



Bacterial Community Composition and Heavy-Metal Adaptation in Soils of a Bulgarian Gold-Copper Mining Region

Joonseok Chong*

Department of Environmental Microbiology, Sofia University, Sofia, Bulgaria

DESCRIPTION

Mining environments are characterized by substantial changes in soil structure, mineral composition, water availability and chemical conditions. Gold-copper extraction can introduce elevated concentrations of metals into surrounding soils through exposed geological materials, waste deposits, dust movement and drainage. These altered environments can strongly influence microorganisms living in the soil [1]. Bacteria are particularly important because they participate in decomposition, nutrient cycling, mineral transformation and organic matter turnover. Their community composition may therefore provide valuable information about how soil ecosystems respond to prolonged metal exposure. Heavy metals such as copper, lead, zinc, cadmium, arsenic and other potentially toxic elements can impose strong physiological pressure on microorganisms. Some metals are essential micronutrients at low concentrations but become harmful when their availability increases. Copper, for example, participates in important cellular processes but can interfere with proteins, membranes and oxidative balance at excessive levels [2].

Bacterial populations exposed to contaminated soils may consequently experience selection favouring organisms capable of tolerating or transforming these elements. The bacterial community in a mining-affected soil is not necessarily uniform. Metal concentration can vary substantially over short distances depending on geological characteristics, waste distribution, drainage patterns and vegetation [3]. Areas close to mine residues may therefore support microbial communities different from those found in less affected soils. Soil pH organic carbon, moisture, texture and nutrient availability also influence bacterial distribution and can interact with metal toxicity. The combined effect of these environmental factors determines which bacterial groups can persist under particular conditions [4].

Bacterial adaptation to heavy metals can involve several biological mechanisms. Some microorganisms reduce metal

toxicity by limiting uptake through the cell membrane, while others actively transport toxic ions out of the cell. Metals can also be immobilized through binding to extracellular substances or cellular components [5]. Certain bacteria can transform metals into chemical forms with different mobility or toxicity. Production of extracellular polymeric substances may provide an additional protective barrier by binding metal ions before they reach sensitive cellular structures. Long-term exposure can also influence the genetic characteristics of bacterial populations. Resistance-related genes may occur on chromosomes or mobile genetic elements, including plasmids and transposons. These elements can facilitate the movement of adaptive traits among microorganisms when environmental conditions favor their persistence [6]. Consequently, mining environments may function as selective habitats in which metal-tolerance characteristics become more common within portions of the microbial community.

Characterizing bacterial communities can be approached through culture-based and molecular methods. Traditional cultivation can reveal organisms capable of growing under selected environmental conditions, while Deoxy Ribonucleic Acid (DNA) -based profiling can provide a broader picture of bacterial diversity, including microorganisms that are difficult to cultivate [7]. Sequencing of taxonomic marker regions can help identify bacterial groups present in different soil samples. Functional genetic analysis can further provide information about pathways associated with metal resistance, stress responses and environmental adaptation. A notable feature of metal-contaminated soils is the potential enrichment of bacterial groups capable of surviving under chemically stressful conditions. Taxa associated with mineral transformation, stress tolerance and nutrient cycling may become relatively more abundant, whereas metal-sensitive organisms may decline [8-10]. However, contamination does not act independently of other soil characteristics. Organic matter can bind certain metals and reduce their bioavailability, while changes in pH can increase or decrease metal solubility. Therefore, total metal concentration

Correspondence to: Joonseok Chong, Department of Environmental Microbiology, Sofia University, Sofia, Bulgaria, Email: joonseok.chong@envmicrobio.bg

Received: 30-Aug-2025, Manuscript No. JDMGP-25-32410; **Editor assigned:** 02-Sep-2025, PreQC No. JDMGP-25-32410; **Reviewed:** 16-Sep-2025, QC No. JDMGP-25-32410; **Revised:** 22-Sep-2025, Manuscript No. JDMGP-25-32410; **Published:** 30-Sep-2025, DOI: 10.35248/2153-0602.25.16.397

Citation: Chong J (2025). Bacterial Community Composition and Heavy-Metal Adaptation in Soils of a Bulgarian Gold-Copper Mining Region. J Data Mining Genomics Proteomics. 16:397.

Copyright: © 2025 Chong J. 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.

alone may not accurately describe the biological pressure experienced by microorganisms.

CONCLUSION

The bacterial community can also influence the environmental behavior of metals. Microbial metabolism may alter mineral surfaces, promote precipitation, dissolve particular compounds or change the chemical form of metal ions. These processes can affect whether metals remain immobilized in soil or become available for movement into water and biological systems. Microorganisms are consequently both responders to contamination and potential contributors to the transformation of contaminants. Understanding microbial adaptation in Bulgarian gold-copper mining areas has ecological significance because contaminated soils may remain altered for long periods after intensive extraction activities decline. Bacterial community information can help indicate the degree of ecological disturbance and identify microorganisms with potential roles in natural attenuation. Metal-tolerant bacteria may also possess useful biochemical characteristics for environmental applications, including bioremediation approaches designed to immobilize or transform contaminants. At the same time, the presence of metal-resistant bacteria should not automatically be interpreted as evidence of ecological recovery. A community dominated by tolerant organisms may reflect persistent environmental stress rather than restoration of normal soil function.

REFERENCES

1. Maze EA, Booth G, Limon G, Belij-Rammerstorfer S, Tchakarova SR, Alexandrov T, et al. Serological cross-reactivity between Crimean-Congo haemorrhagic fever virus and Nairobi sheep disease virus glycoprotein C. *Front Immunol.* 2025;15:1423474.
2. Estrada-Peña A, Palomar AM, Santibáñez P, Sánchez N, Habela MA, Portillo A, et al. Crimean-Congo hemorrhagic fever virus in ticks, Southwestern Europe, 2010. *Emerg infect dis.* 2012;18(1):179.
3. Mancuso E, Toma L, Polci A, d'Alessio SG, Di Luca M, Orsini M, et al. Crimean-Congo hemorrhagic fever virus genome in tick from migratory bird, Italy. *Emerg infect dis.* 2019;25(7):1418.
4. Ahmeti S, Berisha L, Halili B, Ahmeti F, von Possel R, Thomé-Bolduan C, et al. Crimean-congo hemorrhagic fever, Kosovo, 2013-2016. *Emerg infect dis.* 2019;25(2):321.
5. Duh D, Nichol ST, Khristova ML, Saksida A, Hafner-Bratkovič I, Petrovec M, et al. The complete genome sequence of a Crimean-Congo hemorrhagic fever virus isolated from an endemic region in Kosovo. *Virology.* 2008;5(1):7.
6. Midilli K, Gargılı A, Ergonul O, Elevation M, Ergin S, Turan N, et al. The first clinical case due to AP92 like strain of Crimean-Congo hemorrhagic fever virus and a field survey. *BMC infectious diseases.* 2009;9(1):90.
7. Sherifi K, Rexhepi A, Berxholi K, Mehmedi B, Gecaj RM, Hoxha Z, et al. Crimean-Congo hemorrhagic fever virus and *Borrelia burgdorferi* sensu lato in ticks from Kosovo and Albania. *Front Vet Sci.* 2018;5:38.
8. Cronin P, Joyce SA, O'toole PW, O'connor EM. Dietary fibre modulates the gut microbiota. *Nutrients.* 2021;13(5):1655.
9. Youssefian S, Rahbar N. Molecular origin of strength and stiffness in bamboo fibrils. *Sci rep.* 2015;5(1):11116.
10. De Paepe K, Verspreet J, Courtin CM, Van de Wiele T. Microbial succession during wheat bran fermentation and colonisation by human faecal microbiota as a result of niche diversification. *ISME J.* 2020;14(2):584-596.
1. Maze EA, Booth G, Limon G, Belij-Rammerstorfer S, Tchakarova SR, Alexandrov T, et al. Serological cross-reactivity between Crimean-