
RECENT RESEARCH ACTIVITIES

Use of biphenyl/polychlorinated biphenyl-degrading bacteria for the production of useful aromatic compounds

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Most of aromatic compounds sourced from nature are derived from plant lignin. Lignin is a recalcitrant aromatic heteropolymer; however, some species of basidiomycetes, collectively known as white-rot fungi, can degrade lignin in wood. When these fungi partially degrade lignin, many of its degradation products, containing lignin-derived aromatic compounds, are released into natural environments. Especially, in soil environments, there are a large number of bacteria grown on lignin-derived aromatic compounds.

On the other hand, so far we have isolated 14 biphenyl-utilizing/degrading bacteria, belonging to the genera *Pseudomonas* and *Rhodococcus*, from various environmental samples. Because these bacteria can also co-metabolically degrade polychlorinated biphenyls (PCBs), xenobiotic compounds known as one of the most serious environmental pollutants, we have extensively studied on biochemical and genetic bases of biphenyl/PCB degradation [1]. Furthermore, we have recently performed the whole genome sequencing of these biphenyl/PCB-degrading bacteria and compared their genomes with those of other xenobiotic compound-degrading bacteria [2-10]. Interestingly, the genome analyses revealed that these biphenyl/PCB-degrading bacteria possess various catabolic genes involved in the degradation of lignin-derived aromatic compounds, as well as xenobiotic aromatic compounds. In fact, some of the sequenced bacteria were able to grow well on lignin-derived aromatic compounds as the sole sources of carbon and energy. These findings show that many aromatic compound-catabolic genes may be functionally expressed in the presence of lignin-derived aromatic compounds.

In this study, we focus on the production of useful aromatic compounds from wood biomass, such as lignin-derived aromatic compounds, by molecular breeding of aromatic compound-catabolic genes from the biphenyl/PCB-degrading bacteria. We are now trying to screen and identify useful genes and proteins from these bacteria using genomics and proteomics technologies.

References

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