**Papers for Review**

***Genome sequencing and population genomics in non-model organisms***

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**“The Omics Era of biology”**

* Three major developments in past century: the modern synthesis, emergence of molecular biology, and the “omics” era. 30-year intervals. Start of genomics was 1990s.
* Study of complete repertoire of traits = behaviourome and phenome

**“Status of genome sequences”**

* Accumulation of genome sequences of wild species to use genome information for ecology and evolution.
* Genome sequences include transposable elements, tandem arrays of similar sequence (centromeres and telomers), and other deviant structures that are resistant to being sequenced.
* Understand the inference that a “whole genome sequence” actually means DNA sequence currently obtainable.
* More repetitive = more difficult

**“Example of progress: avian genome sequences”**

* Contig building is the core of shotgun sequencing,
* Merging contigs into scaffolds in high-throughput sequencing uses info from read-pairs
* Scaffolding is a problem when both ends are repetitive DNA.

**“Genome sequences and evolutionary genetics”**

* Linkage between advantageous allele and deleterious allele in neighboring alleles hinders spread of favorable variant.
* Recombination rate is high = focal loci is less vulnerable to opposing forces.
* SO adaptive evolution should be higher at sites with higher recombination rates
* GC biased gene conversion… genomic region with higher recombination should have higher GC content. Stronger in larger populations.

**“Comparative genomics and molecular evolution”**

* Purifying selection reduces genetic diversity, both at sites under direct selection and at linked neutral sites (*The Effect of Strong Purifying Selection on Genetic Diversity*)
* Scaled selection coefficients are higher = larger fraction of genome conserved.
* Genetic structure and signatures of selection in grey reef sharks (Carcharhinus amblyrhynchos)
* Detecting signatures of positive selection in non-model species using genomic data
* The search for loci under selection: trends, biases and progress
* Signatures of positive selection and local adaptation to urbanization in white-footed mice (Peromyscus leucopus)
* Genomic signatures of extensive inbreeding in Isle Royale wolves, a population on the threshold of extinction
* Whole-genome sequencing of eight goat populations for the detection of selection signatures underlying production and adaptive traits