

# The Extent of Positive and Negative Selection in Noncoding Regions of the Genome of *Capsella grandiflora*.

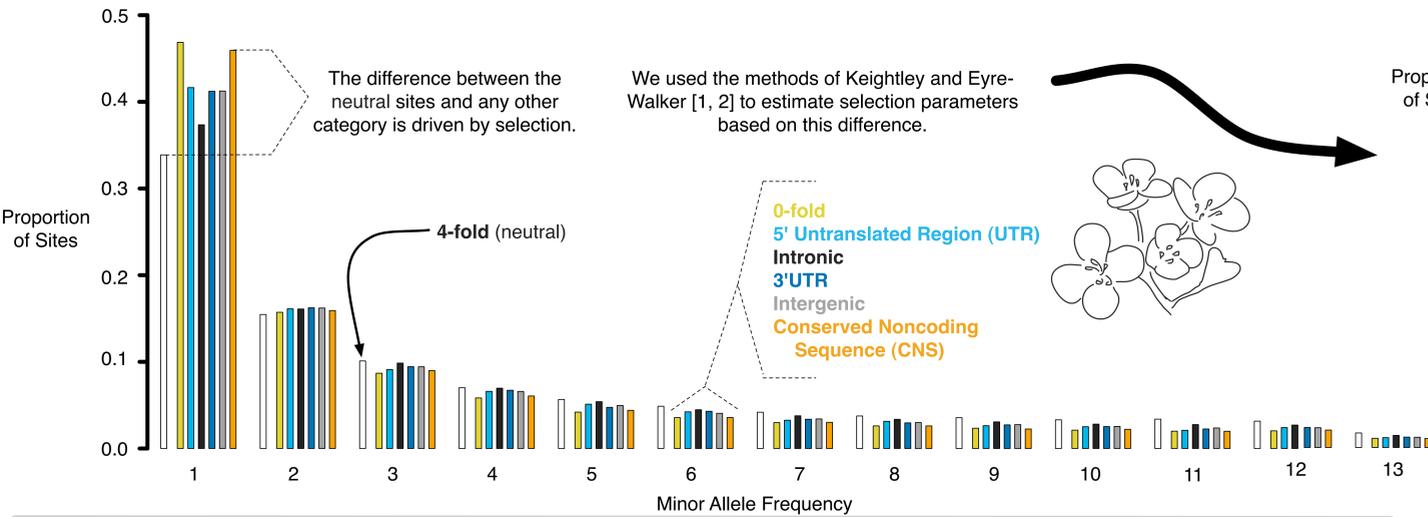
Robert J Williamson<sup>1\*</sup>, Emily B Josephs<sup>1</sup>, Adrian Platts<sup>2</sup>, Stephen I Wright<sup>1</sup>

1. Department of Ecology and Evolutionary Biology, University of Toronto

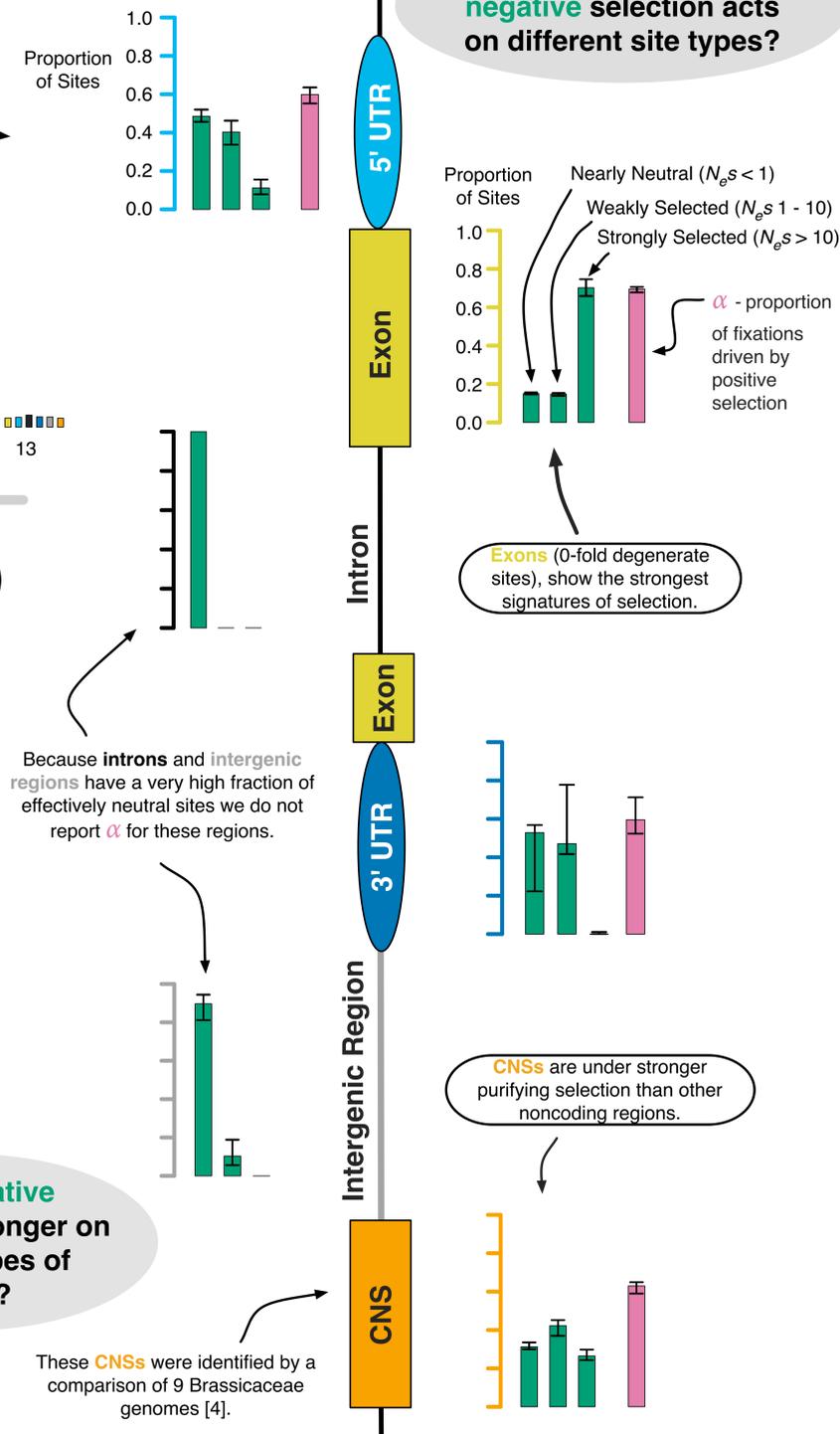
2. Department of Biology, McGill University

Data from *Drosophila* indicates that a large proportion of non-coding DNA is conserved and under positive selection, while in humans a large proportion is neutral, although there are many conserved non-coding sequences (CNS) associated with each gene. To date, little is known about the extent of genome-wide selection in plants. To explore this, we used whole genome resequencing and transcriptome sequencing of *C. grandiflora*, an obligate outcrosser closely related to *Arabidopsis*. We show that the coding regions of this species' genome are under both very strong positive and negative selection, while most non-coding DNA is neutrally evolving. However, CNSs show signatures of both purifying and positive selection; additionally, CNSs are enriched around loci that show little variation in expression level between individuals suggesting that these regions are important in regulating gene expression.

## What does selection look like in noncoding regions of the *C. grandiflora* genome?



## 1. How much positive and negative selection acts on different site types?

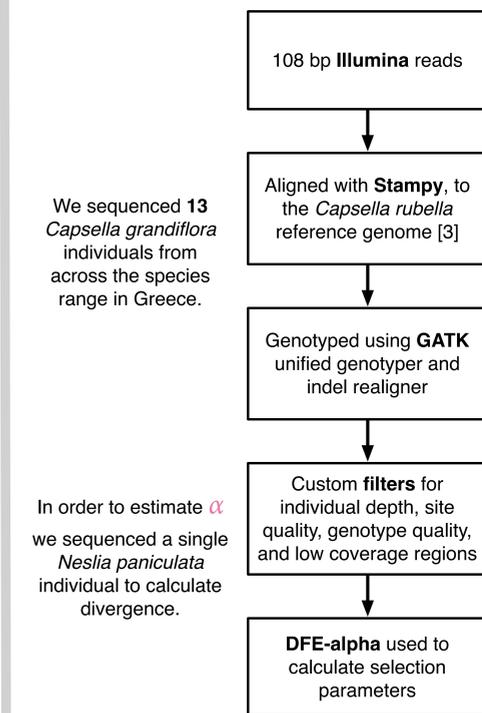


## What is our dataset?

*Capsella grandiflora* is an obligate outcrosser with a large long-term stable effective population size. The species also has little population structure. These attributes make this system ideal for studying selection in a natural population.

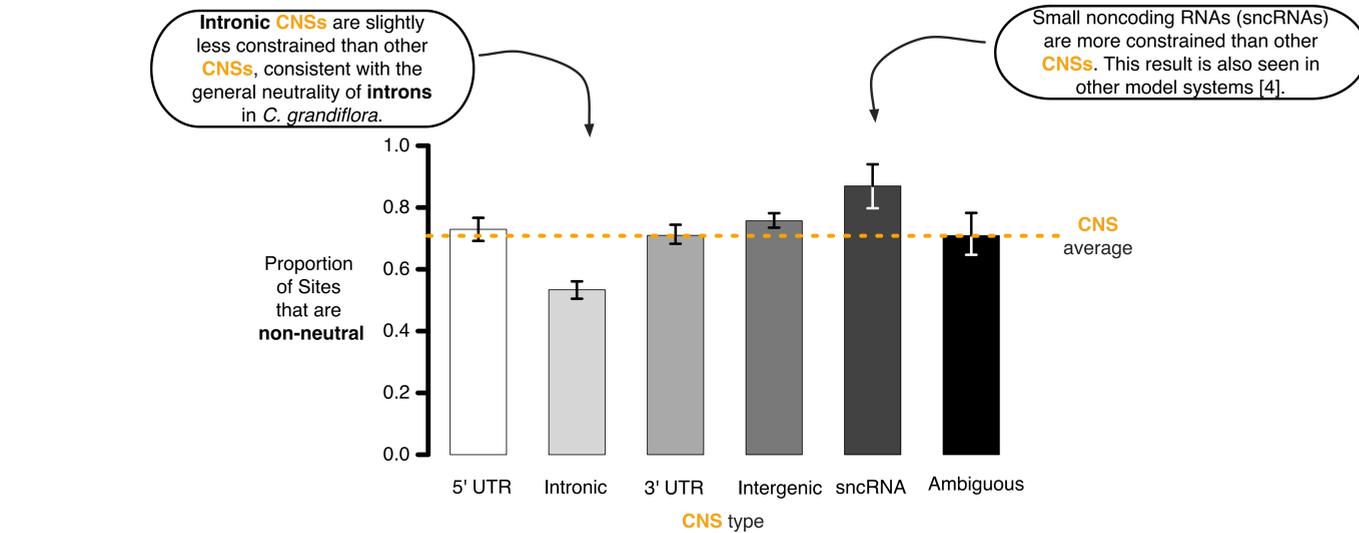


## How was the data processed?



## References

- Methods**
- Keightley & Eyre-Walker (2007) *Genetics*
  - Eyre-Walker & Keightley (2009) *MBE*
  - Slotte et al. (2013) *Nat Genet*
- Brassicaceae CNSs**
- Haudry et al. (2013) *Nat Genet*
- Drosophila data**
- Andolfatto (2005) *Nature*
  - Casillas et al. (2007) *MBE*
- Mouse data**
- Halligan et al. (2011) *MBE*
  - Kousathanas et al. (2011) *MBE*
- Human data**
- Torgerson et al. (2009) *PLoS Genet*



## 3. Overall we see...

- Less negative selection in noncoding regions than in some animal systems.
- Both positive and negative selection are strong on CNSs, but less so than protein coding regions.
- Certain CNS categories are more constrained than others.

## 2. Is negative selection stronger on certain types of CNSs?

These CNSs were identified by a comparison of 9 Brassicaceae genomes [4].

## How do these results compare to other species?

