Current Trends in Bioremediation and Biodegradation: Stable Isotope Probing

Gerald K Sims*

Department of Entomology Plant Pathology and Weed Science, New Mexico State University, Las Cruces, New Mexico 88011, USA

Diverse groups of microorganisms are involved in biodegradation of organic contaminants, and these organisms vary widely in adaptations and responses to in situ conditions, which can complicate managing bioremediation projects involving indigenous organisms. Though the vast majority of soil microorganisms (about 99 %) have yet to be successfully cultivated, it often is not necessary to know the identities of active degraders to succeed in bioremediation, since the field as it is known generally evolved in the absence of such information about most sites. However, would bioremediation proceed differently with knowledge of the identity of active degraders at a given site? Until recently, it has not often been a question worthy of discussion, given the difficulty of establishing such information, but that is changing with the advent of tools designed for that purpose. Among the recent advancements in ecological methods, applications of stable isotope probing, stand out for providing the potential to establish the identity of microorganisms involved in biodegradation in situ.

Microbial ecologists presently use the term, Stable Isotope Probing (SIP), to refer to various techniques based on isotopic labeling of microbial biomarkers used for microbial identification (usually 13C), followed by analysis of labeled biomarkers to identify the organisms assimilating substrate. Though SIP is not the only tool that allows such analysis it is particularly well-suited for soils and biodegradation research. Typical biomarkers include phospholipid fatty acids, DNA, and RNA, with nucleic acid SIP generally the most informative due to the extensive 16S rRNA database (>120,000 sequences) available for searching. DNA- and RNA-based SIP are accomplished with the same basic protocol [1]. A community is exposed to a labeled, then a sample is extracted to recover nucleic acids and nucleic acids are separated by density gradient centrifugation and the heavy fractions ultimately are sequenced for identification. An increase in the Buoyant Density (BD) of enriched nucleic acids is considered evidence the sequence came from an active degrader.

The DNA-SIP method has been applied to assimilation of numerous substrates, such as naphthalene [2] phenol [3], methanol [4], methane [5], propionate [4], methyl bromide, methyl chloride [6], pentachlorophenol [7], ammonium [8], and 2,4-D [9]. Obviously, SIP methods are subject to the weaknesses of molecular methods (nucleic acid recovery, PCR bias, etc.) and incubation time may result in cross-feeding if too long or insufficient labeling if too short.

As SIP becomes more and more commonplace, it may no longer be necessary to work in the dark when managing bioremediation of contaminated sites. It may now be time to begin asking the question, how will this information see practical use in management of contaminated sites?

References