

## Humic acid affecting pentachlorophenol biodegrading microorganisms in soil deciphered by stable isotope probing coupled with high-throughput sequencing approaches

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Humic substances (HSs) are ubiquitous in soils and can be reversibly oxidized and reduced by acting as redox mediators and impacting a direct effect on the biodegradation of organic pollutants. However, the roles of HSs on specific microbial taxa that are responsible for organic pollutant degradation remain unclear. In this work, the effect of three humic acids (HAs), extracted from forest (CBHA), paddy (PSHA) and peat (YNHA) soils on the microbial community involved in pentachlorophenol (PCP) anaerobic biodegradation were investigated by high throughput sequencing and stable isotope probing (SIP) approaches. The results showed that all HA samples accelerated the biotransformation processes of PCP, with the highest rate obtained in YNHA group. Illumina sequencing revealed that *Desulfovibrio* and *Clostridium* were the dominant functional bacteria for PCP dechlorination. During the subsequent mineralization process of PCP, HAs had substantial effects on the diversity and abundance of microbial communities and several taxa were enriched in the <sup>13</sup>C heavy fractions compared with <sup>12</sup>C heavy fractions. Without HA, *Methanobacterium* and *Spartobacteria* exhibited a significant increase in <sup>13</sup>C heavy fractions. *Methanosarcina* and OP11 were the dominant PCP degraders in microcosms when amended with CBHA, whereas *Burkholderia* and *Methanobacterium* were the key PCP degraders in PSHA- and YNHA-amended experimental microcosms. These findings extend our knowledge of the diversity and ubiquitous nature of HSs-utilizing microorganisms involved in PCP degradation and could provide scientific support for developing in situ bioremediation technologies for HSs-rich soils contaminated by PCP.