



Rapid evolution of W chromosome repeat content in *Heliconius* butterflies



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Introduction: Why study the W Chromosome?

- The Y/W chromosome stands out as different compared to the rest of the genome
 - filled with repetitive elements
 - very low in gene content
- The Y/W chromosome is very difficult to assemble and evolves very quickly
- The toxic Y/W chromosome hypothesis for sex differences in ageing
- W chromosome in Lepidoptera
 - we chose to study *Heliconius* butterflies



Heliconius hecale



Heliconius numata



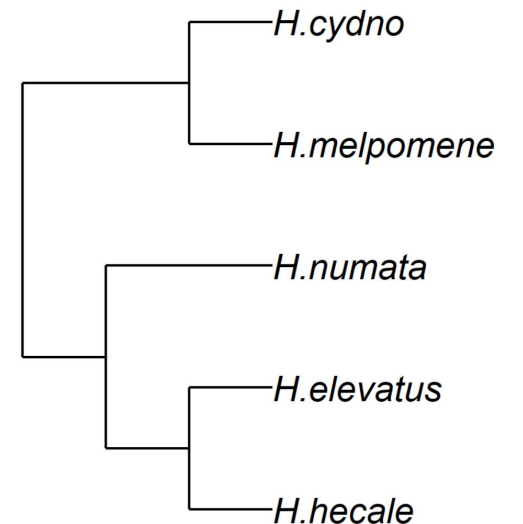
Heliconius elevatus



Heliconius cydno



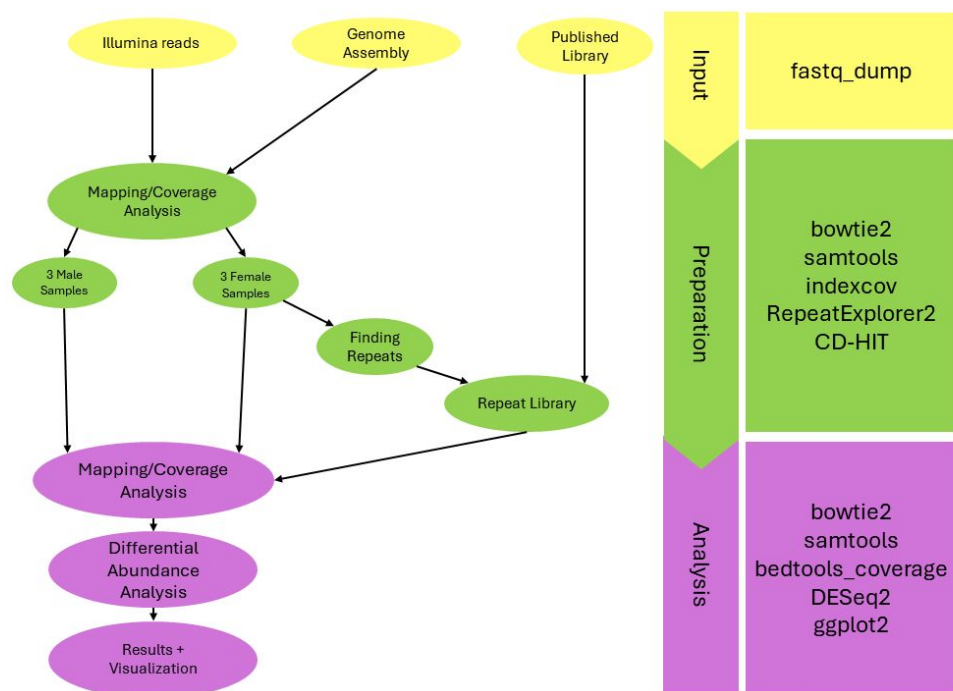
Heliconius melpomene





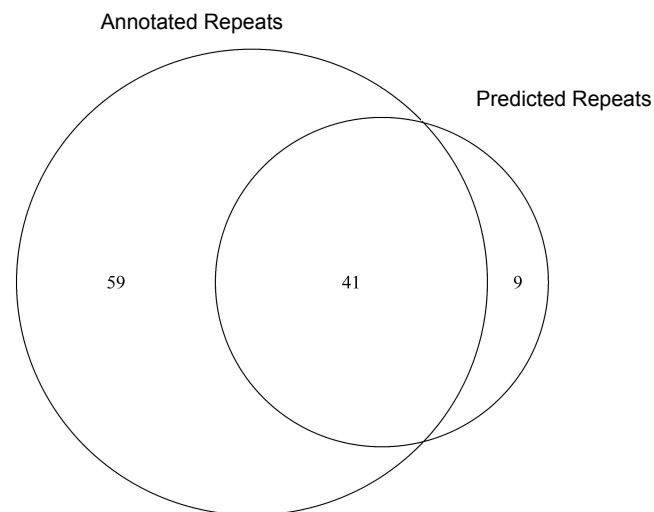
Our Method of Analysis

- Conducting an analysis based on the coverage depth of unassembled reads
- Looking for repeats that are enriched in females, putatively on the W chromosome



Proof of Concept:

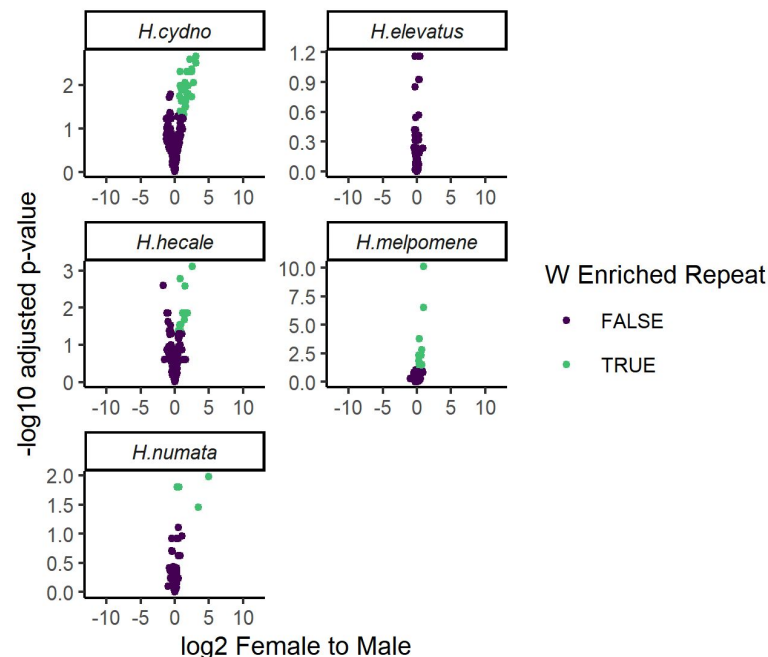
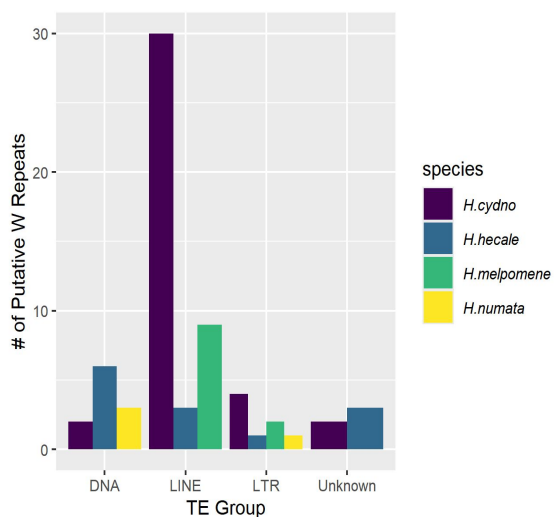
- Monarch results show large overlap between predicted W repeats and repeats annotated in the W chromosome assembly





Results and Conclusions

- No significant repeats on *Heliconius elevatus*
- Almost no overlap in repeats between species
- Different groups of repeats form the majority of putative W repeats in each species



- Future analysis
 - More comprehensive reference repeat library

