ABSTRACT

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The Odom laboratory investigates how tissue-specific transcriptional and post-transcriptional programs are globally controlled by combining high-throughput techniques with hepatocytes and hepatocellular carcinoma as model cell types. In the last five years, we have shown that relationships between TF functionality and conservation of TF binding in vertebrates are complex and unpredictable (Schmidt 2010a; Stefflova 2013; Ballester 2014). Previously we have shown that DNA sequence variation is the ultimate driver of regulatory evolution by using a previously existing mouse model of Downs syndrome carrying human chromosome 21 to place human genetic sequence into mouse diet, lifestyle, epigenetic machineries, developmental processes, and nuclear concentration of transcription factors (Wilson 2008). Our more recent exploration using this mouse has revealed how human repeat elements have latent regulatory potential that is unmasked in the heterologous mouse nucleus (Ward 2013). In this talk, I also will be discussing our recent large-scale investigation of enhancer evolution across mammalian space (Villars 2015).