**Papers for Review**

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

**Hans Ellegren**

**Review , 2014**

**“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

Genome sequencing and conservation genomics in the Scandinavian wolverine population

Population genomics for wildlife conservation and management