

enterobactin. Ferri-enterobactin shows a Δ -*cis* configuration, with the synthetic ferri-*enantio*-enterobactin based on D-Ser Λ -*cis*-configuration (256).

Escherichia coli and *Salmonella enterica* produce a derivative of enterobactin, salmochelin S4, where two of the aromatic rings are β -C-glucosylated in the 5-position (Fig. 7, 23). Also glycosylated degradation products or precursors (monomer: salmochelin SX, dimers: S1 and S5, linear trimer: S2) could be isolated (31, 135, 247). Salmochelin S4 is identical with pacifarin, a compound active against salmonellosis (378), and SX with pacifarinic acid, glucosylated DHB-serine (247).

From *Corynebacterium glutamicum* the siderophore corynebactin was obtained (41). It differs from enterobactin in being composed of three DHB-Gly-L-Thr units (Fig. 7, 24). Later the same siderophore was found to be produced also by *Bacillus subtilis* and named bacillibactin (223). Its complexation constant is $\sim 10^{48}$ (84). The monomeric unit DHB-Gly-Thr was isolated from *Bacillus licheniformis* (357a).

Azospirillum brasilense under iron starvation produces spirilobactin. Hydrolysis yields DHB, ornithine, and serine of unknown chirality in a ratio of 1:1:1. The molecular mass was not determined and hence it is not known whether spirilobactin forms a (cyclic) trimer. Iron uptake was studied with the $^{59}\text{Fe}^{3+}$ complex (10).

Erwinia chrysanthemi (278) and *Serratia marcescens* (101) produce N^2 -DHB-D-Lys-L-Ser named chrysobactin. The structure was confirmed by synthesis. At physiological pH values 2 or 3 chrysobactin residues are associated with Fe^{3+} (280).

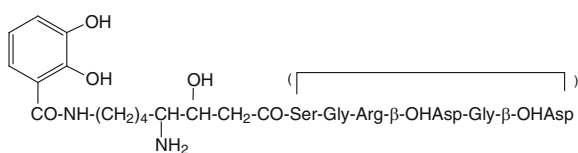
From *Chryseomonas luteola* in addition to chrysobactin a derivative (chrysomonin) was isolated where C-6 of the DHB unit is substituted with the N-atom of a pyridinium cation. Chrysomonin could be synthesized from chrysobactin (*1a*).

Amonabactins (**25**) were found to be excreted by *Aeromonas hydrophila* (355, 356) and by *Pseudomonas stutzeri* (398). They are based on the peptides Lys-Lys-Phe and Lys-Lys-Trp; N⁶ of the first L-Lys residues is derivatized by DHB or by a DHB-Gly residue, and that of the second L-Lys by a DHB group (Table 3). At high pH values and excess ligand a (Fe³⁺)₂Lig₃ complex is formed, while at neutral pH a 1:1 ratio prevails with H₂O molecules satisfying the remaining coordination sites. The 2:3 complex is preferentially Δ-configured, and the 1:1 complex is achiral (357). Model uptake studies with *Aeromonas* were performed with ⁵⁵Fe³⁺ and a ¹⁴C-labeled artificial synthetic siderophore. They demonstrate a modified shuttle mechanism. An iron-free siderophore molecule is strongly bound to the receptor protein and Fe³⁺ exchange occurs between an approaching ferri-siderophore and the bound one, which then is transported into the cell (337); cf. the pyoverdins (Sect. 2.1).

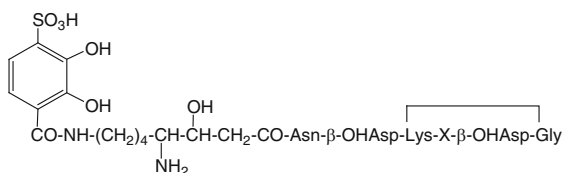
Alterobactin A is a cyclodepsipeptide from *Alteromonas luteoviolacea*, with N⁸-DHB-(4S),8-diamino-(3R)-hydroxy-octanoyl-D-Ser-Gly-L-Arg-L-threo-3-hydroxy-Asp-Gly-L-threo-3-hydroxy-Asp having an ester bond between the C-terminal carboxyl group and Ser. It is accompanied by its hydrolysis product alterobactin B (Fig. 8, **26**, **27**) (298). Alterobactin A forms a 1:1 complex with Fe³⁺ with an

Table 3. Amonabactins (**25**)

R ¹ -NH-(CH ₂) ₄ -CH(NH ₂)-CO-NH-CH(COR ₂)-(CH ₂) ₄ -NH-DHB		
Name	R ¹	R ²
Amo T 789	DHB-Gly	D-Trp
Amo P 750	DHB-Gly	D-Phe
Amo T 732	DHB	D-Trp
Amo P 693	DHB	D-Phe



26: with ester bond between OHAsp and Ser
27: without ester bond between OHAsp and Ser



28: X = Lys, **29:** X = Arg

Fig. 8. Alterobactins (**26**, **27**), pseudoalterobactins (**28**, **29**)

degradation and NMR studies (335, 336) as containing 3-hydroxy fatty acid residues and putrescine that blocks the C-terminus, with acyl = R-CHOH-CH₂-CO (R = CH₃, C₃H₇, C₅H₁₁).

33 acylOHO_{rn}-OHA_{sp}-Ser-formylOHO_{rn}-NH-(CH₂)₄-NH₂

The three ornibactins are accompanied by minor components, which contain an additional oxygen atom. Their structure has not been investigated. Ornibactins are the main siderophores of a series of *Burkholderia* strains accompanied in part by pyochelin (Sect. 5) and cepabactin (Sect. 6) (235). A further *B. cepacia* siderophore is cepaciachelin (Sect. 3.2) (15). The iron acquisition by the various siderophores of *B. cepacia* has been discussed in detail (359).

From *Nocardia* strains several closely related compounds (nocobactins, formobactin, amamistatins) were isolated that contain three typically Fe³⁺ binding sites, two hydroxamate units, and a hydroxyphenyloxazole structure (cf. Sect. 3.2 below). The C-terminus is *N*-hydroxy-*cyclo*-Lys bound to a long chain 3-hydroxy fatty acid, whose hydroxy group is esterified by *N*⁶-acyl-*N*⁶-hydroxy-Lys, the α-amino group of which is bound to 2-*o*-hydroxyphenyl-5-methyl-oxazole-4-carboxylic acid (Table 4). For the amamistatins the configuration of the cyclic lysine was determined as L, the open one as D, and that of C-3 of the fatty acid as (S). The involvement in the iron metabolism was not investigated.

Structurally related with the nocobactin family are the mycobactins and carboxy-mycobactins (the latter were also referred to as exochelins, Sect. 2.5 (128)) from *Mycobacterium* spp. For reviews see (85, 331, 369). They have the same basic skeleton as the nocobactins, but the 4,5-double bond of the oxazole ring is saturated. A series of differently substituted representatives has been isolated (see Table 5). The major group comprises mixtures carrying saturated and unsaturated long-chain fatty acid residues as substituents of the hydroxamic acid unit formed by the *N*⁶-amino group of lysine. For some ("J", M, and N), the fatty acid residues are located in the chain, as for the nocobactins. Representatives of the MAIS group (*Mycobacterium avium*, *M. intracellulare*, *M. scrofulaceum*) possess two long

Table 4. The nocobactin family

Compound	R ¹	R ²	R ³	R ⁴	References
nocobactin NA	H	C ₉ H ₁₉ , C ₁₁ H ₂₃	CH ₃	H	(294, 295)
formobactin	CH ₃	C ₉ H ₁₉	H	H	(252)
amamistatin A	CH ₃	C ₇ H ₁₅	H	H	(191, 341)
amamistatin B	CH ₃	C ₇ H ₁₅	H	OCH ₃	(191, 341)

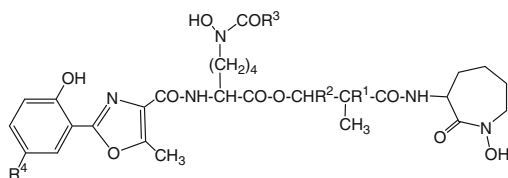
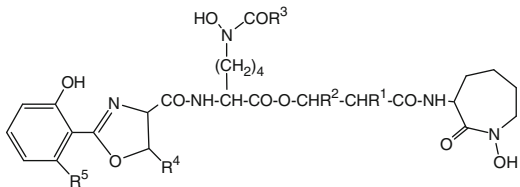


Table 5. The mycobactin family (adapted from (369))


Mycobactin	R ¹	R ²	R ³	R ⁴	R ⁵	References
A	H	CH ₃	C ₁₃	H	CH ₃	(332)
F	H	CH ₃	C ₉₋₁₇	CH ₃	H	(332)
H	H	CH ₃	C _{17,19}	CH ₃	CH ₃	(381)
J	CH ₃	CH(CH ₃) ₂	C ₁₅	H	H	(224)
“J”	CH ₃	b	a	CH ₃	H	(18)
P	CH ₃	C ₂ H ₅	C ₁₃₋₁₉	H	CH ₃	(329)
R	CH ₃	C ₂ H ₅	C ₁₉	H	H	(332)
S	H	CH ₃	C ₁₃₋₁₉	H	H	(381)
T	H	CH ₃	C ₁₄₋₂₁	H	H	(330)
M	CH ₃	C ₁₄₋₁₇	CH ₃	CH ₃	H	(332)
N	CH ₃	C ₁₄₋₁₇	C ₂ H ₅	CH ₃	H	(332)
MAIS	CH ₃	b	a	H	H	(18)
	CH ₃	b	a	CH ₃	H	(18)
carboxy	H	CH ₃	c	H	H	(128)
	H	CH ₃	c	CH ₃	H	(128)
	CH ₃	C ₂ H ₅	d	CH ₃	H	(199, 292)

a – unsaturated alkyl chain, b – saturated alkyl chain, c – saturated and unsaturated dicarboxylic acid methyl ester, d – unsaturated dicarboxylic acid

chain fatty acid residues. The stereochemistry of most chiral centers has been determined. For the Fe³⁺ complex of mycobactin P an X-ray analysis is available (157). For the carboxymycobactins the residues R³ in Table 5 are saturated or unsaturated alkyl groups with terminal carboxyl groups or their methyl esters.

Transvalencin Z (245a) from *Nocardia transvalencis* could be a precursor or side product of mycobactin biosynthesis, possibly acquired from a vagabonding gene. It comprises the left part of the serine/salicylic acid based molecules (Table 5 R⁴ = R⁵ = H) and ends with N⁶-formyl-Lys (R³ = H, no N-hydroxy group). The stereochemistry of the two chiral centers was not determined. Transvalencin Z seems not to bind Fe³⁺.

Iron uptake of *Mycobacterium smegmatis* involving mycobactin S was studied with ⁵⁵Fe³⁺ (293). Mycobactin is not given off into the surrounding medium but is located instead in the lipid envelope of the cell and is active in the trans-membrane transport of Fe³⁺ (taxi mechanism). Iron is released at the inside of the membrane by a reductive mechanism. There is some evidence that salicylic acid is the extracellular siderophore.

Corrugatin (34) (Fig. 9) is the siderophore of *Pseudomonas corrugata* (302). It was also found as secondary siderophore of several pyoverdinin producing *Pseudomonas* strains as *P. fluorescens*, occasionally in slightly modified forms such as

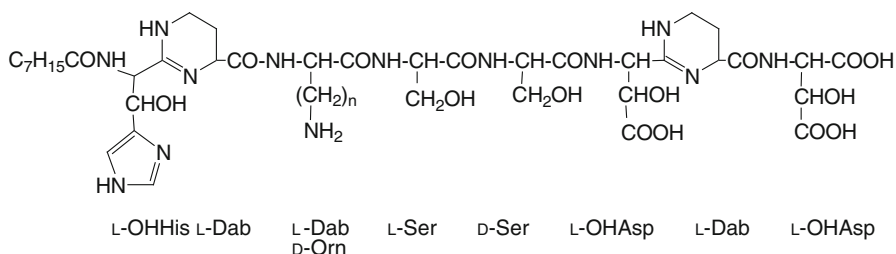


Fig. 9. Corrugatin ($n = 2$, L-Dab) (**34**) and omicorrugatin ($n = 3$, D-Orn) (**35**)

- 36:** RCO-OHAsp-Dab-Ser-acetylOHOrn-Ser-acetylOHOrn
37: RCO-OHAsp-Ser-Ser-Gln-acetylOHOrn-Ser-acetylOHOrn
38: RCO-acetylOHOrn-acetylOHOrn-Ser-acetylOHOrn (2 D-, 1L-Orn, L-Ser)
39: RCO-OHAsp-Ser-Gln-Ser-acetylOHOrn-Dhb-Ser-cOHOrn

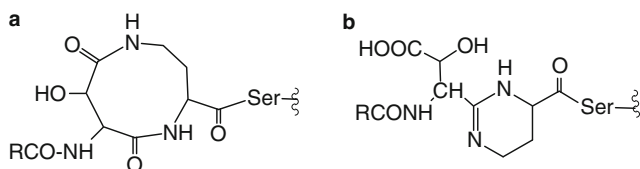


Fig. 10. Amphiphilic marine siderophores

omicorrugatin (**35**) where one Dab is replaced by Orn (**218**), or with OHHis instead of OHAsp as the C-terminus (*S. Matthijs*, unpublished).

A group of amphiphilic siderophores was isolated from marine bacteria (**410**), the marinobactins (Fig. 10, **36**), from *Marinobacter* sp., aquachelins (Fig. 10, **37**), from *Halomonas aquamarina* (**215**, **217**), the amphibactins (Fig. 10, **38**), from *Vibrio* sp. (**216**), and the loihichelins (Fig. 10, **39**), from *Halomonas* sp. (**150**). They all comprise series of related molecules differing in the nature of the saturated or unsaturated fatty acid (for amphibactins and loihichelins also 3-hydroxy fatty acids) linked to the N-terminus (see also ochrobactins and synechobactins, Sect. 4.1). Structure elucidations were effected by spectroscopic methods and degradation studies. For the marinobactins a N-terminal nine-membered lactam ring was suggested to be formed by an amide bond between the carboxyl group of Asp and the C-4 amino group of Dab (Fig. 10, **a**). It may be suggested that rather a condensation with the amide carbonyl group had occurred (Fig. 10, **b**; cf. Chart 1). This would keep the α -hydroxycarboxyl grouping of OHAsp intact, which acts as a binding site for Fe^{3+} and is essential for photolytic degradation. The rather scarce structural data presented do not allow a decision to be made. The siderophores show a strong affinity to lipid membranes (**389**). The Fe^{3+} complexes of aquachelins and marinobactins suffer degradation under sunlight irradiation. For the Fe^{3+} -aquachelin complexes the formation of Fe^{2+} , of hydrophobic and of hydrophylic cleavage

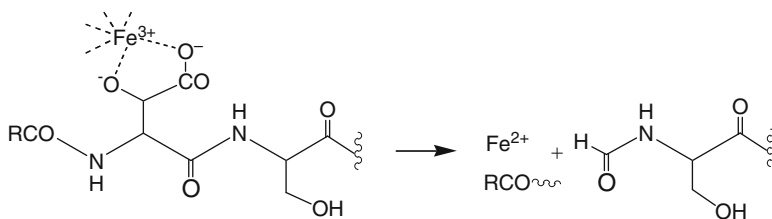


Chart 2. Light-induced degradation of Fe^{3+} -aquachelins

products was observed. For the latter a *N*-formyl-Ser terminus was suggested based on mass spectral data (Chart 2) (12). There is evidence that this type of photolytic degradation is common for siderophores containing α -hydroxycarboxyl ligands (13, 150, 401).

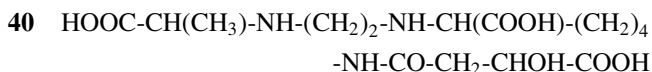
2.9. *Pseudomonas mendocina* Siderophores

From *Pseudomonas mendocina* five siderophores were isolated by chromatography. They are reported to have identical molecular masses of 1,152 Da (the also reported (3a) value of 929 Da is an error; *L. E. Hersman*, private communication) and an identical amino acid composition, which has not been revealed (141a). Color reactions show the presence of a hydroxamate, but not of a catecholate grouping. A gene analysis suggests a partial sequence acyl-Asp-Dab-Ser-formylOHOrn-Ser-formylOHOrn where asparagine could be OHAsp and the C-terminal ornithine cOHOrn (9b). In which way the five isomeric siderophores with identical molecular masses differ from each other is not clear.

3. Siderophores Based on Diamino- and Triaminoalkane Skeletons

3.1. *Rhizobactin*

Rhizobactin (40) is the siderophore of *Rhizobium meliloti* (328). It contains one α -hydroxycarboxylic acid and two α -amino acid units as probable binding sites for Fe^{3+} . Acid hydrolysis yields *inter alia* L-malic acid. The stereochemistry of the other two chiral centers is not known.



3.2. Catecholate Siderophores

For other catecholate siderophores, see the peptide-based siderophores above (Sect. 2.7) and the citric acid derivatives below (Sect. 4.3); for a review on syntheses, see (24), for a general review, (38).

The tricatecholate siderophore protochelin (41) (Fig. 11) was obtained from a methanol – bacterium (351). Subsequently it was also found to be produced by *Azotobacter vinelandii* (72, 360) together with its constituents 2,3-dihydroxybenzoic acid, azotochelin (bis-DHB lysine) (70) and aminochelin (mono-DHB cadaverine) (273). Cepaciachelin from *Burkholderia cepacia* (15) lacks the DHB residue from the aminochelin part of protochelin. The amino acid in all compounds is L-lysine. *Azotobacter vinelandii* shows an interesting rationale when confronted with a deficiency in iron supply. At concentrations $>7 \mu\text{M}$, 2,3-dihydroxybenzoic acid is secreted, between 3 and $7 \mu\text{M}$, the di- and tricatecholate siderophores are produced, and at still lower concentrations, it is resorted to azotobactin D (see above Sect. 2.2) (72). Myxochelin A from *Angiococcus disciformis* (197) and *Nonomuraea pusilla* (239a) can be considered as a reduction product of azotochelin (lysinol instead of Lys). The absolute configuration of lysinol (*S*) was determined by synthesis. Both antipodes show about the same antitumor activity (239a).

Pistillarin was first isolated from *Clavariadelphus pistillaris* and from several *Ramaria* spp. (Basidiomycetes) (334). Recently, it was found to be produced also by the marine fungus *Penicillium bilaii* (56). Like siderochrome II below it is a spermidine derivative substituted only at the terminal NH_2 -groups (N^1, N^{10} -di-(3,4-dihydroxy)benzoyl-spermidine). Its synthesis and that of siderochrome II was reported, their siderophore activity and their complexation with Fe^{3+} (1:1 complexes) was investigated (102, 299). A derivative of pistillarin substituted at all three amino functions has not been reported yet.

When DHB is bound to serine or threonine cyclization may occur resulting in an oxazoline ring (*cf.* above anachelin, Sect. 2.3, and mycobactins, Sect. 2.8). It has been discussed whether the oxazoline nitrogen atom may act as a ligand site (see below, (303)). This would explain why DHB is replaced by a salicylic acid residue in some cases.

To this group of siderophores belong photobactin (42a) from *Photobacterium luminescens* (Fig. 12) (66), derived from 1,4-diaminobutane substituted by DHB and by cyclized DHB-Thr ($^1\text{H-NMR}$ data indicate that the substituents of the oxazoline ring are in *trans* positions; the absolute stereochemistry is not known),

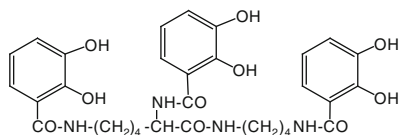


Fig. 11. Protochelin (41)

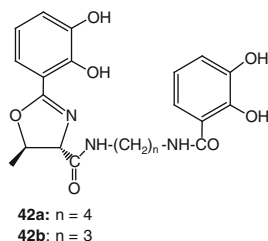


Fig. 12. Photobactin (**42a**), serratiochelin (**42b**)

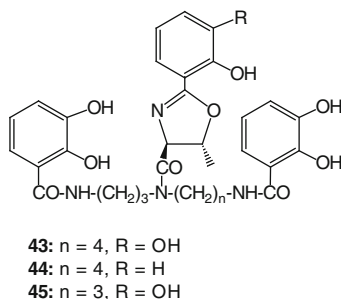


Fig. 13. Agrobactin (**43**), parabactin (**44**), fluvibactin (**45**)

and its lower homolog serratiochelin (**42b**) from *Serratia marcescens* derived from 1,3-diaminopropane. Its structure including the absolute stereochemistry (L-Thr) was confirmed by synthesis (101).

Spermidine derivatives are agrobactin from *Agrobacterium tumefaciens* (Fig. 13, **43**) (268), for which the structure was confirmed by X-ray analysis (109) and synthesis of the hydrolyzed form (DHB-Thr) agrobactin A (283), and parabactin (Fig. 13, **44**) from *Paracoccus denitrificans* (284). Two syntheses are reported for parabactin (28, 28c, 255) (see Sect. 8.3). The open form (parabactin A) as well as the precursors 2,3-dihydroxybenzoic acid and a compound with a free central NH group (N^1 , N^{10} -di-DHB-spermidine, siderochrome II) were also found (347). The 1:1 Ga^{3+} /Lig complex shows Λ -*cis* configuration (28a). Parabactin also forms a 1:1 complex with Fe^{3+} (347) for which the structure was investigated by X-ray photoelectron and electron spin resonance spectroscopy. In particular, the question as to whether the oxazoline nitrogen acts as a binding site has been discussed. An experimental proof seemed not to be possible (303).

Iron transport was studied using the $^{55}\text{Fe}^{3+}$ - and ^3H -complexes of parabactin (25). After a quick uptake of 10% of both labels there was a continuing steady uptake of $^{55}\text{Fe}^{3+}$ while the amount of ^3H remained constant. This could either mean that after binding to the cell surface $^{55}\text{Fe}^{3+}$ only is transferred into the cell (“taxi mechanism”) or there is a fast re-export of the ligand. A decision in favor of the

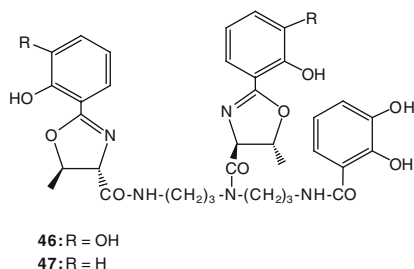


Fig. 14. Vibriobactin (**46**), vulnibactin (**47**)

taxi-mechanism could be reached by offering the Ga^{3+} complex of [^3H]-parabactin (Ga^{3+} cannot be released reductively in the cell and hence a re-export of the ligand is not possible). The uptake curve resembled that of ferri- [^3H]-parabactin: a small amount of complex is bound to the cell surface, but there is no transport of the ligand in the cell. This is in agreement with temperature studies (30 and 4°C). While the uptake of $^{55}\text{Fe}^{3+}$ decreases that of ^3H is not influenced.

Fluvibactin (Fig. 13, **45**) from *Vibrio fluvialis* (391) differs from agrobactin by replacement of spermidine by norspermidine. Also here the precursor with a free central NH group could be isolated. Vibriobactin from *Vibrio cholerae* (Fig. 14, **46**) contains two cyclized DHB-Thr substituents (129). Syntheses of agrobactin, fluvibactin and vibriobactin are published (26, 30, 308). In vulnibactin from *Vibrio vulnificus* (Fig. 14, **47**) (264) two DHB groups are replaced by salicylic acid units. The precursor with a free central NH group was also found.

3.3. Hydroxamic Acid Siderophores

Bisucaberin (**48**) from *Alteromonas haloplanktis* (181) is a cyclic dimer of succinyl- (*N*-hydroxycadaverin) (348); cf. the cyclic trimer proferrioxamine E (Table 6).



In putrebactin from *Shewanella putrefaciens* (201) cadaverine is replaced by putrescine (**49**, R = H). For the cyclic trimer, see proferrioxamine X₂ in Table 6. The arctic *S. gelidimarina* living in a habitat with extremely low iron supply produces a cell-associated hydroxamic acid siderophore with the mass 977 Da for $[\text{M}+\text{H}]^+$ of unknown structure (274).

Alcaligin from *Alcaligenes denitrificans* (260) and from *Bordetella* spp. (244) is a cyclic dimer of succinyl-*N*¹,3*S*-dihydroxyputrescine (**49**, R = H) confirmed by synthesis (402).

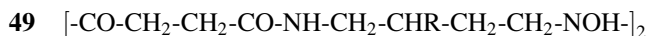


Table 6. Structures and nomenclature of proferrioxamines (pFO) (adapted from (110))^a

$\text{H}_2\text{N}-(\text{CH}_2)_m-\text{NOH}-\text{CO}-\text{CH}_2-\text{CH}_2-\text{CO}-\text{NH}-(\text{CH}_2)_n-\text{NOH}-\text{CO}-\text{CH}_2-\text{CH}_2-\text{CO}-\text{NH}-(\text{CH}_2)_o-\text{NOH}-\text{CO}-\text{CH}_2-\text{CH}_2-\text{CO}-\text{NH}-(\text{CH}_2)_p-\text{NOH}-\text{CO}-\text{CH}_2-\text{CH}_2-\text{COOH}$									
pFO	cyclic	m	n	o	p	N-terminus	C-terminus	Abbreviation	References
A ₁	–	5	5	4	0	–	Ac	pFO _{554Ac}	(185a)
A ₂	–	5	4	4	0	–	Ac	pFO _{544Ac}	(185a)
B	–	5	5	5	0	–	Ac	pFO _{555Ac}	(30e)
D ₁	–	5	5	5	0	Ac	Ac	Ac-pFO _{555Ac}	(185b)
D ₂	+	4	5	5	0	–	Suc	pFO _{455c}	(185a)
E ^b	+	5	5	5	0	–	Suc	pFO _{555c}	(155a, 186)
G ₁ ^c	–	5	5	5	0	–	Suc	pFO ₅₅₅	(186a)
G _{2a}	–	5	5	4	0	–	Suc	pFO ₅₅₄	(115)
G _{2b} ^c	–	5	4	5	0	–	Suc	pFO ₅₄₅	(115)
G _{2c} ^c	–	4	5	5	0	–	Suc	pFO ₄₅₅	(115)
H	–	5	5	0	0	Suc	Ac	Suc-pFO _{55Ac}	(1)
T ₁	+	5	5	5	5	–	Suc	pFO _{5555c}	(115)
T ₂	+	4	5	5	5	–	Suc	pFO _{4555c}	(115)
T ₃	+	3	5	5	5	–	Suc	pFO _{3555c}	(115)
X ₁	+	4	4	5	0	–	Suc	pFO _{445c}	(115)
X ₂	+	4	4	4	0	–	Suc	pFO _{444c}	(115, 398)
X ₇	+	3	5	5	0	–	Suc	pFO _{355c}	(115, 398)

^aStructures were not established for C and F (R_f values and physical constants) (30d), T₄-T₆, and X₈, X₉ (mass spectra) (115)

^bIdentical with norcardamin (186, 338)

^cAccompanied by “truncated” compounds without the terminal succinic acid unit (G₁₁, G_{2bt}, G_{2ct}) (115, 398)

Alcaligin forms at pH 2.0 a 1:1 and at pH 6.0 a 2:3 Fe-to-ligand complex. The structure (Plate 3) of the (Fe³⁺)₂Lig₃ complex was studied by X-ray analysis (156). One ligand bridges two metal ions while the remaining two are coordinated with a single Fe³⁺ each. The metal centers show Λ -configuration.

Alcaligin E from *Alcaligenes eutrophus* is described from color tests as a phenolic siderophore (126a). According to a recent publication (90a) it is identical with staphyloferrin B, a citrate siderophore (Sect. 4.2). No further information is given to resolve these discrepancies.

A group of related siderophores comprises the desferri- or deferriferrioxamines (occasionally abbreviated as desferrioxamines) or proferrioxamines. Originally they were obtained from Actinomycetes, mainly *Nocardia* and *Streptomyces* spp. (187) and later found to be produced also by *Erwinia* spp. (several representatives) (e.g. (30a, 113, 115, 180)), *Arthrobacter simplex* (B), *Chromobacterium violaceum* (E) (246a), and by *Pseudomonas stutzeri* (several) (229a, 246, 398). They consist of three (or in rare cases four) mono-*N*-hydroxy-1,4-diaminobutane (putrescine), mono-*N*-hydroxy-1,5-diaminopentane (cadaverine) or (rarely) mono-*N*-hydroxy-1,3-diaminopropane units connected by succinic acid links. The hydroxylated terminus carries an acetyl or a succinyl (as in the structural formula heading Table 6)

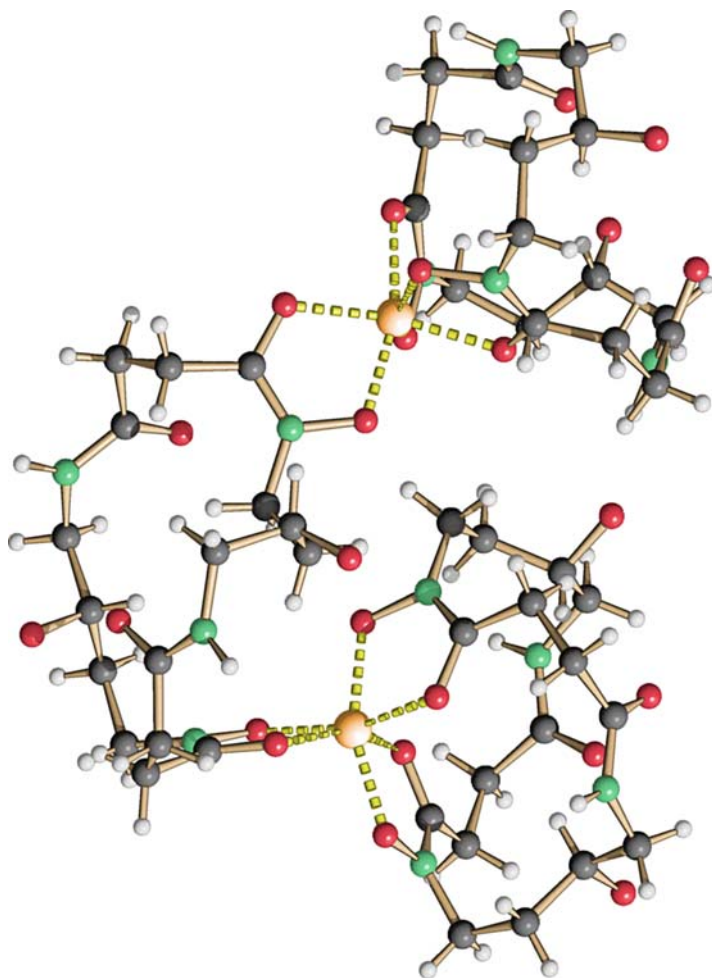


Plate 3. X-ray structure of ferri-alcigin (ferri-49)

residue, and in the latter case the free carboxyl group and the free N-terminus may form a macrolactam. The terminal acid residue can also be missing (referred to as “truncated”) (115, 398). By feeding of suitable diamino precursors to the culture medium unnatural analogs can be obtained (111, 194, 227). At *pH* values above 6.5 (Fe^{3+})₂Lig₃ complexes prevail, in more acidic media Fe^{3+} Lig is formed (194). The crystals of the Fe^{3+} Lig complexes of ferrioxamine D₁ and E are racemic mixtures of Λ -*cis* and Δ -*cis* coordination isomers (154, 366a). The outer membrane receptor protein of *Erwinia amylovora* was structurally determined (180). Siderophore activity was demonstrated for ⁵⁵Fe-labeled ferrioxamine E (30a). For the mass spectrometric analysis, see (112a).

Originally the various natural representatives had been designated by capital letters, but later a nomenclature system was proposed (110). In short, the indices and modifications as listed in Table 6 ($p = 0$ means that the entire fourth diaminoalkane-succinyl unit is missing) are grouped around the acronym pFO. The system is essentially self-explanatory; for details and possible extensions see the original publication.

4. Citrate Siderophores

For a review, see (39). Some citrate siderophores are accompanied by cyclic imide structures formed by the loss of water from the central carboxyl group and a lateral amide NH (Chart 3). They are usually designated by an A following the name of the siderophore. Free citric acid can be a true siderophore, e.g. for *Bradyrhizobium* spp. (205), *Pseudomonas aeruginosa* (213), and *Mycobacterium smegmatis* (228a). The mode of the uptake differs. *Bradyrhizobium* and *Pseudomonas* incorporate ferric citrate but *Pseudomonas* shows also a citrate mediated Fe^{2+} uptake, while in the case of *Mycobacterium* no citrate enters the cell. Ferric citrate is a complex system depending on the pH of the solution and the relative concentration of the two constituents (333a, 333b). In an acidic milieu equimolar concentrations form $[\text{FeCit}]^-$, at about pH 4 polymerization starts resulting at pH 8–9 in an insoluble complex with an iron hydroxide core and citrate ions bound to the surface. With a citrate excess species like $[\text{FeCit}_2]^{5-}$ are discussed.

It should be mentioned that the central carbon atom of citric acid becomes chiral when the two peripheral carboxy groups are substituted differently (examples will be found below). For enzyme reactions it is a prochirality center. This has been shown for vibrioferrin (58) and staphyloferrin B (59).

4.1. Siderophores with Two Hydroxamic Acid Units

In siderophores of this series, 1,3-diaminopropane, 1,5-diaminopentane, or lysine (by its α -amino group) is connected to the outer two carboxyl groups of citric acid.

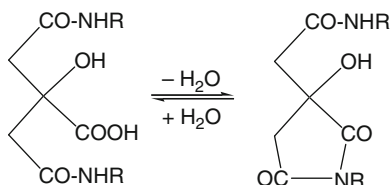


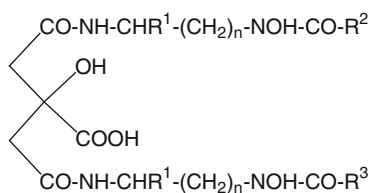
Chart 3. Cyclization of citrate siderophores to amidic structures

These spacers, in turn, are acylated and derivatized by a *N*-hydroxy group thus forming hydroxamic acids. For a synthesis concept see (404).

Schizokinen (Fig. 15, 50) was first isolated from *Bacillus megaterium* (53), subsequently from *Ralstonia solanacearum* (43), *Rhizobium leguminosarum* (339), and several species of the cyanobacterium *Anabena* (e.g. (326)). It was named after its cell division promoting effect observed with *Bacillus* cultures (200). Its structure was elucidated by degradation and spectral data and confirmed by synthesis (43, 202, 237, 248). For a compilation of details on structural data the review (39) should be consulted. Both natural and synthetic schizokinen is accompanied by the cyclized schizokinen A (43, 202, 237, 248). Schizokinen forms a 1:1 complex with Fe^{3+} , but at the central hydroxy group acetylated schizokinen yields $(\text{Fe}^{3+})_2\text{Lig}_3$. This proves that the central unit is one of the binding sites (285). Also *N*-deoxy-schizokinen from *Bacillus megaterium* lacking one hydroxamic acid unit still binds Fe^{3+} (158). Whether it acts as a siderophore is not known.

The schizokinen-mediated Fe^{3+} transport in *Bacillus megaterium* was studied by double labelling with ^{59}Fe and ^3H (8). At 37°C, uptake of ^{59}Fe and of ^3H are parallel during the first 30 sec, then that of ^{59}Fe continues until it levels off after 2 min, while that of [^3H]-schizokinen drops to a low constant level. At 0°C, uptake of both labels reaches this low level which is obviously due to the binding of the ferri-siderophore to the cell surface. At 37°C, transport into the cell, release of iron, and re-export of the ligand follow. Apparently a shuttle mechanism takes place, cf. the experimental results obtained with parabactin (Sect. 3.2) indicative of a taxi mechanism.

Arthrobactin (Fig. 15, 51) was obtained from *Arthrobacter* spp. and originally described as the growth factor of *A. terregens*, the “terregens factor” (51). Its structure was elucidated (207) and confirmed by synthesis (202). Also the structure



50: $\text{R}^1 = \text{H}$, $\text{R}^2 = \text{R}^3 = \text{CH}_3$, $n = 2$

51: $\text{R}^1 = \text{H}$, $\text{R}^2 = \text{R}^3 = \text{CH}_3$, $n = 4$

52: $\text{R}^1 = \text{H}$, $\text{R}^2 = \text{R}^3 = (E)\text{-CH=CH-(CH}_2\text{)}_4\text{-CH}_3$, $n = 2$

53: $\text{R}^1 = \text{COOH}$, $\text{R}^2 = \text{R}^3 = \text{CH}_3$, $n = 4$

54: $\text{R}^1 = \text{COOH}$, $\text{R}^2 = \text{R}^3 = (E)\text{-CH=CH-C}_6\text{H}_5$, $n = 4$

55: $\text{R}^1 = \text{COOH}$, R^2 and R^3 alkyl or alkenyl groups, $n = 4$

56: $\text{R}^1 = \text{H}$, $\text{R}^2 = \text{CH}_3$, $\text{R}^3 = (E)\text{-CH=CH-(CH}_2\text{)}_6\text{-CH}_3$, $n = 2$

57: $\text{R}^1 = \text{H}$, $\text{R}^2 = \text{CH}_3$, $\text{R}^3 = \text{alkyl groups}$, $n = 2$

Fig. 15. Citrate siderophores with two hydroxamic acid units

of acinetoferrin from *Acinetobacter haemolyticus* was established (Fig. 16, **52**) (265) and confirmed by synthesis (375). It shows strong interaction with lipid membranes like the marine liposiderophores above (211) (Sect. 2.8).

Aerobactin (Fig. 15, **53**) was first isolated from *Aerobacter* (*Enterobacter*) *aerogenes* (126), *Enterobacter cloacae* (368) and subsequently from various enterobacteria such as *Escherichia* (376), *Salmonella* (225), *Shigella* (277), *Yersinia* (340), but also from *Erwinia carotovora* (163), *Pseudomonas* sp. (52) and *Vibrio* spp. (141, 266). Aerobactin is an important virulence factor for enterobacteria (75). Aerobactin contains L-lysine. A synthesis is described (222). The bright orange Fe^{3+} complex was investigated in detail (predominant Λ configuration in solution, stability constant, redox potential) (138). Fe^{3+} transport was studied by double labelling (^{59}Fe and ^3H) (8). The results corresponded to those obtained with schizokinen. Aerobactin binds to the same receptor as the bacteriocin cloacin DF13 and thus alleviates the growth inhibiting effect of the latter (368).

Nannochelin C (Fig. 15, **54**) from the myxobacterium *Nannocystis exedens* contains two L-Lys and two (*E*)-cinnamic acid units. The reported mono- and di-methyl esters (nannochelin B and A) may be artifacts from the work-up (198). A synthesis is described (29) (see Sect. 8.4). The ochrobactins (Fig. 15, **55**) isolated from the sea-shore bacterium *Ochrobactrum* sp. (214) with the spacer L-lysine are membrane active due to the fatty acid residues (saturated C_8 and (*2E*)-unsaturated C_8 and C_{10}); cf. lipopeptidic siderophores in Sect. 2.8.

Rhizobactin 1021 (Fig. 15, **56**) (for rhizobactin, see diaminoalkane-based siderophores, Sect. 3.1) from *Rhizobium meliloti* (281), contains an acetyl and an (*E*)-decenoyl group. Its Fe^{3+} complex in aqueous solution is Λ -configured and forms an equilibrium between a monomeric and a dimeric form that can be separated by chromatography. A synthesis is described (404).

Synechobactins (Fig. 15, **57**) from the cyanobacterium *Synechococcus* (165), contain an acetyl and C_{12^-} , C_{10^-} , and C_8 -saturated acid residues and thus belong to the amphiphilic marine siderophores (cf. Sect. 2.8). Both rhizobactin 1021 and the synechobactins are substituted unsymmetrically. Hence, for each, the central C-atom of citric acid is chiral, but its stereochemistry has not been determined.

Awaitins are synthetic homologs of siderophores (A: **53**, $n = 3$; B: **50**, $n = 3$; C: **53**, $n = 2$) "awaited" to be found in nature, so far without success (405).

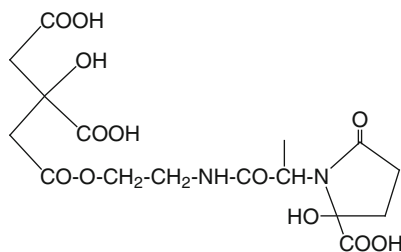


Fig. 16. Vibrioferrin (cyclic form) (**58**)

4.2. Siderophores with 2-Oxoglutaric Acid Units

N-Alkylated 2-oxoglutaric acid derivatives cyclize at neutral pH values to two epimeric 5-carboxy-5-hydroxy-2-oxopyrrolidine structures (Chart 4). In this way, α -hydroxycarboxylic acid groupings are formed that can act as ligand sites for Fe^{3+} .

Vibrioferrin (**58**, Fig. 16) was isolated from *Vibrio parahaemolyticus*. The stereochemistry of the central citric acid C-atom is *R*, that of the alanine part is *S* as shown by stereospecific synthesis (411). Iron uptake was studied with $^{55}Fe^{3+}$ proving that vibrioferrin acts as a siderophore despite the fact that it has only five ligand sites, the two α -hydroxy acids and the free citric acid carboxyl group. Possibly a solvent molecule satisfies the eighth octahedral position (393, 411). Vibrioferrin is also formed by *Marinobacter* spp. It is a weak Fe^{3+} chelator (complexing constant 10^{24}). Its Fe^{3+} complex is very susceptible to photodegradation by oxidative decarboxylation of the cyclized 2-oxoglutaric acid unit yielding a succinimide ring. This species cannot bind Fe^{3+} . The concomitantly formed Fe^{2+} (*cf.* Chart 2) is reoxidized to fairly soluble Fe^{3+} hydroxo complexes, which are readily taken up by the bacteria (410).

Staphyloferrin B (**59**, Fig. 17) is produced together with staphyloferrin A (see below Sect. 4.4) by *Staphylococcus hyicus* and other staphylococci (94, 131), by *Ralstonia eutropha* (250) (= *Cupriavidus metallidurans* (90a)). Comparison of its CD spectrum with those of model compounds suggests the (*S*)-configuration of the central citric acid C-atom. Mass spectral investigations show a 1:1 Fe^{3+} -to-ligand ratio, and NMR studies of the Ga^{3+} complex confirm the participation of the two α -hydroxy- and of the α -amino acid functions in complex formation. Uptake studies with $^{55}Fe^{3+}$ showed that staphyloferrin B acts as a siderophore, but it is less efficient than staphyloferrin A.

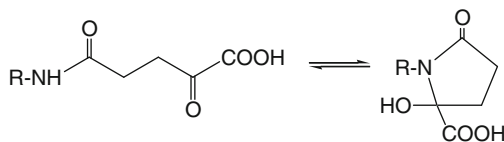


Chart 4. Cyclization of 2-oxoglutaric acid substituents

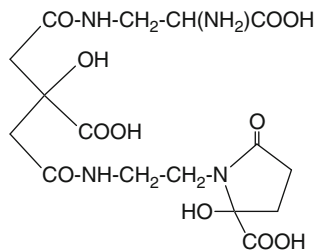


Fig. 17. Staphyloferrin B (cyclic form) (**59**)

Achromobactin (**60**, Fig. 18) is produced by *Erwinia chrysanthemi* in addition to chrysoabactin (see above under the catecholate siderophores, Sect. 2.7). It has two chiral centers, a L-Dab unit and the central citric acid C-atom (not determined) (249). Recently, achromobactin was also found to be produced by *Pseudomonas syringae* (30b), a very versatile bacterial species (see pyoverdine, Sect. 2.1, and yersiniabactin, Sect. 5).

4.3. Siderophores with Two Catecholate Units

In petrobactin, spermidine residues are bound to citric acid substituted with 3,4-dihydroxybenzoyl (27), and not 2,3-dihydroxybenzoyl units (Fig. 19, **61**), as assumed originally (14). One or both of the substituents can carry a sulfonic acid group in the 2-position of the aromatic ring (Fig. 19, **62** and **63**) (142, 149); cf. also (40). Petrobactin was originally obtained from *Marinobacter hydrocarbonoclasticus* (14) and subsequently from *Bacillus anthracis* (195, 382), *B. cereus* and *B. thuringiensis* (195a), its sulfonated derivatives from *Marinobacter* spp. It is probably identical with the incompletely characterized anthrachelin (123).

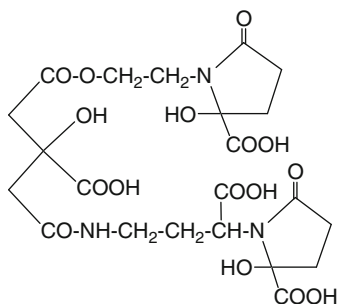
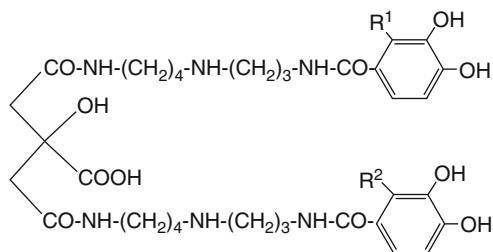


Fig. 18. Achromobactin (cyclic form) (**60**)



61: $R^1 = R^2 = H$

62: $R^1 = H, R^2 = SO_3H$

63: $R^1 = R^2 = SO_3H$

Fig. 19. Petrobactin (**61**), petrobactin monosulfonic acid (**62**), petrobactin disulfonic acid (**63**)

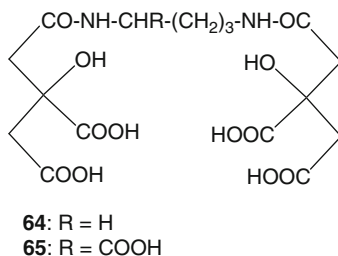


Fig. 20. Rhizoferrin (**64**), staphyloferrin A (**65**)

4.4. Siderophores with Two Citric Acid Units

(*S,S*)-(enanti)-Rhizoferrin (Fig. 20, **64**) was obtained from *Ralstonia pickettii* (251). It is the optical antipode of the fungal (*R,R*)-rhizoferrin first isolated from *Rhizopus microsporus* (93) and subsequently found to be a common siderophore of Zygomycetes (358). It is accompanied by two dehydration products, which are due to the formation of one or two imide rings (*cf.* Chart 3). UV spectral studies revealed that rhizoferrin forms a 1:1 Fe^{3+} -to-ligand complex despite the fact that it has only two α -hydroxy acid binding sites (95). NMR studies of the Ga^{3+} complex proved the twofold symmetry of the complex and showed that only the carboxyl groups, but not the hydroxy groups are deprotonated between *pH* 5.5 and 9.0. The Fe^{3+} complex is chiral and shows Λ -configuration (58). Uptake studies suggest a shuttle mechanism (61). While *Ralstonia* accepts both antipodes with equal rates *Rhizopus* shows a clear preference for its native (*R,R*)-enantiomer (251).

Staphyloferrin A (Fig. 20, **65**) is a second siderophore of *Staphylococcus* spp. (226). D-Ornithine connects the two citric acid parts. Due to the unsymmetrical link the central C-atoms of the citric acid units are chiral, but their stereochemistry has not been determined. Another consequence of the asymmetric structure is that two mono- and one di-dehydration products are observed. Staphyloferrin A forms a 1:1 Fe^{3+} -to-ligand complex, which is preferentially Λ -configured. For steric considerations only *cis*-(*SR'*) or *cis*-(*RS'*) arrangements can be considered. Uptake experiments with ^{55}Fe showed that it is a true siderophore (193).

4.5. Legiobactin

Legionella pneumophila produces a siderophore named legiobactin, which shows no catecholates or hydroxamate reactions (206). Enzymatic studies suggest a citrate structure in agreement with the data obtained by mass spectrometry (molecular mass *ca.* 350 Da) and NMR (three carbonyl and ten aliphatic C atoms). It is not clear yet as to whether legiobactin is essential for the iron acquisition in the aqueous habitat of the bacterium or during lung infection (2, 65).

5. Pyochelin and Related Structures

This group comprises condensation products of salicylic acid with cysteine giving a thiazoline ring. For a review, see (310). Some structurally related compounds will also be mentioned here. Salicylic acid isolated from *Burkholderia (Pseudomonas) cepacia* was named azurochelin (333). It was found to act as a siderophore, e.g. for *Pseudomonas fluorescens* (230) and *P. syringae* (178); see also *Mycobacterium smegmatis* (Sect. 2.8). For details on the siderophore activity of salicylic acid, see (359).

The structure of pyochelin (for a detailed bibliography, see (37)), a secondary siderophore of *Pseudomonas aeruginosa* and of *Burkholderia cepacia* was established (73) as 2-(2-*o*-hydroxyphenyl-2-thiazolin-4-yl)-3-methylthiazolidine-4-carboxylic acid. It consists of a mixture of two easily interconvertible stereoisomers (pyochelin I and II) differing in the configuration of C-2''. They can be separated by chromatography, but in methanolic solution (not in DMSO) the equilibrium (ca. 3:1) is restored quickly. For a discussion of the mechanism of isomerization, see (37, 317).

The relative and absolute stereochemistry (4'*R*,2''*R*,4''*R*) of pyochelin I (Fig. 21, 66) were established by an X-ray analysis of its Fe³⁺ complex (316). Fe³⁺ is associated with the phenolate and the carboxylate oxygen ions and with the two nitrogen atoms. Two of these units are bridged by an acetate ion and a water molecule satisfying the remaining two ligand loci of Fe³⁺ (Plate 4). However, by titration a (Fe³⁺)/pyochelin ratio of 1:2 has been determined at pH 2.5 (370). This may be due to a partial protonation of the complexing sites. From *Burkholderia cepacia*, a mixed complex was obtained comprising Fe³⁺/pyochelin/cepabactin 1:1:1 (see Sect. 6 below) (188). An X-ray analysis has been performed of ferri-pyochelin bound to its outer membrane receptor (67a). Pyochelin II has the configuration (4'*R*,2''*S*,4''*R*). It does not complex Fe³⁺ (140).

Several syntheses resulting in mixtures of stereoisomers (C-4' and C-2'') have been developed (6, 301, 397) (Sect. 8.5). *Pseudomonas fluorescens* CHA0 produces *enantio*-pyochelin (394). The two optical antipodes are not accepted reciprocally by the two *Pseudomonas* species.

Pyochelin is a non-ribosomal condensation product of salicylic acid with two molecules of cysteine (289). Intermediates with one cysteine unit are aeruginic acid (Fig. 21, 67) first isolated from *Pseudomonas aeruginosa* (390), and (+)-(*S*)-4,5-dihydroaeruginic acid, from *Pseudomonas fluorescens* (57). Detailed studies (274a) suggest that *N*-hydroxybenzoyl-L-cysteine bound to the synthetase

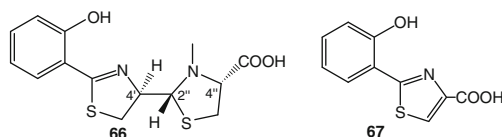


Fig. 21. Pyochelin I (66), aeruginic acid (67)

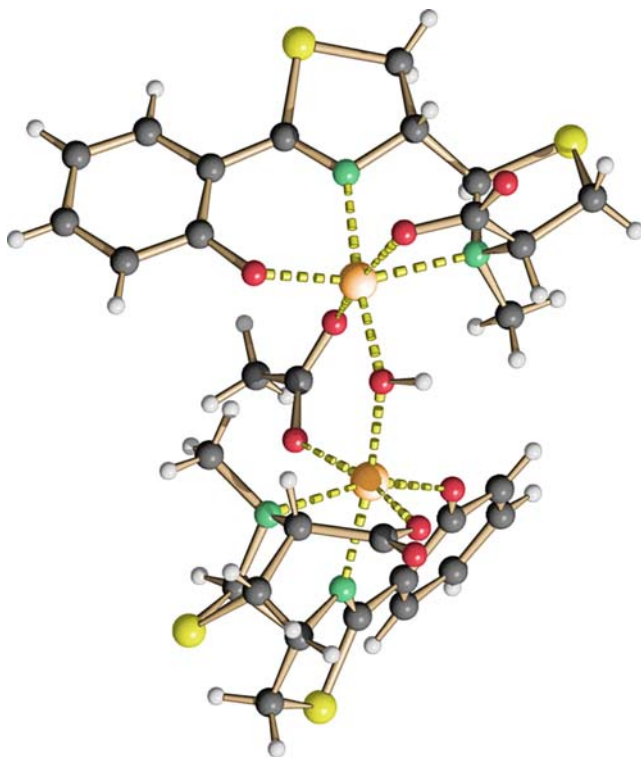


Plate 4. X-ray structure of ferri-pyochelin I (ferri-66)

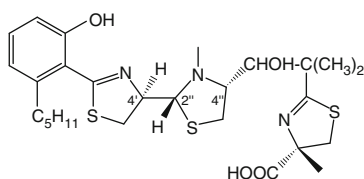


Fig. 22. Micacocidin (68)

racemizes, that bound dihydroaeruginoic acid is still a racemate, and that in the further steps only the 4'(*R*) isomer is used.

Micacocidin (Fig. 22, 68) from *Pseudomonas* sp. complexes Fe^{3+} and other metal ions (189, 190). Whether it acts as a siderophore has not been investigated. A stereospecific synthesis was elaborated (161, 161a), but the same isomerization problems at C-4' and C-2'' were encountered as had been observed with pyochelin (see Note 14 in (161)).

Yersiniabactin (Fig. 23, 69) was obtained from *Yersinia* spp., and is produced also by *Pseudomonas syringae* (49) and *Escherichia coli* (178). Its structure was elucidated independently by two groups and given the names yersiniabactin (96)

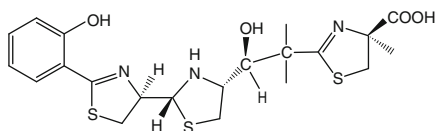


Fig. 23. Yersiniabactin (**69**)

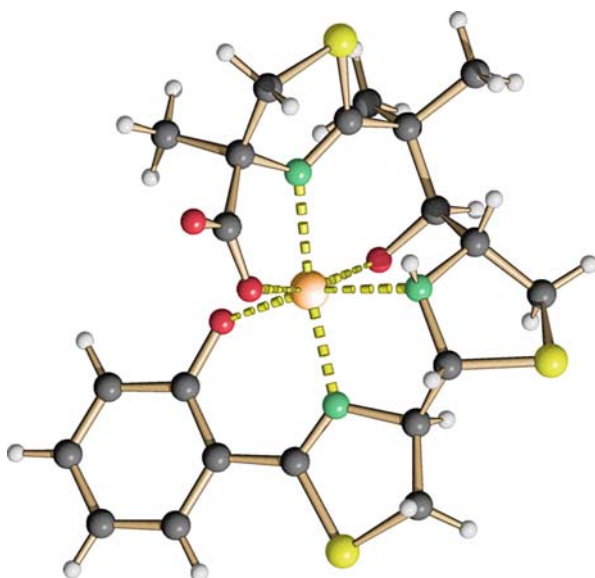


Plate 5. X-ray structure of ferri-yersiniabactin (ferri-**69**)

and yersiniophore (**64**). The configurations of the four chiral centers were not determined, but epimerization probably at C-10 (corresponding to C-2'' of pyochelin) was indicated. A recent X-ray analysis (Plate 5) of the Fe^{3+} complex (**238**) established the absolute stereochemistry [N-2 (*R*), C-9 (*R*), C-10 (*R*) as for pyochelin, C-12 (*R*), C-13 (*S*), C-19 (*S*)], with Δ -configuration.

Anguibactin (Fig. 24, **70**) from *Vibrio anguillarum* (**171**) contains DHB condensed with Cys (stereochemistry not determined). It is accompanied by a biosynthetic by-product (**311**) without the histamine part as its methyl ester.

6. Miscellaneous Siderophores

Desferri-ferrithiocin from *Streptomyces antibioticus* (Fig. 25, **71**) (**4**, **254**) is structurally related to the pyochelin group. It is (*S*)-configured and forms a $\text{Fe}^{3+}\text{Lig}_2$ complex (**131a**).

Cepabactin (Fig. 25, **72**) from *Burkholderia cepacia* (**232**) forms a $(\text{Fe}^{3+})\text{Lig}_3$ complex (**386**) and a mixed Fe^{3+} complex with pyochelin (Sect. 5).

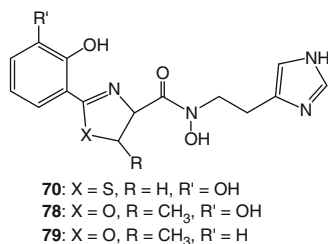


Fig. 24. Anguibactin (70), pre-acinetobactin (78), pre-pseudomonine (79)

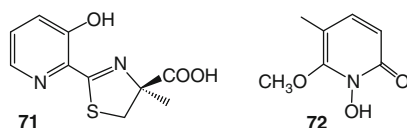


Fig. 25. Desferri-ferrithiocin (71), cepabactin (72)

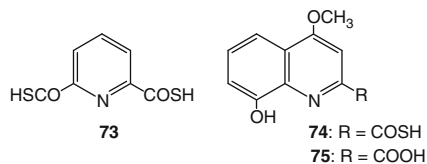


Fig. 26. Pyridine-di(monothiocarboxylic acid) (73), thioquinaldic (74), quinaldic acid (75)

Pyridine-2,6-di(monothiocarboxylic acid) (Fig. 26, 73) [for a review, see (36), *cf.* also (37)] was obtained from *Pseudomonas putida* (262) and later from *Pseudomonas stutzeri* (203). It forms a brown Fe^{3+} complex and a blue Fe^{2+} complex (both FeLig_2) (143), which may be accompanied by complexes carrying two additional cyanide ions (145). An X-ray analysis (Plate 6) of the Fe^{3+} complex of 73 shows a distorted octahedral symmetry (143). There is evidence that a sulfenic acid residue (-CO-SOH) is the biosynthetic link between -COOH and -COSH (144).

From iron-deficient cultures of *Pseudomonas fluorescens*, 8-hydroxy-4-methoxy-monothioquinaldic acid (thioquinolobactin) together with the corresponding quinaldic acid (quinolobactin) (Fig. 26, 74 and 75), could be isolated (258). Quinolobactin can act as an alternative siderophore of *Pseudomonas fluorescens* (245), although it is the hydrolysis product of the thioacid (220). Its synthesis and complex formation as $(\text{Fe}^{3+})\text{Lig}_2$ was described (98).

Pseudomonine (Fig. 27, 76) is produced by *Pseudomonas fluorescens* strains (7, 228) and by *P. entomophila*, where it can act as a secondary siderophore (209). The substituents on C-4 and C-5 of the isoxazolinone ring are in *trans* positions (311). The complex formation has not been studied. *In vitro* enzyme-catalyzed synthesis studies (311, 388) showed that initially the intermediate pre-pseudomonine (Fig. 24, 79) is formed, which non-enzymatically rearranges to pseudomonine.

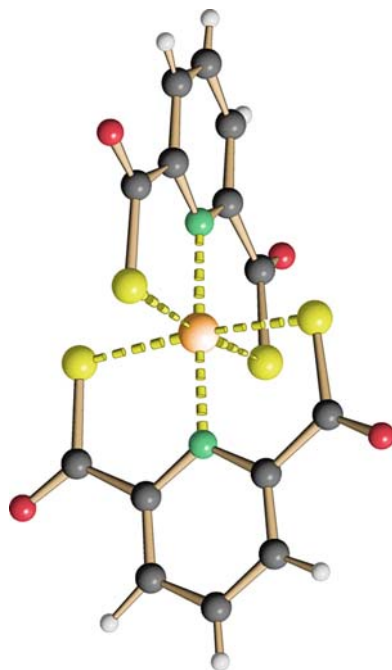


Plate 6. X-ray structure of the Fe^{3+} -complex of **73**

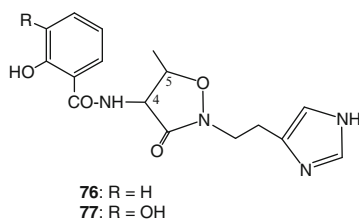


Fig. 27. Pseudomonine (**76**), acinetobactin (**77**)

An analogous set of studies demonstrated that acinetobactin from *Acinetobacter baumannii* ([392](#)) has actually the structure **77** shown in Fig. [27](#) and that the one originally proposed (Fig. [24](#), **78**) is that of pre-acinetobactin. In contrast, the thiazoline ring of anguibactin (Fig. [24](#), **70**) (see above Sect. 5) is stable. Acinetobactin forms a 1:1 complex with Fe^{3+} .

Domoic acid (Fig. [28](#), **80**) ([263](#)) is a neuro-phyco toxin responsible for the mortality of wildlife and for amnesic shellfish poisoning (ASP) of humans during algal bloom. Domoic acid was first isolated from the red alga *Chondria armata* (“domoi” in Japanese), and it is produced also by diatoms, such as *Pseudo-nitzschia* spp. For the latter, evidence has been presented that it is involved in iron acquisition ([307](#)).

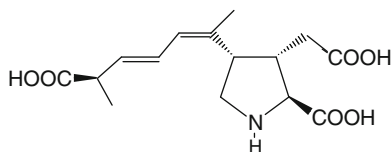


Fig. 28. Domoic acid (**80**)

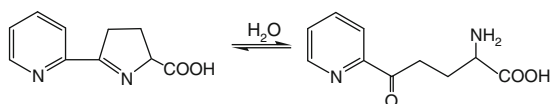


Chart 5. Proferrosamin A (**81**)

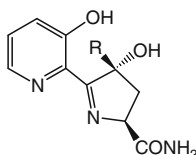


Fig. 29. Siderochelin A (R = CH₃) (**82**), B (C-3 epimer) (**83**) and C (R = C₂H₅) (**84**)

The smallest hydroxamate siderophore is *N*-methyl-*N*-thioformylhydroxylamine, CH₃-N(OH)-CHS, named thioformin (*100*) or fluopsin (*325*). The synthesis was described (CH₃-N(OH)-CHO + P₂S₅ or CH₃-N(OH)-H + HCSSK) (*100, 166a*). It forms a purple Fe³⁺Lig₃ complex. *Pseudomonas mildenbergii* produces *N*-methyl-*N*-phenylacetylhydroxylamine (CH₃-N(OH)-CO-CH₂-C₆H₅) (*159*), which also forms a purple Fe³⁺ complex.

7. Fe²⁺ Binding Ligands

Pseudomonas roseus fluorescens (*288*), *Pseudomonas* GH (*324*) and *Erwinia rhapontici* (*113*) produce pro-ferrosamine A (**81**), also named pyrimine, which forms a red (Fe²⁺)Lig₃ complex. Under acidic conditions, an open form of pro-ferrosamine A prevails, which cannot bind Fe²⁺ (Chart 5). Pro-ferrosamine B is probably an artifact produced by condensation of pro-ferrosamine A with CHO-COOH. Pro-ferrosamine A is essential for iron uptake by *Pseudomonas* (*367*) and for the pathogenicity of *Erwinia* (*114*).

Structurally closely related is the *Nocardia* metabolite, siderochelin, for which the structure and relative and absolute stereochemistry were all established by X-ray crystallography (*208, 267*). It is a mixture of two epimers A and B (Fig. 29, **82** and **83**). Siderochelin C, with an ethyl residue (Fig. 29, **84**), was obtained from a different actinomycete, tentatively identified as *Streptoalloteichus* sp. (*239*).

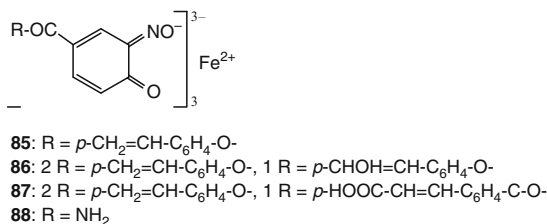


Fig. 30. Ferroverdins

The green pigments produced by *Streptomyces* spp. chelating Fe²⁺ with *o*-nitrosophenolate residues are occasionally referred to as siderophores, but whether they are really involved in iron metabolism has not been investigated. Ferroverdin A (**11**) forms a (Fe²⁺)Lig₃ complex (**55**), with the ligand being *p*-vinylphenyl-3-nitroso-4-hydroxybenzoate (Fig. 30, **85**). In ferroverdin B and C, one of the three ligands is substituted at the vinyl group (Fig. 30, **86** and **87**) (**346**, **361**). From *Streptomyces murayamaensis*, a precursor of ferroverdin was obtained (Fig. 30, **88**) (**69**).

For a further chelator of Fe²⁺, see pyridine-2,6-di(monothiocarboxylic acid) above (Sect. 6).

8. Selected Syntheses

In this section the syntheses of several typical siderophores will be presented in a summarized form pointing out interesting features.

8.1. *Anachelin H* (**10**)

The challenge lay in the stereochemically correct synthesis of the polyketide part of the molecule. Starting from L-serine (**89**) (Chart 6) by C₂-elongation steps, reduction of the obtained keto functions including adequate protection and deprotection, and introduction of the salicylic acid residue the four stereoisomeric 3,5-diols (**90**) were obtained. Comparison of the ¹H-NMR data with those of anachelin (**10**) showed that the isomer with (3*R*,5*S*,6*S*) configuration was the correct starting material.

The chromophore part was prepared from Boc-protected *N,N*-dimethyl-L-DOPA (**91**), reduction to the diamine **92** and tellurium-mediated oxidative ring closure (**93**). The free amino group of **94** was coupled with protected L-Ser and L-Thr-D-Ser (**95**) and then the two constituent parts were connected and deprotected yielding **10** (**121**).

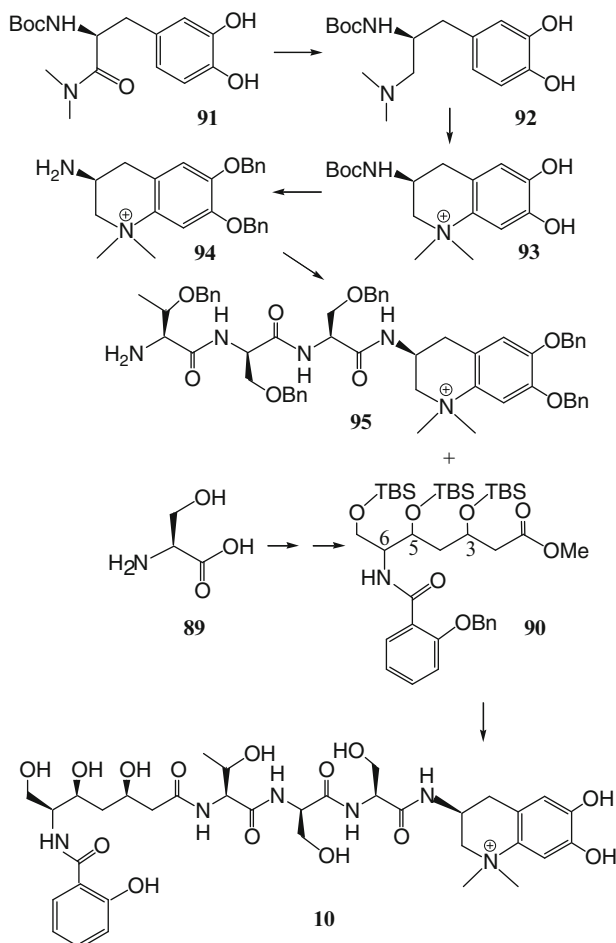


Chart 6. Synthesis scheme of anachelin H (**10**)

8.2. *Alterobactin* (**26**)

Several building blocks were prepared separately (Chart 7). Methyl *trans*-cinnamate gave by *Sharpless* enantiocontrolled dihydroxylation a diol from which by a series of stereo- and regioselective transformations (**96**) and Ru-catalyzed oxidation for transformation of the phenyl into a carboxyl group accompanied by adequate protection (**97**) and deprotection steps the protected OHAsp derivative **98** was obtained.

The protected (*S*)-4,8-diamino-3-oxooctanoic acid **99** was reduced with NaBH₄, the resulting mixture of diastereomers was separated and the (3*R*,4*S*)-product was derivatized with benzylated DHB (**100**). Then derivatized D-Ser-Gly was added and the serine OH-group was esterified with the protected OHAsp (**101**). The Gly carboxyl group was finally set free.

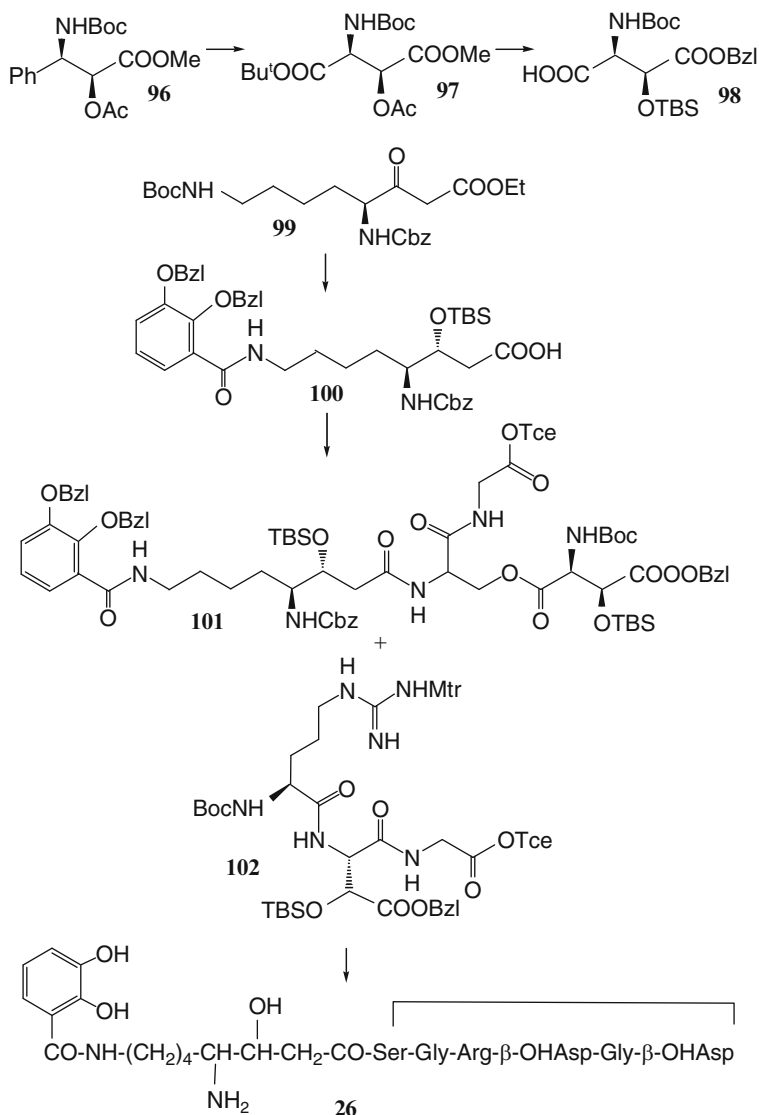


Chart 7. Synthesis scheme of alterobactin (**26**)

The synthesis of the remaining part of the molecule started from a condensation of protected Gly with the OHAsp derivative **98**, and subsequently with protected Arg (**102**). In the resulting protected tripeptide the Boc group from the Arg residue was removed. Connection of the two building blocks between Gly and Arg was followed by ring closure between Ser and Gly. Deprotection yielded finally alterobactin (**26**) (**83**).

8.3. Parabactin (44)

Here the critical step is the formation of the oxazoline ring. Both the stereochemistry of the two chiral centers and its acid lability had to be considered. Two approaches have been published. They can be modified for other members of this class.

The terminal NH_2 -groups of N^5 -benzylspermidine (Chart 8) were acylated with 2,3-dimethoxybenzoyl chloride and the benzyl group was removed by hydrogenolysis (28b). N^1, N^{10} -bis(2,3-dimethoxy)benzoylspermidine (**103**) was then reacted with protected L-threonine (**104**). The Boc group was removed with CF_3COOH and the methoxy groups were cleaved with BF_3 (**105**). Subsequent reaction with 2-hydroxybenzimidazole (**106**) gave parabactin (**44**) (28, 28c).

In the second synthesis (Chart 9) of **44** the carboxyl group of benzoyl-protected salicylic acid was activated by transformation into the 1,2-thiazolidine-2-thione derivative **107** and reacted with D-threonine. The methyl ester was debenzoylated reductively (**108**). Treatment with SOCl_2 resulted in cyclization accompanied by stereoinversion of C_β of threonine. The resulting *cis*-oxazoline derivative **109** was epimerized at C_α with $\text{C}_2\text{H}_5\text{ONa}$. Subsequent hydrolysis of the ester function gave the *trans*-carboxylic acid **110** which was reacted with N^1, N^{10} -bis(benzyloxy-carbonyl)spermidine by treatment with phenylbis-(2-thioxo-1,3-thiazolidine-3-yl)phosphinoyl (**111**). The remaining steps leading to **44** (removal of the N-protecting

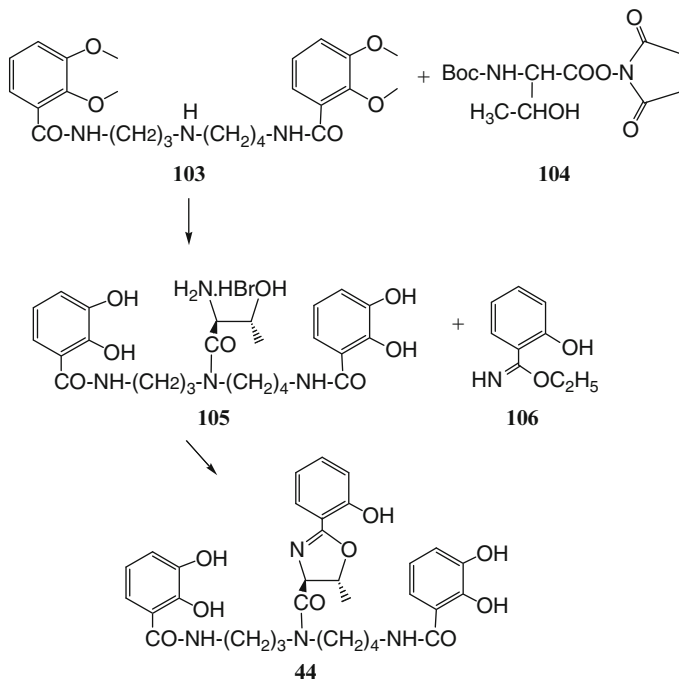


Chart 8. Synthesis I of parabactin (**44**)

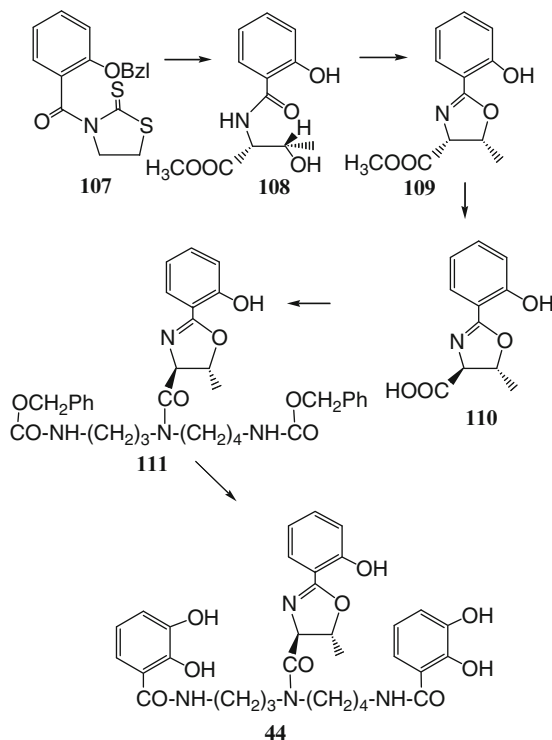


Chart 9. Synthesis II of parabactin (**44**)

groups, reaction with 2,3-diacetoxybenzyl chloride and cleavage of the acetoxy groups) were standard operations (255).

In a recent modification of the second synthesis (308) effected for fluvibactin (**45**) an *o*-xylene protection group was proposed (reaction of 2,3-dihydroxybenzoic acid methyl ester with 1,2-di(bromomethyl)benzene) which could be removed later by hydrogenolysis. The formation of the oxazoline ring from protected DHB-L-threonine methyl ester was achieved with Mo(VI) catalysts (e.g. (NH₄)₂MoO₄) without affecting the chiral centers. Derivatization of the primary amino groups of norspermidine with the protected DHB methyl ester was catalyzed by Sb(OC₂H₅)₃.

8.4. Nannoachelin A

For the condensation with the properly derivatized lysine part (**112**) 3'-*tert*-butyl-1,5-di-*N*-hydroxysuccinimidyl citrate (**113**) was used (Chart 10). It was prepared from 1,5-dimethyl citrate by reaction with *tert*-butyl acetate, alkaline hydrolysis of the methyl ester and coupling with *N*-hydroxysuccinimide by DCCI (237).

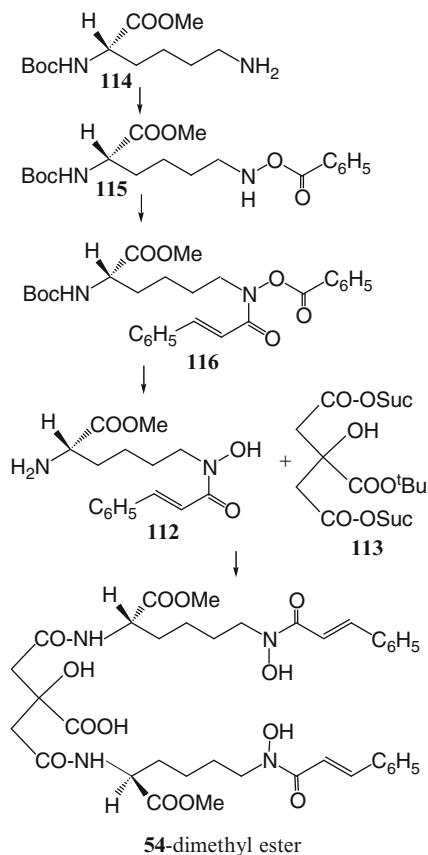


Chart 10. Synthesis of nannochelin A (**54**-dimethyl ester)

For the synthesis of the lysine part (**112**) N^2 -Boc-L-lysine methyl ester (**114**) was treated with benzoylperoxide/ Na_2CO_3 (**115**) and subsequently with *trans*-cinnamoyl chloride yielding **116**. The hydroxamate ester was deprotected with $\text{NH}_3/\text{CH}_3\text{OH}$ at -23°C and the Boc group was removed with CF_3COOH . Condensation with the citric acid 3-*tert*-butyl ester was effected with $(\text{C}_2\text{H}_5)_3\text{N}$. After cleavage of the ester with CF_3COOH nannochelin A (**54**-dimethyl ester) was obtained (**29**). The difficulties in the synthesis lay in the various functional and protecting groups, which had to be introduced and removed in a deliberate sequence.

8.5. Pyochelin

The problem encountered with all published syntheses (**6**, **301**, **397**) is the non-stereospecific formation of C-4' and the facile conversion of C-2''. The common approach (Chart **11**) consists in the reaction of 2-hydroxybenzoinitrile (**117**) with

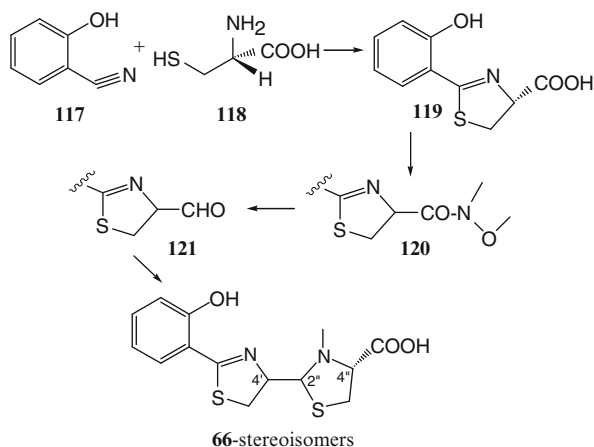


Chart 11. Synthesis of pyochelin stereoisomer mixture

L-cysteine (**118**) giving dihydroaeruginic acid (**119**), reduction of the carboxyl group to the aldehyde **121** and condensation of the latter with L-N-methyl-cysteine. Details will be given for the procedure worked out by Zamri and Abdallah (397). The first condensation step was effected in a phosphate buffer (pH 6.4) to minimize epimerization at C-4'. Then the carboxyl group was reacted with N,O-dimethylhydroxylamine (**120**) using diethylcyanophosphonate as condensation agent. Reduction with LiAlH_4 yielded the aldehyde **121**, which then was treated with L-N-methyl-cysteine. A mixture of the four stereoisomers of (**66**), ($4'R,2''S,4''R$), ($4'S,2''S,4''R$), ($4'R,2''R,4''R$), ($4'S,2''R,4''R$) in a ratio of 2:1:2:5 was obtained.

9. Epilog

The history of siderophores actually began towards the end of the nineteenth century when laboratories engaged in bacteriological research observed that certain bacterial cultures showed a green fluorescence, and when in 1891 the first attempts were reported to isolate the fluorescent pigment (later named pyoverdine, Sect. 2.1) produced by *Bacterium fluorescens liquefaciens* (*Pseudomonas fluorescens*), although it was not before 1978 that J.-M. Meyer demonstrated its being involved in the iron transport into the bacterial cell (37). Pyoverdins were among the centers of interest during the last decades, and other preferred topics were the fungal siderophores (Sect. 2.6), and more recently the marine lipopeptides (Sect. 2.8).

This review is mainly concerned with structural aspects of siderophores and their iron transport, intended to give a status report of what has been achieved up to late-2009. But the fields of interest in siderophores are much wider, spreading into

- genetics (identification of the genes responsible for the synthesis of the siderophores and their receptors (e.g. (403, 409)),

- medicine (siderophores as virulence factors (*e.g.* (75)), but serving also as carriers for antibiotics in a Trojan Horse strategy (*e.g.* (35a)),
- agriculture (starving phytopathogenic bacteria by binding iron (*e.g.* (187b, 406)),
- environmental problems (binding heavy metal ions (*e.g.* (90a)), degrading detrimental compounds (*e.g.* (205a)), mobilizing uranium and *trans*-uranium elements in contaminated soils (*e.g.* (242a)),

just to mention some areas. The diversity of scientific journals to be found in the References Section gives an idea of where information on siderophores can be hidden.

Structural work may take its time. Examples are *Pseudomonas mendocina* (Sect. 2.9) where the first structural data were reported in 2000 and the next pertinent publication appeared in 2008, or *Legionella pneumophila* (Sect. 4.5) whose legiobactin was first characterized in 2000, further details followed in 2007 and 2009, with loose ends in both cases. Only partially characterized siderophores are mentioned wherever data were available in order to stimulate further work. This would be worthwhile: siderophore research is a fascinating branch of natural products chemistry promising sometimes surprising results (*e.g.* (311, 388)).

Acknowledgement Many thanks are due to Dr. J. Neudörfl for preparing the Plates with siderophore X-ray structures. Data bases for the X-ray structures: Plate 1: FEPSBC 10; 3: TEQKQV; 4: YELJOP; 5: VENPAC; 6: CUHGUH.

Appendix

Table 7. Pyoverdins Isolated from *Pseudomonas* spp.

P.	Name	Peptide chain ^{a,b,c,d}	Mass ^e	References ^f
(a) Complete or fairly complete structures				
<i>Pyoverdins with a C-terminal cOHOrn</i>				
6 amino acids				
<i>f</i>	Ps (= B10 ^h)	ϵ Lys-OHAsp-Ala-aThr-Ala-cOHOrn	989	(352–354)
<i>f</i>	Py 9AW ⁿ	Ser-Lys-OHHis-aThr-Ser-cOHOrn	1043	(42)
<i>ap</i>	Py 4a ^l (= Py SB83)	Ala-Lys-Thr-Ser-AcOHOrn-cOHOrn	1046	(47)
<i>p</i>	iPy BTP1	Asp-Ala-Asp-AcOHOrn-Ser-cOHOrn	1047	(168)
7 amino acids				
<i>f</i>	Py PL7	Ser-AcOHOrn-Ala-Gly-aThr-Ala-cOHOrn	1046	(16)
<i>f</i>	Py BTP2	Ser-Val-OHAsp-Gly-Thr-Ser-cOHOrn	1049	(270)
<i>p</i>	Py G4R	Asp-Orn-(OHAsp-Dab)-Gly-Ser-cOHOrn ⁱ	1073	(33, 309)
	Py 2908	Ser-Orn-OHAsp-Ser-Ser-Ser-cOHOrn	1088	(373)
<i>ae</i>	Py T II ^g (=27853)	Ser-FoOHOrn-Orn-Gly-aThr-Ser-cOHOrn ^{bb}	1091	(350)
<i>f</i>	Py PL8	Lys-AcOHOrn-Ala-Gly-aThr-Ser-cOHOrn	1103	(16)

Table 7. (continued)

<i>P.</i>	Name	Peptide chain ^{a,b,c,d}	Mass ^e	References ^f
<i>p</i>	Py 11370	Asp- ϵ Lys-OH <u>Asp</u> - <u>Ser</u> -Ala- <u>Ser</u> - cOHOrn	1106	(48)
<i>p</i>	iPy 90-33	Asp-Lys-Thr-OH <u>Asp</u> -Thr-a <u>Thr</u> - cOHOrn 8 amino acids	1164	(345)
<i>p</i>	Py 90-51	Asp- ϵ Lys-OH <u>Asp</u> -Ser-Gly-a <u>Thr</u> -Lys- cOHOrn 9 amino acids	1234	(343)
<i>c, au</i>	Py Pau ^u	<u>Ser</u> -AcOHOrn-Gly-a <u>Thr</u> -Thr-Gln-Gly- <u>Ser</u> -cOHOrn	1277	(21)
<i>f</i>	Py 2392 (= A6 ^h)	<u>Lys</u> -AcOHOrn-Gly-a <u>Thr</u> -Thr-Gln-Gly- <u>Ser</u> -cOHOrn	1318	(23)
<i>p</i>	Ps 589A ^o	Asp- ϵ Lys-OH <u>Asp</u> - <u>Ser</u> -Thr- <u>Ala</u> - <u>Glu</u> - <u>Ser</u> -cOHOrn	1336	(279)
<i>p</i>	Py 2461 (=L1 ^h , WCS358 ^h)	Asp- ϵ Lys-OH <u>Asp</u> -Ser-a <u>Thr</u> - <u>Ala</u> -Thr- <u>Lys</u> -cOHOrn ^{cc}	1349	(365)
<i>ap</i>	Py 3b ^t	Asp-(AcOHOrn-Dab)-Thr-Ala-Thr-Thr- Gln-cOHOrn 10 amino acids	1358	(349)
<i>f</i>	Py 2798 (=W ^{aa})	(<u>Ser</u> -Dab)-Gly-Ser-OH <u>Asp</u> -Ala-Gly- <u>Ala</u> -Gly-cOHOrn	1187	(78)
<i>f</i>	Py 17400	<u>Ala</u> - <u>Lys</u> -Gly-Gly-OH <u>Asp</u> -(<u>Gln</u> -Dab)- <u>Ser</u> -Ala-cOHOrn ^t	1299	(77)
<i>p</i>	Py 1,2	Ser-Thr- <u>Ser</u> -Orn-OH <u>Asp</u> -(<u>Gln</u> -Dab)- <u>Ser</u> -a <u>Thr</u> -cOHOrn	1405	(130)
<i>f</i>	Py 1,3	<u>Ala</u> - <u>Lys</u> -Gly-Gly-OH <u>Asp</u> -(<u>Gln</u> -Dab)- Gly-Ser-cOHOrn	1285	(125)
<i>t</i>	Py 2192	<u>Ser</u> -Lys-Ser- <u>Ser</u> -Thr- <u>Ser</u> -AcOHOrn- Thr- <u>Ser</u> -cOHOrn	1424	(78)
<i>p</i>	iPy 90-44	Asp-Lys-AcOHOrn-Thr- <u>Ser</u> - <u>Ser</u> -Gly- <u>Ser</u> - <u>Ser</u> -cOHOrn ^s 11 amino acids	1408	(344)
<i>f</i>	Py 51W	<u>Ala</u> - <u>Lys</u> -Gly-Gly-OH <u>Asp</u> - <u>Gln</u> - <u>Ser</u> -Ala- Gly-a <u>Thr</u> -OHOrn	1375	(371)

^aIn part (a) D-amino acids are underlined; a broken line indicates either that the stereochemistry of the amino acid has not been determined or that a specific amino acid occurs both in the D- and the L-form, but a localization of the the two enantiomers has not been effected. In part (b) D-amino acids are indicated only when data are available from the literature

^bAbbreviations: *P*, *Pseudomonas*; *ae*, *aeruginosa*; *ap*, *aptata*; *as*, *asplenii*; *au*, *aureofaciens*; *c*, *costantini*; *ci*, *cichoriae*; *en*, *entomophila*; *f*, *fluorescens*; *li*, *libanensis*; *m*, *marginalis*; *mo*, *monteilii*; *p*, *putida*; *pa*, *palleroniana*; *r*, *rhodesiae*; *s*, *syringae*; *t*, *tolaasii*; *Ps*, pseudobactin; *Py*, pyoverdin; *iPy*, isopyoverdin; amino acids: 3-letter code - in addition: OHAsp, *threo*- β -hydroxy-Asp; OHHis, *threo*- β -hydroxy-His; OHOrn, *N*⁵-hydroxy-Orn; Ac(Fo,Bu)OHOrn, *N*⁵-acetyl (formyl, (R)- β -hydroxy-butryl) OHOrn; cOHOrn, *cyclo*-OHOrn (3-amino-1-hydroxy-piperidone-2); aThr, *allo*-Thr

^cAmino acids are bound to the chromophore or to the preceding amino acid by their α -amino group or in the case of Lys occasionally by its ϵ -amino group (indicated as ϵ Lys)

Table 7. (continued)

P.	Name	Peptide chain ^{a,b,c,d}	Mass ^e	References ^f
		12 amino acids		
<i>f</i>	Py GM	<u>Ala-Lys-Gly-Gly-OH</u> <u>Asp-Gln-Ser-Ala-</u>	1430	(242)
	Py 1547	<u>Ala-Ala-Ala-cOH</u> <u>Orn-Ser-Lys-Ala-AcOH</u> <u>Orn-Thr-Ala-Gly-Gln-Ala-Ser-Ser-OH</u> <u>Orn</u>	1547	(304)
<i>Pyoverdins with a C-terminal cyclo-tetra- or tripeptide</i>				
		cyclo-tetrapeptide		
<i>f</i>	Py G173	<u>Ser-Ala-AcOH</u> <u>Orn-(Orn-Asp-</u>	1175	(363)
	Py 96-312	<u>Ser-Ser-FoOH</u> <u>Orn-(Lys-FoOH</u> <u>Orn-Lys-</u>	1190	(315)
	Py 96.188	<u>Ser-Lys-FoOH</u> <u>Orn-(Lys-FoOH</u> <u>Orn-Glu-</u>	1232	(379)
		<u>Ser)</u>		
<i>ae</i>	Py C-E (= PAO1 ^h , ATCC 15692, Pa)	<u>Ser-Arg-Ser-FoOH</u> <u>Orn-(Lys-FoOH</u> <u>Orn-</u>	1333	(35, 81)
	Py 95-275 (= BTP7 ^h)	<u>Thr-Thr)</u> <u>Ser-Ser-FoOH</u> <u>Orn-Ser-Ser-(Lys-</u>	1364	(342)
		<u>FoOH</u> <u>Orn-Lys-Ser)</u>		
<i>f</i>	Py 12	<u>Ser-Lys-Gly-FoOH</u> <u>Orn-Ser-Ser-Gly-</u>	1520	(124)
		<u>(Lys-FoOH</u> <u>Orn-Glu-Ser)</u>		
		cyclo-tripeptide		
<i>f</i>	Py 13525 ^m	<u>Ser-Lys-Gly-FoOH</u> <u>Orn-(Lys-FoOH</u> <u>Orn-</u>	1160	(146)
		<u>Ser)</u>		
<i>pa</i>	Py 96-318	<u>Ser-Orn-FoOH</u> <u>Orn-Ser-Ser-(Lys-</u>	1263	(315)
		<u>FoOH</u> <u>Orn-Ser)</u>		
<i>f</i>	Py 18-1	<u>Ser-Lys-Gly-FoOH</u> <u>Orn-Ser-Ser-Gly-</u>	1391	(3)
		<u>(Lys-FoOH</u> <u>Orn-Ser)</u>		
<i>Pyoverdins with a C-terminal cyclodepsipeptide or a free carboxyl group</i>				
		6 amino acids		
<i>a</i>	PS 6.10	<u>Ala-Orn-OH</u> <u>Asp-Dab-AcOH</u> <u>Orn-Lys</u>	1091	(46)
		7 amino acids		
<i>ae</i>	Py R'	<u>(Ser-Dab)-FoOH</u> <u>Orn-Gln-FoOH</u> <u>Orn-</u>	1046	(305)
		<u>Gly)</u>		

^dParentheses indicate either a cycle formed by an amide or ester bond between the carboxyl group of the C-terminal amino acid and a side chain functionality of another amino acid or the condensation product of the NH₂ groups of Dab with the amide carbonyl group of the preceding amino acid giving a tetrahydropyrimidine ring (see Chart 1)

^eNominal molecular mass for a Py or iPy chromophore with a succinic acid side chain; the exact mass is about 0.5 Da higher

^fReferences to complete structure elucidations. For further details see (37)

^gProbably identical with the pyoverdinin of *Pseudomonas aeruginosa* ATCC 9027 (212)

^hThe structure published originally had to be corrected or amended; literature references to the originally proposed structure may be found in (37)

ⁱAccompanied by the not cyclized Dab form (M + 18)

^jAccompanied by a non-cyclic pyoverdinin with the same amino acid sequence

^kFor this pyoverdinin an ε-amino Lys linkage was claimed but not substantiated. It is probably identical with the pyoverdinin from *P. putida* 9AW where a α-amino Lys linkage was established
^l*P. aptata* is a pathovar of *P. syringae*. The same pyoverdinin was found produced by *P. fluorescens* SB83 (20). The identification of *P. aptata* may, therefore, be questioned (*cf.* also (179))

Table 7. (continued)

<i>P.</i>	Name	Peptide chain ^{a,b,c,d}	Mass ^e	References ^f
<i>ci</i>	PaB	εLys-OH <u>Asp</u> -Thr-(Thr-Gly-OH <u>Asp</u> -Ser)	1093	(50)
<i>s</i>	Py 19310	εLys-OH <u>Asp</u> -Thr-(Thr-Ser-OH <u>Asp</u> -Ser) ^j	1123	(179)
<i>ae</i>	Py R (=Pa6)	(Ser-Dab)-FoOH <u>Orn</u> -Gln-Gln-FoOH <u>Orn</u> -Gly 8 amino acids	1173	(127)
<i>p</i>	Ps A214 (= Ps 39167)	Ser-AcOH <u>Orn</u> -Ala-Gly-(Ser-Ala-OH <u>Asp</u> -Thr) ^l	1134	(365)
<i>f</i>	Py P19 (= Ps 7 SR1 ^h , Ps A 225)	Ser-AcOH <u>Orn</u> -Ala-Gly-(Ser-Ser-OH <u>Asp</u> -Thr) ^l	1150	(372)
<i>ch</i>	Py D-TR133	Asp-FoOH <u>Orn</u> -Lys-(Thr- <u>Ala</u> - <u>Ala</u> -FoOH <u>Orn</u> - <u>Ala</u>) ^{j,x}	1230	(17)
<i>f</i>	Py I-III	Asn-FoOH <u>Orn</u> -Lys-(Thr- <u>Ala</u> - <u>Ala</u> -FoOH <u>Orn</u> -Lys)	1286	(287)
<i>f</i>	CHAO	Asp-FoOH <u>Orn</u> -Lys-(Thr- <u>Ala</u> - <u>Ala</u> -FoOH <u>Orn</u> -Lys) 9 amino acids	1287	(387)
<i>p</i>	Py C	Asp-BuOH <u>Orn</u> - <u>Dab</u> -Thr-Gly-Ser-Ser-OH <u>Asp</u> -Thr	1370	(319)
<i>p</i>	Py BTP16	Asp-BuOH <u>Orn</u> - <u>Dab</u> -Thr-Gly-Ser-Ser-OH <u>Asp</u> -Thr ^v 10 amino acids	1370	(271)
<i>as</i>	Py fuscovaginae	εLys-OH <u>Asp</u> -Ala-(Thr- <u>Dab</u> -Gly-Gly-Thr-(OH <u>Asp</u> - <u>Dab</u>))	1316	(49a, 231)

(b) Partial or tentative structures*Pyoverdins with a C-terminal cOHOrn*

<i>p</i>	Thai	(Ser-Dab)-Thr-Ser-AcOH <u>Orn</u> -cOH <u>Orn</u>	1016	(306)
<i>f</i>	Py 244 ^k	Ser-εLys-OHHis-aThr-Ser-cOH <u>Orn</u>	1043	(132–134)
<i>p</i>	Py 12633 ^o	Asp-Lys-OH <u>Asp</u> -Ser-Thr-Ala-Glu-Ser-cOH <u>Orn</u>	1336	(80)

Pyoverdins with a C-terminal cyclo-tetra- or tripeptide cyclo-tetrapeptide

<i>f</i>	D47	Ser- <u>Orn</u> -FoOH <u>Orn</u> -(Lys-FoOH <u>Orn</u> -Glu-Ser)	1218	(119)
<i>r</i>	L25	Ser-Lys-FoOH <u>Orn</u> -Ser-Ser-Gly-(Lys-FoOH <u>Orn</u> -Ser-Ser)	1421	(119)

^mThe same pyoverdin was isolated from *P. chlororaphis* ATCC 9446 (146) and CNR15 (162). The reported isolation from *P. putida* KT2440 (297) is the result of a mix-up of strains (*J.-M. Meyer*, private communication)

ⁿProbably identical also with that from *P. fluorescens* 244

^oThe Py 589A is probably identical with the pyoverdin Py Pp 12633

^pEither the preliminary structural work or the identification of the strains may be questioned since screening of a large number of *P. aeruginosa* strains revealed the existence of only three siderovars characterized by the production of the pyoverdins Py C-E, Py R and Py Pa TII (234) plus probably of a mutant of Py R (R' (305)). Py Pa 15152 was shown to be identical with Pa D above (20)

^qThe structural proposals are tentative; Orn/Asn and Lys/Gln have the same mass, Lys may be incorporated in the peptide chain by its α- or its ε-amino group

Table 7. (continued)

<i>P.</i>	Name	Peptide chain ^{a,b,c,d}	Mass ^e	References ^f
<i>m</i>	G 76	cyclo-tripeptide Ser-Ser-FoOHOrn-Ser-Ser-(Lys- FoOHOrn-Ser)	1236	(119)
	DSM 50106	Ser-Lys-Gly-FoOHOrn-Ser-Ser-Gly- (Orn- FoOHOrn-Ser)	1377	(119)
<i>Pyoverdins where only limited mass spectral data are available^g</i>				
<i>p</i>	Py GS43	Lys-OHAsp-Ser-Ser-Ser-cOHOrn	1007	(231)
<i>li</i>	Py 96.195	Ala-Orn-OHAsp-Ser-Orn-Ser-cOHOrn	1091	(231)
	Py G 85	Ser-Lys-OHAsp-Ser-Orn-Ser-cOHOrn	1121	(231)
	Py G 76	Ser-Ser-FoOHOrn-Ser-Ser-Lys- (FoOHOrn-Ser)	1236	(231)
	Py HR6	Asp-ε-Lys-OHAsp-Ser-Ser-Thr-Thr- Thr-cOHOrn	1238	(231)
	LBSA1	Asp-Arg-AcOHOrn-Lys-Ser-Asp- cOHOrn	1260	(231)
<i>mo</i>	iPy Lille 1	Asp-Lys-AcOHOrn-Ala-Ser-Ser-Gly- Ser-cOHOrn	1291	(231)
<i>f</i>	Py G153	Ser-Lys-Ala-Ser-Ser- AcOHOrn-Ser- Ser-cOHOrn	1293	(231)
<i>en</i>	L48	Ala-Asn-Dab-OHHis-Gly-Gly-Ala-Thr- Ser-cOHOrn	1298	(219)
<i>p</i>	Py G172	Ala-Lys-Dab-OHAsp-Thr-Gly- OHAsp- Gly-Thr-Thr - H ₂ O	1335	(231)
<i>f</i>	Pf0-1	Ala-AcOHOrn-Orn-Ser-Ser-Ser-Arg- OHAsp-Thr	1381	(231)
<i>p</i>	90-136/ G 168	Ser-Lys-Ser-Ser-Thr-Thr-AcOHOrn- Ser-Ser-cOHOrn	1424	(231)
	IB3	Ser-Ala-Thr-Gln-Orn-AcOHOrn-Thr- Thr-Ala-Ser-Thr-Ala-Ala-cOHOrn	1764	(231)
<i>Various pyoverdins with incomplete structural data</i>				
<i>ae</i>	Py UNK ^p	Ser-Thr-Ser-Gly-OHOrn-OHOrn		(107)
<i>ae</i>	Pa 15152 ^p	2 Arg, 2 Orn, 3 Ser, 3 Thr		(107)
<i>p</i>	Py Pm	OHAsp, Lys, OHOrn, 2 Ser, 3 Thr		(212a)
<i>s</i>	Py Ps	Lys, OHOrn, 3 Ser, 3 Thr		(362)
<i>s</i>	Py PSS ^z	2 OHAsp, Lys, 2 Ser, 2 Thr		(68)
	<i>P. mildenbergii</i>	Glu, Lys, Ser, Thr ^w		(259)

^rThe reported amino acid composition cannot be correct. The minimum molecular mass calculated from it is about 120 u higher than the molecular mass determined by mass spectrometry. Also the amino acids acting as ligands for Fe³⁺ are missing

^s2 D-ser, 2 L-Ser

^tContains 2 Thr and one aThr. The amino acid analysis of the corresponding ferribactin gave D-Ala, L-Asp, L-Dab, D- and L-Glu, L-Orn, D-aThr, L-Thr and D-Tyr

^uThe same pyoverdin was isolated from *P. tolaasii* NCBBP 2192 (*P. constantinii*); the fact that the strain designated as *P. aureofaciens* does not produce phenazines casts doubts on the correct identification (364)

^v1 Thr, 1 aThr

^wRatios of 1:1:2:4 and 1:2:3:5 are reported for the pyoverdins from two strains of *P. mildenbergii*; for the second one a blocked N-terminus was demonstrated

^x1 D-Ala, 2L-Ala; the pyoverdin D-TR 133 is accompanied by a small amount of a pyoverdin where the second Ala is replaced by Gly

Table 7. (continued)

<i>P.</i>	Name	Peptide chain ^{a,b,c,d}	Mass ^e	References ^f
<i>p</i>	Py A1	Asx, Glx, 3 Gly, His, Lys, 4 Ser, Thr, Val ^f		(32)
<i>f</i>	BTP9 ^y	2 Lys, 2 FoOHOrn, 5 Ser		(269)
<i>p</i>	BTP14 ^{aa}	Asx, Dab, Glx, Gly, Orn, 2 Ser, Thr, aThr		(269)

^yProbably identical with the pyoverdins of BTP7 and BTP16 (private communication Dr. *M. Ongena*, Liège)

^zProbably identical with the pyoverdin Py 19310

^{aa}Identical with pyoverdin W mentioned in (79) (private communication Dr. *J.-M. Meyer*, Strasbourg)

^{bb}Accompanied by a variety with one AcOHOrn (187a)

^{cc}Accompanied by a small amount of a pyoverdin where Ala is replaced by Gly

Notes Added in Proof

Section 2.5

Coelichelin from *Streptomyces coelicolor* comprises $D\text{-}N^5\text{-formyl-}N^5\text{-hydroxy-Orn-D-aThr}$ bound to N^5 of $L\text{-}N^5\text{-hydroxy-Orn}$ whose N^2 is acylated by $D\text{-}N^5\text{-formyl-}N^5\text{-hydroxy-Orn}$ (412).

Section 2.6

Erythrochelin from *Saccharopolyspora erythraea* is a coprogen-type siderophore (Table 2) with $Ac^1 = \mathbf{i}$ and $Ac^2 = D\text{-Ser-D-}N^2, N^5\text{-diacetyl-}N^5\text{-hydroxy-Orn}$ (413).

Section 2.7

The transport system of *Bacillus subtilis* accommodates the Fe^{3+} complexes of enterobactin (Δ -configured), *enantio-D*-enterobactin and of corynebactin (bacillibactin) (both Λ). Since only Λ complexes can be bound to the receptor a configurational change from Δ to Λ is induced. Only the natural ferri-*L*-siderophores can be degraded enzymatically (399, 408).

From *Nocardia tenerifensis* the heterobactin JBIR-16 was obtained (30, R = DHB). The stereochemistry of the two Orn residues was not established. By mass spectrometry a 1:1 Fe^{3+}/Lig ratio was determined for the red complex (407).

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