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*Pseudomonas aeruginosa* is an opportunistic bacterium known for its high level of resistance to antibiotics and disinfectants which contributes to increased morbidity and mortality following infection. One well-studied context of *P. aeruginosa* infection is cystic fibrosis, where the bacterium forms persistent biofilms in the lungs. *P. aeruginosa* ATCC 39324 is commonly used to investigate biofilm formation and antimicrobial resistance mechanisms. Preliminary analysis of an existing transcriptomics data set comparing starved vs non-starved *P. aeruginosa* ATCC 39324 was performed using the EPI2ME Labs wf-transcriptomes workflow, comparing RNA reads from each sample to the well-characterized *P. aeruginosa* PAO1 reference genome. This analysis found that only one gene, *PA4581.1*, was detected exclusively in the starved samples. Conversely, the gene *rpII* was detected exclusively in the non-starved samples. These findings suggest potential transcriptional differences between long-term starved and non-starved *P. aeruginosa*. To understand more about these differences, *P. aeruginosa* ATCC 39324 that had been subjected to long-term starvation was compared to a non-starved wild-type ATCC 39324 culture. Starved and non-starved specimens were sampled at multiple time points following reintroduction to growth conditions: initial, 15 minutes, 30 minutes, 3 hours, 24 hours, and 1 week. Total RNA was extracted from each time point for sequencing using Oxford Nanopore Technologies. Additionally, crystal violet assays were performed to analyze the effects of starvation on biofilm formation. (This work was supported by NIH Grant P20GM103434 to the West Virginia IDeA Network for Biomedical Research Excellence and was made possible by funding from NASA West Virginia Space Grant Consortium).