

Microbial Metabolism of Quinoline and Related Compounds

XVII. Degradation of 3-Methylquinoline by *Comamonas testosteroni* 63

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Dedicated to Prof. Dr. A. Butenandt on the occasion of his 90th birthday

Summary: A bacterial strain which utilizes 3-methylquinoline as sole source of carbon, nitrogen and energy was isolated from activated sludge. On the basis of its morphological and physiological characteristics, this isolate was classified as *Comamonas testosteroni*. Four metabolites of 3-methylquinoline degradation were isolated from the culture supernatant

and identified as 3-methyl-2-oxo-1,2-dihydroquinoline, 6-hydroxy-3-methyl-2-oxo-1,2-dihydroquinoline, 5,6-dihydroxy-3-methyl-2-oxo-1,2-dihydroquinoline and 2,5,6-trihydroxy-3-methylpyridine. Based on these results, a degradation pathway for 3-methylquinoline is proposed.

Key terms: Degradation of 3-methylquinoline, 3-methyl-2-oxo-1,2-dihydroquinoline, 5,6-dihydroxy-3-methyl-2-oxo-1,2-dihydroquinoline, 2,5,6-trihydroxy-3-methylpyridine, *Comamonas testosteroni*.

Quinoline, methylquinolines and other *N*-heterocyclic compounds occur in shale oil^[1], and they are found as common contaminants in many aquifers affected by fossil fuel processing activities, in groundwater near landfills containing azaarene-contaminated solid wastes and near creosote wood preservation facilities^[2–9].

Since some of these compounds are suspected to be carcinogenic^[3,10,11], the discharge of them causes health effects and environmental damage. Assessment of the hazard posed by quinoline and its derivatives requires the knowledge of its microbial transformation or degradation.

Several investigators demonstrated the microbial transformation of quinoline under both anaerobic^[9,12–17] and aerobic^[13,14,18–31] conditions.

In contrast to the thoroughly investigated catabolism of quinoline^[23–25,27], comparatively few data are available on the metabolism of methylquinolines. Pereira

et al.^[8,9] reported that complete degradation of 4-methylquinoline under anaerobic conditions only occurs in the presence of an additional carbon source. Under methanogenic conditions, 6-, 7-, and 8-methylquinoline were transformed to the corresponding 2-hydroxylated products in anoxic freshwater sediment^[17].

Concerning the aerobic metabolism of methylquinolines, a quinoline-degrading strain of *Pseudomonas aeruginosa* was found to hydroxylate 6-, 7-, and 8-methylquinoline, but not 2-methyl, 4-methyl, or 2,6-dimethylquinoline. *Pseudomonas putida* strain QP was capable to hydroxylate only 8-methylquinoline^[29]. A quinoline-degrading *Pseudomonas putida* strain was adapted to utilize 6-methylquinoline as sole source of carbon and energy, but this organism did not degrade 2-, 4-, 7-, or 8-methylquinoline^[32].

Rhodococcus sp. CHS^[31], *Pseudomonas* sp. strain MPQ^[29], an *Alcaligenes* and an *Arthrobacter* strain^[33,34]

Abbreviations:

TLC, Thin-layer chromatography; DMSO, dimethylsulfoxide.