

> *Sci Total Environ.* 2023 Sep 1:889:164285. doi: 10.1016/j.scitotenv.2023.164285. Epub 2023 May 19.

Soil polluted with nano ZnO reveals unstable bacterial communities and decoupling of taxonomic and functional diversities

R Dinesh ¹, C P Sreena ¹, T E Sheeja ², I P Vijesh Kumar ¹, R Praveena ¹, Sona Charles ¹, V Srinivasan ¹, K Jayarajan ¹, V Sajith ³, K P Subila ¹, P Haritha ¹

Affiliations [+](#) expand

PMID: 37209750 DOI: 10.1016/j.scitotenv.2023.164285

Abstract

Due to relentless production and disposal of nano zinc oxide (nZnO), it has become critical to comprehend the serious risks large-scale accumulation of nZnO pose to bacterial communities in soil. The primary objective was to evaluate the changes in bacterial community structure and associated functional pathways through predictive metagenomic profiling and subsequent validation through Quantitative Realtime PCR in soil spiked with nZnO (0, 50, 200, 500 and 1000 mg Zn kg⁻¹) and similar levels of bulk ZnO (bZnO). The results revealed that soil microbial biomass-C, -N, -P, soil respiration and enzyme activities decreased markedly at higher ZnO levels. The alpha diversity decreased with increasing ZnO level, with more impact under nZnO, while beta diversity analyses indicated a distinct dose- dependent separation of bacterial communities. The dominant taxa including Proteobacteria, Bacteroidetes, Acidobacteria and Planctomycetes significantly increased in abundance, while Firmicutes, Actinobacteria and Chloroflexi decreased in abundance with elevated nZnO and bZnO levels. Redundancy analysis indicated that changes in bacterial community structure instilled a greater dose- rather than size- specific response on key microbial parameters. Predicted key functions did not show a dose- specific response, and at 1000 mg Zn kg⁻¹, methane metabolism as well as starch and sucrose metabolism were attenuated, while functions involving two component systems and bacterial secretion systems were enhanced under bZnO indicating better stress avoidance mechanism than under nZnO. Realtime PCR and microbial endpoint assays confirmed the metagenome derived taxonomic and functional data, respectively. Taxa and functions that varied substantially under stress were established as bioindicators to predict nZnO toxicity in soils. Taxon-function decoupling indicated that the soil bacterial communities deployed adaptive mechanisms under high ZnO, with lesser buffering capacity and resilience of communities under nZnO.

Keywords: Metabolic quotient; Metal oxide nanoparticles; Predictive metagenomic profiling; Soil enzyme activity; Soil microbial biomass; Soil pollution.

Copyright © 2023 Elsevier B.V. All rights reserved.

[PubMed Disclaimer](#)

Conflict of interest statement

Declaration of competing interest The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Similar articles

[New insights into bacterial Zn homeostasis and molecular architecture of the metal resistome in soil polluted with nano zinc oxide.](#)

Raghavan D, Patinharekkara SC, Elampalay ST, Payatatti VKI, Charles S, Veeraraghavan S, Kadiyalath J, Vandana S, Purayil SK, Prasadam H, Anitha SJ.

Ecotoxicol Environ Saf. 2023 Sep 15;263:115222. doi: 10.1016/j.ecoenv.2023.115222. Epub 2023 Jul 6. PMID: 37418939

[Metagenomics indicates abundance of biofilm related genes and horizontal transfer of multidrug resistant genes among bacterial communities in nano zinc oxide polluted soil.](#)

Dinesh R, Sreena CP, Sheeja TE, Charles S, Srinivasan V, Sajith V, Subila KP, Haritha P.

Sci Total Environ. 2023 Feb 10;859(Pt 1):160032. doi: 10.1016/j.scitotenv.2022.160032. Epub 2022 Nov 10. PMID: 36370776

[Soil pH effects on the toxicity of zinc oxide nanoparticles to soil microbial community.](#)

García-Gómez C, Fernández MD, García S, Obrador AF, Letón M, Babín M.

Environ Sci Pollut Res Int. 2018 Oct;25(28):28140-28152. doi: 10.1007/s11356-018-2833-1. Epub 2018 Aug 1. PMID: 30069782

[Ecological life strategies of microbes in response to antibiotics as a driving factor in soils.](#)

Sharma U, Rawat D, Mukherjee P, Farooqi F, Mishra V, Sharma RS.

Sci Total Environ. 2023 Jan 1;854:158791. doi: 10.1016/j.scitotenv.2022.158791. Epub 2022 Sep 13. PMID: 36108841 [Review](#).

[Taxonomic Diversity and Functional Traits of Soil Bacterial Communities under Radioactive Contamination: A Review.](#)

FULL TEXT LINKS



ACTIONS

“ Cite

📁 Collections

SHARE



PAGE NAVIGATION

< Title & authors

Abstract

Conflict of interest statement

Similar articles

MeSH terms

Substances

Related information

LinkOut - more resources