Detecting undeclared nuclear fuel cycle activities presents a significant challenge for the nuclear nonproliferation focus. Radionuclide signals in common environments are difficult to detect due to rapid physical and environmental decay. However, radionuclide-contaminated sites can have geochemical characteristics that have been shown to be signatures of nuclear proliferation activities. We hypothesize that radiologically contaminated sites have characteristic microbiomes that can be correlated to chemical signatures in environments associated with specific fuel cycle activities. These microbiomes could potentially act as environmental sensors to monitor nuclear fuel cycle activities, verify nuclear arms nonproliferation and support the safe development of global nuclear energy resources. Samples collected from the Savannah River Site (SRS) and The Oak Ridge Reservation (ORR) field sites are undergoing microbial and geochemical analysis to evaluate the potential for characteristic microbiomes to act as biomonitors of fuel cycle activities and proliferation effluent. Comparison of taxonomic occurrences between the SRS and ORR show 320 (out of ~1200) classified genera are unique to the SRS, with at least 20% of these sequences belonging to acidophilic bacteria. Out of 808 genera identified in the ORR samples, 258 are unique to the site and exhibit an abundance of archaeal and bacterial taxa associated with nitrification and radiation tolerance/resistance. A comparison of SRS and ORR microbial communities with those from the background sites revealed over 180 genera occurring at both the SRS and ORR sites that are absent from the background sites. The potential distinction between nuclear contaminated and non-contaminated sites is supported by analyses conducted by team members from UC-Berkeley that show a statistically significant difference between microbial 16S rRNA sequences from ORR samples when compared to over three thousand soil samples from the Earth Microbiome Project. Data from each site will be integrated to determine how long potential biosensors retain fuel cycle signatures.