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Use of LH-PCR as a DNA fingerprint technique to trace sediment-associated microbial communities from various land uses

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The search for new techniques to effectively and efficiently trace sediment from its source along catchment pathways continues, with a range of new methods being developed and tested annually. A relatively recent approach marries genetic techniques to sediment analysis in order to characterize and differentiate the bacterial populations associated with soil and/or sediment originating from specific locations. Here we present the preliminary results of DNA fingerprint profiles of soil and sediment-associated bacterial communities in and around two different industrial land uses in the central interior of British Columbia, a feedlot and a copper/gold mining site. We assessed the naturally varying 16S rDNA gene using amplicon length heterogeneity-polymerase chain reaction (LH-PCR). Statistical differences between bacterial community profiles were investigated using a suite of methods of which non-metric multidimensional scaling (NMS) and indicator species analysis (ISA) were the most useful. Stronger statistical results were observed for the feedlot data set with spatial differences observed from the source location and within the adjacent creek. Results from the mine site were more difficult to assess although responses were detected in downstream waterways. While bacterial DNA fingerprinting of soil and sediment appears to be a promising tracing technique issues of scale and transferability may limit its use. Lessons learned from this preliminary study will be presented.