

Draft genome sequence of humic substance-degrading *Pseudomonas* sp. PAMC 29040 from Antarctic tundra soil

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천연 복합유기화합물인 부식질을 분해하는 남극 툰드라 토양 *Pseudomonas* sp. PAMC 29040의 유전체 분석

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Pseudomonas sp. PAMC 29040 was isolated from a maritime tundra soil in Antarctica for its ability to degrade lignin and subsequently confirmed to be able to depolymerize heterogeneous humic substance (HS), a main component of soil organic matter. The draft genome sequences of PAMC 29040 were analyzed to discover the putative genes for depolymerization of polymeric HS (e.g., dye-decolorizing peroxidase) and catabolic degradation of HS-derived small aromatics (e.g., vanillate *O*-demethylase). The information on degradative genes will be used to finally propose the HS degradation pathway(s) of soil bacteria inhabiting cold environments.

Keywords: cold-adapted bacteria, degradative enzyme, soil humic substance

Humic substance (HS) is a naturally occurring complex heteropolymer, which is widely distributed in various environments including Arctic and Antarctic tundra soils. HS is composed mainly of aromatic, aliphatic, and phenolic components, which are covalently bound mostly through various types of C-C and C-O-C bonds (Grinhut *et al.*, 2007). Owing to

its complexity and structural similarity to lignin, HS has been considered as modified lignin and thus to be rather recalcitrant to microbial degradation. Although the information on HS bacterial degradation, such as catalytic enzymes, is not sufficient, a degradative pathway has been proposed based on several previous fragmentary studies (Bugg *et al.*, 2011; Kamimura *et al.*, 2017; Kim *et al.*, 2018). It is assumed that HS is depolymerized by bacterial extracellular oxidoreductases, such as dye-decolorizing peroxidases and laccases. The resulting HS-derived small aromatic compounds including various biaryls (e.g., β -aryl ether and biphenyl) are generally funneled into a main metabolite, vanillate, which is *O*-demethylated to produce protocatechuate. As another route, vanillate is decarboxylated into guaiacol, which is subsequently *O*-demethylated to catechol (Alvarez-Rodriguez *et al.*, 2003). Protocatechuate and catechol are further degraded to TCA cycle intermediates (e.g., acetyl-CoA) through *meta*- or *ortho*-cleavage pathway.

A study site (designated KS1) for HS microbial degradation was selected around Kaya Hill near the Korean Antarctic Research Station (King Sejong) on the Barton Peninsula of King George Island on the western Antarctic Peninsula. In January, 2015, a bacterial strain (PAMC 29040) was isolated

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(예, vanillate *O*-demethylase)를 탐색하기 위해 PAMC 29040 게놈 염기서열을 분석하였다. 분석을 통해서 최종 확보한 효소유전자 정보는 저온환경에 서식하는 토양 세균의 부식질 분해경로 제안에 활용될 것이다.

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