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RNA versus DNA Applications for Bioremediation Management

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Background/Objectives. The rapid expansion of molecular biology applications in medical science has led to the democratization of a range of methods, such as quantitative polymer chain reaction (q-PCR) and sequencing. While q-PCR potentially measures the presence of either RNA or DNA, the molecular biology dogma that RNA represents ongoing activity and DNA represents potential activity needs to be evaluated in the context of laboratory and field studies. This is of special importance if the data will be used to estimate biodegradation rates.

Approach/Activities. Laboratory and field systems were established to evaluate whether and how measurements of RNA and/or DNA were able to aid in the prediction of degradation rates. Laboratory studies included batch and column studies fed any of a range of pollutants including ethyl- and methyl-*tert*-butyl ethers, petroleum hydrocarbons, and chlorinated solvents and aromatic compounds (e.g., PCBs). Subsamples were used to extract RNA and DNA, which were either sequenced or had qPCR applied to estimate the quantities different genes (e.g., *vcrA* and the V3-V4 segment of the 16S rRNA gene for *Dehalococcoides*). Chemical compounds were also measured to estimate degradation rates. In field systems, models were usually needed to estimate degradation rates.

Results/Lessons Learned. Correlations between estimated compound degradation rates and the measured quantity of RNA and DNA were established. The relatively rapid response of the transcription process for inducible genes provides information concerning the initial start-up of the molecular machinery, but the high production phase does not last as long as the produced enzymes, for example. The DNA provides some measure of the community response when the specific populations involved in the compound degradation increase over time. The time period for this DNA response depends on the pollutant, the starting population (quality and quantity) and other parameters that influence cell growth (redox, pH, etc.). The process of including this information into predictive models requires understanding how these relationships (between rates and nucleic acids) will be used, i.e., relative ease of incorporating a first-order rate constant or Monod kinetics in existing fate models.