Reductive Dechlorination of Chlordecone Under Anaerobic Conditions: Transformation by KB-1 and Insights from Soil and Sediment Microcosms

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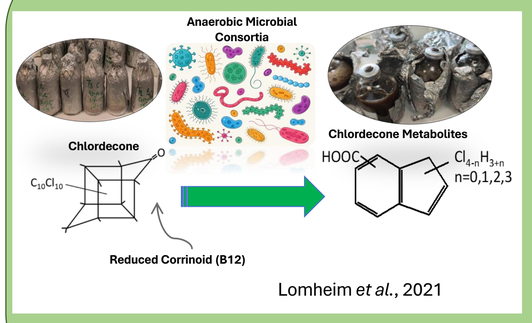
INTRODUCTION



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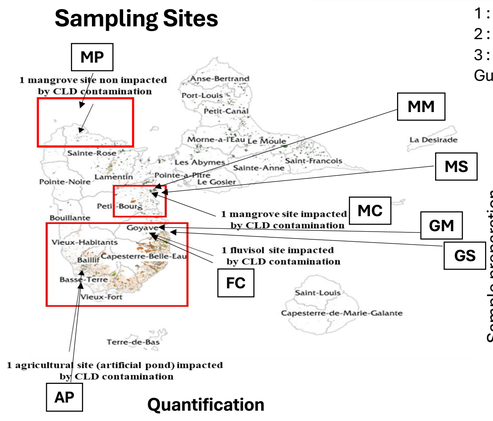
Chlordecone (CLD), a persistent organochlorine pesticide, remains a major environmental and public health concern in the French Caribbean decades after its ban. Its widespread occurrence in soils, sediments, waters, food webs, and human populations reflects its high recalcitrance and ongoing exposure risks. Conventional remediation approaches have shown limited success; however, anaerobic microcosm studies suggest that indigenous microbial communities can promote reductive dechlorination of chlordecone[1,2]. Despite this potential, the microbial taxa and metabolic mechanisms involved remain poorly understood. This study investigates the response of a known culture KB1[3,4] and of indigenous anaerobic microbial communities to biostimulation, focusing on microbial succession, putative chlordecone-transforming taxa, and corrinoid-mediated functions predicted using PICRUSt2 for gene prediction through gene content inference, KEGG Ortholog (KO) annotations, and MetaCyc metabolic pathway reconstruction[5].

La pollution par la chlordécone (CLD), un pesticide organochloré persistant, demeure une préoccupation environnementale et de santé publique majeure dans les Antilles françaises, plusieurs décennies après son interdiction. Sa présence généralisée dans les sols, les sédiments, les eaux, les réseaux trophiques et les populations humaines reflète sa forte récalcitrance et les risques d'exposition persistants. Les approches conventionnelles de remédiation ont montré un succès limité ; cependant, des études en microcosmes anaérobies suggèrent que les communautés microbiennes autochtones peuvent favoriser la déchloration réductrice de la chlordécone[1,2]. Malgré ce potentiel, les taxons microbiens et les mécanismes métaboliques impliqués restent mal compris. Cette étude examine la réponse d'une culture connue KB1[3,4], et de communautés microbiennes anaérobies autochtones à la biostimulation, en mettant l'accent sur la succession microbienne, les taxons potentiellement impliqués dans la transformation de la chlordécone et les fonctions médiées par les corrinoïdes, prédites à l'aide de PICRUSt2 par inférence du contenu génique, annotation des orthologues KEGG (KO) et reconstruction des voies métaboliques MetaCyc[5].

METHODOLOGY

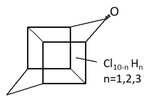
1

Sampling Sites

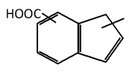


Quantification

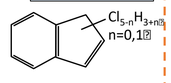
Hydrochlordécones



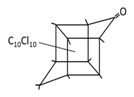
Chloroindènes carboxylés



Chloroindènes



Chlordécone



Approximate quantification

Chemical Analysis

1 : Gas phase
2 : Surface water from the sampling sites
3 : CLD-contaminated soil from Guadeloupe, 2022 (=**Inoculum**)

Sample preparation

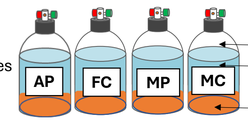
Mixed bacterial culture (**KB1**)



Strictly anaerobic

1 : *Dehalococcoides*-enriched cultures
2 : *Dehalobacter*-enriched cultures
3 : *Dehalogenimonas*, *Dehalobacter* and *Dehalococcoides*-enriched cultures

Anaerobic microcosms



Mixed bacterial culture (**MC2**)



Dehalobacter-enriched culture

Chemical extraction



Hexane/Acétone 85:15 v/v

LC-MS analysis



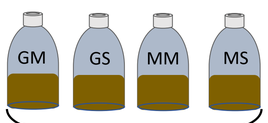
Microbial Community Analysis

2

Sampling Sites:

- Goyave mangrove soil (**GM**)
- Goyave sediment (**GS**)
- Mache-a- Eau mangrove soil (**MM**)
- Mache-a- Eau mangrove sediment (**MS**)
- Gourbeyre fresh water sediment (**ARP**)

Anaerobic Microcosms



Incubation Medium:
- ✓ Artificial groundwater,
- ✓ Chlordecone,
- ✓ $C_3H_3NaO_3$,
- ✓ Vitamins

Sediment

Strictly anaerobic

Incubation Time Points (Months): T0 → T1 → T2 → T3

Sediments from Saline Mangrove

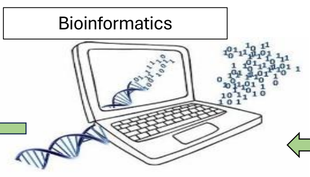
Sediments from Freshwater

Total DNA extraction



Metabarcoding analysIs

Bioinformatics



Bioinformatics Pipeline for 16S DNA Metabarcoding Analysis

3

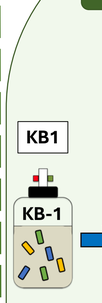
Data import	Data pre-processing	Taxonomic annotation	Microbial diversity analysis	Functional Prediction
Import of FASTQ data into the Qiime2 data format	DADA2 Denoising: data filtering, pruning and normalization, to reduce noise and improve data quality	Taxonomic Assignment (SILVA), Assigning taxonomic identities to DNA sequences using reference databases	Alpha Diversity, Beta Diversity, calculation of species abundance, taxonomic richness, diversity indices and rarefaction curves	PICRUSt2, Predict genes, KEGG Orthologs (KOs), MetaCyc Predict metabolic pathways

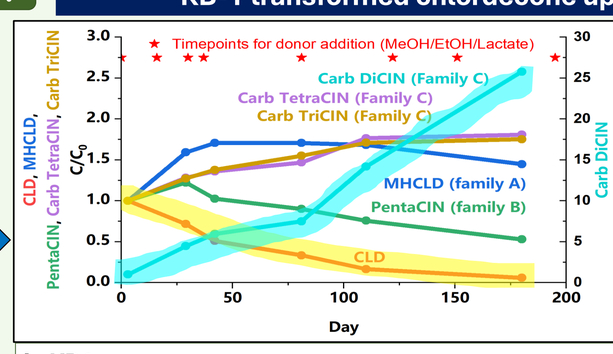
RESULT

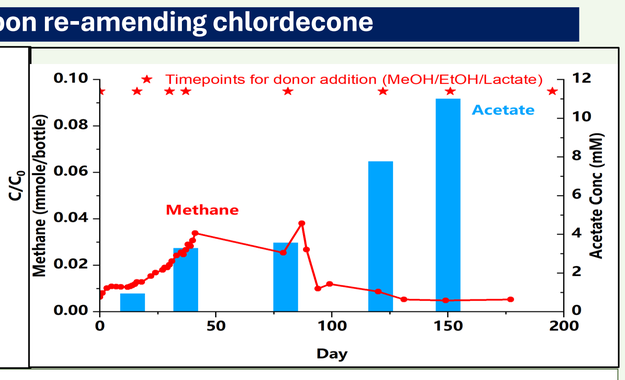
4

KB-1 transformed chlordecone upon re-amending chlordecone

KB1





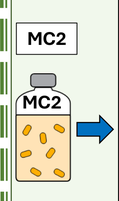


In KB1:

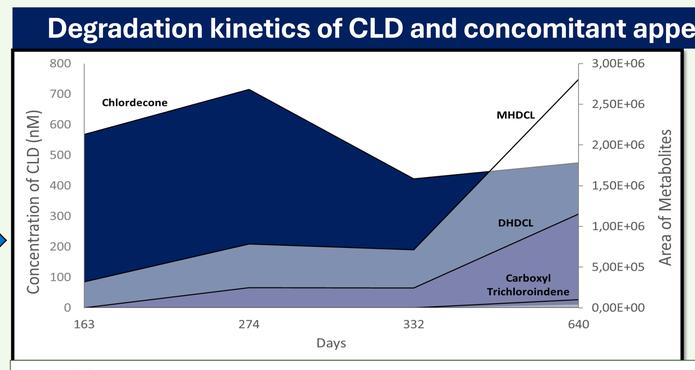
➢ Methane production was measured in the culture, testifying to the strict anaerobic conditions.

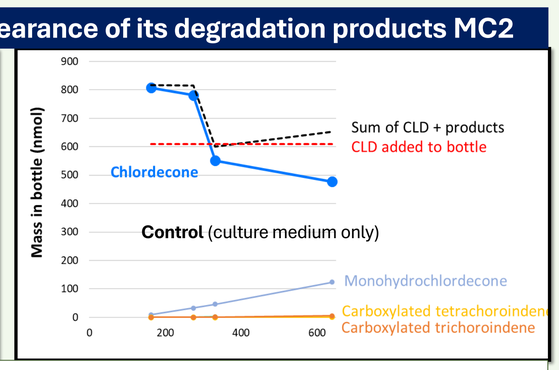
1) Chlordecone is extensively depleted in the culture within 200 days.
2) **Carboxylated dichloroindene (Carb DiCIN) was observed as a dominant transformation product.**

MC2



Degradation kinetics of CLD and concomitant appearance of its degradation products MC2





In MC2:

➢ Methane production was measured in the culture, testifying to the strict anaerobic conditions.

1) This culture enabled dechlorination of around 20% of the CLD in 600 days.
2) The main dechlorination product is monohydrochlordecone
3) Carboxylated dihydrochlordecone and trichloroindene are produced

5

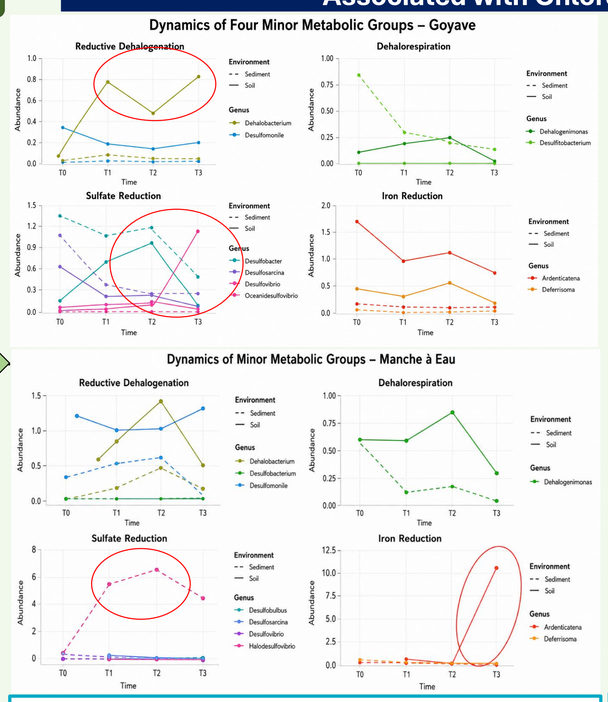
PICRUSt2-Predicted Functional Potential: KEGG Orthologs and MetaCyc Pathways Associated with Chlordecone Transformation

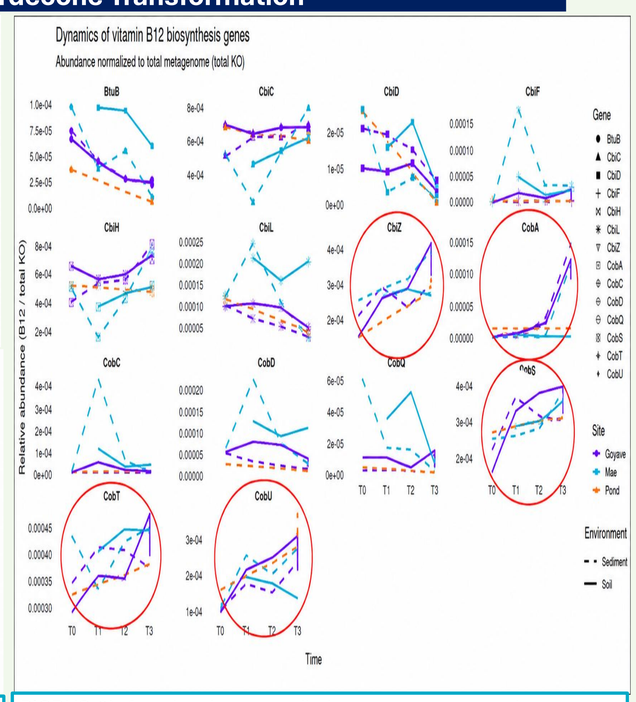
GM

GS

MM

MS





Saline mangroves showed enrichment of putative dehalogenating genera (*Dehalobacterium*, *Desulfomonile*, and *Halodesulfovibrio*), along with sulfur-reducing and iron-reducing taxa.

PICRUSt2's functional gene predictions suggest progressive enrichment of corrinoid biosynthesis and activation pathways (cobA, cobS, cobT, cobU, cbiZ), supporting a potential role for vitamin B12-dependent reductive dechlorination.

CONCLUSIONS-PERSPECTIVES

- Under strict anaerobic conditions, the KB1 culture extensively transformed chlordecone within 200 days, with carboxylated dichloroindene (Carb-DiCIN) emerging as the predominant transformation product.
- The indigenous mixed culture MC2 achieved approximately 20% chlordecone (CLD) dechlorination within 600 days. Monohydrochlordecone was the main transformation product, while carboxylated dihydrochlordecone and trichloroindene were also detected.
- Saline mangrove microcosms showed enrichment of putative dehalogenating genera, including *Dehalobacterium*, *Desulfomonile*, and *Halodesulfovibrio*, along with sulfur-reducing and iron-reducing taxa.
- Functional predictions indicated progressive enrichment of corrinoid biosynthesis and activation pathways (*cobA, cobS, cobT, cobU,* and *cbiZ*), supporting a potential role for vitamin B12-dependent reductive dichlorination
- Perspectives of this work are: Column study with KB1 and stimulation of indigenous bacteria to degrade chlordecone and toxicological profile of metabolites obtained during microbial degradation

- *Dans des conditions strictement anaérobies, la culture KB1 a transformé la chlordécone sur une période de 200 jours, avec le dichloroindène carboxylé (Carb-DiCIN) comme principal produit de transformation.*
- *La culture mixte endogène MC2 a atteint environ 20 % de déchloruration de la chlordécone (CLD) en 600 jours. Le monohydrochlordécone était le principal produit de transformation, tandis que le dihydrochlordécone carboxylé et le trichloroindène ont également été détectés.*
- *Les microcosmes de mangrove saline ont montré un enrichissement en genres bactériens putativement déhalorénants, notamment Dehalobacterium, Desulfomonile et Halodesulfovibrio, ainsi que des taxons réducteurs de soufre et de fer.*
- *Les prédictions fonctionnelles ont indiqué un enrichissement progressif des voies de biosynthèse et d'activation des corrinoïdes (cobA, cobS, cobT, cobU et cbiZ), suggérant un rôle potentiel de la déchlorination réductive dépendante de la vitamine B12.*
- *Les perspectives de ce travail sont les suivantes : étude en colonne avec la culture KB-1 et stimulation des bactéries indigènes afin de favoriser la dégradation de la chlordécone, ainsi que l'établissement du profil toxicologique des métabolites produits au cours de la dégradation microbienne.*

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THANKS TO