Professor Tyrrell Conway, Ph.D., is the regents professor and head of the microbiology and molecular genetics department at Oklahoma State University. Professor Tyrrell Conway currently has about eleven undergraduate researchers working under him on his two main projects at this time. His current areas of study consist of two main goals. One goal is figuring out how Escherichia coli (a type of bacteria) gets its nutrients in the intestine and the other primary goal is comparing how different bacteria in the gut use their genes to compete with each other. All that said the main publication that was discussed during our interview was Professor Tyrrell Conway’s publication entitled Quantitative bacterial transcriptomics with RNA-seq, this article was co-published by James P. Creecy in 2015.

The original work focused on bacteria genes that code for proteins, just like humans do, but before the genes can be used to make proteins, they first have to be read or transcribed into messenger molecules called RNA. In the past, scientists could only look at which genes were being transcribed in bacteria by using techniques that provided a very zoomed-out, blurry picture. Professor Tyrrell Conway described the past technique using the analogy “ It was like trying to watch a movie through a foggy window” he then went on to explain how technology has changed this issue. With a new technique called RNA sequencing (RNA-seq), scientists can get a crystal-clear, zoomed-in view of exactly which genes are being transcribed and how much in bacteria. Not only did this new technology clear the foggy window, but it was like watching it on a giant high-definition screen. The specific publication that was discussed explained how to use RnA-seq data to map out all the start and stop signals, also known as promoters and terminators, that control when genes get transcribed in bacteria. An example of this would be like finding the play and stop buttons on a now-labeled remote. Not only that, RNA-seq lets scientists measure precisely how much gene transcript is being made under different conditions, like when the bacteria is growing quickly versus slowly. It’s like seeing which scenes get played more in a movie. The authors of the article give an example of analyzing a set of co-transcribed genes in E. coli, showing how RNA-seq can tease apart the complex control of when each gene gets transcribed based on different start and stop signals. However, there are still challenges, like precisely pinpointing some of the stop signals for transcription. But, overall, RNA-seq provides an unprecedented, quantitative way to study how bacteria control gene transcription at ultra-high resolution.

This publication lends a great hand in advancing synthetic biology. Which is the ability to dissect and quantify transcriptional control elements like promoters paves the way for building synthetic gene circuits and reprograming bacteria for specialized functions in the future. Some of those functions could include therapeutics, biosensing, and even bioremediation. Professor Tyrrell Conway has and continues to advance molecular studies and helps piece together many puzzles that surround us all.