Expedited evolution of soil bacteria exposed to organic contaminants

<u>Aki Sinkkonen</u>¹, Sari Kauppi¹, Martin Romantschuk¹ and Rauni Strömmer¹

¹ University of Helsinki, Department of Ecological and Environmental Sciences, Niemenkatu 73, 15140 Lahti, Finland. E-mail: aki.sinkkonen@helsinki.fi.

Organic xenobiotics are a worldwide problem. Soil microbes, especially bacteria, are known to be capable of degrading most if not all these contaminants. Despite detailed microbiological knowledge, basic understanding on the ecological factors behind the microbially mediated changes in contaminant concentrations is limited. We tested two hypotheses for which support can be found in the literature: (1) the degradation of organic contaminants is faster in humus soil than in mineral soil and (2) the degradation of organic contaminants is faster in previously contaminated soil than in similar but previously noncontaminated soil. Mesocosms were spiked with either diesel oil or creosote that are organic mixtures, and two two-factor (precontamination, soil type) experiments were performed. In both cases, soil remediation progressed faster in humus soil, as compared to mineral soil (repeated-measures ANOVA). Precontamination, on the other hand, had variable effects on the degradation of the xenobiotics. The results cannot be explained by differences in nutrient availability or soil pH. Humus soil putatively contains natural compounds that are structurally similar to the contaminants used, while bacteria in precontaminated soil may have adapted to cope with the compounds used, regardless of soil type. These results lend support to the first hypothesis indicating that organic matter in soil context is a crucial determinant of soil degradation capacity. Previous direct contact and metabolism of the contaminants (hypothesis 2) does not necessarily leave long-lasting traces in the degradation capacity of the microbial community, and is therefore of secondary importance. We have also investigated soil bacteria in our mesocosms by using DGGE and 454-sequencing. The hypothesis is that an increase in the frequency of certain bacterial taxa can be associated with enhanced degradation in humus soil. Our results support the view that bacterial evolution and bioremediation are expedited in contaminated mineral soils by adding humus.