January 2003 Meeting: Molecular Evolution, Dr. Rebecca Reiss

New Mexicans for Science & Reason heard Dr. Rebecca Reiss (New Mexico Tech) on " Molecular Evolution: Studies in Microbes, Middens, and Man" at our January 11th meeting. Rebecca began by discussing her work on xenobiotics -- bacteria that can metabolize exotic compounds like the dangerous pollutants called dihalogens, which include ethylene dibromide (EDB) and ethylene dichloride (EDC). Reiss mentioned there are 175 sites with such pollutants in New Mexico, described with the acronym LUST - Leaky Underground Storage Tanks. In Reiss's pilot project, levels of EDB and EDC have been monitored at selected LUST sites in New Mexico, and the levels of these compounds have been seen to decrease over time. The best explanation is that it's biotic - bacteria are breaking down these dangerous compounds, and performing a valuable public service. But the rates are quite slow. How can science speed up this process?

That's where the two fields of genomics and proteomics comes in. Genomics is the study of DNA, the genetic material, and its RNA products. RNA, in turn, directs the assemblies of legions of amino acids into long chains called proteins, which are the molecules of both structure (like bone) and activity (like enzymes for digestion). The study of how the amino acid chains fold up and interact with other molecules is called proteomics. So, the question of understanding bioremediation of such compounds involves identifying the particular species involved (and many species of bacteria are lurking there), isolating the responsible genes, or isolating the actual proteins. Rebecca discussed PCR (polymerase chain reaction), which can be used to "amplify" tiny snippets of DNA into measurable amounts. This technique is very useful, but it has its pitfalls - for example, any contamination (DNA from, say, a human handler) can also be amplified to yield a false signal. Reiss's group has studied using 16SrRNA primers to isolate the xenobiotic genes of the dihalogen-consuming bacteria. Another approach is to study the proteins directly, but proteins can't be amplified like genes can with PCR. But, you can examine banded protein stains from pools of hundreds of bacteria, and perhaps even deduce the key proteins for the reaction. If you can, then duplication of the proteins in mass is quite practical. Also, the amino acid sequence can be converted into a DNA sequence, and appropriate DNA primers can be developed, which will lock onto the corresponding genes in the bacterial genomes. Besides the

impressive biology, there are many difficult technical issues involved, such as filtering bacteria from solution, growing bacteria that refuse to be cultured, asnd so forth.

Rebecca also discussed work with middens (dung heaps near houses), and how molecular markers could assist with archaeological studies. She mentioned her work on human evolution and NUMTS (Nuclear-localized mitochondrial DNA's). Our cells have many mitochondria outside the nucleus, busy helping us get enough energy. But, occasionally the DNA from one of these energy powerhouses (which probably were a stand-alone microbe before their assimilation long ago into our eukaryotic cells) can migrate right into the nucleus, where its rate of mutation/evolution slows down. When we compare our DNA with that of other humans, or other primates, we can observe many different NUMTS, because this migration process is still ongoing. NUMTS can be used in forensic analysis; there are so many that comparison of several can indicate how closely related given test DNA is to that of an individual or group.

NMSR thanks Rebecca Reiss for a delightful presentation.