

# Connecting Epigenetics and Phenotypic Variation in Ecology

**Introduction** The influence of epigenetics on phenotypic variation in natural populations is not yet understood. To date, most studies exploring phenotypic variation assume that the evolution of phenotypes by natural selection depends on the presence of genetic variation alone. However, recent work demonstrates that *epigenetic* variation can be inherited across multiple generations and can be at least partially independent of genetic variation. Therefore, genetically homogenous populations may still have the potential for rapid evolution in changing environments if they harbor epigenetic variation that leads to fitness differences among individuals. We do not understand how epigenetics, genetics, and the environment interact to influence phenotypes. **To understand epigenetics and its contribution to phenotypic variation and possibly adaptation, it is critical for ecologists to apply the latest epigenomics approaches to studies of natural populations and their ecological interactions.**

*Methods for exploring links – Combine:*

## Experimental approaches from ecological genetics with Epigenomics tools

### Control for environmental and genetic variation

- **Environmental:** Common garden experiments to separate heritable versus non-heritable variation
- **Genetic:** Use individuals with **identical genomes** (clonal, eusocial) or develop **selection lines** and perform specific **hybrid crosses**

### DNA methylation measurement

- Methylation-sensitive AFLP markers (uses restriction enzymes)
- Bisulfite sequencing techniques (whole genome or reduced representation methods such as BsRADseq)

### Combining approaches: Baerwald *et al* 2016

- Studied migratory propensity in *Oncorhynchus mykiss*, a plastic trait that may be affected by epigenetic regulation of gene expression.
- They used a **double haploid cross** of migratory and resident fish to reduce genetic variability. Also minimized environmental noise by raising the lines in a **common environment**. Using **reduced representation bisulphate sequencing**, they measured genome-scale DNA methylation of F2 siblings.
- **Results:** Found 57 differentially methylated regions between migratory and resident fish (many of which were in transcriptional regulatory regions), suggesting a relationship between epigenetic variability and divergence in migratory propensity.



**Top: resident Bottom: migratory**

### Causality: Experimental manipulation of DNA methylation

- **in vivo methyltransferase inhibiting agents** [Con: side effects of the chemical treatments can complicate interpretation]
- **Knock out mutants** with compromised DNA methylation machinery [Con: difficult for non-model species]

### Case study: Wilschut *et al* 2016

- Studied a clonal lineage of a dandelion. Clones from different field sites had heritable differences in flowering times. These differences were correlated with inherited differences in MS-AFLP marker profiles.
- Used zebularine to inhibit DNA methylation: **differences in flowering times between the clones were significantly reduced.**



**Next Steps** Recent studies describing associations between epigenetic and phenotypic variation have advanced our understanding of ecological epigenetics however, they do not reveal *mechanisms*. Incorporating expression analyses may be a way forward. Ecology has largely focused on DNA methylation. Improving methods to explore other epigenetic modifications may lead to important insights. Future work exploring interactions between epigenetics, genetics, and the environment will provide a more complete understanding of phenotypic variation in natural populations.

**References** Baerwald *et al* Mol. Ecol. (2016) 25, 1785–1800. Bossdorf *et al* Ecol. Letters. (2008) 11, 106–115. Verhoeven *et al* Mol. Ecol. (2016) 25, 1631–1638. Wilschut *et al* Mol. Ecol. (2016) 25, 1759–1768.