**“Understanding epigenetic regulation in bacteria – one base at a time”**

News and views type of essay. Write for a non-science reader.

<http://www.nature.com/ncomms/2015/150615/ncomms8438/full/ncomms8438.html>

***Short abstract***

DNA methylation (addition of a –CH3 group to one of the four bases, A, C, G or T) is one way by which the expression of genes is controlled in all organisms. Research has also demonstrated several additional roles of DNA methylation in bacteria, such as recognition of foreign DNA, and antibiotic resistance. Bacterial populations also acquire epigenetic heterogeneity to better withstand rapid changes in their environment. Profiling the bacterial methylome at single-cell resolution can provide insights into how bacterial populations evolve and maintain phenotypic plasticity. Single molecule sequencing can be adapted to identify DNA methylation patterns at single cell resolution. This adapted technology is presented in the paper by Beaulaurier et al in their 2015 paper. The authors propose SMALR (single-molecule modification analysis of long reads), a technique that combines Single Molecule Real-Time (SMRT) DNA sequencing of long reads with an iterative loop over the smaller ‘subreads’ spanning each long read, thereby improving detection of methylated bases.

***Background description (including challenges remaining to be solved)***

***Description of research (including methods used and results obtained)***

***Discussion (Provide your comments on the work)***

**Figures and Tables**

**References**