Sex-Biased Genome Evolution

Melissa A. Wilson
Arizona State University, USA

Abstract

The human sex chromosome evolved from a pair of homologous autosomes, and are unlike any other pair of chromosomes within the human genome. While many parts of the X and Y chromosomes have diverged from one another, there are still some regions that share significant sequence homology, and others, the pseudoautosomal regions, that still undergo homologous recombination in genetic males. This unique evolutionary history results in technical challenges for genome alignment analysis of next-generation sequencing data. I will present an overview of the evolutionary history of the human X and Y, how this leads to technological challenges, and then present new methodology to improve genomic and transcriptomic analyses of the sex chromosomes. I will then discuss how we're using this to study sex differences in gene expression.