FATE II

Reductive Dechlorination of Chlorinated Dibenzo-p-dioxins by a Bacterial Consortium Isolated from Lake Ketelmeer Sediment

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Introduction

The sediment of Lake Ketelmeer (a sedimentation area of the river Rhine in the Netherlands) sediment is contaminated with high levels of chlorinated aromatic compounds such as chlorobenzenes (CBs), PCBs, PCDFs and PCDDs. These compounds are generally assumed to be persistent. However an anaerobic enrichment culture, isolated from these sediments, has been shown to be capable of dechlorinating some CBs and some PCBs under anaerobic conditions [1]. The question arises whether this culture is also able to dechlorinate dioxins. In the present study, the dechlorinationpathway of 1,2,3,4-TeCDD, as a model, with the same culture has been examined.

Methods

The culture was enriched from Lake Ketelmeer sediments on a minimal medium, in the presence of lactate as an electron donor and hexachlorobenzene (HCB) as an electron acceptor. After this culture had dechlorinated all of the HCB, dioxins were added; each dioxin to a separate batch. Control incubations were also made, by pasteurization (20 min at 75°C), 24 h incubation at room temperature and sterilization (3 h at 121°C), of an active HCB-dechlorinating culture, after which dioxins were added.

The following dioxins were used in separate batch experiments: 1,2,3,4-TeCDD; 1,2,3-TrCDD; 1,2,4-TrCDD. Both trichlorinated dioxins had been identified as metabolites of 1,2,3,4-TeCDD in an earlier experiment [2,3]. Each dioxin was added in high concentrations in order to be able to analyze its metabolites. At appropriate time intervals, samples were taken in triplicate and after clean-up with acid/base silica gel columns, analyzed with GC-ECD and GC-MSD using a DB5 column (30 m x 0.32 mm). Each metabolite was positively identified on GC-MSD by comparison with authentic standards.

Results

This enrichment culture was capable of reductively dechlorinating about half the initial concentration of ± 500 nM 1,2,3,4-TeCDD in 18 days. The metabolites which were identified are 1,2,4-TrCDD and a smaller amount of 1,2,3-TrCDD. Also, 1,3-DCDD and a smaller amount of 2,3-TrCDD were identified. Both these latter two metabolites could be products of the dechlorination of 1,2,4-TrCDD and 1,2,3-TrCDD. Trace amounts of 2-MCDD were identified with GC-MS. This metabolite could be a product of both 1,3-DCDD and 2,3-DCDD. No metabolites were found in the control incubations.

From the separate incubations with 1,2,4-TrCDD and 1,2,3-TrCDD the dechlorination pathway is further clarified. 1,3-DCDD was identified as a metabolite from both 1,2,3-TrCDD and 1,2,4-TrCDD. 2,3-DCDD was identified only as a metabolite from 1,2,3-TrCDD. Also an other monochlorinated dioxin was identified with GC-MSD: 1-MCDD. This metabolite could only be a product of 1,3-DCDD. 2-MCDD was identified only as a product of 2,3-DCDD.

These results indicate that the pathway for dechlorination of 1,2,3,4-TeCDD by the consortium is as shown in fig.1.

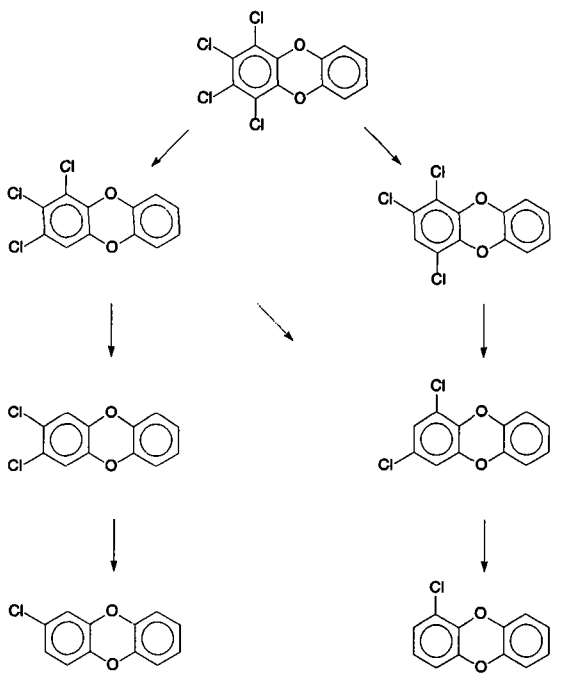

Fig. 1. Dechlorination pathway of 1,2,3,4-TeCDD.

This consortium is thus able to dechlorinate lower chlorinated dioxins. The ability of one consortium to dechlorinate three classes of compounds is not a general phenomenon [4]. The results show a relatively fast dechlorination of a lower chlorinated dioxin to monochlorinated dioxins. The dechlorination-pattern suggest that also more toxic products (2,3,7,8-substituted) could potentially be formed from higher chlorinated dioxins. Dechlorination of higher chlorinated dioxins and furans has also been reported [5].

References

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