



Data in Brief

Metagenomic exploration of microbial community in mine tailings of Malanjkhand copper project, India



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ABSTRACT

Mine tailings from copper mines are considered as one of the sources of highly hazardous acid mine drainage (AMD) due to bio-oxidation of its sulfidic constituents. This study was designed to understand microbial community composition and potential for acid generation using samples from mine tailings of Malanjkhand copper project (MCP), India through 16S rRNA gene based amplicon sequencing approach (targeting V4 region). Three tailings samples (T1, T2 and T3) with varied physicochemical properties selected for the study revealed distinct microbial assemblages. Sample (T3) with most extreme nature (pH < 2.0) harbored *Proteobacteria*, *Actinobacteria*, *Chloroflexi* while the samples (T1 and T3) with slightly moderate nature (pH < 4.0 and > 3.0) exhibited abundance of *Proteobacteria*, *Fimicutes*, *Actinobacteria* and/or *Nitrospirae*. Metagenomic sequences are available under the BioProject ID PRJNA361456.

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Specifications

Organism/cell line/tissue	Mine tailings sediment
Sex	Not applicable
Sequencer or array type	Ion Torrent S5 Platform
Data format	Raw data: FASTQ file
Experimental factors	Environmental samples
Experimental features	16S rRNA gene amplicon (V4 region) sequencing using Ion Torrent platform and diversity analysis using QIIME 1.9.0
Consent	Not applicable
Sample source location	Tailing dam of Malanjkhand copper project, Balaghat district, M.P., India. T1 (N21°59.105' E080°42.423"), T2 (N21° 59.096" E080° 42.427") and T3 (N21° 59.915" E 080°42.081")

1. Direct link to deposited data

<https://www.ncbi.nlm.nih.gov/bioproject/361456>

2. Experimental design, materials and methods

Mine tailings are considered as a major source of acid mine drainage (AMD) due to the microbial bio-oxidation of sulfidic constituents [1].

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Mine tailings are characterized with low –pH, – organic matters and other nutrients, as well as high concentrations of toxic metals and sulfate which pose a severe environmental threat [2 and 3]. Several studies have been conducted worldwide to understand microbial community composition within mine tailings and their metabolic role in biogeochemical cycles of acid generation using either clone library/cultivation or pyrosequencing based approach [3,4,5,6,7,8, and 9]. In recent years, advances in semiconductor based next generation sequencing technology has shown high promises to gain better insights into the microbial community structure and dynamics in natural ecosystems. Numerous studies have been conducted to understand the microbial community structure and function of AMD ecosystem [10,11,12,13,14,15 and 16]. However, dynamics of microbial community composition from mine tailings (source) to the generation of AMD (product) remains less explored. This study was designed to target unexplored mine tailings of Malanjkhand copper project (MCP), Asia's biggest copper mine, situated in Balaghat district of Madhya Pradesh, India to analyze in-depth microbial community composition and their potential role in acid generation.

2.1. Sampling, DNA extraction and sequencing

Tailing sediments (T1 and T2) were collected from tailing dam and its seepage point (T3) of MCP during April 2014 (T1 and T3) and September 2016 (T2). Samples were collected in sterile container and stored at 4 °C, till further analysis. Metagenome was extracted from 0.25 g of each sample using Power soil DNA isolation kit (MoBio laboratories) according to the manufacturer protocol; quantified in Qubit 3.0

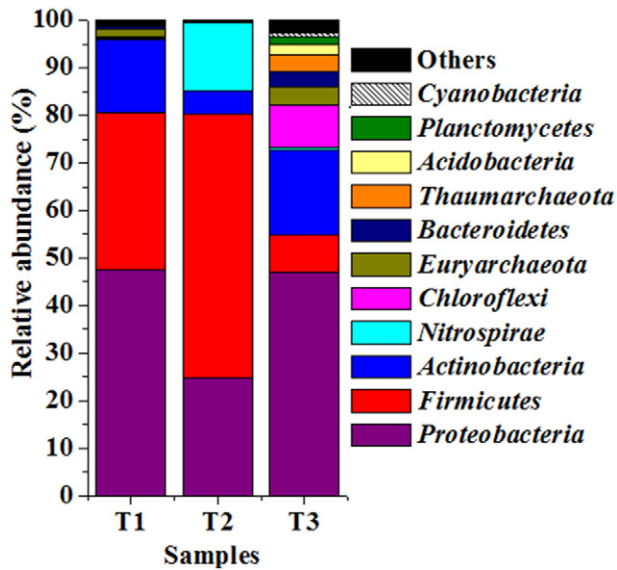


Fig. 1. Distribution of taxa at phylum level across the samples (cumulative abundance > 0.5%).

fluorometer (Invitrogen, Thermo Fisher Scientific) and V4 region of 16S rRNA gene was amplified with V4 specific primers [17]. Each forward primer was tagged with 10–12 bp barcode for multiplexing during sequencing run. PCR was performed in 25 μ l of reaction using Amplitaq Gold 360 Master Mix (Invitrogen, Thermo Fisher Scientific), 40 pico mole each fusion primers and 10–50 ng of template DNA. PCR amplified

products (V4 amplicons libraries) were extracted using E gel base system (Invitrogen, Thermo Fisher Scientific). Purified amplicons were processed and sequenced in Ion S5 sequencer.

2.2. Bioinformatic processing of 16S rRNA gene sequence and diversity analysis

Total 0.97 million raw reads were obtained after sequencing. These reads were analyzed in QIIME pipeline [18]. Quality filtering was performed using `split_libraries.py` to remove primers, sequences with homopolymers run of >6 bp and read length beyond the range of 230–300 bp. Minimum 3 primer mismatches were allowed in this step due to degeneracy of primer set. The output files from three samples were merged together and `pick_closed_reference_otus.py` was used to pick OTUs, assign taxonomy and create OTU table against a SILVA 119 reference database (www.arb-silva.de/documentation/release-119). Number of OTUs was obtained using `alpha_diversity.py`. Agglomerative hierarchical clustering on the abundance of major genera (cumulative abundance > 0.5%) were performed with weighted pair group average (WPGA) clustering method using Bray–Curtis dissimilarity distance matrix in XLSTAT 2014 software.

Out of 0.7 million operational reads (obtained after quality filtering), 0.58 million reads were assigned to taxonomy using closed reference method. Alpha diversity indicator revealed that T1 was highly diverse (OTUs 4885) followed by T3 (OTUs 3776) and T2 (OTUs 211). Sample (T3) with most extreme nature (pH < 2.0) harbored *Proteobacteria*, *Actinobacteria* and *Chloroflexi* while the samples (T1 and T2) with slightly moderate nature (pH < 4.0 and >3.0) exhibited abundance of *Proteobacteria*, *Firmicutes*, *Actinobacteria* and/or *Nitrospirae*. Archaeobacterial phyla, *Euryarchaeota* and *Thaumarchaeota* were abundant in the extreme sample (T3) and accounted for 7.2% of total assigned reads. (Fig. 1).

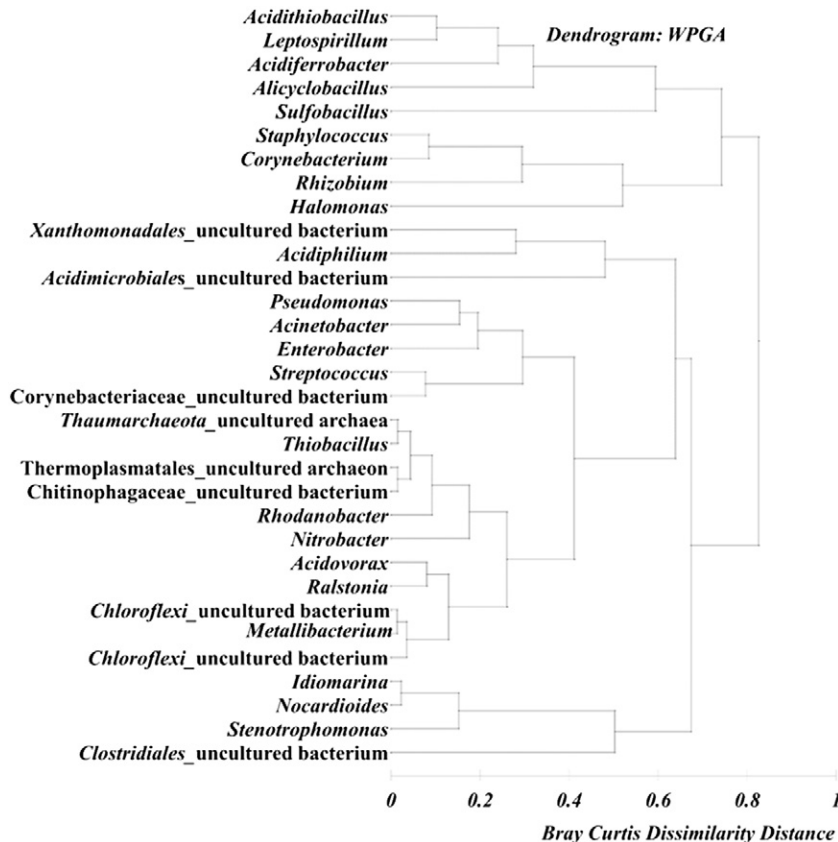


Fig. 2. Weighted pair average group based hierarchical clustering with Bray-Curtis dissimilarity distance matrix of major abundant genera (cumulative abundance > 0.5%) across the samples.

T1 and T2 samples showed commonality with presence of genera *Sulfobacillus* and *Alicyclobacillus*. T1 showed specific abundance of *Halomonas*, *Corynebacterium*, *Staphylococcus*, *Rhizobium*, *Acinetobacter* and *Stenotrophomonas* while T2 harbored *Leptospirillum*, *Acidithiobacillus*, *Acidiferrobacter* and *Acidiphilium*. In contrast, T3 sample showed distinct abundance of *Ralstonia*, *Metallibacterium*, *Acidovorax*, *Rhodanobacter*, uncultured-*Chloroflexi*, -*Chitinophagaceae*, -*Thermoplasmatales*, -*Thaumarcheota* and *Thiobacillus*. Hierarchical clustering on abundance of these genera across the samples was also evident in Fig. 2, indicating distinct patterns of assemblage among the organisms with common metabolic/biogeochemical functions. Detection of major genera such as *Sulfobacillus*, *Leptospirillum*, *Acidithiobacillus*, *Acidiferrobacter*, *Metallibacterium*, *Acidiphilium* and *Alicyclobacillus* in the tailings samples indicates the intrinsic acid generation potential of the microbial community. Observed variation in community composition among the samples could be attributed to the prevalent physicochemical conditions and their role in shaping the community structure. This study provides an insight into the microbial community structure and their relation to biogeochemistry of copper mine tailings.

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References

- [1] A. Schippers, A. Breuker, A. Blazejak, K. Bosecker, D. Kock, T.L. Wright, The biogeochemistry and microbiology of sulfidic mine waste and bioleaching dumps and heaps, and novel Fe (II)-oxidizing bacteria. *Hydrometallurgy* 104 (3) (2010) 342–350.
- [2] M.O. Mendez, J.W. Neilson, R.M. Maier, Characterization of a bacterial community in an abandoned semiarid lead-zinc mine tailing site. *Appl. Environ. Microbiol.* 74 (12) (2008) 3899–3907.
- [3] G.L. Tan, W.S. Shu, K.B. Hallberg, F. Li, C.Y. Lan, W.H. Zhou, L.N. Huang, Culturable and molecular phylogenetic diversity of microorganisms in an open-dumped, extremely acidic Pb/Zn mine tailings. *Extremophiles* 12 (5) (2008) 657–664.
- [4] D. Kock, A. Schippers, Geomicrobiological investigation of two different mine waste tailings generating acid mine drainage. *Hydrometallurgy* 83 (1) (2006) 167–175.
- [5] N. Diaby, B. Dold, H.R. Pfeifer, C. Holliger, D.B. Johnson, K.B. Hallberg, Microbial communities in a porphyry copper tailings impoundment and their impact on the geochemical dynamics of the mine waste. *Environ. Microbiol.* 9 (2) (2007) 298–307.
- [6] D. Kock, A. Schippers, Quantitative microbial community analysis of three different sulfidic mine tailing dumps generating acid mine drainage. *Appl. Environ. Microbiol.* 74 (16) (2008) 5211–5219.
- [7] L.N. Huang, W.H. Zhou, K.B. Hallberg, C.Y. Wan, J. Li, W.S. Shu, Spatial and temporal analysis of the microbial community in the tailings of a Pb-Zn mine generating acidic drainage. *Appl. Environ. Microbiol.* 77 (15) (2011) 5540–5544.
- [8] L.X. Chen, J.T. Li, Y.T. Chen, L.N. Huang, Z.S. Hua, M. Hu, W.S. Shu, Shifts in microbial community composition and function in the acidification of lead/zinc mine tailings. *Environ. Microbiol.* 15 (9) (2013) 2431–2444.
- [9] P.K. Dha, P. Sar, Microbial communities in uranium mine tailings and mine water sediment from Jaduguda U mine, India: a culture independent analysis. *J. Environ. Sci. Health A 6* (2014 May 49).
- [10] K.B. Hallberg, D.B. Johnson, Biodiversity of acidophilic prokaryotes. *Adv. Appl. Microbiol.* 49 (2001) 37–84.
- [11] B.J. Baker, J.F. Banfield, Microbial communities in acid mine drainage. *FEMS Microbiol. Ecol.* 44 (2) (2003) 139–152.
- [12] G.L. Tan, W.S. Shu, K.B. Hallberg, F. Li, C.Y. Lan, L.N. Huang, Cultivation-dependent and cultivation-independent characterization of the microbial community in acid mine drainage associated with acidic Pb/Zn mine tailings at Lechang, Guangdong, China. *FEMS Microbiol. Ecol.* 59 (1) (2007) 118–126.
- [13] E. González-Toril, E. Llobet-Brossa, E.O. Casamayor, R. Amann, R. Amils, Microbial ecology of an extreme acidic environment, the Tinto River. *Appl. Environ. Microbiol.* 69 (8) (2003) 4853–4865.
- [14] G.K. Druschel, B.J. Baker, T.M. Gihring, J.F. Banfield, Acid mine drainage biogeochemistry at Iron Mountain, California. *Geochem. Trans.* 5 (2) (2004) 13.
- [15] P.N. Bertin, A. Heinrich-Salmeron, E. Pelletier, F. Goulhen-Chollet, F. Arsène-Ploetze, S. Gallien, V. Bonnefoy, Metabolic diversity among main microorganisms inside an arsenic-rich ecosystem revealed by meta- and proteo-genomics. *ISME J.* 5 (11) (2011) 1735–1747.
- [16] J.L. Kuang, L.N. Huang, L.X. Chen, Z.S. Hua, S.J. Li, M. Hu, W.S. Shu, Contemporary environmental variation determines microbial diversity patterns in acid mine drainage. *ISME J.* 7 (5) (2013) 1038–1050.
- [17] S.T. Bates, D. Berg-Lyons, J.G. Caporaso, W.A. Walters, R. Knight, N. Fierer, Examining the global distribution of dominant archaeal populations in soil. *ISME J.* 5 (5) (2011) 908–917.
- [18] J.G. Caporaso, J. Kuczynski, J. Stombaugh, K. Bittinger, F.D. Bushman, E.K. Costello, G.A. Huttley, QIIME allows analysis of high-throughput community sequencing data. *Nat. Methods* 7 (5) (2010) 335–336.