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The abundance of health-associated bacteria is altered in PAH polluted soils - Implications for health in urban areas?

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Abstract

© 2017 Parajuli et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited. Long-term exposure to polyaromatic hydrocarbons (PAHs) has been connected to chronic human health disorders. It is also well-known that i) PAH contamination alters soil bacterial communities, ii) human microbiome is associated with environmental microbiome, and iii) alteration in the abundance of members in several bacterial phyla is associated with adverse or beneficial human health effects. We hypothesized that soil pollution by PAHs altered soil bacterial communities that had known associations with human health. The rationale behind our study was to increase understanding and potentially facilitate reconsidering factors that lead to health disorders in areas characterized by PAH contamination. Large containers filled with either spruce forest soil, pine forest soil, peat, or glacial sand were left to incubate or contaminated with creosote. Biological degradation of PAHs was monitored using GC-MS, and the bacterial community composition was analyzed using 454 pyrosequencing. Proteobacteria had higher and Actinobacteria and Bacteroidetes had lower relative abundance in creosote contaminated soils than in non-contaminated soils. Earlier studies have demonstrated that an increase in the abundance of Proteobacteria and decreased abundance of the phyla Actinobacteria and Bacteroidetes are particularly associated with adverse health outcomes and immunological disorders. Therefore, we propose that pollution-induced shifts in natural soil bacterial community, like in PAH-polluted areas, can contribute to the prevalence of chronic diseases. We encourage studies that simultaneously address the classic “adverse toxin effect” paradigm and our novel “altered environmental microbiome” hypothesis.

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