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Profiling of bacterial community structure on Asian dust particles by T-RFLP

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Key words: Asian dust, bacteria, T-RFLP

INTRODUCTION: Dust storms originating in the arid regions of Asia usually occur from late winter through spring, and more than one million tons of dust per year is transported to distant locations such as the Korean Peninsular and Japan by the prevalent westerly winds (Asian dust events; Kosa). The major dust sources are considered to be the arid regions in China. We supposed that these soil particles could be carriers of microbes. In order to clarify the dynamics of microbes moving with these dust events, bacterial communities in soil in Chinese arid regions and those on Asian dust particles were examined by culture-independent approaches.

MATERIALS AND METHODS: Soil samples were collected from the Loess plateau, Taklamakan desert, and Gobi desert. Asian dust particles were collected in Beijing. The volume of bacterial cells transported to Beijing was determined by real-time PCR quantification with the eubacterial primer set. Bacterial community structures were examined by T-RFLP analysis based on the bacterial rRNA gene. RESULTS AND DISCUSSION: The volume of bacterial cells on Asian dust particles was estimated as 10^{13} - 10^{16} cells/km²/month. MDS analysis following T-RFLP demonstrated that the community structures of bacteria on these Asian dust particles were similar with those of Taklamakan desert and Loess plateau. These findings show that bacterial cells can "travel" by atmospheric transport of soil. These bacteria would be expected to affect the microbial ecosystem in Eastern Asian countries when severe dust events occur.

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Effect of copper nonylphenol sulfonate on soil microbial communities

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Copper nonylphenol sulfonate (NPS-Cu) is a bactericidal agent used for the agricultural practice. The fate of NPS-Cu in the soil is not yet studied fully and it was also unknown whether the biodegradation of NPS-Cu resulted in the production of estrogenic nonylphenol. The purpose of this study was to analyze the effect of NPS-Cu on soil microbial communities and the degradation of NPS-Cu in the soil environment. A soil sample (20g) was collected from the Field Science Center, Ibaraki University College of Agriculture and incubated with NPS-Cu at 30°C for 30 days. Practically, during the incubation, a solution of NPS-Cu was repeatedly added to the soil sample (final concentration, 0.08mg/g) every 5 days. The concentration of NPS-Cu was determined by the methylenblue colorimetric method. The degradation products of NPS-Cu were analyzed by HPLC. Soil bacterial communities were analyzed by extracting soil DNA and the subsequent T-RFLP analysis of the PCR-amplified 16s rDNA. The degradation product was detected and identified as methane sulfinic acid by HPLC analysis. The incubation of soil with NPS-Cu resulted in a large decrease in soil bacterial diversity and the predominance of *Lysobacter* sp. and a bacterium belonging to *Xanthomonadaceae*.

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