

Interactive
Comment

Interactive comment on “Response of soil microorganisms to radioactive oil waste: results from a leaching experiment” by P. Galitskaya et al.

Anonymous Referee #3

Received and published: 27 February 2015

The manuscript by Galitskaya and coauthors tackles the response of soil microorganisms to oil and/or radionuclides through leaching column experiments coupled to the estimation of microbial activity and changes in the microbial community structure by means of PCR-SCCP analysis. The results are analyzed with MDS analysis concluding that the negative effects of radioactive oil wastes are mainly due to the hydrocarbon fraction than to the radionuclides.

My main concern with this manuscript is that is too focused on the response of the microorganisms to the radioactive oil waste without providing good experimental evidences. The authors use a toxicity test based only in *Bacillus* sp., which is probably a standardized test but does not provide evidences of how the microbial community as whole is affected by the oil or radioactive compounds. Same thing applies to the cellu-

Full Screen / Esc

Printer-friendly Version

Interactive Discussion

Discussion Paper



Interactive
Comment

lase activity and metabolic quotient. The microbial community will change, obviously, upon amendment with the oil + radioactive waste of with the radioactive waste, mainly due to the presence of accessible (or more recalcitrant) compounds of the oil waste, but that doesn't mean the microbial population suffers from a toxic effect (not proven at least with the methods applied here). As mentioned by the authors in this version (page 32, lines 5 to 12), the hydrocarbon contamination normally leads to a change in the microbial composition favoring those able to degrade these compounds. Thus, the fingerprinting method used DOES NOT prove that the community structure was "affected" by the waste addition, but rather that there was a shift in the community, which is of a common sense to me. To actually prove that the microbial community is affected by these compounds you could have prepare microcosms with sterile soil and add a mixture of known microbial strains known to be present in these soils and see how the presence of the contaminant would affect their activity (e.g. changes in the 16S rRNA gene expression). In general the methods are out of date and the conclusions too adventurous considering the experimental design.

Interactive comment on Biogeosciences Discuss., 12, 1753, 2015.

[Full Screen / Esc](#)

[Printer-friendly Version](#)

[Interactive Discussion](#)

[Discussion Paper](#)

