

First chromosome scale genomes of ithomiine butterflies (Nymphalidae: Ithomiini): comparative models for mimicry genetic studies

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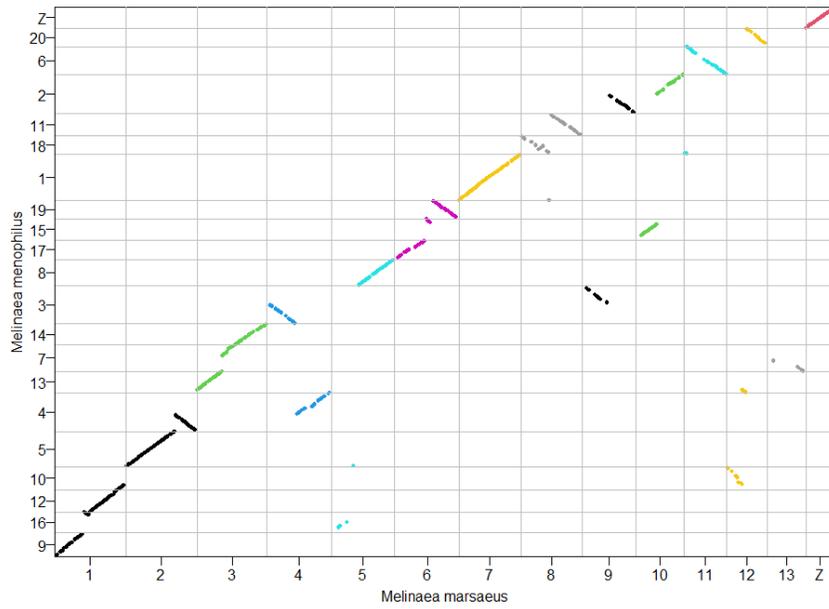
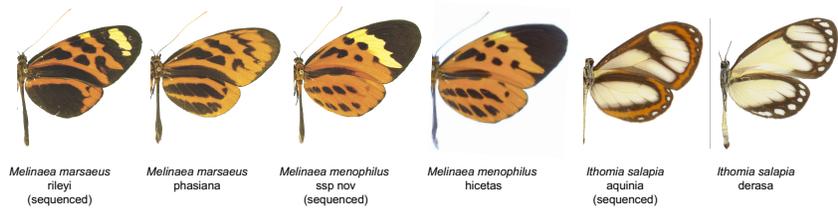
Abstract

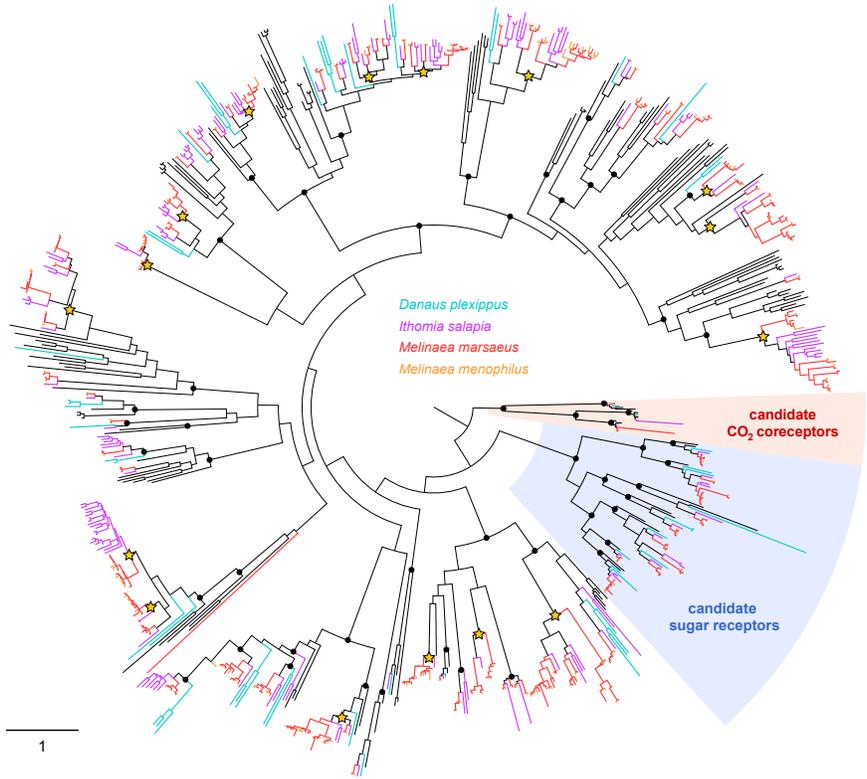
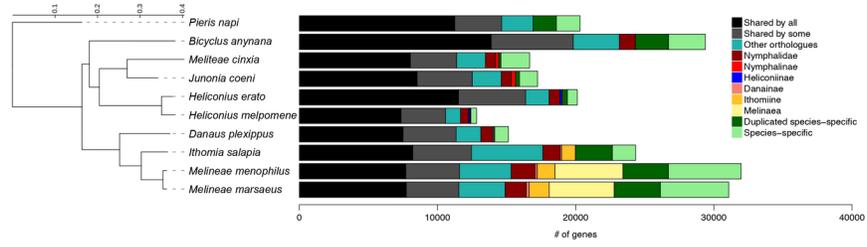
The ithomiine butterflies (Nymphalidae: Danainae) represent the largest known radiation of Mullerian mimetic butterflies. They dominate by number the mimetic butterfly communities, which include species such as the iconic neotropical *Heliconius* genus. Despite recent studies carried out on ithomiine ecology and genetic structure, no reference genome was available for the tribe. Here, we generated high-quality, chromosome-scale genome assemblies of two *Melinaea* species, *Melinaea marsaeus* and *Melinaea menophilus*, and a draft genome of *Ithomia salapia*. We obtained genomes with a size ranging from 396 Mb to 503 Mb across the three species and scaffold N50 of 40.5 Mb and 23.2 Mb for the two chromosome-scale assemblies. Using collinearity analyses we identified massive rearrangements between the two closely related *Melinaea* species. A detailed annotation of transposable elements and genes was performed, resulting in the identification of 24,341, 31,081 and 31,976 genes in *I. salapia*, *M. marsaeus* and *M. menophilus*, respectively. We used a specialist annotation to target chemosensory genes, which is crucial for host plant detection and mate recognition in mimetic species. A comparative genomic approach revealed independent gene

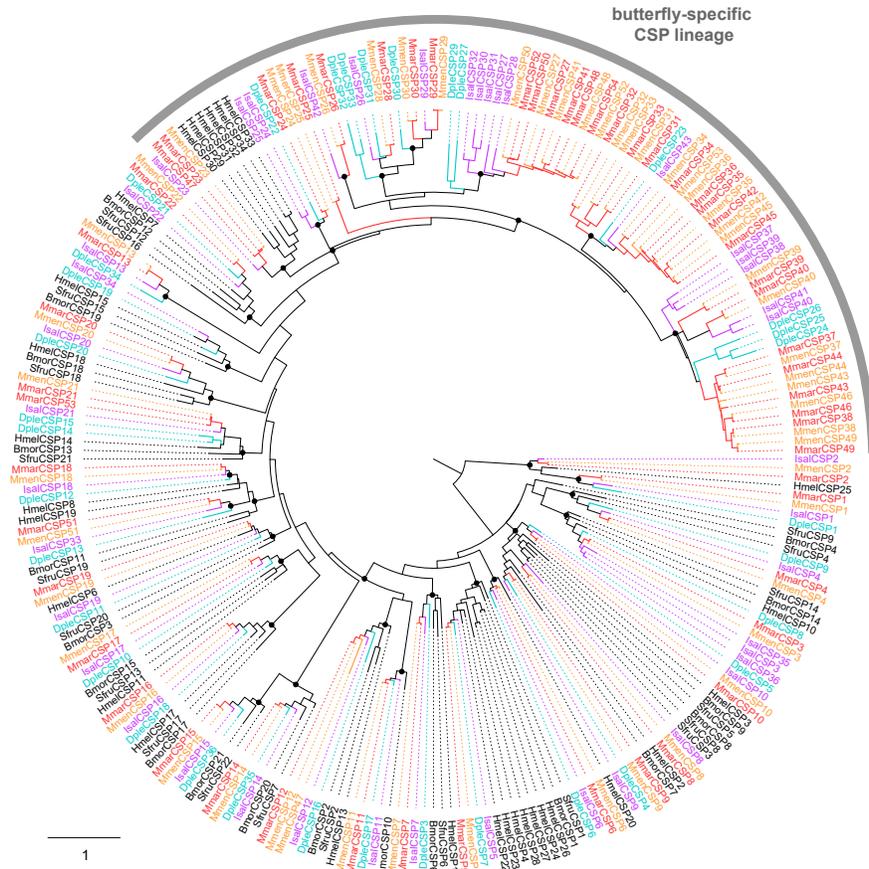
expansions in ithomiines and particularly in gustatory receptor genes. These first three genomes of ithomiine mimetic butterflies constitute a valuable addition and a welcome comparison to existing biological models of mimicry, such as *Heliconius*, and will enable further understanding of the mechanisms of adaptation and the genetic bases underpinning mimicry.

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