VANDERBILT SCHOOL OF MEDICINE | Basic Sciences

Emily Hodges, PhD

Assistant Professor, Department of Biochemistry
Vanderbilt Genetics Institute and Vanderbilt Ingram Cancer Center

emily.hodges@vanderbilt.edu
615-875-9991
https://lab.vanderbilt.edu/hodges-lab

Biosketch

Dr. Hodges received her Ph.D. in Functional Genomics from the Karolinska Institute, where she developed high-throughput approaches to investigate the function of newly discovered proteins in mammalian cell culture models. She completed her postdoctoral training at Cold Spring Harbor Laboratory where she pioneered chip-based DNA capture methods that allow rapid targeted sequencing of protein coding genes and ancient DNAs to enable profiling of DNA mutations. Her lab utilizes next-generation DNA sequencing to understand the role of chemical, so-called "epigenetic" DNA modifications in both gene regulation and functional specialization of different blood cell types, and how epigenetic variability can lead to disease susceptibility in immune disorders and cancer.

Key Publications

"De novo DNA demethylation and noncoding transcription define active intergenic regulatory elements," *Genome Research*, Oct 23(10):1601-14, 2013

"Directional DNA methylation changes and complex intermediate states accompany lineage specificity in the adult hematopoietic compartment," *Molecular Cell*, 44(1):17-28, 2011

"Targeted investigation of the Neanderthal genome by array-based sequence capture," *Science*, 328(5979):723-5, 2010

"How epigenetic traits are passed from generation unto generation "

Research in the Hodges Lab **strives to understand how epigenetic features shape human genomes**. We study this relationship on two levels; first, we are interested in **how chemical modifications of DNA, DNA methylation, are established during the specialization of developing cell types**. Second, we are interested in the **relationship between genetics, DNA methylation state (epitype), and how this relationship affects cellular function (phenotype).**

I. DNA methylation of genomic sequence elements in differentiating cells

Gene regulatory elements called "enhancers" are docking sites for protein-DNA interactions that control gene expression. They are the nodes of complex gene interaction networks that direct cell fate specification and maintain tissue homeostasis. Furthermore, they are believed to be a driving force behind the diversification of organisms. DNA methylation is an important component of this process but **little is understood about how patterns of DNA methylation are established during development. Projects in our lab address these questions utilizing innovative biochemical, functional genomic and bioinformatic approaches.**

II. Human methylation variation and disease susceptibility

Enhancers display higher DNA methylation variability between species and human individuals than other genomic elements. These differential patterns of enhancer methylation may reflect individual differences in gene regulation and disease susceptibility. **We integrate our understanding of cell-type specific DNA methylation patterns with genetic and phenotype information from the electronic health record to triangulate specific functional relationships between genetic variation and disease risk.**