Microbial organisms are ubiquitous in nature, and their sensitivity to environmental conditions makes them suitable candidates for monitoring environmental contamination, such as radionuclides produced by nuclear reactors. Thus, microbial communities can serve as bio-sensors, and machine-learning approaches have been used to predict environmental conditions from microbial community composition. Mechanistic knowledge can also be leveraged to inform such predictions, as microbes may respond predictably to environmental contaminants. Microbial isolate phenotyping provides complementary mechanistic insight into the growth sensitivity of individual organisms to environmental contaminants. Here, we introduce an approach to integrate this mechanistic information into amplicon sequencing based machine learning models to improve prediction performance and interpretability. Our approach maps isolate phenotype information to field sequences through a phylogenetic-tree based transformation. A generative statistical model is then used to simulate training data samples that encapsulate the isolate phenotype information, and can be combined with field sequencing data to reduce model variance. Our approach is shown to sharpen feature contributions from select bacterial strains and improve predictions of dominant chemical contaminants in nuclear waste contaminated groundwater samples.