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***“Conservation or Flexibility of the Epigenome in  
Ultraconserved Non-coding Elements by  
Comparing 60 Species.”***

Ultraconserved noncoding elements (UCNEs) constitute less than 1 Mb of vertebrate genomes and are impervious to selection induced mutation. About 4000 UCNEs exist in vertebrate genomes, sharing greater than 95% sequence identity between human and chicken. Despite extreme sequence conservation over 400 million years of vertebrate evolution, it is currently unknown whether epigenetic characteristics within these regions are similarly conserved. Here we assess both interspecies and interindividual variation in DNA methylation in these regions. Here we surveyed UCNEs with high CpG density in 56 species. Similarly, we determined the inter-tissue range of methylation within a single species, the mouse. To look for variability within a population, we tested DNA methylation within a human panel, along with the commonly used LINE1 transposon. Over all species, global methylation as assessed via mass-spectrometry was found to be inversely correlated to hydroxymethylation across 60 vertebrates. In UCNEs, DNA methylation is flexible, conserved between related species, and relaxed from the underlying sequence selection pressure, while remaining heritable through speciation.

**Thursday, September 21, 2017**

**3:00 p.m.**

**Room TBA**