

Bacterial diversity of the abandoned Mamut Copper Mine in Sabah, Malaysia and its correlation with copper contamination

ABSTRACT

Aims: The former Mamut Copper Mine, acid mine drainage site represents an anthropogenic altered landscape characterized by its acidic topsoil which is contaminated primarily with copper. Even though the mining operation was ceased at 1999, the bacterial diversity in this area has never been investigated. This study was conducted to ascertain the bacterial diversity of this abandoned copper mine and correlate it to the copper concentration in the soil. **Methodology and results:** Soil samples were collected from 7 sites near the mine pit and the vicinity. Soil samples were assessed for soil copper elemental concentration using inductively coupled plasma optical emission spectrometry and bacteria were isolated via serial dilution followed by culture on nutrient agar plates. Phylogenetic analysis was done based on the full-length sequences of 16S rRNA gene. Twenty-four phylotypes were obtained from the 7 locations which originated from the phyla Firmicutes, Actinobacteria, Bacteroidetes and Proteobacteria. The results of the study indicated that site 2 (6.030223°; 116.658030°), located in between the mine pit and the mine factory with a copper concentration of 88.96 ppm, possessed the most diverse bacterial community with a Shannon diversity index (H) of 1.68, evenness (EH) of 0.94 and richness (S) of 6. **Conclusion, significance and impact of study:** Current study revealed that there was a positive correlation between the copper concentration and the H index and the richness, but this was not reflected in the evenness. This is the first report of bacterial diversity from the former Mamut Copper Mine site. The data provided a valuable insight for the future monitoring of the bacterial community in this ecologically important niche.