

# 1,2-二氯苯污染環境下比較土壤微生物組成結構之的潛在變化

## Compositions of soil microbes in soil with high 1,2-DCB concentrations.

國立台灣大學生物環境系統工程研究所

碩士班學生

黃玟婷

Wen-Ting Huang

助理教授

蕭友晉

Yo-Jin Shiau

### 摘 要

含氯有機化合物是工業中重要的溶劑。然而，它們大多對人體和環境具有高毒性。由於穩定性和緻密的非水相，一旦釋放到土壤和地下水系統中，它們幾乎不會被生物降解。

本研究試圖評估不同碳源和營養源的 1,2-二氯苯污染在微觀世界中土壤微生物群落的潛在變化。通過使用即時聚合酶連鎖反應(real-time Polymerase Chain Reaction, real-time PCR) 和次世代定序(Next Generation Sequencing, NGS)技術進行微生物體分析。

該研究表明，產甲烷菌最有可能在厭氧和貧營養環境中分解 1,2-二氯苯的微生物。然而，反硝化細菌，如假單胞菌屬、鞘氨醇單胞菌屬和黃單胞菌科、假單胞菌科以及芽孢桿菌科，一旦環境中存在可用氮源，它們可能在分解 1,2-二氯苯中發揮重要作用。這些結果表明，外部氮源對於未來生物修復的污染場地很重要。

關鍵詞: 次世代定序，1,2-二氯苯，土壤污染，微生物生態學，反硝化細菌，產甲烷菌

### Abstract

Chlorinated organisms are important solvents in industry. However, most of them are highly toxic to the environments. Because these organisms are relatively stable in the environment and can settle into the soil and groundwater system, they can hardly be biodegraded once they are released into the environments.

This study tried to evaluate the changes of microbial composition in 1,2-DCB contaminated soils with real-time PCR and next generation sequencing. The results showed that methanogens may be the microorganisms that most likely decompose 1,2-DCB in anaerobic and oligotrophic environments.

In addition, *Pseudomonas*, *Sphingomonas*, and some genus belong to

*Xanthomonadaceae*, *Pseudomonadaceae* and *Bacillales* families may also play important role in decomposing 1,2-DCB once N sources are available. These results indicate that external N sources are important in contaminant sites for future bioremediation.

Keyword: next generation sequence , 1,2-DCB , soil pollution , microbial ecology , denitrier , methanogen