

New technique gives researchers closer look at epigenetics

Scientists from the Icahn School of Medicine at Mount Sinai have developed a new technique to more precisely analyze bacterial populations, to reveal epigenetic mechanisms that can drive virulence. The new methods hold the promise of a potent new tool to offset the growing challenge of antibiotic resistance by bacterial pathogens. The research was published today in the journal *Nature Communications*, and conducted in collaboration with New York University Langone Medical Center and Brigham and Women's Hospital of Harvard Medical School.

The information content of the genetic code in DNA is not limited to the primary nucleotide sequence of A's, G's, C's and T's. Individual DNA bases can be chemically modified, with significant functional consequences. In the bacterial kingdom, the most prevalent base modifications are in the form of DNA methylations, specifically to adenine and cytosine residuals. Beyond their participation in host defense, increasing evidence suggests that these modifications also play important roles in the regulation of gene expression, virulence and antibiotic resistance.

'The application of this [new technique](#) will enable a more comprehensive characterization of the functions of DNA methylation and their impact on bacterial physiology. Resolving nucleotide modifications at the single molecule, single nucleotide level, especially when integrated with other single molecule- or single cell-level data, such as RNA and protein expression, will help resolve regulatory relationships that govern higher order phenotypes such as drug resistance' said Eric Schadt, Ph.D., founding director of the Icahn Institute and professor of genomics at the Icahn School of Medicine at Mount Sinai. 'The approach we developed can also be used to analyze DNA viruses and human mitochondrial DNA, both of which present significant epigenetic heterogeneity.'

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis. Read full, original post: [Scientists develop new technique for analyzing the epigenetics of bacteria](#)