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Microbial community diversity as a potential bioindicator of AMD and steel plant effluent in a channelled valley bottom wetland

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ABSTRACT:

Freshwater resources in semi-arid countries are under constant threat from pollution. One of the major pollutants is acid mine drainage (AMD), which not only lowers the pH of the water, but contains high sulphuric acid and high metal concentrations. Bacteria and algae are the first organisms to respond to stressors such as reduced pH and high metal concentrations. The bacterial community in a natural freshwater wetland impacted by AMD and steel plant effluent was identified, with the objective to include bacterial indicator communities in an ecotoxicological screening tool for wetland ecosystem health estimation. Five study sites at the Grootspruit canal valley bottom wetland in Mpumalanga, South Africa, were identified as case study areas which include a reference site and four AMD-impacted sites displaying various degrees of degradation. Physical, chemical and microbiological parameters were measured at each site. The bacterial community was sampled from both the water column and bottom sediment and subjected to next-generation sequencing for identification. The bacterial diversity was high, even at the most impacted sites. The phyla that were predominant in all the samples were the alpha-, beta- and gamma-Proteobacteria and Bacteriodetes. The bacterial based bio-assessment tool scored the reference site as mostly unaffected by anthropogenic impacts, while the AMD and steel plant effluent-impacted sites were classified as modified to severely modify. The outcome of the study showed that the proposed bacterial bioindicators can potentially be employed as part of the ecotoxicological screening tool to determine wetland ecosystem health.