**Week 4: Evolution of genomic architecture**

|  |  |
| --- | --- |
| **18 groups** | **75+ participants** |

**Summary**: Groups discussed how genetic architecture (chromosomal inversions and alleles of small effect) can affect local adaptation based on papers by Kirkpatrick and Barton 2006 (*Genetics*) and Yeaman 2015 (*American Naturalist*).

**1. What kind of genomic architecture to expect to evolve under high gene flow?**

* When adaptive inversions occur, they should reach fixation despite high gene flow due to suppression of recombination
  + If >1 adaptive alleles are captured in inversion, more likely to reach fixation.
  + Any post-zygotic barrier or recombination prevention that is adaptive should maintain high fitness despite influx of maladaptive alleles
* Traits governed by many, small effect genes may be more adaptable, but less likely to reach fixation given likelihood that other processes mitigate each gene’s impact.
  + In high gene flow, stable maintenance of allelic polymorphism could be prevented by gene swamping or mutation rates
  + Despite not reaching fixation, polygenic traits may still affect adaptive divergence.

**2. How does genomic architecture constrain adaptation?**

* Inversions may allow for high fitness given one environmental change, but produce populations that may be resistant to subsequent environmental changes
  + May not be able to take advantage of introduction of novel, adaptive alleles
  + May reduce genetic variation available for selection to act upon.
* Variability among polygenic traits may provide sufficient standing genetic variation to facilitate adaptation, but the ability of these genes to propagate through population more likely to be constrained by high gene flow.
  + Low mutation rates, reduced standing genetic variation, and decreased genetic redundancy may reduce adaptability of polygenic traits.

**3. What are the implications of different genomic architectures for our ability to study adaptation using genomic data?**

* Detection of these architectural changes is difficult, so may be overlooked.
  + Large effect genes have gotten more attention (Fst outliers)
  + GWAS approach (Berg and Coop 2014) suggested to improve detection but requires large sample size and may produce false positives.
* Likelihoods of phenomena unknown but likely vary according to different genome sizes, complexity, structure as well as gene flow, time scale, migration/selection balance, etc.

**Key Unknowns:**

* Ability to answer questions about genetic architecture contingent on the prevalence and impact of adaptive changes in genetic architecture in nature
  + Presently unknown how often inversions occur, the extent genes of small effect and inversions affect phenotype, etc.
  + Do not know, as we often cannot detect with current methods
* If we capture a pattern of evolution in response to historic evolutionary process, can we use that understanding to make accurate future predictions?