

Study on humic substances degradation by a microbial consortium from subarctic tundra soil

Dockyu Kim^{a*}, Ha Ju Park^a, Sungjin Nam^a, Seok Cheol Kim^a, and Hyoungseok Lee^b

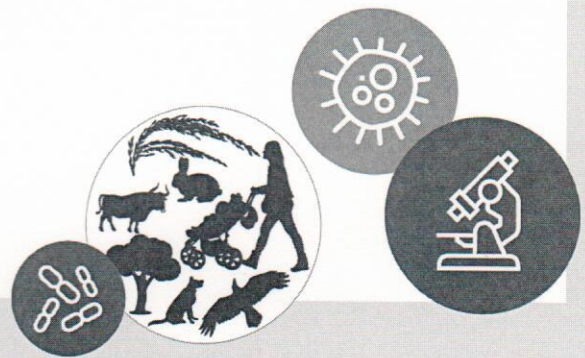
^aDivision of Polar Life Sciences, Korea Polar Research Institute, Incheon 21990, Republic of Korea

^bUnit of Polar Genomics, Korea Polar Research Institute, Incheon 21990, Republic of Korea

The largest constituent of soil organic matter, humic substances (HS), is naturally present as aromatic heteropolymers, with a composition similar to lignin. The microbes in a sample of subarctic tundra soil (Alaska, USA) were able to degrade humic acids (HA, a major component of HS) during microcosm experiments at a low temperature of 5°C, which is similar to natural soil temperature during the thawing period (average temperature of 5.6°C at a depth of 20 cm). The relative abundance of HA decreased to approximately 71% compared with the non-incubated soil control (100%). The microbes, however, were unable to degrade HA at 25°C, which is in the ideal soil temperature range for planting most plants. When enriched at 15°C in liquid mineral medium provided with HA as a sole carbon source, the HA-enriched microbial consortium was metabolically activated to degrade abundant soil carbons (e.g., 4-hydroxy benzoic acid and D-cellobiose) and completely degraded 2-methoxy phenols (ferulic and vanillic acids), which are lignin-derived mono-aromatics. Our data indicate that the microbial consortium of Alaska tundra soil, which dominantly contains phylum Proteobacteria (specifically, class Betaproteobacteria), is cold-adapted and symbiotically degrades HS, possibly via a bacterial lignin-catabolic pathway in which vanillic acid is a main metabolite. To our knowledge, this is the first report describing a HS-degradative pathway at the microbial consortium level.



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P05 Physiology

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Dockyu Kim¹, Ha Ju Park¹, Sungjin Nam¹, Seok Cheol Kim¹, and Hyungseok Lee²

¹Division of Polar Life Sciences, Korea Polar Research Institute, Incheon 21990, Republic of Korea

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P06 Microbial Ecology

Harmful algal community and co-occurring species in relation to the algal temporal stability in river-connected lakes

Min Sung Kim¹, Keun Hee Kim², Soon Jin Hwang², Tae Kwon Lee¹

¹Department of Environmental Engineering, Yonsei University, Wonju, Republic of Korea

²Department of Environmental Health Science, Kon Kuk University, Seoul, Republic of Korea

Stability, which calculate how much community fluctuate over time, is an important index to interpret ecological features. Recent studies have interested in the effects of algae-bacterial interactions, water qualities and climate changes on the harmful algal bloom (HAB), but the relationship between the stability of algal structure and HAB have been scarcely studied. Here, we collected nine-year time series datasets of algal community compositions, water qualities and regional factors in six river-connected lakes (the North Han River, South Korea) to examine the effects of the stability of algal communities on the co-occurrence network and frequency of HABs. We calculated the stability of the algal communities in each lake and could classify into high (HL) and low stable lakes (LL). The complexity of the co-occurrence networks was significantly lower in LL (density: 0.038) than HL (density: 0.066). The network in LL is built around the cyanobacterial harmful algae, *Mycrocystis* and *Dolichospermum*, whereas *Scenedesmus* (green algae) and *Cymbella* (diatom) are the main pillars of the network in HL. The abundance of algal species correlated with network degree ($R^2 = 0.34$) in LL, but not in HL ($R^2 = 2.8e^{-7}$), indicating that algae-algae interactions were highly conserved in HL regardless of algal abundances. These results confirmed the algal abundances in LL were strongly associated with water qualities. Taken together, our result will take a step toward understanding the concept of the algal stability suggesting a new perspective on HABs.