Developing a bacterial consortium for improving the quality of mining-contaminated water.

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The bio/remediation of water sources contaminated by mining activity has become a priority in water stressed countries such as South Africa. The closure mine option that involves flooding opencast mines creates pit lakes to avoid the oxidation of exposed minerals (e.g., pyrite) is a prominent problem. Rock-water interactions and indigenous microorganisms thrive in these aquatic ecosystems triggering the acidification (FeS_2 minerals) or alkalinisation ($CaCO_3$ minerals) of the water and toxic metals weathering, deteriorating the water quality. Bioremediation techniques has been extensively used to remediate these water sources. However, the performance of the microorganism(s) in bioremediation is quite variable consequently, can be inefficient. This may result from the consortia being assembled without considering the origin and ecology of the constituent microorganisms. Here this study uses networking analysis to understand the establishment/survival microbial consortia from seven alkaline pit lakes from coal mines, providing a graphic visualization of potential relationships between microbes in a holistic manner, which settled the bases to design an optimal consortium. The pit lakes water presents hydro-geochemistry of alkaline mine drainage with pH between 4.02 and 6.20, with the oxic conditions, Eh ranged between $86.33 - 190.57$ mV and high salt concentrations such as Ca, Mg, Na, K, Cl, and mainly SO_4 ($\sim= 6000$ mg/L). Additionally, principal component analysis distinguished several groups based on chemical composition. The α diversity indices also showed that the communities were significantly different ($p < 0.05$) between the pit lakes. Principal coordinates analysis proves that the microbial communities were distinct between and within groups (PERMANOVA $p < 0.05$; PERMDISP, $p = 0.001$, respectively). At genus level the major bacterial taxa were *Algoriphagus*, *Candidatus*, and *Luteolibacter*. Even though their abundance were low across all pit lakes, the *Allorizobium* and *Pseudomonas* genus were core species in the network's biggest modules. They have high tolerance for metals, participate in their reduction and inducing ureolysis for metal precipitation [1,2]. Overall, we demonstrated the potential of exploring inter-taxa correlations and identification of key species in the pit lakes to design an efficient consortium for their treatment.

1. Huang et al., (2016), Technol, 370–378.
2. Fagorzi et al., (2018), Genes (Basel), 542.