

Microbial Metabolism of Pyridine, Quinoline, Acridine, and Their Derivatives under Aerobic and Anaerobic Conditions

JEAN-PIERRE KAISER,† YUCHENG FENG, AND JEAN-MARC BOLLAG*

Laboratory of Soil Biochemistry, Center for Bioremediation and Detoxification,
The Pennsylvania State University, University Park, Pennsylvania 16802

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INTRODUCTION

Two-thirds of known organic chemicals contain heterocyclic structures (70, 73). Heterocyclic aromatic compounds exist naturally in biological systems as electron carriers, nucleotides, energy storage molecules, mycotoxins, and alkaloids. Synthetic heterocyclic aromatic compounds are used as industrial solvents, dyes, explosives, pharmaceuticals, and pesticides. Waste materials containing large amounts of heterocyclic aromatic compounds are generated by the mining industry, coal tar- and oil shale-processing operations, wood-preserving facilities, and chemical manufacturing plants.

Because of their heterocyclic structure, these chemicals are more soluble in water than are their homocyclic analogs and can be more easily transported to groundwater. Despite the potentially serious consequences of such contaminants, insufficient research has been conducted to determine their fate in the environment (7, 8, 30). Therefore, it is important that we gain a clearer understanding of the processes by which they are degraded and the types of microorganisms involved.

Pyridine and its derivatives are important representatives of heterocyclic compounds. The pyridine ring is a major constituent of natural plant alkaloids, pyridoxyl derivatives, and coenzymes such as nicotinamides. Nicotine, anabasine, and cavadin are produced by plants and animals and were used as natural pesticides for many years. The herbicides paraquat, diquat, and picloram also contain the pyridine ring structure.

Microbial transformation of pyridine and its derivatives has been reviewed by Kost and Modyanova (68), Shukla (104), and Sims and O'Loughlin (112). In this review we present information currently available concerning the microbial metabolism of pyridine, quinoline, acridine, and their derivatives under aerobic and anaerobic conditions, with emphasis on metabolic pathways.

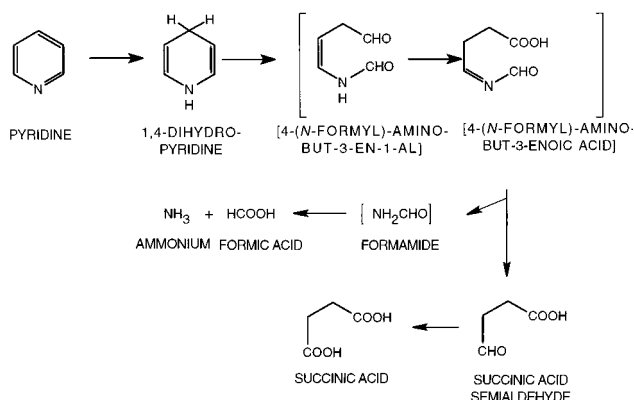
TRANSFORMATION OF PYRIDINE

Although research has shown that a number of organisms are capable of transforming heterocyclic aromatic compounds, the mechanism of cleavage of the pyridine ring remains unclear. In early work, Shukla (101) isolated from soil a *Corynebacterium* sp. and a *Brevibacterium* sp. capable of degrading pyridine. Cells grown on pyridine were unable to transform monohydroxylated pyridines. Similar observations were reported for *Nocardia* strain Z1. Hydroxylated pyridine derivatives were never observed during the transformation of pyridine (51). Further investigations with *Corynebacterium* sp. showed that formic acid and ammonium were formed and released into the culture medium during the degradation of pyridine and that in the presence of semicarbazide as an inhibitor, succinic acid semialdehyde accumulated as an intermediate product (108). Similar results were obtained for *Brevibacterium* sp. (109), with succinic acid semialdehyde and pyruvic acid accumulating in the presence of arsenite. Subsequently, Sims et al. (116) isolated from soil a *Micrococcus luteus* species which oxidized pyridine. Only aliphatic intermediates of pyridine metabolism were identified; therefore, the initial steps of ring cleavage remained uncertain.

Watson and Cain (140) investigated the metabolic pathways of pyridine biodegradation by *Bacillus* strain 4. When this spe-

* Corresponding author. Mailing address: 129 Land and Water Bldg., University Park, PA 16802. Phone: (814) 863-0843. Fax: (814) 865-7836. Electronic mail address: jmbollag@psu.edu.

† Present address: Swiss Federal Laboratories for Materials Testing and Research, CH-9001 St. Gallen, Switzerland.

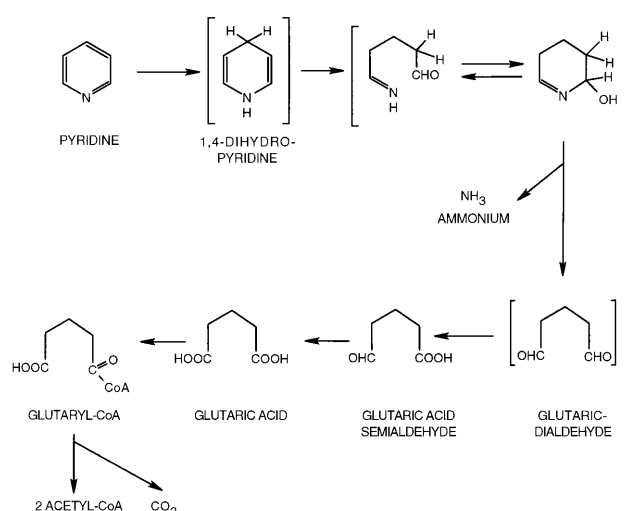
FIG. 1. Transformation of pyridine by *Bacillus* strain 4 (140).

cies was grown in the presence of semicarbazide as an inhibitor, several carbonyl compounds derived from pyridine, including succinic acid semialdehyde, accumulated. The products of *Bacillus* strain 4 were similar to those obtained during the transformation of pyridine by *Corynebacterium* and *Brevibacterium* spp. Mutants of *Bacillus* strain 4 deficient in succinic acid semialdehyde dehydrogenase were unable to grow on pyridine. In the presence of cyanide, further oxidation of formic acid (a by-product of pyridine metabolism) was inhibited, and formic acid accumulated in the culture broth. Experiments with [2-¹⁴C]pyridine showed that formic acid was derived from the carbon 2 atom of the heterocyclic ring. Formamide was not detected in the culture medium. The formation of succinic acid and formic acid from the carbon 2 atom of the pyridine ring indicates a ring fission between carbons 2 and 3. The metabolic steps in the transformation of pyridine to succinic acid semialdehyde by *Bacillus* strain 4 remain somewhat speculative but may follow the pathway suggested in Fig. 1.

Watson and Cain (140) also studied the transformation of pyridine by *Nocardia* strain Z1 and found that glutaric acid semialdehyde was produced as an intermediate product. The formation of an intermediate product with five carbon atoms indicates that the pyridine ring must be cleaved between the heteroatom and carbon 2. Therefore, the authors proposed a pathway for the metabolism of pyridine by *Nocardia* strain Z1 as outlined in Fig. 2.

Subsequently, Shukla and Kaul (110) isolated from soil a *Nocardia* sp. which was capable of transforming pyridine, pyridine-*N*-oxide, and 2-hydroxypyridine. In the presence of semicarbazide, transformation of pyridine resulted in the formation of succinic acid semialdehyde as an intermediate product. This *Nocardia* sp. followed a pyridine metabolic pathway similar to that reported by Watson and Cain (140) for *Bacillus* strain 4, including cleavage of the heterocyclic aromatic ring between carbons 2 and 3.

Ronen and Bollag (93) reported that an *Alcaligenes* sp. was able to rapidly mineralize pyridine under denitrifying conditions. The ratio of pyridine to nitrate strongly affected the pyridine metabolism. In further studies, the *Alcaligenes* sp. was reinoculated into a subsurface sediment and found to mineralize 10 μg of pyridine per g (94). Kaiser and Bollag (60) studied the transformation of pyridine by sewage sludge under aerobic, denitrifying, and sulfate-reducing conditions. Pyridine was degraded within 9 days under aerobic conditions and mineralized under denitrifying and sulfate-reducing conditions. The amounts of nitrate and sulfate that were utilized were 79

FIG. 2. Transformation of pyridine by *Nocardia* strain Z1 (140). CoA, coenzyme A.

and 85% of the amounts predicted from stoichiometric equations, respectively.

TRANSFORMATION OF HYDROXYLATED PYRIDINES

Houghton and Cain (51) reported that several *Achromobacter* spp. can transform monohydroxylated pyridines. 2- and 3-hydroxypyridine were transformed to 2,5-dihydroxypyridine, whereas 4-hydroxypyridine was converted to 3,4-dihydroxypyridine. After a short lag period, isolated bacteria growing on 2-hydroxypyridine were also able to transform 3-hydroxypyridine and vice versa. The 4-hydroxypyridine-degrading organisms were unable to transform 2- or 3-hydroxypyridine. In a continuation of this work, Cain et al. (15) reported that when 2- and 3-hydroxypyridine were oxidized to 2,5-dihydroxypyridine, production of maleamic acid occurred through ring cleavage. Cell extracts accumulated maleamic and formic acids and a small amount of ammonium, the latter probably formed by deamination of maleamic acid. The resulting maleic acid was further transformed to fumaric acid. Subsequently, Khanna and Shukla (62) reported that 2,5-dihydroxypyridine accumulated during the transformation of 3-hydroxypyridine by a gram-negative bacterium isolated from soil.

Gupta and Shukla (32) and Kolenbrander et al. (65) have described an *Arthrobacter* sp. which degrades 2-hydroxypyridine. During transformation of this pyridine derivative, a blue pigment, which was probably the result of 2,3,6-trihydroxypyridine condensation, appeared in the culture medium. Further degradation of 2,3,6-trihydroxypyridine involved the production of maleamic acid, maleic acid, and pyruvic acid as intermediate products. Similar observations were reported by Ensign and Rittenberg (19). The authors suggested that during the metabolism of 2-hydroxypyridine, a tripyridinol was produced, and that the blue pigment was generated from its oxidation. At low substrate concentrations, no pigment formation occurred, indicating that the excess substrate was shunted to a side reaction leading to formation of the pigment.

Considering all of the foregoing observations together, we propose the pathway for transformation of 2-hydroxypyridine presented in Fig. 3. It is likely that 3-hydroxypyridine is metabolized in a similar manner.

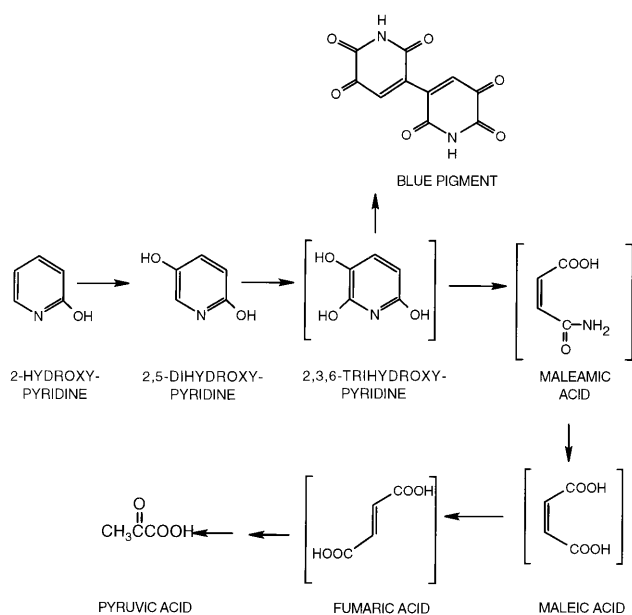
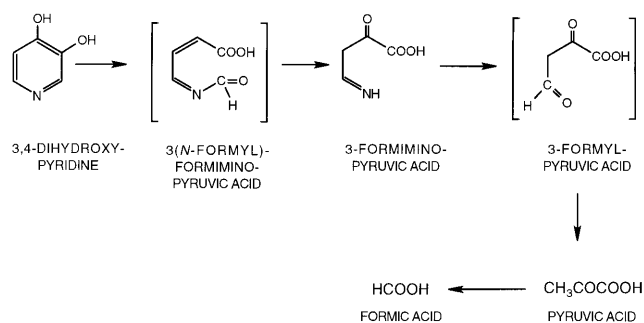


FIG. 3. Transformation of 2-hydroxypyridine (110).

Both dioxygenase and monooxygenase activities have been observed during the transformation of hydroxylated pyridines. The stoichiometry for the reaction between 2,5-dihydroxypyridine and oxygen in the presence of crude cell extracts of the *Achromobacter* sp. suggested that a dioxygenase was involved in the degradation process (15). However, degradation of 2-hydroxypyridine by cell extracts of various *Arthrobacter* spp. suggested monooxygenase activity (66). Enzymatic oxidation of 2-hydroxypyridine required molecular oxygen and NADH, each in equimolar amounts with respect to the substrate. The enzyme was stimulated by flavin mononucleotide but not flavin adenine dinucleotide (FAD) or riboflavin and was inhibited by the flavin analog quinacrin.

Kolenbrander and Weinberger (66) investigated the location of degradative genes for the transformation of 2-hydroxypyridine. In *Arthrobacter crystallopoietes*, the degradative gene appears to be carried by a plasmid; consequently, over time, the bacterium loses the ability to degrade 2-hydroxypyridine, because the plasmid is not always passed on during propagation. However, in *A. pyridinolis* and *A. viridescens*, the genes responsible for 2-hydroxypyridine metabolism are located on the chromosome.

As noted above, 4-hydroxypyridine is transformed via 3,4-dihydroxypyridine (52). Studies with $H_2^{18}O$ demonstrated that in the presence of $NADP^+$ or an artificial dye (methylene blue), the oxygen used for oxidation of 4-hydroxypyridine to 3,4-dihydroxypyridine by the enzyme 4-hydroxypyridine-3-hydroxylase was derived from water (141). Watson et al. (142) reported that cell extracts of an *Agrobacterium* sp. transformed 3,4-dihydroxypyridine into 3-formiminopyruvic acid, pyruvic acid, two molecules of formic acid, and ammonium. The identification of 3-formiminopyruvic acid as an intermediate restricted the possibility of ring cleavage to the bonds between carbons 2 and 3 or carbons 5 and 6. Since ring fission between unsubstituted atoms is rare, fission between carbons 2 and 3 is the most likely site. The ring cleavage mechanism we propose for the metabolism of 3,4-dihydroxypyridine by the *Agrobacterium* sp. is shown in Fig. 4. The lack of a requirement for NADH or other cofactors and the absolute requirement for

FIG. 4. Proposed ring cleavage mechanism for 3,4-dihydroxypyridine by an *Agrobacterium* sp. (142).

molecular oxygen during the metabolism of 3,4-dihydroxypyridine suggested that the enzyme responsible for this reaction was a dioxygenase.

Metabolism of hydroxylated pyridines under anaerobic conditions has been studied only rarely. Kaiser and Bollag (60) investigated the degradation of monohydroxypyridines under denitrifying and sulfate-reducing conditions by a mixed culture obtained from sewage sludge.

3-Hydroxypyridine was metabolized after a lag period of 2 months, whereas 2- and 4-hydroxypyridines were not transformed. This finding suggests that 3-hydroxypyridine is metabolized by a pathway different from that for 2- and 4-hydroxypyridine under these conditions.

TRANSFORMATION OF CARBOXYLATED PYRIDINES

2-Carboxypyridine

The metabolism of 2-carboxypyridine (2-picolinic acid) transformation started with a hydroxylation at position 6 of the heterocyclic aromatic ring, leading to 6-hydroxypicolinic acid. This oxidation could occur anaerobically in the presence of methylene blue and was unaffected by pyridine nucleotides, indicating that the oxygen was supplied by water and not by molecular oxygen (16, 126).

In addition to 6-hydroxypicolinic acid, other metabolites such as 3,6-dihydroxypicolinic acid and 2,5-dihydroxypyridine were isolated during the metabolism of 2-picolinic acid by a *Bacillus* sp. (103). 6-Hydroxypicolinic acid and 2,5-dihydroxypyridine were also found in the culture medium during transformation of 2-picolinic acid by another unidentified gram-negative coccus isolated from soil (111).

Bacillus cells caused α -oxoglutaric acid to accumulate in the culture medium when inhibited with arsenite. However, when cell growth was only partially inhibited with arsenite, pyruvic acid was produced (107). Tate and Ensign (125, 126) reported that picolinic acid-grown resting cells of *Arthrobacter picolinophilus* oxidized 6-hydroxypicolinic acid to carbon dioxide, ammonium, and water. Ohsugi et al. (78) reported that a bacterium isolated from soil utilized 2-picolinic acid, producing dicarboxylic acids with two-, five-, six-, seven-, and nine-carbon chains. The authors suggested that these dicarboxylic acids were precursors in the biosynthesis of desthiobiotin and found that desthiobiotin was also produced during the transformation of 2-picolinic acid.

Figure 5 shows the proposed pathway for metabolism of 2-picolinic acid.

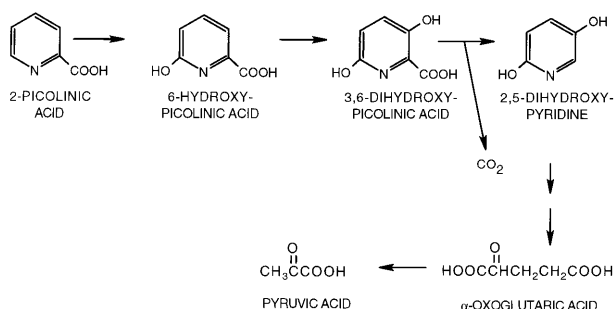


FIG. 5. Proposed metabolism of 2-picolinic acid (107).

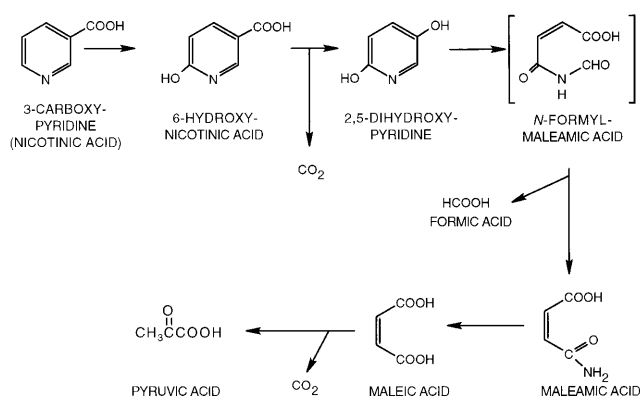
3-Carboxypyridine

3-Carboxypyridine (nicotinic acid) is the most frequently investigated of the pyridine derivatives. Hughes (52) reported that many strains of *Pseudomonas fluorescens* are able to oxidize nicotinic acid, with 6-hydroxynicotinic acid being the first intermediate product formed. Experiments with cell extracts demonstrated that during the transformation of nicotinic acid to 6-hydroxynicotinic acid, the oxygen of the hydroxyl group was derived from water and not from molecular oxygen (55, 59).

Further investigations into the oxidation of nicotinic acid by a strain of *P. fluorescens* were conducted by Behrman and Stanier (5). In agreement with Hughes (52), they showed that hydroxylation at carbon 6 was the first step in the pathway. The second step was an oxidative decarboxylation producing 2,5-dihydroxypyridine. The ring of 2,5-dihydroxypyridine was then cleaved oxidatively to yield maleamic acid and formic acids. Hydrolytic deamination of maleamic acid generated maleic acid, an isomer of fumaric acid. It was proposed that ring cleavage occurred between carbons 5 and 6, although the *N*-formylmaleamic acid was not detected. When appropriate concentrations of arsenite were present, pyruvic acid was present among the end products. All of the reactions except the initial hydroxylation step were catalyzed by soluble enzymes. Similar results were obtained by Gauthier and Rittenberg (25, 26), who investigated the 2,5-dihydroxypyridine oxygenase from *Pseudomonas putida* N9. In these experiments, 2,5-dihydroxypyridine was oxidized to equivalent amounts of maleamic acid and formic acid, with the consumption of 1 mol of oxygen. The enzyme did not require NADH, and the reaction did not proceed anaerobically in the presence of an electron acceptor. The incorporation of $^{18}\text{O}_2$ into maleamic acid and formic acid clearly implicated a dioxygenase in the ring cleavage step.

Gupta and Shukla (33) isolated from soil a *Sarcina* sp. which was capable of metabolizing nicotinic acid. Resting cells grown on nicotinic acid accumulated 6-hydroxynicotinic acid and pyruvic acid. Under restricted aeration, 2,5-dihydroxypyridine accumulated in the culture medium. Thus, this *Sarcina* sp. appeared to metabolize nicotinic acid via a pathway similar to that described for *P. fluorescens*. On the basis of intermediates formed during the transformation of nicotinic acid by *P. fluorescens*, the pathway presented in Fig. 6 was proposed (33).

Ensign and Rittenberg (20) isolated from soil a *Bacillus* sp. which oxidized nicotinic acid by a pathway different from that postulated for *Pseudomonas* spp. Resting cells of the organism oxidized nicotinic acid via 6-hydroxynicotinic acid and 2,6-dihydroxynicotinic acid. The latter compound was further transformed to 2,3,6-trihydroxypyridine via oxidative decarboxylation followed by ring cleavage and the formation of maleamic acid. A blue pigment was produced during the oxidation

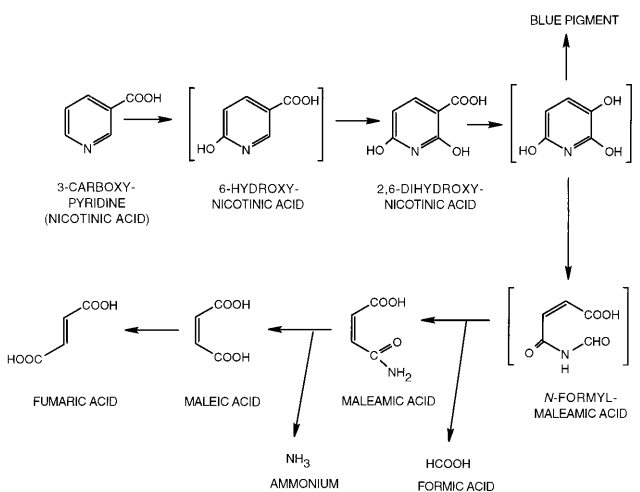
FIG. 6. Proposed pathway for the transformation of nicotinic acid by *Pseudomonas fluorescens* (33).

of nicotinic acid; it was formed via nonenzymatic oxidation of 2,3,6-trihydroxypyridine.

Hirschberg and Ensign (40) purified enzymes from the *Bacillus* sp. that hydroxylated nicotinic acid and 6-hydroxynicotinic acid to 2,6-dihydroxynicotinic acid, but it was not possible to separate the nicotinic acid-hydroxylating enzyme from the 6-hydroxynicotinic acid-hydroxylating enzyme. This indicated either that two distinct enzymes with very similar properties existed or that one multifunctional enzyme complex was responsible for both activities. Further investigations showed that both hydroxyl groups incorporated into 2,6-dihydroxynicotinic acid during the transformation of nicotinic acid were derived from water (41). The proposed pathway for the metabolism of nicotinic acid by the *Bacillus* sp. is shown in Fig. 7.

Additional experiments with 6-hydroxypyridine demonstrated that this compound served as an inducer of the enzyme for nicotinic acid metabolism. The lag period before the appearance of the hydroxylase activities was shorter when 6-hydroxynicotinic acid was added to the cells (42).

The transformation pathway for nicotinic acid under anaerobic conditions differs from that described above for *Pseudomonas* and *Bacillus* spp. under aerobic conditions. The first step in the degradation of nicotinic acid by both aerobic and anaerobic organisms appears to be the same, i.e., the forma-

FIG. 7. Proposed pathway for the transformation of nicotinic acid by a *Bacillus* sp.

tion of 6-hydroxynicotinic acid, but thereafter the pathways diverge. Harary (36–38) reported that a *Clostridium* sp. transformed nicotinic acid to produce propionic acid, acetic acid, carbon dioxide, and ammonium. 6-Hydroxynicotinic acid was proposed as an intermediate product. Stoichiometric conversion of nicotinic acid and the oxidizing agent methylene blue led to 6-hydroxynicotinic acid and reduced methylene blue. The hydroxylation of nicotinic acid to 6-hydroxynicotinic acid was a reversible reaction catalyzed by an enzyme which appeared to be a FAD-containing nonheme iron protein that used triphosphopyridine nucleotide as the ultimate electron acceptor (47).

Tsai et al. (129), also working with *Clostridium* spp., reported that in the presence of pyruvic acid, several intermediate products accumulated in the medium, including 6-hydroxynicotinic acid, 1,4,5,6-tetrahydro-6-oxonicotinic acid, and α -methylene-glutaric acid. Pyruvic acid supplied the electrons for the further metabolism of 6-hydroxynicotinic acid. Subsequent experiments showed that nicotinic acid was converted to equimolar amounts of propionic acid, acetic acid, carbon dioxide, and ammonium and that the following compounds were sequential intermediates: 6-oxonicotinic acid, 1,4,5,6-tetrahydro-6-oxonicotinic acid, α -methylene-glutaric acid, methylitaconic acid, dimethylmaleic acid, and pyruvic acid (121). An enzyme requiring reduced ferredoxin or reduced methyl viologen dye as the electron donor was partially purified from a *Clostridium* sp. and found to catalyze the reversible reduction of 6-hydroxynicotinic acid to 1,4,5,6-tetrahydro-6-oxonicotinic acid (48). Methylitaconic acid was identified as the intermediate in the conversion of α -methylene-glutaric acid to dimethylmaleic acid, and the enzyme catalyzing this reaction was isolated and characterized as a vitamin B₁₂-coenzyme-dependent α -methylene-glutarate mutase (71). The formation of methylitaconic acid is therefore B₁₂ dependent, accounting for the high levels of B₁₂ compounds found in cells cultured on medium in which nicotinic acid serves as the major carbon, nitrogen, and energy source.

When 1,4,5,6-tetrahydro-6-oxonicotinic acid was incubated with a crude enzyme extract of a *Clostridium* sp., 2-formylglutaric acid was produced and α -methylene-glutaric acid was converted to dimethylmaleic acid (130). This reaction may involve cleavage of the bond between carbons 3 and 4 and attachment of carbon 3 to carbon 5. Taking into account the above-described intermediates produced during transformation of nicotinic acid by *Clostridium* spp., a pathway for nicotinic acid metabolism under anaerobic conditions was proposed (Fig. 8) (130).

Experiments with [2-¹⁴C]nicotinic acid indicated that the labeled carbon was almost equally distributed between the methyl groups of propionic and acetic acids. The isotope from either [6-¹⁴C]nicotinic acid or [7-¹⁴C]nicotinic acid was distributed almost equally between carbon dioxide and the carboxy group of propionic acid (72, 82). The distribution of radioactivity supported the proposed pathway for *Clostridium* spp., which involves cleavages between carbon 6 and the nitrogen atom, between carbons 3 and 4, and between carbon 2 and the nitrogen atom (Fig. 8), leading to the formation of four end products, propionic acid, acetic acid, carbon dioxide, and ammonium.

Imhoff-Stuckle and Pfennig (58) isolated from marine mud sediment another anaerobic bacterium, characterized as *Desulfococcus niacini* sp. nov., which utilized nicotinic acid as an electron donor and carbon source. This bacterium used sulfur as well as thiosulfate and sulfite as the electron acceptor, and all of them were reduced to sulfide. In contrast to the *Clostridium* sp. reported above, *Desulfococcus niacini* oxidized nic-

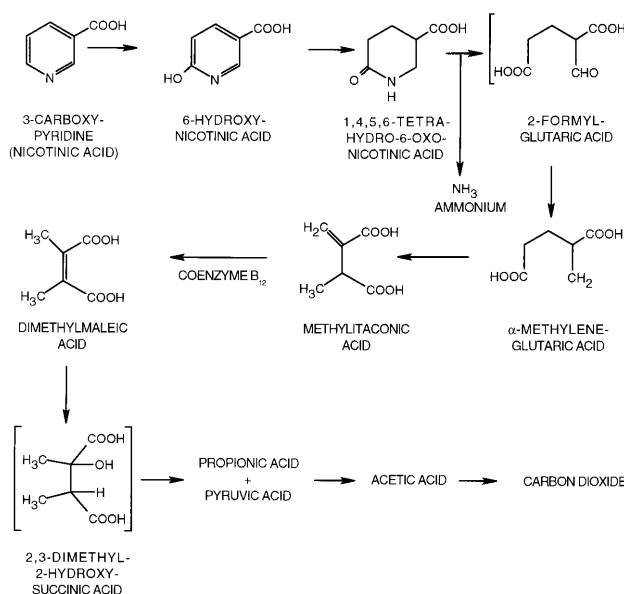


FIG. 8. Proposed pathway for the transformation of nicotinic acid by a *Clostridium* sp. (130).

otinic acid to carbon dioxide and ammonium, but neither propionic acid nor acetic acid was generated as an end product.

4-Carboxypyridine

The initial step in the transformation of 4-carboxypyridine (isonicotinic acid) appears to be hydroxylation at carbon 2. Gupta and Shukla (34) found that 2-hydroxyisonicotinic acid was produced during the metabolism of isonicotinic acid by a *Sarcina* sp. and suggested 2,6-dihydroxyisonicotinic acid (citrazinic acid) as a further intermediate product. Ensign and Rittenberg (21) showed that growing cultures of a soil bacterium produced 2,6-dihydroxyisonicotinic acid. Cells growing on isonicotinic acid were simultaneously adapted to growth on 2,6-dihydroxyisonicotinic acid, indicating that the metabolism of isonicotinic acid involved hydroxylation of the pyridine ring at the two alpha positions. Dihydroxyisonicotinic acid formed a blue pigment by chemical oxidation, similar to that observed during the transformation of 2,6-dihydroxypyridine by the *Pseudomonas* sp. Singh and Shukla (119) observed that a *Bacillus* sp. isolated from soil was able to grow on isonicotinic acid. Incubation of resting cells with arsenite led to the accumulation of succinic acid semialdehyde during isonicotinic acid transformation. The pathway depicted in Fig. 9 was proposed for the metabolism of isonicotinic acid by various microorganisms.

The metabolism of isoniazid (isonicotinic acid hydrazide) evidently occurs in a similar way. Gupta and Shukla (35) re-

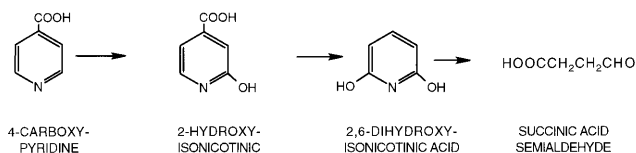


FIG. 9. Proposed pathway for the transformation of isonicotinic acid by various microorganisms.

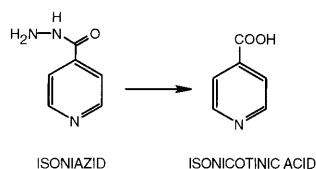


FIG. 10. Transformation of isoniazid to isonicotinic acid.

ported that a *Sarcina* sp. was able to utilize isoniazid as well as isonicotinic acid as sole source of carbon, nitrogen, and energy. It has been reported that in addition to a *Sarcina* sp., some *Bacillus* spp. have the ability to transform both isoniazid and isonicotinic acid (118).

Fishbain et al. (23) reported that *Mycobacterium smegmatis* transformed isoniazid to equivalent amounts of isonicotinic acid and hydrazine. Therefore, it was postulated that isoniazid was metabolized by these organisms through a pathway similar to that proposed for isonicotinic acid. The conversion of isoniazid to isonicotinic acid is shown in Fig. 10.

Pyridine-2,6-Dicarboxylic Acid

Arima and Kobayashi (4) demonstrated that an *Achromobacter* sp. oxidized pyridine-2,6-dicarboxylic acid (2,6-dipicolinic acid) to carbon dioxide, ammonium, and water. Further investigations showed that 3-hydroxydipicolinic acid was an intermediate product of 2,6-dipicolinic acid transformation, which was further degraded to α -ketoglutaric acid and oxalic acid (64). Oxalic acid is an end product of 2,6-dipicolinic acid and is directly produced from it. Incubation of resting cells of the *Achromobacter* sp. growing on α -ketoglutaric acid produced no oxalic acid, because α -ketoglutaric acid is not an end product of oxalic acid.

Phthalate-degrading bacteria isolated from marine sediments were reported to metabolize pyridinedicarboxylic acids (3, 127, 128). As well as *Achromobacter* sp. and the various phthalic acid-degrading marine bacteria, a *Bacillus brevis* strain has been reported to be able to grow on 2,6-dipicolinic acid (117). Strain CC9M partially oxidized 2,6-dipicolinic acid to produce 2,3-dihydroxypicolinic acid, which can be further degraded upon exposure to sunlight (3).

Seyfried and Schink (100) studied the anaerobic transformation of 2,6-dipicolinic acid by a defined coculture of two bacteria from marine sediment. 2,6-Dipicolinic acid was transformed to propionic acid, acetic acid, carbon dioxide, and ammonium. The dipicolinic acid-fermenting bacterium could be cultivated only in coculture with another bacterium which oxidized acetic acid to carbon dioxide. The aerobic and anaerobic pathways for transformation of 2,6-dipicolinic acid are shown in Fig. 11.

TRANSFORMATION OF ALKYL PYRIDINES

The initial step of microbial transformation of alkylpyridines may occur on the aromatic ring or the alkyl substituent. Oxidation of the heterocyclic ring results in the formation of pyridine-*N*-oxide or hydroxypyridines. Oxidation of the side chain leads to the formation of hydroxyalkyl pyridines.

Korosteleva et al. (67) found that *Pseudomonas* sp. strain KM-3 transformed 3-methylpyridine (3-picoline) to 3-hydroxymethylpyridine by oxidizing the alkyl group. In addition, nicotinic acid was identified as one of the metabolic products. The authors proposed a metabolic pathway for the further transformation of nicotinic acid by this *Pseudomonas* sp. similar to that described for *Pseudomonas fluorescens*, even though

expected metabolites such as 2,5-dihydroxypyridine and maleic acid were not detected. The proposed pathway for the transformation of 3-methylpyridine is presented in Fig. 12.

Several *Curvularia* spp., as well as *Cunninghamella blakesleena*, *Sporotrichum sulfurescens*, and *Pseudomonas* sp. strain AM-1, were found to hydroxylate 2,6-dimethylpyridine to 2-methyl-6-hydroxymethylpyridine. *Sporotrichum sulfurescens* further metabolized 2-methyl-6-hydroxymethylpyridine to form small quantities of 2,6-dihydroxymethylpyridine (18). No other metabolites have been reported for the subsequent transformation of 2,6-dihydroxymethylpyridine; however, it may be further oxidized to 2,6-dipicolinic acid, which can then be degraded by one of the proposed pathways for this compound.

Oxidation of the alkyl substituent has also been shown during the transformation of alkylpyridines by fungi. A group of Russian scientists proposed the use of a microbiological procedure instead of chemical methods to produce isomeric hydroxyalkylpyridines (75, 133). Various fungi grown in medium containing carbon sources other than alkylpyridines were able to catalyze the initial hydroxylation of alkylpyridines, but no further reactions took place. Modyanova et al. (75) found that fungi which hydroxylate dialkylbenzenes (*Beauveria bassiana* VKM F-2533, *Aspergillus sclerotiorum* JMJ 56673, and *Aspergillus niger* NRRL 3228) and steroids (*Tiefimella hyalospora*, *Abisidia orchidis* 6, *Rhizopus nigricans* 7, and *Trichothecium roseum* 27) also carried out side chain oxidation of methylpyridines and dimethylpyridines. 2-, 3-, and 4-methylpyridines were transformed to 2-, 3-, and 4-hydroxymethylpyridines, respectively, and only one methyl group of dimethylpyridines was hydroxylated. Vorob'eva et al. (133) studied the hydroxylation of ethylpyridines by microscopic fungi. 2-Ethylpyridine was transformed to 2-(1-hydroxyethyl)pyridine, 2-(2-hydroxyethyl)pyridine, and 2-ethylpyridine-*N*-oxide. *Beauveria bassiana* VKM F-2533, *Beauveria* sp. strain 12, and *Penicillium* sp. strain 13 transformed 2-ethylpyridine to the optically active 2-(1-hydroxyethyl)pyridine with yields of 59.7, 7.0, and 10%, respectively. *Aspergillus awamori* VNIIG VUD T-2 and *Scopulariopsis brevicaulis* formed 2-(2-hydroxyethyl)pyridine from 2-ethylpyridine with yields of 30 to 40%.

Several studies indicate that the initial transformation of alkylpyridines takes place on the pyridine ring. Kost et al. (69) investigated the microbial transformation of 2,6-dimethylpyridine by bacteria, fungi, and yeasts. 2,6-Dimethylpyridine was transformed to 2,6-dimethylpyridine-*N*-oxide. The low concentration of 2,6-dimethylpyridine-*N*-oxide which accumulated in the culture media indicated that this product was further transformed by the microorganisms involved.

Feng et al. (22) investigated the transformation of ethylpyridines by a mixed culture of aerobic bacteria. Oxidation of the pyridine was found to have occurred, since 6-ethyl-2(1H)-pyridone and 4-ethyl-2(1H)-pyridone were determined to be intermediate products of 2- and 4-ethylpyridine degradation, respectively. The presence of 4-ethyl-2-pyridone suggests that reduction of the pyridine ring also occurred.

Shukla (102) reported that resting cells of an *Arthrobacter* sp. accumulated succinic acid semialdehyde and pyruvic acid during the transformation of 2-methylpyridine (2-picoline) in the presence of an inhibitor (semicarbazide). Because no other intermediate products were reported, the metabolic path for transformation of 2-picoline remains unknown.

A few researchers studied the transformation of alkylpyridines under anaerobic conditions. Transformation of 3- and 4-picoline by a microbial population under sulfate-reducing conditions was investigated by Kaiser et al. (61). In the presence of sulfate, 3- and 4-picoline (0.4 mM) were transformed

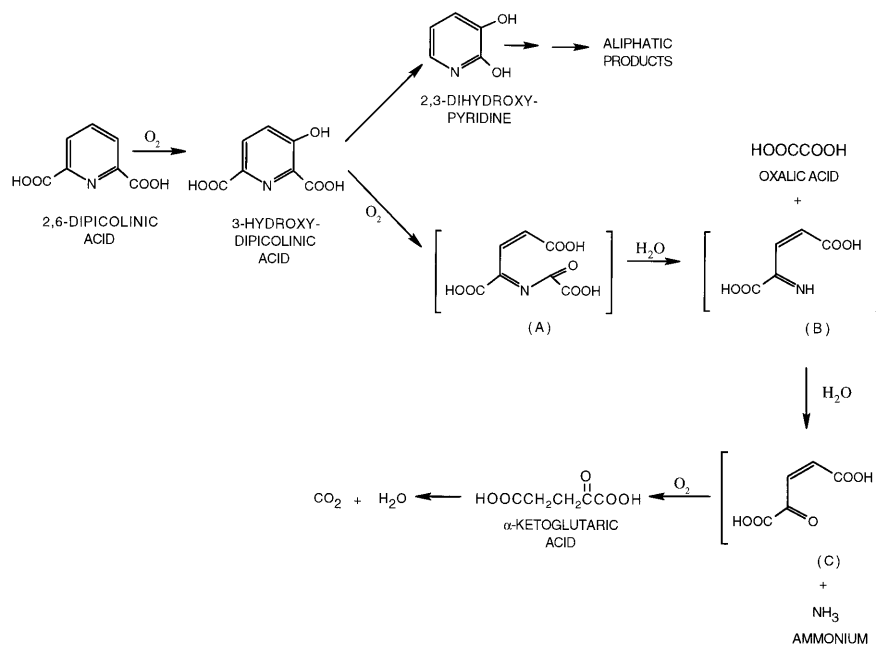


FIG. 11. Pathways for the transformation of 2,6-dipicolinic acid under aerobic and anaerobic conditions. The postulated compounds A, B, and C could not be found in the culture medium because they might be unstable (64).

within 30 days. A metabolite identified as 2-hydroxy-4-picoline accumulated during the transformation of 4-picoline. The 3- and 4-picoline-degrading culture could transform benzoic acid; however, 2-picoline, dimethylpyridines, and trimethylpyridines were not degraded.

Rogers et al. (91) investigated the transformation of various alkylpyridines in the presence of a soil inoculum under both aerobic and anaerobic conditions. Biodegradation rates under aerobic but not anaerobic conditions were greatly affected by the specific ring substitution of structural isomers. Unfortunately, no information was provided about possible intermediate products formed during the metabolism of these alkylpyridines.

TRANSFORMATION OF CHLORINATED PYRIDINES

Behrman and Stanier (6) investigated the transformation of halogenated nicotinic acids. 2-Fluoro-, 5-fluoro-, and 5-chloronicotinic acid were transformed to their 6-hydroxy derivatives by whole cells of *Pseudomonas fluorescens* N-9, but 5-bromonicotinic acid could not be oxidized. The findings for 2-fluoro- and 5-fluoronicotinic acid are in agreement with those of Hughes (53).

Two products were isolated from the culture medium after the transformation of 5-fluoronicotinic acid by *P. fluorescens* N-9. These were probably fluorine-substituted intermediates which could not be further metabolized because the site of enzyme action was blocked by the fluorine atom. Behrman and

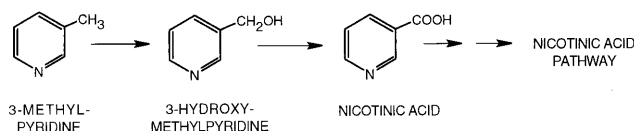


FIG. 12. Transformation of 3-methylpyridine (67).

Stanier (6) suggested that the two compounds were fluorocitric acid and acetic acid.

Chlorpyrifos [*O,O*-diethyl-*O*-(3,5,6-trichloro-2-pyridyl)phosphorothioate] is a pyridine-based herbicide. The pathway of chlorpyrifos degradation in soil has been reported to involve both chemical and microbiological processes (87). The major products were the hydrolysis products, 3,5,6-trichloro-2-pyridinol and 3,5,6-trichloro-2-methoxy-pyridine, and carbon dioxide. In soils in which 3,5,6-trichloro-2-pyridinol did not accumulate, large quantities of carbon dioxide were produced, suggesting that chlorpyrifos metabolism involved cleavage of the heterocyclic aromatic ring (86). However, no reports were available concerning a ring cleavage mechanism for 3,5,6-trichloro-2-pyridinol. Racke et al. (86) used the most-probable-number technique to study the microorganisms that utilize 3,5,6-trichloro-2-pyridinol as the sole carbon and energy sources. However, when soils that rapidly degrade 3,5,6-trichloro-2-pyridinol were used as an inoculum, no microorganisms were isolated, suggesting that transformation of 3,5,6-trichloro-2-pyridinol occurs through a cometabolic process.

TRANSFORMATION OF NICOTINE

Early work by Frankenburg and Vaitekunas (24) with microorganisms isolated from the surface of tobacco seeds indicated that nicotine is transformed by various pathways, with both the pyridine and pyrrolidine rings being attacked. This finding was subsequently confirmed by several investigators working with a variety of different organisms. The pathways are depicted in Fig. 13 and 14.

Hochstein and Rittenberg studied the transformation of nicotine by strain PP-34 (45, 46). They found that 6-hydroxynicotine was formed and further transformed to 6-hydroxy-*N*-methylmyosmine by dehydrogenation of the pyrrolidine ring (Fig. 13). The hydroxylation of nicotine to 6-hydroxynicotine required 0.5 mol of oxygen per mol of nicotine; however, the

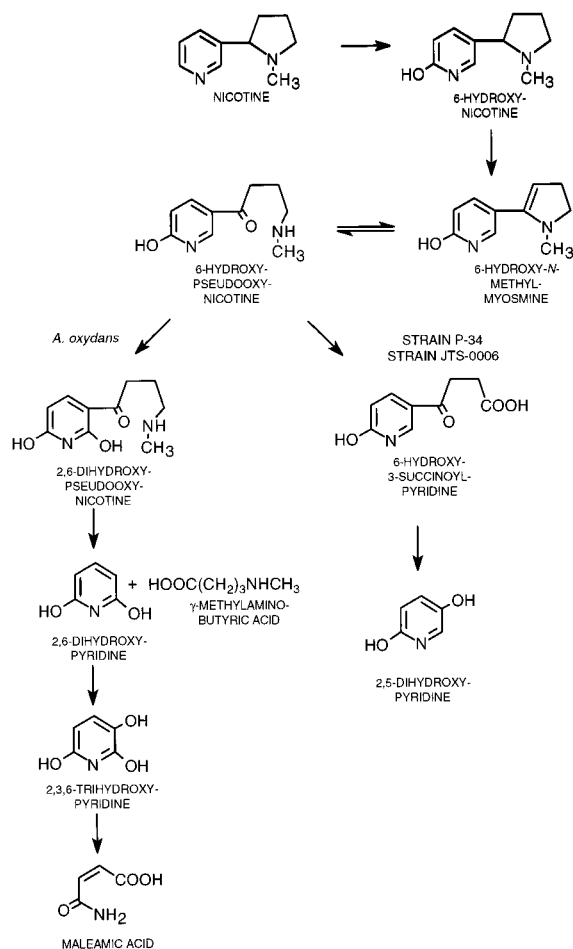


FIG. 13. Proposed pathway for the metabolism of nicotine by *Arthrobacter oxydans* (27).

product contained 1 mol of oxygen, indicating that the oxygen originated from water rather than from molecular oxygen (43).

Maeda et al. (74) reported that another bacterial strain, JTS-0006, followed a pathway for the transformation of nicotine similar to that reported by Hochstein and Rittenberg (46). During nicotine transformation, 6-hydroxynicotine, 6-hydroxy-*N*-methylmyosmine, and 6-hydroxypseudooxynicotine were detected in the culture medium (Fig. 13).

Hochstein and Dalton (44) isolated from *Arthrobacter oxydans* a nicotine oxidase which incorporated oxygen from water into nicotine to form 6-hydroxynicotine. This nicotine oxidase was conceived as a two-headed enzyme carrying out the dissimilar functions of hydration followed by oxidation. 6-Hydroxypseudooxynicotine was isolated after a one-step oxidation reaction of 6-hydroxynicotine (46). 6-Hydroxypseudooxynicotine was further oxidized to 2,6-dihydroxypseudooxynicotine (88, 89). Further transformation of 2,6-dihydroxypseudooxynicotine yielded 2,6-dihydroxypyridine and γ -methylaminobutyric acid (27) (Fig. 13). A monooxygenase catalyzed the transformation of 2,6-dihydroxypyridine to 2,3,6-trihydroxypyridine (50). In the presence of oxygen and the absence of a catalyzing enzyme, this trihydroxypyridine showed a rapid spontaneous oxidation and formed a blue pigment. In the presence of crude cell extracts of *A. oxydans*, this pigment was not formed and 2,3,6-trihydroxypyridine was converted by a cleavage enzyme

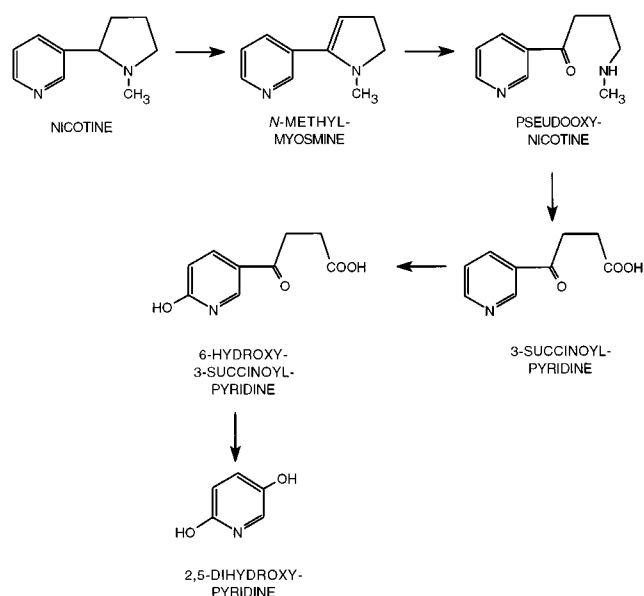


FIG. 14. Proposed pathway for the transformation of nicotine by a *Pseudomonas* sp., bacterial strain P-34, and strain JTS-0006 (28, 74).

to maleamic acid. The purification of this inducible oxidase that catalyzed the oxidation of 2,6-dihydroxypyridine required reduced pyridine nucleotide; this indicated that the enzyme was a monooxygenase (49). The authors suggested that the conversion of 2,6-dihydroxypyridine to maleamic acid involved at least two enzymes, the oxidase and the enzyme cleaving the aromatic ring.

It had been reported that 2,6-dihydroxypseudooxynicotine, an unstable intermediate product of 6-hydroxypseudooxynicotine, was further transformed to 2,6-dihydroxy-*N*-methylmyosmine by a nonenzymatic reaction in the absence of a proper enzyme fraction (27, 88, 89). 2,6-Dihydroxy-*N*-methylmyosmine was not further metabolized and appeared to be a metabolic artifact in the main pathway of nicotine degradation by *A. oxydans*, arising only because of the incomplete enzyme system used (88, 89).

The *Pseudomonas* sp. studied by Wada (134, 135) can metabolize both nicotine and nornicotine. Nornicotine and nicotine differ only with respect to substituents in position 1 of the pyrrolidine ring (-H for nornicotine and -CH₃ for nicotine). During the transformation of nornicotine, 6-hydroxymyosmine and 3-succinoyl-6-hydroxypyridine were detected in the culture medium. The formation of 6-hydroxymyosmine indicated that this *Pseudomonas* sp. used a metabolic pathway which involved a hydroxylation of the heterocyclic aromatic ring prior to transformation to pseudooxynicotine. The same bacterium used a different pathway to degrade nicotine.

Several microorganisms were reported to transform nicotine by first modifying the pyrrolidine ring (Fig. 14). Gherna and Rittenberg (28) reported that a *Pseudomonas* sp. was able to oxidize nicotine, *N*-methylmyosmine, pseudooxynicotine, 3-succinoylpyridine, and 6-hydroxy-3-succinoylpyridine. Cells of this *Pseudomonas* sp. adapted to nicotine were simultaneously adapted to the oxidation of 2,5-dihydroxypyridine (28). Thus, the authors suggested a cleavage at the 3' position of 6-hydroxy-3-succinoylpyridine with the formation of 2,5-dihydroxypyridine and succinic acid.

Wada and Yamasaki (136) reported that during the transformation of nicotine by bacteria isolated from soil, a different

set of products, *N*-methylmyosmine, pseudooxynicotine, and 3-succinoylpyridine, could be detected. The *Pseudomonas* sp. which metabolized both nicotine and nornicotine transformed nicotine by attacking the pyrrolidine ring first; pseudooxynicotine, 3-succinoylpyridine, and 3-succinoyl-6-hydroxypyridine were found as metabolites of nicotine degradation.

Achromobacter nicotinophagum metabolized nicotine via two different pathways (56). During the exponential growth phase, nicotine was metabolized to 6-hydroxynicotine and then further metabolized to aliphatic products. When the cells stopped dividing, the metabolism of nicotine to aliphatic products was inhibited and nicotine was transformed by an alternate pathway via pseudooxynicotine and 3-succinoylpyridine to 6-hydroxy-3-succinoylpyridine. No further transformation of 6-hydroxy-3-succinoylpyridine could be detected.

Strain JTS-0006 was reported to be able to use nicotine-*N*-oxide as the sole carbon and nitrogen source (74). Pseudooxynicotine and 3-succinoylpyridine were detected as intermediate products in the growing-cell culture. The formation of these metabolites indicated that the bacterial strain JTS-0006 transformed nicotine-*N*-oxide through a pathway similar to that described for the metabolism of nicotine by *Pseudomonas* spp.

TRANSFORMATION OF OTHER PYRIDINE DERIVATIVES

Nitrogen Substituents

Vaughan et al. (132) reported that 3-cyanopyridine (3-pyridine-carbonitrile) was hydrolyzed to nicotinic acid and ammonium by *Nocardia rhodochrous*. Ammonium was utilized for growth, whereas nicotinic acid was not further metabolized. An *Escherichia coli* strain transformed nicotinamide in a similar manner (131), producing nicotinic acid and ammonium.

N-Substituted Derivatives

As discussed in the section on transformation of hydroxylated pyridines (above), Shukla and Kaul (110) described a *Nocardia* sp. which was able to transform pyridine, pyridine-*N*-oxide, and 2-hydroxypyridine. Transformation of pyridine-*N*-oxide under limited aeration resulted in the accumulation of 2-hydroxypyridine. In the presence of arsenite, pyruvic acid was produced during the transformation of pyridine-*N*-oxide and 2-hydroxypyridine. However, 2-hydroxypyridine was never produced during the degradation of pyridine. The authors suggested, therefore, that pyridine transformation follows a pathway different from that of pyridine-*N*-oxide, with pyridine being transformed via the pathway described for *Bacillus* strain 4 and pyridine-*N*-oxide being oxidized via 2-hydroxypyridine to 2,5-dihydroxypyridine. The formation of a blue pigment (probably the condensation of 2,3,6-trihydroxypyridine) indicated that a trihydroxypyridine derivative was produced prior to ring fission by the *Nocardia* sp. For the complete transformation of pyridine-*N*-oxide, a pathway similar to that described above for degradation of 2-hydroxypyridine (Fig. 3) was proposed.

Several studies have also been undertaken to investigate the transformation of 4-carboxy-1-methylpyridinium chloride, a photolytic product of paraquat. Wright and Cain (143) reported the isolation of *Achromobacter* strain D, which utilized 4-carboxy-1-methylpyridinium chloride as the sole source of carbon and nitrogen. This *Achromobacter* sp. cleaved the pyridine ring by a multienzyme reaction sequence and liberated methylamine, which was further oxidized to ammonium and carbon dioxide. Later investigations on the degradation of

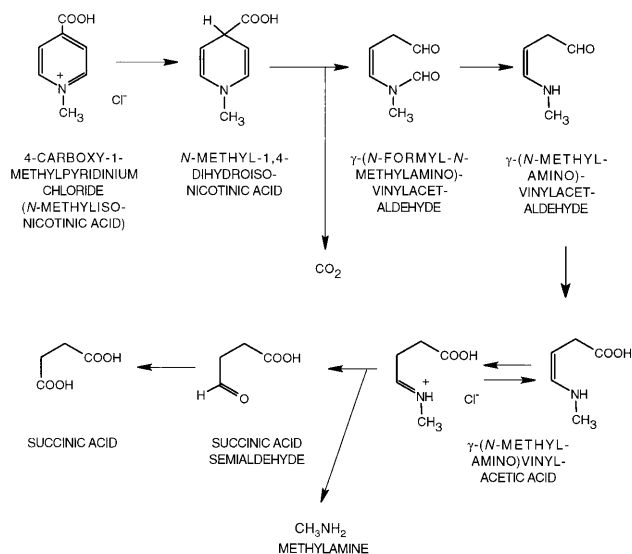


FIG. 15. Transformation of 4-carboxy-1-methylpyridinium chloride by *Achromobacter* strain D (146).

4-carboxy-1-methylpyridinium chloride showed that in addition to methylamine and carbon dioxide, succinic acid and formic acid were produced as end products (144, 145). The oxygen-requiring step consumed 1 mol of oxygen per mol of 4-carboxy-1-methylpyridinium chloride, consistent with direct oxidative cleavage (by a dioxygenase) of the partially reduced pyridinium ring. Radioisotopic experiments indicated that ring cleavage must occur between carbons 2 and 3 of the heterocyclic ring. The *N*-formyl group was hydrolyzed to formic acid, while γ -(*N*-formyl-*N*-methylamino)vinylacetaldehyde was hydrolyzed to its corresponding acid, γ -(*N*-methylamino)vinylacetic acid. These reactions were followed by another hydrolysis step, leading to the formation of succinic acid semialdehyde and methylamine. Experiments with cell extracts of the *Achromobacter* sp. and ^{14}C -labeled 4-carboxy-1-methylpyridinium chloride showed that the carbon dioxide was derived from the 4-carboxyl group and the methylamine was derived from the *N*-methyl group of the substrate (146). Succinic acid most probably originated from the carbon 3 to carbon 6 atoms of the heterocyclic ring, whereas formic acid originated from carbon 2. According to these intermediate products, a pathway was proposed for the transformation of 4-carboxy-1-methylpyridinium chloride by *Achromobacter* strain D as shown in Fig. 15.

Orpin et al. (79, 81), studying *Achromobacter* strain 4C1, proposed a different pathway for the transformation of *N*-methyl-4-carboxypyridine (*N*-methylisonicotinic acid) (Fig. 16). In contrast to *Achromobacter* strain D, this bacterium appeared to remove the methyl group before ring fission occurred. The authors suggested that *N*-methyl-4-carboxypyridine was hydroxylated at position 2 to form 2-hydroxy-*N*-methylisonicotinic acid, which was then demethylated to 2-hydroxy-4-carboxypyridine. These two steps were not demonstrated by enzyme assays, but 2-hydroxy-4-carboxypyridine was hydroxylated by the crude cell extract to 2,6-dihydroxy-4-carboxypyridine. Maleamic acid was deaminated and maleic acid was isomerized to fumaric acid by soluble enzyme systems. The cells of this soil bacterium were grown on 2-hydroxyisonicotinic acid with an oxygen consumption of 0.5 mol per mol of substrate transformed. This indicated that the oxygen source for this hydroxylation reaction was water.

Orpin et al. (80) also studied a gram-negative rod-shaped

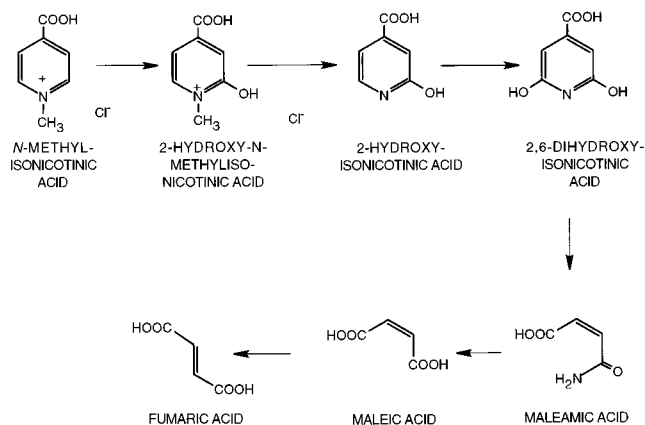


FIG. 16. Proposed pathway for the metabolism of *N*-methylisonicotinic acid by *Achromobacter* strain 4C1 (79, 81).

bacterium that transformed pyridine-2-carboxamide (picolineamide), a photolytic product of diquat. During the transformation of pyridine-2-carboxamide, 2,5-dihydroxypyridine was released into the culture medium. Cultures inhibited by arsenite accumulated 6-hydroxypicolinic acid and pyruvic acid. Cell extracts of the bacterium transformed picolineamide into picolinic acid, picolinic acid to 6-hydroxypicolinic acid, 2,5-dihydroxypyridine to maleamic and formic acids, and maleamic acid to fumaric acid (Fig. 17).

Mimosine, β -[*N*-(3-hydroxy-4-oxopyridyl)]- α -aminopropionic acid, is a nonprotein amino acid which is found in tropical plants and induces toxic effects in ruminants and monogastric animals (17). Bacteria isolated from the rumen of sheep have been found to transform mimosine to 3-hydroxy-4(1H)pyridone and 2,3-dihydroxypyridine, which were further degraded by a wide range of ruminal bacteria (17). In addition, Allison et al. (2) identified and characterized four strains of obligate

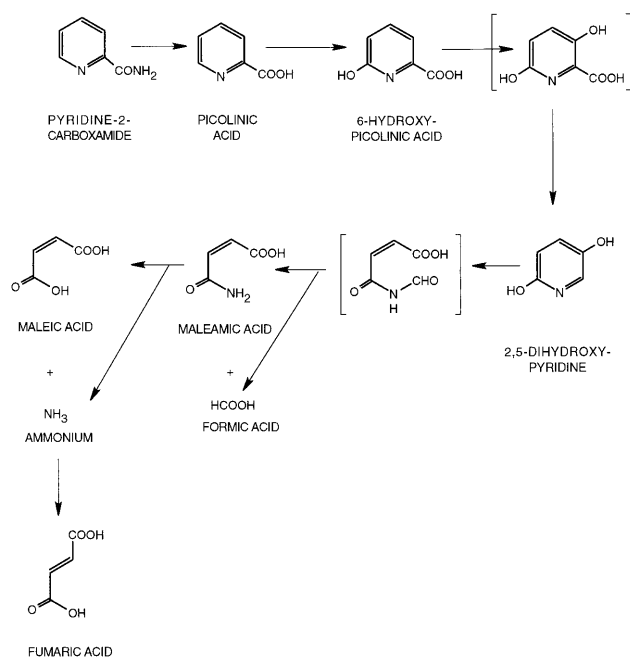


FIG. 17. Proposed pathway for the metabolism of pyridine-2-carboxamide (81).

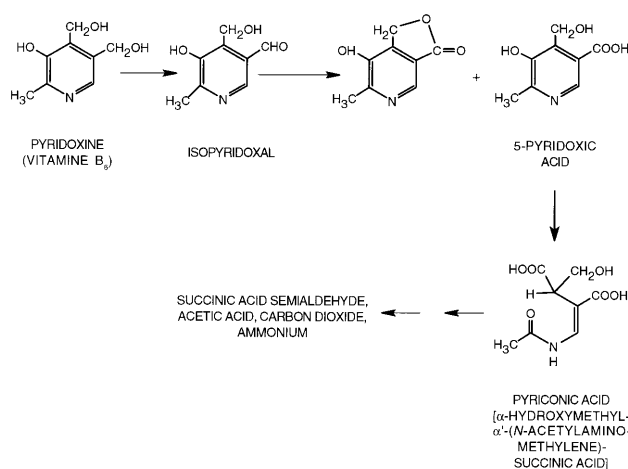


FIG. 18. Proposed pathway for the transformation of pyridoxine by *Pseudomonas* strain IA (13, 120).

anaerobic bacteria that degraded 3-hydroxy-4(1H)pyridone and 2,3-dihydroxypyridine. These isolates did not fit into any existing taxon; therefore, a new genus and species, *Synergistes jonesii*, were proposed.

Pyridoxine

Pyridoxine (vitamin B₆) was metabolized by two strains of *Pseudomonas* strains IA and MA-1, by related but different pathways. *Pseudomonas* strain IA oxidized pyridoxine via isopyridoxal and 5-pyridoxic acid (or its lactone) to pyronic acid [α -hydroxymethyl- α' -(*N*-acetylamino)methylene)succinic acid] and further to carbon dioxide and ammonium (13, 57, 90). The transformation of pyridoxine to isopyridoxal was catalyzed by a FAD-dependent enzyme isolated from *Pseudomonas* strain IA. This enzyme used 2,6-dichloroindophenol but not oxygen as the hydrogen acceptor (122). Sparrow et al. (120) found that the transformation of 5-pyridoxic acid to pyronic acid was catalyzed by an oxygenase in the presence of a reductant. The open-chain product (pyronic acid) could be obtained only with purified oxygenase preparations; in crude cell extracts of *Pseudomonas* strain IA, this product was rapidly converted to succinic acid semialdehyde, acetic acid, carbon dioxide, and ammonium. The proposed pathway for transformation of pyridoxine by *Pseudomonas* strain IA is given in Fig. 18.

Pseudomonas strain MA-1 oxidized pyridoxine by a pathway with analogous reaction mechanisms to those described above; however, the intermediate products formed were different. Pyridoxine was oxidized via pyridoxal, 4-pyridoxic acid lactone, 4-pyridoxic acid, 2-methyl-3-hydroxy-5-formylpyridine-4-carboxylic acid, 2-methyl-3-hydroxypyridine-4,5-dicarboxylic acid, 2-methyl-3-hydroxypyridine-5-carboxylic acid, α -(*N*-acetylamino)methylene)succinic acid, succinic acid semialdehyde, acetic acid, carbon dioxide, and ammonium (13), as shown in Fig. 19. The transformation of pyridoxine to 4-pyridoxic acid was catalyzed by a FAD-dependent enzyme isolated from *Pseudomonas* strain MA-1. This pyridoxine-4-dehydrogenase utilized either oxygen or 2,6-dichloroindophenol as the hydrogen acceptor (122). A DPN⁺ (diphosphopyridine nucleotide)-specific pyridoxal dehydrogenase from *Pseudomonas* strain MA-1 oxidized pyridoxal to 4-pyridoxalacetone (14), which in turn was cleaved to 4-pyridoxic acid by a second enzyme, 4-pyridoxalacetone. The ring cleavage of 2-methyl-3-hydroxypyri-

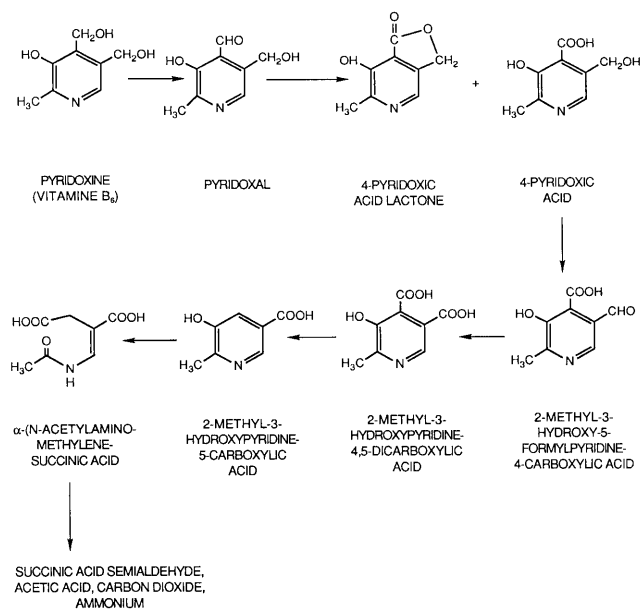


FIG. 19. Proposed pathway for the transformation of pyridoxine by *Pseudomonas* strain MA-1 (13).

dine-5-carboxylic acid was catalyzed by a DPNH-dependent oxygenase (120). The metabolite α -(*N*-acetylamino)methylene succinic acid accumulated only in the presence of purified oxygenase preparations (77). The two *Pseudomonas* oxygenases, FAD-dependent pyridoxine-4-dehydrogenase and DPNH-dependent pyridoxal dehydrogenase, responsible for the ring cleavage showed similar mechanisms, although they differed in their specificity toward the reductant and substrate.

Comparative Transformation Rates of Pyridine Derivatives

The fate of heterocycles in nature is dependent on their structure, concentration, and chemical and physical properties, as well as the physical, chemical, and microbiological properties of the environment (31). Experiments were conducted with batch cultures and soil suspensions, using various pyridine derivatives as substrates. These studies showed that pyridinecarboxylic acids had the highest transformation rate, followed by monohydroxypyridines, methylpyridines, aminopyridines, and chloropyridines (114, 115). Carboxyl substituents at any position of the pyridine ring stimulated decomposition more than did any other substituent, whereas chlorosubstituted pyridines showed the lowest degradation rate (76).

TRANSFORMATION OF QUINOLINE AND ITS DERIVATIVES

Quinoline can be transformed by microorganisms under both aerobic and anaerobic conditions (1, 12, 29, 99). Although many bacteria are capable of transforming quinolines, most quinoline-degrading organisms are *Pseudomonas* spp. There are several possible pathways for the transformation of quinoline.

Grant and Al-Najjar (29) isolated from garden soil a bacterium which could use quinoline as the sole carbon and nitrogen source. The authors suggested that the initial step in the transformation of quinoline by whole cells involved a hydroxylation at position 2 of the heterocyclic aromatic ring, leading to 2-hydroxyquinoline. Further transformation included additional

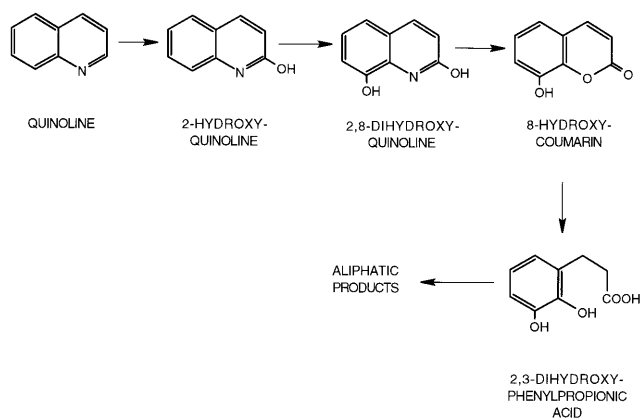


FIG. 20. Transformation of quinoline by a *Pseudomonas* sp. (105, 106).

hydroxylation steps leading to 2,6-dihydroxyquinoline and a trihydroxyquinoline (probably 2,5,6-trihydroxyquinoline).

The degradation of quinoline by *Pseudomonas aeruginosa* QP and *P. putida* QP also occurred via hydroxyquinolines (1). Moreover, a limited number of methylquinolines were hydroxylated by these two species but no further transformation of the hydroxylated products occurred. 2-Methylquinoline was not metabolized, since the methyl group at position 2 apparently blocked the formation of the hydroxyquinoline. However, the authors isolated a new strain of *Pseudomonas* (MQP) which was able to transform 2-methylquinoline, leading to the formation of hydroxylated methylquinolines and other unidentified metabolites.

Shukla (105) isolated from sewage an aerobic gram-negative motile bacterium which was identified as a *Pseudomonas* sp. and was found to degrade quinoline by an alternate pathway. 2-Hydroxyquinoline and 8-hydroxycoumarin were found in the culture medium and were further metabolized. Quinoline-adapted cells were also able to transform these two compounds without a lag phase, providing additional support for their intermediate role in the metabolism of quinoline. Further research demonstrated that 2,8-dihydroxyquinoline and 2,3-dihydroxyphenylpropionic acid were additional intermediate products (106). Arsenate-inhibited cells accumulated 2-hydroxyquinoline and pyruvic acid in the culture medium. The proposed pathway for metabolism of quinoline by this *Pseudomonas* sp. is presented in Fig. 20.

Boyd et al. (11) investigated the transformation of azarenes such as quinoline, isoquinoline, quinazoline, and quinoxaline by a mutant strain of *Pseudomonas putida*, which transformed naphthalene to form its *cis*-dihydrodiol metabolite. This bacterium transformed both the homocyclic and the heterocyclic moieties of quinolines. When the attack occurred on the homocyclic ring, the corresponding *cis*-hydrodiol derivatives were found in the culture medium, along with monohydroxylated derivatives such as 8-hydroxyquinoline or 5-hydroxyisoquinoline. The authors proposed that oxidation by a dioxygenase resulted in the formation of *cis*-hydrodiol derivatives and oxidation by a monooxygenase resulted in the formation of monohydroxylated derivatives via the areneoxide intermediates. *P. putida* also hydroxylated the heterocyclic ring to yield 3-hydroxyquinoline, 4-hydroxyquinazoline, and 5-hydroxyquinoxaline. Hydroxylation of the heterocyclic ring was suggested by the following evidence: (i) an unstable *cis*-dihydrodiol metabolite formed on the heterocyclic ring; and (ii) a spontaneous dehydration of this *cis*-dihydrodiol metabolite re-

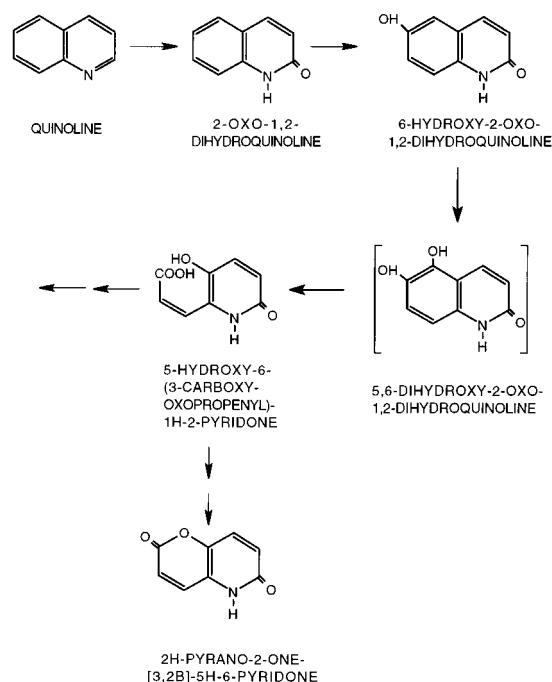


FIG. 21. Proposed pathway for the transformation of quinoline by *Rhodococcus* strain B1 (98).

sulted in the formation of 3-hydroxyquinoline, which led to anthranilic acid (2-aminobenzoic acid). Detection of anthranilic acid as a metabolite in the culture medium during the transformation of quinoline by *P. putida* suggested that cleavage of the heterocyclic ring had occurred.

Schwarz et al. (98) investigated quinoline catabolism by several bacterial strains, and two different degradation pathways for quinoline in different microorganisms were proposed. 2-Oxo-1,2-dihydroquinoline, 8-hydroxy-2-oxo-1,2-dihydroquinoline, 8-hydroxycoumarin, and 2,3-dihydroxy-phenylpropionic acid were found as intermediates of quinoline transformation by *Pseudomonas fluorescens* 3 and *Pseudomonas putida* 86. This finding agrees with the results reported by Shukla (105). In the culture medium of a *Rhodococcus* strain (B1), 2-oxo-1,2-dihydroquinoline, 6-hydroxy-2-oxo-1,2-dihydroquinoline, and 5-hydroxy-6-(3-carboxy-3-oxopropenyl)-1H-2-pyridone were identified (Fig. 21). Ruger et al. (95) isolated four metabolites of quinoline in a *Pseudomonas putida* K1 culture: 2H-pyrano-2-one-[3,2b]-5H-6-pyridone and the above three metabolites found in the pathway of *Rhodococcus* strain B1.

Biodegradation of methylquinolines has been reported by several researchers. Aislabie et al. (1) indicated that *Pseudomonas aeruginosa* was able to hydroxylate 6-, 7-, and 8-methylquinoline but not 2- and 4-methylquinoline or 2,6-dimethylquinoline. The specific sites of hydroxylation, however, were not determined. The degradation pathway of 2-methylquinoline by an *Arthrobacter* sp. was reported by Hund et al. (54), with the following intermediate products being isolated from the culture medium and identified: 1H-4-oxoquinoline, *N*-acetylisatoic acid, *N*-acetylthranilic acid, anthranilic acid, 3-hydroxy-*N*-acetylthranilic acid, and catechol. Schach et al. (96) investigated the transformation of 3-methylquinoline by *Comamonas testosteroni* 63 isolated from activated sludge. Four metabolites of 3-methylquinoline degradation were isolated and identified as 3-methyl-2-oxo-1,2-dihydroquinoline, 6-hydroxy-3-methyl-2-oxo-1,2-dihydroquinoline, 5,6-dihydro-

3-methyl-2-oxo-1,2-dihydroquinoline, and 2,5,6-trihydroxy-3-methylpyridine. Ruger et al. (95) studied the degradation of 4-methylquinoline by *Pseudomonas putida* K1. Four metabolites of 4-methylquinoline degradation were isolated and identified as 4-methyl-2-oxo-1,2-dihydroquinoline, 8-hydroxy-4-methyl-2-oxo-1,2-dihydroquinoline, 7,8-dihydroxy-4-methyl-2-oxo-1,2-dihydroquinoline, and 6-hydroxy-5-(2-carboxyethyl)-4-methyl-1H-2-pyridone. Ring cleavage occurred between C-7 and C-8. The proposed degradation pathway of 4-methylquinoline is different from that of quinoline by the same organism, since the quinoline ring structure was cleaved between C-5 and C-6.

Pseudomonas putida 33/1 was able to degrade 1H-4-oxoquinoline via 1H-3-hydroxy-4-oxoquinoline, *N*-formylanthranilic acid, anthranilic acid, and catechol (10). 6-Hydroxyquinoline could be degraded by *Pseudomonas diminuta* 31/1 Fa1 and *Bacillus circulans* 31/2 A1 via 6-hydroxy-2-oxo-1,2-dihydroquinoline (9). 1-Oxo-1,2-dihydroisoquinoline was found as the product of the first step in the degradation of isoquinoline by *Alcaligenes faecalis* Pa and *P. diminuta* 7 (92). *Microbacterium* sp. strain H2, *Agrobacterium* sp. strain 1B, and *Pimelobacter simplex* 4B and 5B degrade quinoline-4-carboxylic acid, forming 2-oxo-1,2-dihydroquinoline-4-carboxylic acid and 8-hydroxycoumarin-4-carboxylic acid (97).

Under both field and laboratory conditions, Pereira et al. (84, 85) investigated the anaerobic transformation of quinolines in groundwater contaminated by wood-treatment chemicals. Quinoline, isoquinoline, methylquinolines, and acridines were found in the groundwater samples. The presence of oxygenated analogs of quinolines in the anaerobic zones demonstrated that the transformation of quinoline occurred under anaerobic conditions and involved hydroxylation at position 2 of the heterocyclic ring. This indicated that these anaerobic microorganisms used a pathway for the transformation of quinoline similar to that described above for aerobic bacteria. Studies with $H_2^{18}O$ showed that the oxygen for the hydroxylation reaction was derived from water (83).

Wang et al. (138, 139) demonstrated that a methanogenic consortium transformed quinoline in an anaerobic filter. After an acclimation period of 6 months, methane production was 85% of the expected amount, indicating that quinoline could be completely transformed under anaerobic conditions. Unfortunately, no further intermediates were reported, and the pathway of quinoline metabolism under anaerobic conditions remains unknown. Brockman et al. (12) isolated two gram-negative bacteria from deep subsurface sediments. The growing cell cultures of both organisms mineralized quinoline under aerobic conditions and transformed quinoline to soluble intermediates under anaerobic conditions. Both organisms contained four plasmids of identical size, ranging from 50 to 440 kb.

As previously discussed, most quinoline-degrading organisms are *Pseudomonas* spp. These bacteria are also able to transform the quinoline derivative kynurenic acid (2-carboxy-4-hydroxyquinoline). Hayaishi et al. (39) reported that a partially purified enzyme preparation from a tryptophan-adapted *Pseudomonas* sp. produced L-glutamic acid and acetic acid from kynurenic acid. Further investigations showed that an enzyme derived from this *Pseudomonas* sp. catalyzed the transformation of kynurenic acid to 7,8-dihydroxykynurenic acid (124).

In a separate report, Taniuchi and Hayaishi (123) indicated that a cell extract of *Pseudomonas fluorescens* degraded kynurenic acid in the presence of NAD. L-Glutamic acid, L-alanine, acetic acid, and carbon dioxide were formed as the major end products. A compound identical to 7,8-dihydroxykynurenic acid-7,8-diol was also formed. This compound

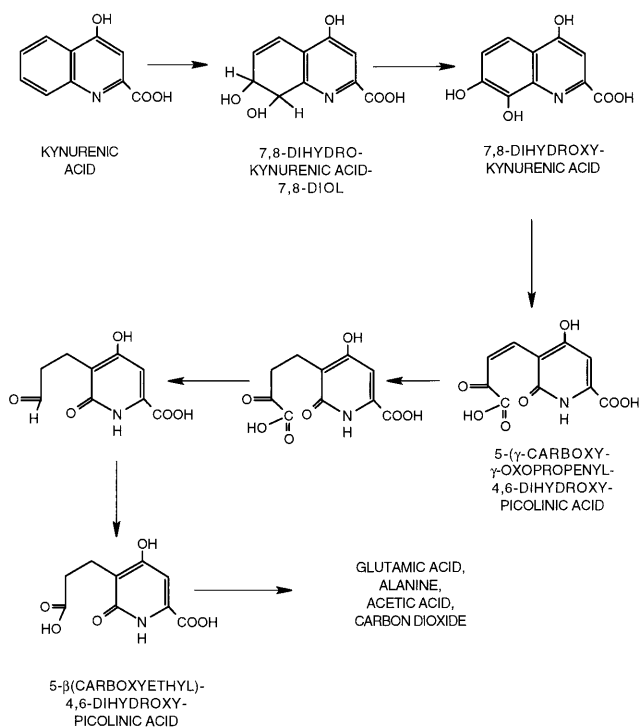


FIG. 22. Proposed pathway for the transformation of kynurenic acid (123).

was dehydrogenated by a partially purified enzyme to 7,8-dihydrokynurenic acid. The identified intermediate products suggested that ring fission occurred on the homocyclic ring. The proposed pathway for kynurenic acid is presented in Fig. 22.

Kynurenic acid was transformed by an *Aerococcus* sp. in a manner similar to that of the *Pseudomonas* sp. described above (16); i.e., 5-(γ -carboxy- γ -oxopropenyl)-4,6-dihydroxypicolinic acid and 5- β -(carboxyethyl)-4,6-dihydroxypicolinic acid were isolated from the culture medium. Transformation of 5- β -(carboxyethyl)-4,6-dihydroxypicolinic acid by an *Aerococcus* cell extract resulted in the formation of α -ketoglutaric acid, glutamate, aspartate, and pyruvic acid.

TRANSFORMATION OF ACRIDINE AND ITS DERIVATIVES

Acridine, a three-ring nitrogen heterocycle, has many properties similar to those of pyridine and quinoline. Knezovich et al. (63) studied anaerobic transformation of acridine in a laboratory microcosm by using three different inocula: a stabilized mixed culture growing on ferulic acid originally from anaerobic sewage sludge, and sulfate-reducing and methanogenic aquifer materials from two sites in a groundwater aquifer contaminated by landfill leachate. Acridine (1 to 6 mg/ml) was degraded under denitrifying, sulfate-reducing, and methanogenic conditions in 1 to 3 weeks. Benzoic acid was one of the key aromatic intermediates. A tentative pathway of anaerobic acridine transformation was proposed. It began with oxidation of either the benzene or the pyridine ring and thereafter followed the common degradation pathway for oxidized aromatic compounds: oxidation, reduction, decarboxylation, ring cleavage, and the breakdown of aliphatic products.

Pereira et al. (84) reported that acridine, 7,8-bezoquinoline, and carbazole were found in an aquifer contaminated by wood

treatment chemicals. Although quinolines at this site were transformed by the indigenous microbial population, acridine and benzoquinoline were not.

CONCLUSIONS

A large variety of organisms including eubacteria, yeasts, and fungi are capable of metabolizing and cleaving homocyclic and heterocyclic aromatic compounds (137). As summarized in this review, many different microbial species are capable of degrading pyridinic and aza-arenic compounds under aerobic and anaerobic conditions.

Pyridine is a benzene-like compound with one carbon atom replaced by a nitrogen atom. The pyridine ring is susceptible to reduction, as demonstrated by the functions of pyridine nucleotides in metabolism (104). Unlike its homocyclic analog, the mechanism of pyridine ring cleavage is not fully understood. Ring fission of benzene proceeds with the introduction of two hydroxyl groups *ortho* to each other, followed by *ortho* or *meta* cleavage. Formation of hydroxypyridine, however, has not been observed during pyridine transformation. The metabolism of hydroxylated and carboxylated pyridines seems to be initiated by hydroxylation: degradation of hydroxylated pyridines occurs via di- and trihydroxypyridine derivatives prior to ring fission.

Carboxylated pyridines have been the most frequently investigated pyridine derivatives. Transformation of pyridines carboxylated at position 2 seems to occur through hydroxylation at positions 3 and 6 followed by decarboxylation to yield a dihydroxypyridine derivative prior to ring cleavage. Similar observations have been reported for the metabolism of 4-carboxypyridine (isonicotinic acid). For 3-carboxypyridine (nicotinic acid), the events leading to ring cleavage follow one of three pathways: (i) transformation to a di- or trihydroxypyridine with the carboxyl group being replaced by a hydroxyl group, (ii) initial hydroxylation at position 6 followed by reduction of the heterocyclic ring, or (iii) initial hydroxylation at position 6 followed by formation of 2,5-dihydroxypyridine and *N*-formylmaleamic acid.

Alkyl- and chloropyridines represent two of the largest classes of pyridines present in the environment (112). Transformation of methylated pyridine derivatives begins with hydroxylation of the substituent to form a methoxypyridine derivative; the substituent is then further oxidized to a carboxyl group, thus forming a carboxylated pyridine derivative. However, laboratory experiments with 4-ethylpyridine under aerobic conditions indicated another mechanism of ring cleavage. The compound may be initially hydroxylated at position 2 to form 4-ethyl-2(1H) pyridine. Prior to oxidation of the side chain, the ring may be cleaved between the heteroatom and the carbon atom in position 2 (22).

Nicotine transformation can occur by various pathways. Both the pyridine ring and the pyrrolidine ring of nicotine can be attacked, but attack of the pyrrolidine ring leading to a di- or trihydroxypyridine occurs most frequently.

The initial step in the transformation of quinoline derivatives can occur on either the heterocyclic or the homocyclic ring. In one reported study, quinoline transformation by a *Pseudomonas* sp. started with transformation at position 2 followed by a second hydroxylation at position 8, leading to 2,8-dihydroxyquinoline. This compound was transformed to 8-hydroxycoumarin prior to ring fission. On the other hand, transformation of kynurenic acid by *Pseudomonas fluorescens* was initiated by hydroxylations at the homocyclic aromatic ring leading to 7,8-dihydroxypyridine. Fission of the homo-

cyclic ring then occurred, leading to 5-(γ -carboxy- γ -oxopropenyl)-4,6-dihydroxypicolinic acid.

It should be noted that under aerobic conditions, the oxygen atom of the hydroxyl group incorporated into the pyridine and quinoline metabolites is often derived from water, whereas in the case of homocyclic aromatics, the oxygen atom is derived from molecular oxygen. In addition, reduction of the pyridine ring during transformation was frequently observed.

During the transformation of pyridine derivatives, the production of some pigments has been observed. A blue pigment appeared when trihydroxypyridine was metabolized; this pigment was characterized as 4,5,4',5'-tetrahydroxy-3,3'-diazadiphenoquinone-(2,2') (108). It did not seem to be of metabolic significance (21) and was not produced when cells grew on pyridine (101). A yellow pigment was produced when *Micrococcus luteus* was grown on pyridine as the carbon source; it was identified as riboflavin and was not directly synthesized from pyridine (113).

Despite the large number of studies conducted so far, our knowledge of this important class of chemicals is still sparse. Many bacteria have been described which degrade pyridine and its derivatives, but little research has been done, e.g., on the genetics of pyridine metabolism. More studies must also be conducted to elucidate the transformation of these chemicals in the environment.

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