EEOB 8896:

Genomics of Adaptation

## AUTUMN 2019

## INSTRUCTORS: LISLE GIBBS & ANDREAS CHAVEZ

# Potential topics

## Methods for discovering adaptive loci

## Rapid adaptation

## Genomic basis of fitness (linking genotype/phenotype/fitness)

## GWAS studies in non-model populations for identifying loci associated with adaptive traits

## Admixture mapping studies in non-model populations for identifying loci associated with adaptive traits

## QTL mapping studies for identifying loci associated with adaptive traits

## Landscape genomics (Identify loci associated with environmental variation)

## Epigenomics (role of epigenes in adaptive phenotypic variation)

## Comparative genomics for studying convergent evolution

## Value of adaptation genomics in conservation biology

# “foundational or review” papers for background

### Charlesworth, D., Barton, N.H. and Charlesworth, B., 2017. The sources of adaptive variation. Proceedings of the Royal Society B: Biological Sciences, 284(1855), p.20162864.Nielsen, R., 2005. Molecular signatures of natural selection. Annu. Rev. Genet., 39, pp.197-218.

### Charlesworth, B. and Charlesworth, D., 2018. Neutral variation in the context of selection. Molecular biology and evolution, 35(6), pp.1359-1361.

### Nielsen, R., 2009. Adaptionism—30 years after Gould and Lewontin. Evolution: International Journal of Organic Evolution, 63(10), pp.2487-2490.

### Hoban, S., Kelley, J.L., Lotterhos, K.E., Antolin, M.F., Bradburd, G., Lowry, D.B., Poss, M.L., Reed, L.K., Storfer, A. and Whitlock, M.C., 2016. Finding the genomic basis of local adaptation: pitfalls, practical solutions, and future directions. The American Naturalist, 188(4), pp.379-397.

### Barrett, R.D. and Hoekstra, H.E., 2011. Molecular spandrels: tests of adaptation at the genetic level. Nature Reviews Genetics, 12(11), p.767.

### Luikart, G., Kardos, M., Hand, B.K., Rajora, O.P., Aitken, S.N. and Hohenlohe, P.A., 2018. Population genomics: advancing understanding of nature. In Population Genomics (pp. 3-79). Springer, Cham.

### Tiffin, P. and Ross-Ibarra, J., 2014. Advances and limits of using population genetics to understand local adaptation. Trends in ecology & evolution, 29(12), pp.673-680.

### Savolainen, O., Lascoux, M. and Merilä, J., 2013. Ecological genomics of local adaptation. Nature Reviews Genetics, 14(11), p.807.

### Yeaman, S., 2015. Local adaptation by alleles of small effect. The American Naturalist, 186(S1), pp.S74-S89.

### Yeaman, S. and Whitlock, M.C., 2011. The genetic architecture of adaptation under migration–selection balance. Evolution: International Journal of Organic Evolution, 65(7), pp.1897-1911.

### Tigano, A. and Friesen, V.L., 2016. Genomics of local adaptation with gene flow. Molecular Ecology, 25(10), pp.2144-2164.

### Radwan, J. and Babik, W., 2012. The genomics of adaptation. Proc. R. Soc. B, 279, pp. 5024-5028.

### Stapley, J., Reger, J., Feulner, P.G., Smadja, C., Galindo, J., Ekblom, R., Bennison, C., Ball, A.D., Beckerman, A.P. and Slate, J., 2010. Adaptation genomics: the next generation. Trends in ecology & evolution, 25(12), pp.705-712.

# Some Key questions/ideas to think about during course

### Does adaptation occur through rapid fixation of new mutations or draws from standing genetic variation?

#### If latter, how is standing variation maintained?

#### Does this differ between organisms or traits?

#### How does genetic architecture influence the trait and distribution of fitness effects?

#### Genetic architecture:

##### Number of genes

##### Interactions between alleles of various loci (epistasis)

###### Can affect the chances the beneficial alleles will spread.

##### Degree to which a gene affects multiple traits (pleiotropy)

###### May constrain adaptive evolution

##### Interactions between genotype and environment, if any?

#### How fast can adaptation happen?

### Importance of protein-coding vs. cis-regulatory adaptive changes?

### Accounting for demographic processes, e.g., population subdivision when searching for genomic regions under selection.

#### Population structure can increase the variance in the statistics used to detect selection, thus leading to more false-positives in outlier scan studies.

### How do we find adaptive alleles?

#### Adaptive alleles are those that have a functional effect on a phenotypic trait that in turn produces an increase in fitness. (connects genotype, phenotype, fitness).

#### Also, important to know the agent of selection.

#### Strengths and limitations of experimental studies of selection?

### Loci of adaptation?

#### How common are QTLs (quantitative trait loci) or QTNs (quantitative trait nucleotides) of large effect?

#### Most complex traits are polygenic (lots of genes of small effect)

##### Small effect genes are more difficult to discover.

### Genomics of adaptive change: hard (from new mutations) and soft sweeps (from standing genetic variation)

#### The effectiveness of selection is impacted heavily by effective population size and recombination rate.

##### Adaption process can be expected to differ between taxonomic groups due to differences in these parameters

### Parallel evolution

#### How probable is the same genetic variant recruited for adaptation in closely related lineages (evolution is repeatable)?

#### What about in more distantly related lineages?

### Evolution of the genome

#### Genome architecture can shape action of natural selection or its efficiency).

##### Excess DNA (selfish DNA elements) is slightly deleterious

##### In LARGE populations, purifying selection can remove excess DNA more effectively

##### In SMALL populations, excess DNA can accumulate due to drift being a stronger force than purifying selection.

##### BUT, excess DNA has potential to be recruited as adaptive variation

### Gene Duplications

##### Been considered an important source of evolutionary novelty

###### But how can a duplicated copy be maintained initially (dosage concerns).

### Role of adaptation in speciation

#### How does disruptive selection affect the number, size, and extent of clustering of loci involved in reproductive isolation along the genome?

### What environmental variables are most important in structuring populations

#### How to use population genomics to identify ecological variables most important in driving adaptation?

#### Correlating genotype with environmental gradients?

### Role of introgression in adaptation?

#### Is adaptive introgression common or rare?

#### How local adaptation occurs in the face of homogenizing gene flow with other divergent populations?

### The role of epigenetic versus genetic variation in adaptive phenotypic variation.

#### Experimental removal of epigenetic marks in transgenic experiments to determine whether sequence variants have functional relevant effects.

### Studying comparative adaptations with comparative genomics.

#### Conduct GWAS studies across species with convergent traits with the availability of reference genomes and good phylogenies.

##### Look for shared evidence of positive selection?

### How important for conservation biology is it to know the genomics of adaptation?

#### How interchangeable are populations for key adaptations?

#### Can transplanted populations evolve key adaptations?

# Resources from “population genomics” book by Rajora 2019?

From Rajora 2019 “Population Genomics”

|  |  |  |
| --- | --- | --- |
| **Question or objective** | **Genomics approach (example)/software** | **References** |
| Identify candidate adaptive loci by detecting selective sweeps | Genome scan for low heterozygosity regions | Rubin et al. (2010), Axelsson et al. (2013), Kardos et al. (2015b) |
| High differentiation (e.g., FST) outlier regions | Rochus et al. (2018) |
| High gametic disequilibrium | Pérez O’Brien et al. (2014) |
| Shifted site frequency spectrum (high-frequency- derived alleles) | Alachiotis and Pavlidis (2018), Tajima (1989), Fay and Wu (2000), DeGiorgio et al. (2016) |
| Extended haplotype homozygosity | Sabeti et al. (2002, 2007), Voight et al. (2006), |
| Scan for soft selective sweeps (sweeps of alleles that are already present on multiple haplotypes [standing genetic variation] or of positively selected alleles at multiple sites in the same region or gene) | Hermisson and Pennings (2017), Marques et al. (2018), Hodel et al. (2018) |
| Scan for hard selective sweeps (sweeps of new (de novo) positively selected mutations) | Pennings and Hermisson (2006), Betts et al. (2018), Kreiner et al. (2018) |
| **Question or objective** | **Genomics approach (example)/software** | **References** |
| Identify candidate loci underlying local adaptation and speciation | Heritable gene expression profile differences | Christie et al. (2016) |
| Parallel evolution of gene expression | Yeaman et al. (2016) |
| Parallel phenotypic or DNA sequence evolution | Prince et al. (2017) |
| **Question or objective** | **Genomics approach (example)/software** | **References** |
| Identify loci associated with environmental variation (landscape genomics) | Methods testing for gene- environment association can detect subtle signatures of adaptation that are not detectable using genome- wide selection scans | Joost et al. (2007), Coop et al. (2010), Hancock et al. (2011), Rellstab et al. (2015), Rajora et al. (2016), Harrisson et al. (2017), Rougeux et al. (2018), Schmidt et al. (2017) |
| **Question or objective** | **Genomics approach (example)/software** | **References** |
| Detect signatures of poly- genic adaptation | Single vs multiple genes and the genomic basis of fitness | Berg and Coop (2014), Bourret et al. (2014), Brieuc et al. (2015), Laporte et al. (2016), Stölting  et al. (2015), Sork (2016), Yeaman et al. (2016), Rajora et al. (2016), Harrisson et al. (2017) |
| **Question or objective** | **Genomics approach (example)/software** | **References** |
| Identify loci associated with traits within populations | Genome-wide association analysis | Smith and O’Brien (2005), John- ston et al. (2011), Johnston et al. (2013), Barson et al. (2015), Bérénos et al. (2015), Husby et al. (2015) |
| Admixture mapping | Lamichhaney et al. (2015) |

**Tentative Weekly Schedule**:

|  |  |  |
| --- | --- | --- |
| **Date** | **Person** | **Topic** |
| 22-Aug | All | Organizational meeting |
| 29-Aug | Lisle | Challenges in assessing the genomic basis of adaptations |
| 5-Sep | Andreas | Key concepts/questions in studying the genomics of adaptation |
| 12-Sep |  |  |
| 19-Sep |  |  |
| 26-Sep |  |  |
| 3-Oct | Matt Hahn | TBD |
| 10-Oct | Break | No class |
| 17-Oct |  |  |
| 24-Oct |  |  |
| 31-Oct |  |  |
| 7-Nov |  |  |
| 14-Nov | Gideon Bradburd | TBD |
| 21-Nov |  |  |
| 28-Nov | Thanksgiving | No class |
| 5-Dec |  |  |